# STEPHEN WOLFRAM A NEW KIND OF SCIENCE

EXCERPTED FROM

CHAPTER 10

Processes of Perception and Analysis



# Processes of Perception and Analysis

## Introduction

In the course of the past several chapters, we have discussed the basic mechanisms responsible for a variety of phenomena that occur in nature. But in trying to explain our actual experience of the natural world, we need to consider not only how phenomena are produced in nature, but also how we perceive and analyze these phenomena. For inevitably our experience of the natural world is based in the end not directly on behavior that occurs in nature, but rather on the results of our perception and analysis of this behavior.

Thus, for example, when we look at the behavior of a particular natural system, there will be certain features that we notice with our eyes, and certain features, perhaps different, that we can detect by doing various kinds of mathematical or other analysis.

In previous chapters, I have argued that the basic mechanisms responsible for many processes that occur in nature can be captured by simple computer programs based on simple rules. But what about the processes that are involved in perception and analysis?

Particularly when it comes to the higher levels of perception, there is much that we do not know for certain about this. But what I will argue in this chapter is that the evidence we have suggests that the basic mechanisms at work can once again successfully be captured by simple programs based on simple rules. In the traditional sciences, it has rarely been thought necessary to discuss in any explicit kind of way the processes that are involved in perception and analysis. For in most cases all that one studies are rather simple features that can readily be extracted by very straightforward processes—and which can for example be described by just a few numbers or by a simple mathematical formula.

But as soon as one tries to investigate behavior of any substantial complexity, the processes of perception and analysis that one needs to use are no longer so straightforward. And the results one gets can then depend on these processes.

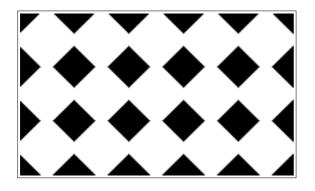
In the traditional sciences it has usually been assumed that any result that is not essentially independent of the processes of perception and analysis used to obtain it cannot be definite or objective enough to be of much scientific value. But the point is that if one explicitly studies processes of perception and analysis, then it becomes possible to make quite definite and objective statements even in such cases.

And indeed some of the most significant conclusions that I will reach at the end of this book are based precisely on comparing the processes that are involved in the production of certain forms of behavior with the processes involved in their perception and analysis.

#### What Perception and Analysis Do

In everyday life we are continually bombarded by huge amounts of data, in the form of images, sounds, and so on. To be able to make use of this data we must reduce it to more manageable proportions. And this is what perception and analysis attempt to do. Their role in effect is to take large volumes of raw data and extract from it summaries that we can use.

At the level of raw data the picture at the top of the facing page, for example, can be thought of as consisting of many thousands of individual black and white cells. But with our powers of visual perception and analysis we can immediately see that the picture can be summarized just by saying that it consists essentially of an array of repeated black diamond shapes.



An example of a picture that our powers of perception and analysis readily allow us to summarize quite succinctly in simple geometrical terms. At the lowest level, however, the picture consists of 24,000 black and white cells.

There are in general two ways in which data can be reduced by perception and analysis. First, those aspects of data that are not relevant for whatever purpose one has can simply be ignored. And second, one can avoid explicitly having to specify every element in the data by making use of regularities that one sees.

Thus, for example, in summarizing the picture above, we choose to ignore some details, and then to describe what remains in terms of its simple repetitive overall geometrical structure.

Whenever there are regularities in data, it effectively means that some of the data is redundant. For example, if a particular pattern is repeated, then one need not specify the form of this pattern more than once—for the original data can be reproduced just by repeating a copy of the pattern. And in general, the presence of regularities makes it possible to replace literal descriptions of data by shorter descriptions that are based on procedures for reproducing the data.

There are many forms of perception and analysis. Some happen quite automatically in our eyes, ears and brains—and these we usually call perception. Others require explicit conscious effort and mathematical or computational work—and these we usually call analysis. But the basic goal in all cases is the same: to reduce raw data to a useful summary form.

Such a summary is important whenever one wants to store or communicate data efficiently. It is also important if one wants to compare new data with old, or make meaningful extrapolations or predictions based on data. And in modern information technology the problems of data compression, feature detection, pattern recognition and system identification all in effect revolve around finding useful summaries of data.

In traditional science statistical analysis has been the most common way of trying to find summaries of data. And in general perception and analysis can be viewed as equivalent to finding models that reproduce whatever aspects of data one considers relevant.

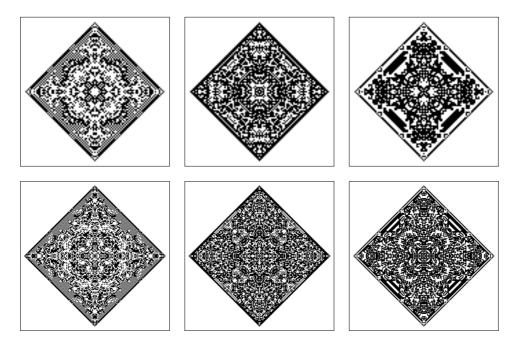
Perception and analysis correspond in many respects to the inverse of most of what we have studied in this book. For typically what we have done is to start from a simple computer program, and then seen what behavior this program produces. But in perception and analysis we start from behavior that we observe, then try to deduce what procedure or program will reproduce this data.

So how easy is it to do this? It turns out that for most of the kinds of rules used in traditional mathematics, it is in fact fairly easy. But for the more general rules that I discuss in this book it appears to often be extremely difficult. For even though the rules may be simple, the behavior they produce is often highly complex, and shows absolutely no obvious trace of its simple origins.

As one example, the pictures on the facing page were all generated by starting from a single black cell and then applying very simple two-dimensional cellular automaton rules. Yet if one looks just at these final pictures, there is no easy way to tell how they were made. Our standard methods of perception and analysis can certainly determine that the pictures are for example symmetrical. But none of these methods typically get even close to being able to recognize just how simple a procedure can in fact be used to produce the pictures.

One might think that our inability to find such a procedure could just be a consequence of limitations in the particular methods of perception and analysis that we, as humans, happen to have developed. And one might therefore suppose that an alien intelligence could exist which would be able to look at our pictures and immediately tell that they were produced by a very simple procedure.

But in fact I very much doubt that this will ever be the case. For I suspect that there are fundamental limitations on what perception and analysis can ever be expected to do. For there seem to be many kinds of



Patterns produced by taking a single black cell, then evolving for 50 and 100 steps according to outer totalistic cellular automaton rules 54, 222 and 374. Despite the simple description that can be given of this procedure, our standard methods of perception and analysis cannot readily deduce this description given just the final pictures shown here.

systems in which it is overwhelmingly easier to generate highly complex behavior than to recognize the origins of this behavior.

As I have discovered in this book, it is rather easy to generate complex behavior by starting from simple initial conditions and then following simple sets of rules. But the point is that if one starts from some particular piece of behavior there are in general no such simple rules that allow one to go backwards and find out how this behavior can be produced. Typically the problem is similar to trying to find solutions that will satisfy certain constraints. And as we have seen several times in this book, such problems can be extremely difficult.

So insofar as the actual processes of perception and analysis that end up being used are fairly simple, it is inevitable that there will be situations where one cannot recognize the origins of behavior that one sees—even when this behavior is in fact produced by very simple rules.

#### **Defining the Notion of Randomness**

Many times in this book I have said that the behavior of some system or another seems random. But so far I have given no precise definition of what I mean by randomness. And what we will discover in this section is that to come up with an appropriate definition one has no choice but to consider issues of perception and analysis.

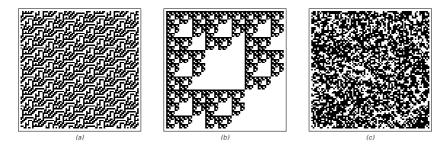
One might have thought that from traditional mathematics and statistics there would long ago have emerged some standard definition of randomness. But despite occasional claims for particular definitions, the concept of randomness has in fact remained quite obscure. And indeed I believe that it is only with the discoveries in this book that one is finally now in a position to develop a real understanding of what randomness is.

At the level of everyday language, when we say that something seems random what we usually mean is that there are no significant regularities in it that we can discern—at least with whatever methods of perception and analysis we use.

We would not usually say, therefore, that either of the first two pictures at the top of the facing page seem random, since we can readily recognize highly regular repetitive and nested patterns in them. But the third picture we would probably say does seem random, since at least at the level of ordinary visual perception we cannot recognize any significant regularities in it.

So given this everyday notion of randomness, how can we build on it to develop more precise definitions? The first step is to clarify what it means not to be able to recognize regularities in something. Following the discussion in the previous section, we know that whenever we find regularities, it implies that redundancy is present, and this in turn means that a shorter description can be given. So when we say that we cannot recognize any regularities, this is equivalent to saying that we cannot find a shorter description.

The three pictures on the facing page can always be described by explicitly giving a list of the colors of each of the 6561 cells that they contain. But by using the regularities that we can see in the first two



Pictures exhibiting different degrees of apparent randomness. Pictures (a) and (b) have obvious regularities, and would never be considered particularly random. But picture (c) has almost no obvious regularities, and would typically be considered quite random. As it turns out, picture (c), like (a) and (b), can actually be generated by a quite simple process. But the point is that the simplicity of this process does not affect the fact that with our standard methods of perception and analysis picture (c) is for practical purposes random.

pictures, we can readily construct much shorter—yet still complete— descriptions of these pictures.

The repetitive structure of picture (a) implies that to reproduce this picture all we need do is to specify the colors in a  $49 \times 2$  block, and then say that this block should be repeated an appropriate number of times. Similarly, the nested structure of picture (b) implies that to reproduce this picture, all we need do is to specify the colors in a  $3 \times 3$ block, and then say that as in a two-dimensional substitution system each black cell should repeatedly be replaced by this block.

But what about picture (c)? Is there any short description that can be given of this picture? Or do we have no choice but just to specify explicitly the color of every one of the cells it contains?

Our powers of visual perception certainly do not reveal any significant regularities that would allow us to construct a shorter description. And neither, it turns out, do any standard methods of mathematical or statistical analysis. And so for practical purposes we have little choice but just to specify explicitly the color of each cell.

But the fact that no short description can be found by our usual processes of perception and analysis does not in any sense mean that no such description exists at all. And indeed, as it happens, picture (c) in fact allows a very short description. For it can be generated just by starting with a single black cell and then applying a simple two-dimensional cellular automaton rule 250 times.

But does the existence of this short description mean that picture (c) should not be considered random? From a practical point of view the fact that a short description may exist is presumably not too relevant if we can never find this description by any of the methods of perception and analysis that are available to us. But from a conceptual point of view it may seem unsatisfactory to have a definition of randomness that depends on our methods of perception and analysis, and is not somehow absolute.

So one possibility is to define randomness so that something is considered random only if no short description whatsoever exists of it. And before the discoveries in this book such a definition might have seemed not far from our everyday notion of randomness. For we would probably have assumed that anything generated from a sufficiently short description would necessarily look fairly simple. But what we have discovered in this book is that this is absolutely not the case, and that in fact even from rules with very short descriptions it is easy to generate behavior in which our standard methods of perception and analysis recognize no significant regularities.

So to say that something is random only if no short description whatsoever exists of it turns out to be a highly restrictive definition of randomness. And in fact, as I mentioned in Chapter 7, it essentially implies that no process based on definite rules can ever manage to generate randomness when there is no randomness before. For since the rules themselves have a short description, anything generated by following them will also have a correspondingly short description, and will therefore not be considered random according to this definition.

And even if one is not concerned about where randomness might come from, there is still a further problem: it turns out in general to be impossible to determine in any finite way whether any particular thing can ever be generated from a short description. One might imagine that one could always just try running all programs with progressively longer descriptions, and see whether any of them ever generate what one wants. But the problem is that one can never in general tell in advance how many steps of evolution one will need to look at in order to be sure that any particular piece of behavior will not occur. And as a result, no finite process can in general be used to guarantee that there is no short description that exists of a particular thing.

By setting up various restrictions, say on the number of steps of evolution that will be allowed, it is possible to obtain slightly more tractable definitions of randomness. But even in such cases the amount of computational work required to determine whether something should be considered random is typically astronomically large. And more important, while such definitions may perhaps be of some conceptual interest, they correspond very poorly with our intuitive notion of randomness. In fact, if one followed such a definition most of the pictures in this book that I have said look random—including for example picture (c) on page 553—would be considered not random. And following the discussion of Chapter 7, so would at least many of the phenomena in nature that we normally think of as random.

Indeed, what I suspect is that ultimately no useful definition of randomness can be based solely on the issue of what short descriptions of something may in principle exist. Rather, any useful definition must, I believe, make at least some reference to how such short descriptions are supposed to be found.

Over the years, a variety of definitions of randomness have been proposed that are based on the absence of certain specific regularities. Often these definitions are presented as somehow being fundamental. But in fact they typically correspond just to seeing whether some particular process—and usually a rather simple one—succeeds in recognizing regularities and thus in generating a shorter description.

A common example—to be discussed further two sections from now—involves taking, say, a sequence of black and white cells, and then counting the frequency with which each color and each block of colors occurs. Any deviation from equality among these frequencies represents a regularity in the sequence and reveals nonrandomness. But despite some confusion in the past it is certainly not true that just checking equality of frequencies of blocks of colors—even arbitrarily long ones—is sufficient to ensure that no regularities at all exist. This procedure can indeed be used to check that no purely repetitive pattern exists, but as we will see later in this chapter, it does not successfully detect the presence of even certain highly regular nested patterns.

So how then can we develop a useful yet precise definition of randomness? What we need is essentially just a precise version of the statement at the beginning of this section: that something should be considered random if none of our standard methods of perception and analysis succeed in detecting any regularities in it. But how can we ever expect to find any kind of precise general characterization of what all our various standard methods of perception and analysis do?

The key point that will emerge in this chapter is that in the end essentially all these methods can be viewed as being based on rather simple programs. So this suggests a definition that can be given of randomness: something should be considered to be random whenever there is essentially no simple program that can succeed in detecting regularities in it.

Usually if what one is studying was itself created by a simple program then there will be a few closely related programs that always succeed in detecting regularities. But if something can reasonably be considered random, then the point is that the vast majority of simple programs should not be able to detect any regularities in it.

So does one really need to try essentially all sufficiently simple programs in order to determine this? In my experience, the answer tends to be no. For once a few simple programs corresponding to a few standard methods of perception and analysis have failed to detect regularities, it is extremely rare for any other simple program to succeed in detecting them.

So this means that the everyday definition of randomness that we discussed at the very beginning of this section is in the end already quite unambiguous. For it typically will not matter much which of the standard methods of perception and analysis we use: after trying a few of them we will almost always be in a position to come to a quite definite conclusion about whether or not something should be considered random.

# **Defining Complexity**

Much of what I have done in this book has been concerned in one way or another with phenomena associated with complexity. But just as one does not need a formal definition of life in order to study biology, so also it has not turned out to be necessary so far in this book to have a formal definition of complexity. Nevertheless, following our discussion of randomness in the previous section, we are now in a position to consider how the notion of complexity might be formally defined.

In everyday language, when we say that something seems complex what we typically mean is that we have not managed to find any simple description of it—or at least of those features of it in which we happen to be interested. But the goal of perception and analysis is precisely to find such descriptions, so when we say that something seems complex, what we are effectively saying is that our powers of perception and analysis have failed on it.

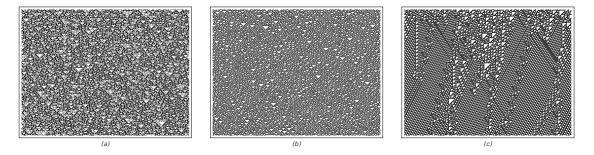
As we discussed two sections ago, there are two ways in which perception and analysis can typically operate. First, they can just throw away details in which we are not interested. And second, they can remove redundancy that is associated with any regularities that they manage to recognize.

The definition of randomness that we discussed in the previous section was based on the failure of the second of these two functions. For what it said was that something should be considered random if our standard methods of perception and analysis could not find any short description from which the thing could faithfully be reproduced.

But in defining complexity we need to consider both functions of perception and analysis. For what we want to know is not whether a simple or short description can be found of every detail of something, but merely whether such a description can be found of those features in which we happen to be interested.

In everyday language, the terms "complexity" and "randomness" are sometimes used almost interchangeably. And for example any of the three pictures at the top of the next page could potentially be referred to as either "quite random" or "quite complex". But if one chooses to look

only at overall features, then typically one would tend to say that the third picture seems more complex than the other two.



Examples of pictures that at an everyday level one might typically describe either as being "quite random" or as being "quite complex".

For even though the detailed placement of black and white cells in the first two pictures does not seem simple to describe, at an overall level these pictures still admit a quite simple description: in essence they just involve a kind of uniform randomness in which every region looks more or less the same as every other. But the third picture shows no such uniformity, even at an overall level. And as a result, we cannot give a short description of it even if we ignore its small-scale details.

Of course, if one goes to an extreme and looks, say, only at how big each picture is, then all three pictures have very short descriptions. And in general how short a description of something one can find will depend on what features of it one wants to capture—which is why one may end up ascribing a different complexity to something when one looks at it for different purposes.

But if one uses a particular method of perception or analysis, then one can always see how short a description this manages to produce. And the shorter the description is, the lower one considers the complexity to be.

But to what extent is it possible to define a notion of complexity that is independent of the details of specific methods of perception and analysis? In this chapter I argue that essentially all common forms of perception and analysis correspond to rather simple programs. And if one is interested in descriptions in which no information is lost—as in the discussion of randomness in the previous section—then as I mentioned in the previous section, it seems in practice that different simple programs usually agree quite well in their ability or inability to find short descriptions.

But this seems to be considerably less true when one is dealing with descriptions in which information can be lost. For it is rather common to see cases in which only a few features of a system may be difficult to describe—and depending on whether or not a given program happens to be sensitive to these features it can ascribe either a quite high or a quite low complexity to the system.

Nevertheless, as a practical matter, by far the most common way in which we determine levels of complexity is by using our eyes and our powers of visual perception. So in practice what we most often mean when we say that something seems complex is that the particular processes that are involved in human visual perception have failed to extract a short description.

And indeed I suspect that even below the level of conscious thought our brains already have a rather definite notion of complexity. For when we are presented with a complex image, our eyes tend to dwell on it, presumably in an effort to give our brains a chance to extract a simple description.

If we can find no simple features whatsoever—as in the case of perfect randomness—then we tend to lose interest. But somehow the images that draw us in the most—and typically that we find the most aesthetically pleasing—are those for which some features are simple for us to describe, but others have no short description that can be found by any of our standard processes of visual perception.

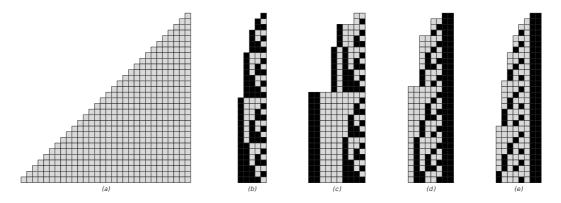
Before the discoveries in this book, one might have thought that to create anything with a significant level of apparent complexity would necessarily require a procedure which itself had significant complexity. But what we have discovered in this book is that in fact there are remarkably simple programs that produce behavior of great complexity. And what this means—as the images in this book repeatedly demonstrate—is that in the end it is rather easy to make pictures for which our visual system can find no simple overall description.

#### **Data Compression**

One usually thinks of perception and analysis as being done mainly in order to provide material for direct human consumption. But in most modern computer and communications systems there are processes equivalent to perception and analysis that happen all the time when data is compressed for more efficient storage or transmission.

One simple example of such a process is run-length encoding—a method widely used in practice to compress data that involves long sequences of identical elements, such as bitmap images of pages of text with large areas of white.

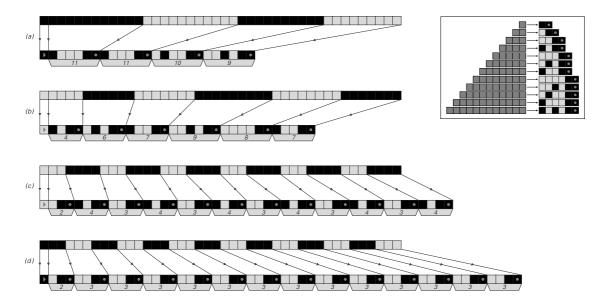
The basic idea of run-length encoding is to break data into runs of identical elements, and then to specify the data just by giving the lengths of these runs. This means, for example, that instead of having to list explicitly all the cells in a run of, say, 53 identical cells, one instead just gives the number "53". And the point is that even if the "53" is itself represented in terms of black and white cells, this representation can be much shorter than 53 cells.



Various representations of numbers from 1 to 30. (a) is unary, in which any given number is represented by a sequence of cells whose length is equal to that number. (b) is ordinary binary or base 2 representation. (c), (d) and (e) are set up to be self-delimiting, so that the end of a number can be recognized purely by looking at the cells within it. (c) is like (b), except that it has a specification of the number of digits at the front. (d) is essentially binary-coded-ternary, with the end of the number indicated by a pair of black cells. (e) uses a non-integer base derived from the Fibonacci sequence, with the property that a pair of black cells can appear only at the end of each number.

Indeed, any digit sequence can be thought of as providing a short representation for a number. But for run-length encoding it turns out that ordinary base 2 digit sequences do not quite work. For if the numbers corresponding to the lengths of successive runs are given one after another then there is no way to tell where the digits of one number end and the next begin.

Several approaches can be used, however, to avoid this problem. One, illustrated in picture (c) at the bottom of the facing page, is to insert at the beginning of each number a specification of how many digits the number contains. Another approach, illustrated in picture (d), is in effect to have two cells representing each digit, and then to indicate the end of the number by a pair of black cells. A variant on this approach, illustrated in picture (e), uses a non-integer base in which pairs of black cells can occur only at the end of a number.

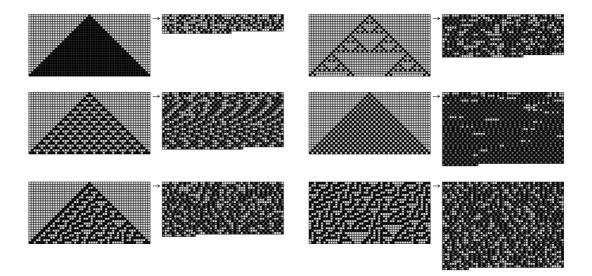


Examples of run-length encoding. In each case the input data is shown on top, and the output is shown below. The arrows between input and output show how the data is broken into runs of identical elements. Each run is then specified by a number, represented as a sequence ending with two black cells, as indicated in the inset picture, and in picture (e) on the facing page. For the first two sets of input data there are enough long runs present that compression is achieved. But for the other two sets no compression is achieved. Note that the first cell in the output is used to specify whether the first run is black or white. In this picture and those that follow, the output consists purely of black and white cells; the gray annotations are included purely as aids to interpretation.

For small numbers, all these approaches yield representations that are at least somewhat longer than the explicit sequences shown in picture (a). But for larger numbers, the representations quickly become much shorter. And this means that they can potentially be used to achieve compression in run-length encoding.

The pictures at the bottom of the previous page show what happens when one applies run-length encoding using representation (e) from page 560 to various sequences of data. In the first two cases, there are sufficiently many long runs that compression is achieved. But in the last two cases, there are too many short runs, and the output from run-length encoding is actually longer than the input.

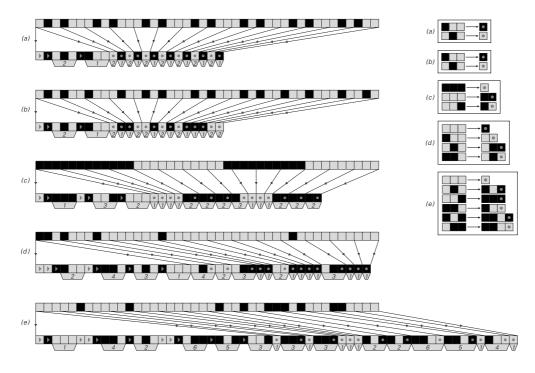
The pictures below show the results of applying run-length encoding to typical patterns produced by cellular automata. When the patterns contain enough regions of uniform color, compression is achieved. But when the patterns are more intricate—even in a simple repetitive way—little or no compression is achieved.



Examples of applying run-length encoding to patterns produced by cellular automata. Successive rows in each original image are placed end to end so as to give a one-dimensional sequence, then run-length encoded, and then chopped into rows again. Compression is typically achieved whenever most of the image consists of regions of uniform color.

Run-length encoding is based on the idea of breaking data up into runs of identical elements of varying lengths. Another common approach to data compression is based on forming blocks of fixed length, and then representing whatever distinct blocks occur by specific codewords.

The pictures below show a few examples of how this works. In each case the input is taken to be broken into blocks of length 3. In the first two cases, there are then only two distinct blocks that occur, so each of these can be represented by a codeword consisting of a single cell, with the result that substantial compression is achieved.

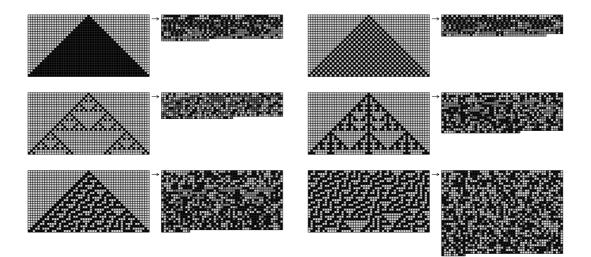


Examples of Huffman coding based on blocks of length 3. In cases (a) and (b), only two possible blocks occur, and these are assigned codewords consisting of a single black cell and a single white cell. In case (c), 3 possible blocks occur, the most common is assigned a codeword consisting of a single white cell, while the others are assigned codewords consisting of two cells. In case (d) 4 out of the 8 possible blocks occur, while in case (e) 6 occur. In all cases, the output begins with a preamble specifying which block is to be represented by which codeword. The blocks appear explicitly in this preamble, and are indicated by numbered tabs. The codewords are represented implicitly by the arrangement of cells shown with arrows. The preamble is followed by the actual codewords representing the data. The codewords are self-delimiting, so that they can be given one after another, with no separator in between.

When a larger number of distinct blocks occur, longer codewords must inevitably be used. But compression can still be achieved if the codewords for common blocks are sufficiently much shorter than the blocks themselves.

One simple strategy for assigning codewords is to number all distinct blocks in order of decreasing frequency, and then just to use the resulting numbers—given, say, in one of the representations discussed above—as the codewords. But if one takes into account the actual frequencies of different blocks, as well as their ranking, then it turns out that there are better ways to assign codewords.

The pictures below show examples based on a method known as Huffman coding. In each case the first part of the output specifies which blocks are to be represented by which codewords, and then the remainder of the output gives the actual succession of codewords that correspond to the blocks appearing in the data. And as the pictures below illustrate, whenever there are fairly few distinct blocks that occur with high frequency, substantial compression is achieved.

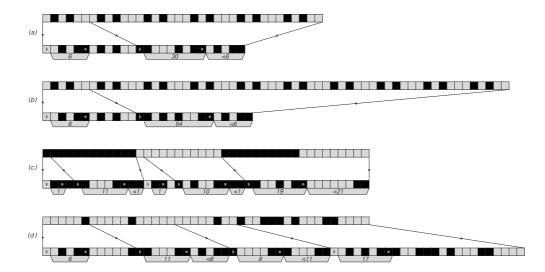


Huffman encoding with blocks of length 6 applied to patterns produced by cellular automata. The maximum possible compression is by a factor of 6; the maximum achieved here is roughly a factor of 3. The difference between the size of the results for the last two examples is mostly a consequence of the presence of large areas of white in the first of them.

But ultimately there is a limit to the degree of compression that can be obtained with this method. For even in the very best case any block of cells in the input can never be compressed to less than one cell in the output.

So how can one achieve greater compression? One approach which turns out to be similar to what is used in practice in most current high-performance general-purpose compression systems—is to set up an encoding in which any particular sequence of elements above some length is given explicitly only once, and all subsequent occurrences of the same sequence are specified by pointers back to the first one.

The pictures below show what happens when this approach is applied to a few short sequences. In each case, the output consists of two kinds of objects, one giving sequences that are occurring for the first time, and the other giving pointers to sequences that have occurred before. Both kinds of objects start with a single cell that specifies their type. This is

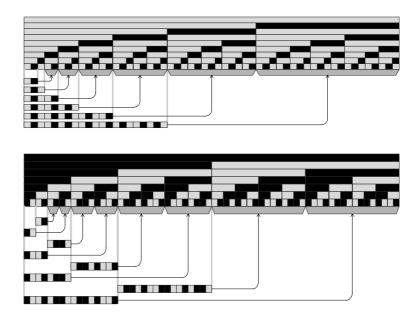


Examples of pointer-based encoding, in which sequences that have occurred once in the data are subsequently specified just by pointers. Each section of output starts with an element which indicates whether what follows is a new sequence, or a pointer to a previous one. After this comes a specification of the length of sequence represented by this section of output, with the number given in the form used for run-length encoding above. Then comes either a literal sequence, or a number giving the offset to where the required sequence last occurred in the data. In the examples shown, pointers are used only for sequences of length at least 6. Pointer-based encoding is similar to the Lempel-Ziv algorithm widely used in practical high-performance general-purpose compression systems.

followed by a specification of the length of the sequence that the object describes. In the first kind of object, the actual sequence is then given, while in the second kind of object what is given is a specification of how far back in the data the required sequence can be found.

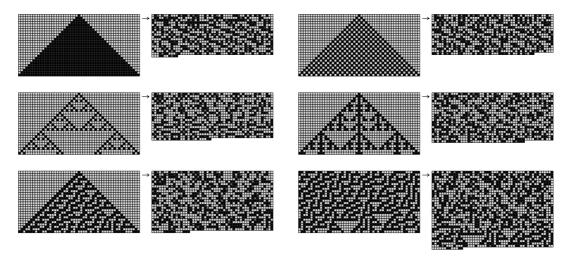
With data that is purely repetitive this method achieves quite dramatic compression. For having once specified the basic sequence to be repeated, all that then needs to be given is a pointer to this sequence, together with a representation of the total length of the data.

Purely nested data can also be compressed nearly as much. For as the pictures below illustrate, each whole level of nesting can be viewed just as adding a fixed number of repeated sequences.



Examples of the pattern of repeats found in purely nested data. As indicated in these pictures, any such data must correspond to the output of a neighbor-independent substitution system (see page 83). In pointer-based encoding, the number of pointers required to represent the data increases essentially like the number of steps in the evolution of the substitution system. Taking into account the length of the representation for each pointer, the compressed form of a nested sequence of length *n* will typically grow in length like  $Log[n]^2$ . (This can be compared with Log[n] growth for a purely repetitive sequence.) Note that actual algorithms for pointer-based encoding will typically find a slightly less regular pattern of repeats than is shown in the pictures here.

So what about two-dimensional patterns? The pictures below show what happens if one takes various patterns, arranges their rows one after another in a long line, and then applies pointer-based encoding to the resulting sequences. When there are obvious regularities in the original pattern, some compression is normally achieved—but in most cases the amount is not spectacular.

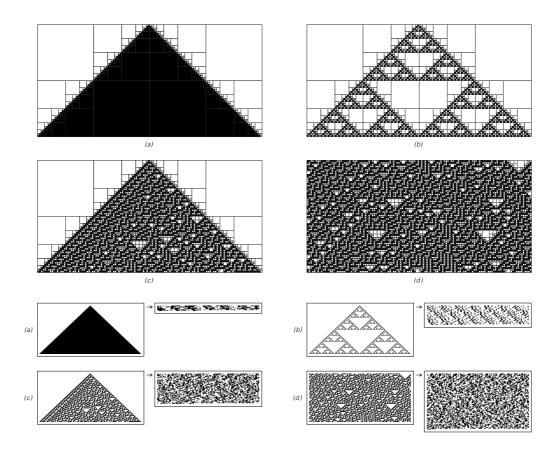


Examples of one-dimensional pointer-based encoding applied to patterns produced by cellular automata. Successive rows in each image are placed end to end so as to get a sequence to which the encoding can be applied. Pointers are used only for repeats that are of length at least 4. In the last example, large regions contain no such repeats, and therefore appear in the output just as they do in the input.

So how can one do better? The basic answer is that one needs to take account of the two-dimensional nature of the patterns. Most compression schemes used in practice have in the past primarily been set up just to handle one-dimensional sequences. But it is not difficult to set up schemes that operate directly on two-dimensional data.

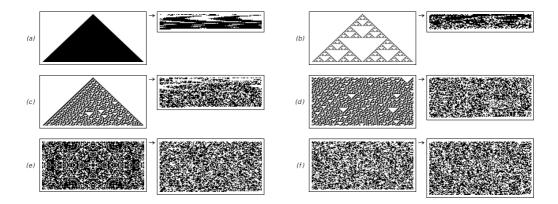
The picture on the next page shows one approach based on the idea of breaking images up into collections of nested pieces, each with a uniform color. In some respects this scheme is a two-dimensional analog of run-length encoding, and when there are large regions of uniform color it yields significant compression.

It is also easy to extend block-based encoding to two dimensions: all one need do is to assign codewords to two-dimensional rather than



Examples of encoding by two-dimensional recursive subdivision. The idea is to use a generalization of a two-dimensional substitution system, in which at each step a square either remains the same or is subdivided into four small squares. The encoding specifies which choice is made at each step for each square. The method is analogous to the quadtree representation sometimes used in computer graphics. The substantial compression seen even in case (c) is a consequence of the large areas of uniform white that are present.

one-dimensional blocks. And as the pictures at the top of the facing page demonstrate, this procedure can lead to substantial compression. Particularly notable is what happens in case (d). For even though this pattern is produced by a simple one-dimensional cellular automaton rule, and even though one can see by eye that it contains at least some small-scale regularities, none of the schemes we have discussed up till now have succeeded in compressing it at all.



Examples of two-dimensional block-based encoding. Each image is broken into  $3 \times 2$  blocks, and codewords are then assigned to these blocks using the Huffman scheme. Note the presence of compression even in case (d). This is a consequence of the fact that the cellular automaton rule allows only certain blocks to appear in the pattern, as illustrated in the picture below. (e) is generated by a two-dimensional cellular automaton; (f) is the sequence that appears on the center column of rule 30.

The picture below demonstrates why two-dimensional block encoding does, however, manage to compress it. The point is that the two-dimensional blocks that one forms always contain cells whose colors are connected by the cellular automaton rule—and this greatly reduces the number of different arrangements of colors that can occur.



Cellular automaton rule 30, and the 3 × 2 blocks which appear in large patterns generated by it. There are a total of  $2^6 = 64$  possible 3 × 2 blocks of black and white cells; the fact that only 24 of them appear in patterns generated by rule 30 is what makes it possible for two-dimensional block-based encoding to compress such patterns.

In cases (e) and (f), however, there is no simple rule for going from one row to the next, and two-dimensional block encoding—like all the other encoding schemes we have discussed so far—does not yield any substantial compression.

Like block encoding, pointer-based encoding can also be extended to two dimensions. The basic idea is just to scan two-dimensional data looking for repeats not of one-dimensional sequences, but instead of two-dimensional regions. And although such a procedure does not in the past appear to have been used in practice, it is quite straightforward to implement. The pictures on the facing page show some examples of the results one gets. And in many cases it turns out that the overall level of compression obtained is considerably greater than with any of the other schemes discussed in this section. But what is perhaps still more striking is that the patterns of repeated regions seem to capture almost every regularity that we readily notice by eye—as well as some that we do not. In pictures (c) and (d), for example, fairly subtle repetition on the left-hand side is captured, as is fourfold symmetry in picture (e).

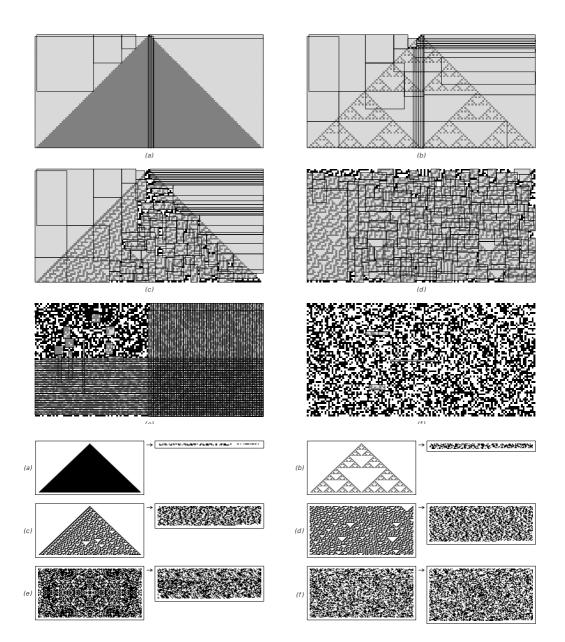
One might have thought that to capture all these kinds of regularities would require a whole collection of complicated procedures. But what the pictures on the facing page demonstrate is that in fact just a single rather straightforward procedure is quite sufficient. And indeed the amount of compression achieved by this procedure in different cases seems to agree rather well with our intuitive impression of how much regularity is present.

All of the methods of data compression that we have discussed in this section can be thought of as corresponding to fairly simple programs. But each method involves a program with a rather different structure, and so one might think that it would inevitably be sensitive to rather different kinds of regularities.

But what we have seen in this section is that in fact different methods of data compression have remarkably similar characteristics. Essentially every method, for example, will successfully compress large regions of uniform color. And most methods manage to compress behavior that is repetitive, and at least to some extent behavior that is nested—exactly the two kinds of simple behavior that we have noted many times in this book.

For more complicated behavior, however, none of the methods seem capable of substantial compression. It is not that no compression is ever in principle possible. Indeed, as it happens, every single one of the pictures on the facing page can for example be generated from very short cellular automaton programs.

But the point is that except when the overall behavior shows repetition or nesting none of the standard methods of data compression



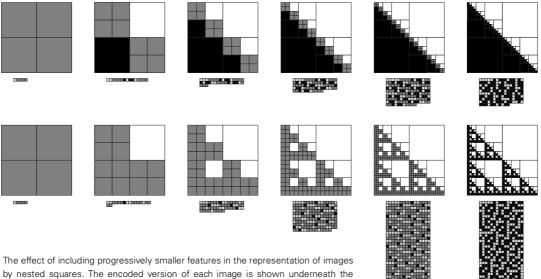
Examples of two-dimensional pointer-based encoding. The gray rectangles in the upper pictures indicate repeated regions that are encoded using pointers. In the particular scheme used here, each of these regions is required to contain at least 25 cells that have not already been encoded using pointers. The images are scanned sequentially and at every point the maximal rectangle extending to the right and down is found that is a repeat of a rectangle previously encountered, and contains the largest number of cells not already encoded using pointers. In many cases this maximal rectangle overlaps those found at subsequent points.

as we have discussed them in this section come even close to finding such short descriptions. And as a result, at least with respect to any of these methods all we can reasonably say is that the behavior we see seems for practical purposes random.

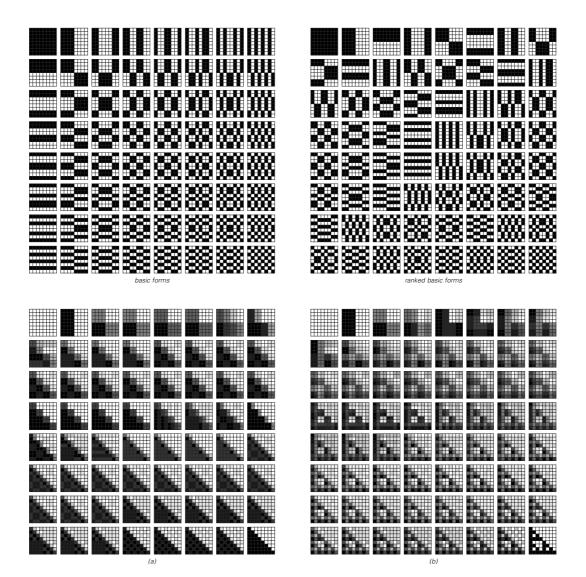
#### Irreversible Data Compression

All the methods of data compression that we discussed in the previous section are set up to be reversible, in the sense that from the encoded version of any piece of data it is always possible to recover every detail of the original. And if one is dealing with data that corresponds to text or programs such reversibility is typically essential. But with images or sounds it is typically no longer so necessary: for in such cases all that in the end usually matters is that one be able to recover something that looks or sounds right. And by being able to drop details that have little or no perceptible effect one can often achieve much higher levels of compression.

In the case of images a simple approach is just to ignore features that are smaller than some minimum size. The pictures below show



by nested squares. The encoded version of each image is shown underneath the image. When smaller squares are included, the amount of data required to specify the image increases rapidly.



Examples of how images can be built up by adding together basic forms consisting of so-called two-dimensional Walsh functions. On the top left the basic forms are given in so-called sequency order. On the top right they are reordered roughly so as to go systematically from coarser to finer. In the bottom arrays of pictures each successive picture is obtained by adding in the corresponding basic form with an appropriate weight. The basic forms shown here have the property of being orthogonal, so that the weight for each form can be deduced simply by multiplying the original image by that form. Note that the forms involve numerical values -1 and +1, corresponding to cells colored white and black. The images shown here are all rescaled so that smallest values are white and largest black. The JPEG method of image compression uses an approach similar to the one shown here, though with basic forms that have continuous levels of gray, rather than just black and white.

what happens if one divides an image into a collection of nested squares, but imposes a lower limit on the size of these squares. And what one sees is that as the lower limit is increased, the amount of compression increases rapidly—though at the cost of a correspondingly rapid decrease in the quality of the image.

So can one do better at maintaining the quality of the image? Various schemes are used in practice, and almost all of them are based on the idea from traditional mathematics that by viewing data in terms of numbers it becomes possible to decompose the data into sums of fixed basic forms some of which can be dropped in order to achieve compression.

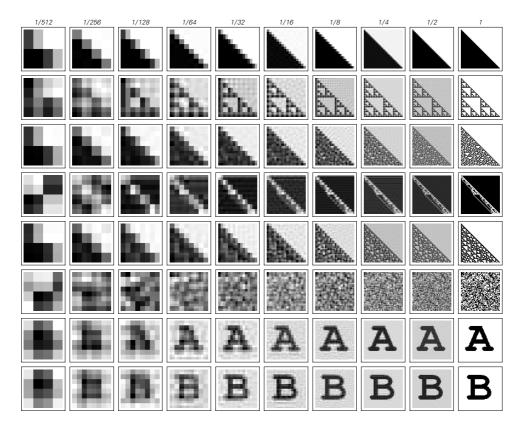
The pictures on the previous page show an example of how this works. On the top left is a set of basic forms which have the property that any two-dimensional image can be built up simply by adding together these forms with appropriate weights. On the top right these forms are then ranked roughly from coarsest to finest. And given this ranking, the arrays of pictures at the bottom show how two different images can be built up by progressively adding in more and more of the basic forms.

If all the basic forms are included, then the original image is faithfully reproduced. But if one drops some of the later forms—thereby reducing the number of weights that have to be specified—one gets only an approximation to the image. The facing page shows what happens to a variety of images when different fractions of the forms are kept.

Images that are sufficiently simple can already be recognized even when only a very small fraction of the forms are included corresponding to a very high level of compression. But most other images typically require more forms to be included—and thus do not allow such high levels of compression.

Indeed the situation is very much what one would expect from the definition of complexity that I gave two sections ago. The relevant features of both simple and completely random images can readily be recognized even at quite high levels of compression. But images that one would normally consider complex tend to have features that cannot be recognized except at significantly lower levels of compression.

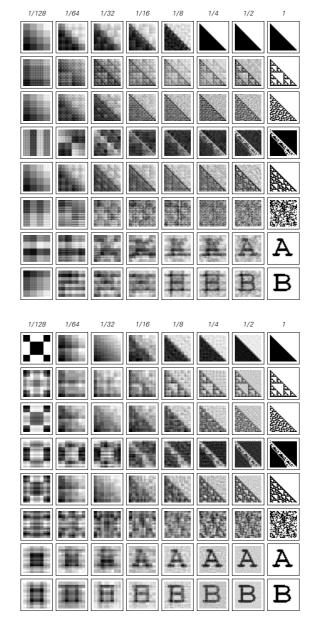
All the pictures on the facing page, however, were generated from the specific ordering of basic forms shown on the previous page. And

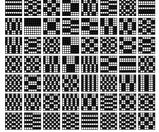


Examples of images obtained by keeping only certain fractions of the complete set of basic forms. In the case of both simple and completely random images, many features are recognizable even with fairly few basic forms—implying that a highly compressed representation can be given.

one might wonder whether perhaps some other ordering would make it easier to compress more complex images.

One simple approach is just to assemble a large collection of images typical of the ones that one wants to compress, and then to order the basic forms so that those which on average occur with larger weights in this collection appear first. The pictures on the next page show what happens if one does this first with images of cellular automata and then with images of letters. And indeed slightly higher levels of compression are achieved. But whatever ordering is used the fact seems to remain that images that we would normally consider complex still cannot systematically be compressed more than a small amount.





Results obtained by deducing optimal orderings of basic forms from collections of images of cellular automata (top) and letters (bottom). The orderings of basic forms are shown on the left, in each case starting with those whose weights are largest in absolute value when averaged over the collection of images. Note that the orderings are shown for 8 × 8 basic forms, while the actual images are 32 × 32. The orderings are deduced respectively from images of the 256 elementary cellular automata, and the 52 upper and lower case letters.

### **Visual Perception**

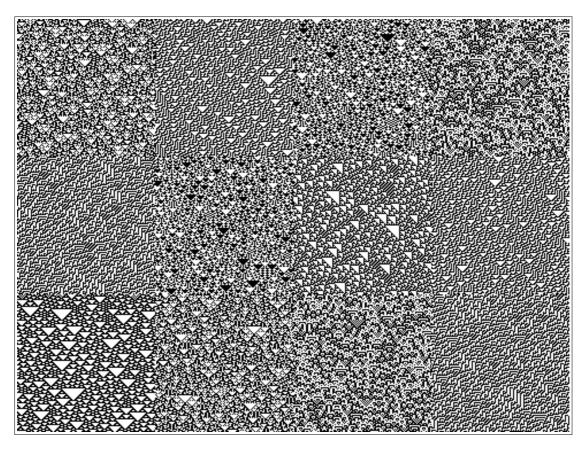
In modern times it has usually come to be considered quite unscientific to base very much just on how things look to our eyes. But the fact remains that despite all the various methods of mathematical and other analysis that have been developed, our visual system still represents one of the most powerful and reliable tools we have. And certainly in writing this book I have relied heavily on our ability to make all sorts of deductions on the basis of looking at visual representations.

So how does the human visual system actually work? And what are its limitations? There are many details yet to be resolved, but over the past couple of decades, it has begun to become fairly clear how at least the lowest levels of the system work. And it turns out—just as in so many other cases that we have seen in this book—that much of what goes on can be thought of in terms of remarkably simple programs.

In fact, across essentially every kind of human perception, the basic scheme that seems to be used over and over again is to have particular kinds of cells set up to respond to specific fixed features in the data, and then to ignore all other features.

Color perception provides a classic example. On the retina of our eye are three kinds of color-sensitive cells, with each kind responding essentially to the level of either red, green or blue. Light from an object typically involves a whole spectrum of wavelengths. But the fact that we have only three kinds of color-sensitive cells means that our eyes essentially sample only three features of this spectrum. And this is why, for example, we have the impression that mixtures of just three fixed colors can successfully reproduce all other colors.

So what about patterns and textures? Does our visual system also work by picking out specific features of these? Everyday experience suggests that indeed it does. For if we look, say, at the picture on the next page we do not immediately notice every detail. And instead what our visual system seems to do is just to pick out certain features which quickly make us see the picture as a collection of patches with definite textures.



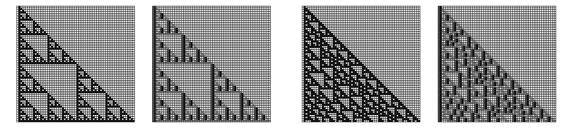
Patches generated by a variety of one-dimensional cellular automaton rules. Each patch is set up to have a roughly equal number of black and white squares. But despite this, our visual system quickly notices that different patches have different textures. And presumably this is because the visual system is automatically identifying particular features in each patch. Everyone appears immediately to be able to see some patches when shown this picture. But after looking at the picture for a while, the boundaries between the patches seem to get somewhat clearer.

So how does this work? The basic answer seems to be that there are nerve cells in our eyes and brains which are set up to respond to particular local patterns in the image formed on the retina of our eye.

The way this comes about appears to be surprisingly direct. Behind the 100 million or so light-sensitive cells on our retina are a sequence of layers of nerve cells, first in the eye and then in the brain. The connections between these cells are set up so that a given cell in the visual cortex will typically receive inputs only from cells in a fairly small area on our retina. Some of these inputs will be positive if the image in a certain part of the area is, say, colored white, while others will be positive if it is colored black. And the cell in the visual cortex will then respond only if enough of its inputs are positive, corresponding to a specific pattern being present in the image.

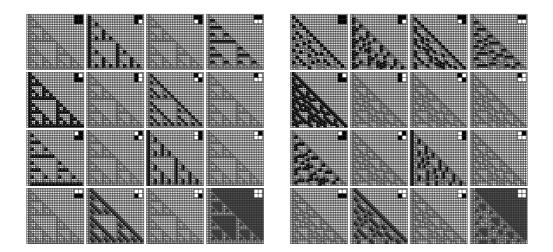
In practice many details of this setup are quite complicated. But as a simple idealization, one can consider an array of squares on the retina, each colored either black or white. And one can then assume that in the visual cortex there is a corresponding array of cells, with each cell receiving input from, say, a  $2 \times 2$  block of squares, and following the rule that it responds whenever the colors of these squares form some particular pattern.

The pictures below show a simple example. In each case the first picture shows the image on the retina, while the second picture shows which cells respond to it. And with the specific choice of rule used here, what effectively happens is that the vertical black edges in the original image get picked out.



Responses to two sample images of cells sensitive to the 2 × 2 template shown on the left. The cells that respond are indicated by darker squares in the second picture in each pair. Such responses occur whenever the 2 × 2 template on the left appears, corresponding to the presence of a vertical black edge. The extraction of features by this kind of simple template matching appears to be a key element in human visual perception—as well as being common in technological image processing. The sample images used here are ones generated by the evolution of elementary one-dimensional cellular automata with rules 60 and 124 respectively.

Neurophysiological experiments suggest that cells in the visual cortex respond to a variety of specific kinds of patterns. And as a simple idealization, the pictures on the next page show what happens with cells that respond to each of the 16 possible  $2 \times 2$  arrangements of black and white squares. In each case, one can think of the results as corresponding to picking out some specific local feature in the original image.

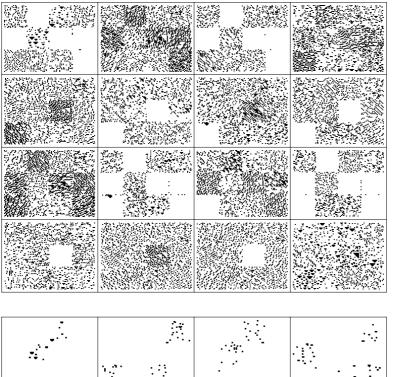


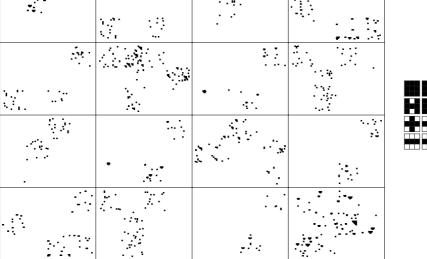
Responses to the sample images from the previous page by types of cells sensitive to each of the local arrangements of black and white squares shown. In each case, one can think of the resulting patterns as being filtered versions of the original images in which only parts that exhibit particular features are kept. The patterns can also be viewed as outputs from a single step in the evolution of two-dimensional block cellular automata in which the rules specify that a block becomes dark if it has the arrangement of cells shown, and becomes light otherwise. The comparative sparsity of dark blocks is a consequence of the fact that at any given position a dark block can occur in only one of the 16 cases shown. The absence of any dark blocks in many of the cases shown can be viewed as a reflection of constraints introduced by the construction of the images from one-dimensional cellular automaton rules.

So is this very simple kind of process really what underlies our seemingly sophisticated perception of patterns and textures? I strongly suspect that to a large extent it is. An important detail, however, is that there are cells in the visual cortex which in effect receive input from larger regions on the retina. But as a simple idealization one can assume that such cells in the end just respond to repeated versions of the basic  $2 \times 2$  patterns.

So with this setup, the pictures on the facing page show what happens with an image like the one from page 578. The results are somewhat remarkable. For even though the average density of black and white squares is exactly the same across the whole image, what we see is that in different patches the features that end up being picked out have different densities. And it is this, I suspect, that makes us see different patches as having different textures.

For much as we distinguish colors by their densities of red, green and blue, so also it seems likely that we distinguish textures by their



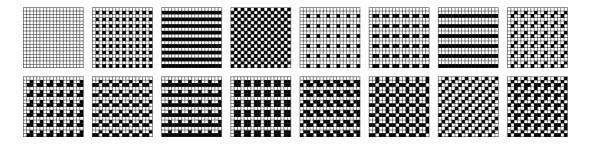


Responses to a smaller version of the image from page 578 by cells sensitive to all 16 possible  $2 \times 2$  blocks, as well as their repetitive  $3 \times 3$  extensions. Patches which appear to have different textures in the original image are seen to contain characteristically different densities of these various blocks. I strongly suspect that it is density differences such as these that allow our visual system to distinguish textures.

densities of certain local features. And the reason that this happens so quickly when we look at an image is no doubt that the procedure for picking out such features is a very simple one that can readily be carried out in parallel by large numbers of separate cells in our eyes and brains.

For patterns and textures, however, unlike for colors, we can always get beyond the immediate impression that our visual system provides. And so for example, by making a conscious effort, we can scan an image with our eyes, scrutinizing different parts in turn and comparing whatever details we want.

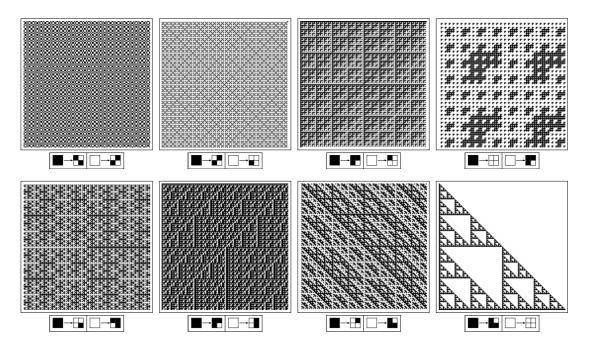
But what kinds of things can we expect to tell in this way? As the pictures below suggest, it is usually quite easy to see if an image is purely repetitive—even in cases where the block that repeats is fairly large.



Examples of all the distinct repetitive patterns that can be formed from arrays of  $2 \times 2$  and  $3 \times 3$  blocks. In every single case the presence of pure repetition is easy to recognize by eye. Note that in a pattern generated by repeating one particular block, there will normally be other blocks that occur with other alignments. Page 215 shows patterns obtained in systems based on constraints in which one effectively requires that only certain blocks or sets of blocks occur.

But with nesting the story is quite different. All eight pictures on the facing page were generated from the two-dimensional substitution systems shown, and thus correspond to purely nested patterns. But except for the last picture on each row—which happen to be dominated by large areas of essentially uniform color—it is remarkably difficult for us to tell that the patterns are nested. And this can be viewed as a clear example of a limitation in our powers of visual perception.

As we found two sections ago, many standard methods of data compression have the same limitation. But at the end of that section I showed that the fairly simple procedure of two-dimensional pointer



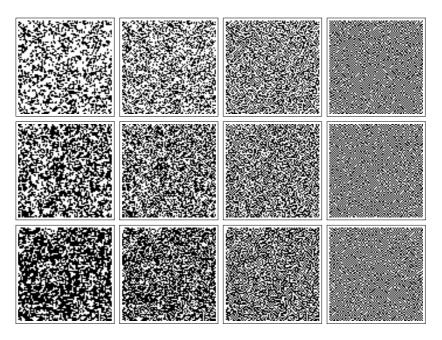
Examples of nested patterns created by following the two-dimensional substitution rules shown. Except for the last examples on each row, it is remarkably difficult to recognize the nested structure in these patterns by eye, even with quite careful scrutiny. The two-dimensional pointer-based encoding scheme from page 571 does however manage to recognize the structure in all cases.

encoding will succeed in recognizing nesting. So it is not that nesting is somehow fundamentally difficult to recognize; it is just that the particular processes that happen to occur in human visual perception do not in general manage to do it.

So what about randomness? The pictures on the next page show a few examples of images with various degrees of randomness. And just by looking at these images it is remarkably difficult to tell which of them is in fact the most random.

The basic problem is that our visual system makes us notice local features—such as clumps of black squares—even if their density is consistent with what it should be in a completely random array. And as a result, much as with constellations of stars, we tend to identify what seem to be regularities even in completely random patterns.

In principle it could be that there would be images in which our visual system would notice essentially no local features. And indeed in



Examples of images that approximate perfect randomness. The second image on each row has squares chosen independently to be black with probabilities 0.4, 0.5 and 0.6 respectively. In the other images various features are added or removed. In the first image on each row, if any square is surrounded by four squares with identical colors, then the square is forced to have the same color. In the third image, any clump of squares with the same color is broken up by reversing the color of the center square. And in the fourth image, the same is done with lines of squares of the same color.

the last two images on each row above all clumps of squares of the same color, and then all lines of squares of the same color, have explicitly been removed. At first glance, these images do in some respects look more random. But insofar as our visual system contains elements that respond to each of the possible local arrangements of squares, it is inevitable that we will identify features of some kind or another in absolutely any image.

In practice there are presumably some types of local patterns to which our visual system responds more strongly than others. And knowing such a hierarchy, one should be able to produce images that in a sense seem as random as possible to us. But inevitably such images would reflect much more the details of our process of visual perception than they would anything about actual underlying randomness.

## **Auditory Perception**

In the course of this book I have made extensive use of pictures. So why not also sounds? One issue—beyond the obvious fact that sounds cannot be included directly in a printed book—is that while one can study the details of a picture at whatever pace one wants, a sound is in a sense gone as soon as it has finished playing.

But everyday experience makes it quite clear that one can still learn a lot by listening to sounds. So what then are the features of sounds that our auditory system manages to pick out?

At a fundamental level all sounds consist of patterns of rapid vibrations. And the way that we hear sounds is by such vibrations being transmitted to the array of hair cells in our inner ear. The mechanics of the inner ear are set up so that each row of hair cells ends up being particularly sensitive to vibrations at some specific frequency. So what this means is that what we tend to perceive most about sounds are the frequencies they contain.

Musical notes usually have just one basic frequency, while voiced speech sounds have two or three. But what about sounds from systems in nature, or from systems of the kinds we have studied in this book?

There are a number of ways in which one can imagine such systems being used to generate sounds. One simple approach illustrated on the right is to consider a sequence of elements produced by the system, and then to take each element to correspond to a vibration for a brief time—say a thousandth of a second—in one of two directions.

So what are such sounds like? If the sequence of elements is repetitive then what one hears is in essence a pure tone at a specific frequency—much like a musical note. But if the sequence is random then what one hears is just an amorphous hiss.

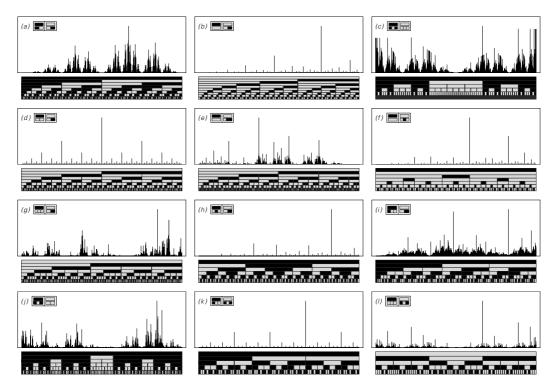
So what happens between these extremes? If the properties of a sequence gradually change in a definite way over time then one can often hear this in the corresponding sound. But what about sequences that have more or less uniform properties? What kinds of regularities does our auditory system manage to detect in these?



A sequence of discrete elements and a possible corresponding waveform for a sound.

The answer, it seems, is surprisingly simple: we readily recognize exact or approximate repetition at definite frequencies, and essentially nothing else. So if we listen to nested sequences, for example, we have no direct way to tell that they are nested, and indeed all we seem sensitive to are some rather simple features of the spectrum of frequencies that occur.

The pictures below show spectra obtained from nested sequences produced by various simple one-dimensional substitution systems. The diversity of these spectra is quite striking: some have simple nested forms dominated by a few isolated peaks at specific frequencies, while others have quite complex forms that cover large ranges of frequencies.

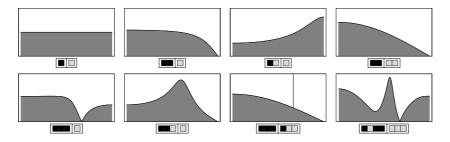


Frequency spectra of nested sequences generated by one-dimensional neighbor-independent substitution systems. The rules are the same as shown on pages 83 and 84. Note the presence of both isolated peaks and complicated background patterns. If a sequence corresponds to a pure tone and repeats every n elements then its spectrum will consist of n/2 equally spaced peaks. Sequences whose spectra contain no dominant peaks typically sound like random noise, although sometimes explicit time variation can be heard, and indeed sequence (c) just sounds like a succession of idealized frog ribbets. Intensity or power spectra are obtained by squaring the quantities shown.

And given only the underlying rule for a substitution system, it turns out to be fairly difficult to tell even roughly what the spectrum will be like. But given the spectrum, one can immediately tell how we will perceive the sound. When the spectrum is dominated by just one large peak, we hear a definite tone. And when there are two large peaks we also typically hear definite tones. But as the number of peaks increases it rapidly becomes impossible to keep track of them, and we end up just hearing random noise—even in cases where the peaks happen to have frequencies that are in the ratios of common musical chords.

So the result is that our ears are not sensitive to most of the elaborate structure that we see in the spectra of many nested sequences. Indeed, it seems that as soon as the spectrum covers any broad range of frequencies all but very large peaks tend to be completely masked, just as in everyday life a sound needs to be loud if it is to be heard over background noise.

So what about other kinds of regularities in sequences? If a sequence is basically random but contains some short-range correlations then these will lead to smooth variations in the spectrum. And for example sequences that consist of random successions of specific blocks can yield any of the types of spectra shown below—and can sound variously like hisses, growls or gurgles.



Frequency spectra for long sequences obtained by concatenating blocks in random orders. Such spectra can be calculated by fairly standard methods from stochastic analysis. The first case shown corresponds to white noise. The second-to-last case always has a black element at every third position, so exhibits a peak at the corresponding repetition frequency.

To get a spectrum with a more elaborate structure requires long-range correlations—as exist in nested sequences. But so far as I can

tell, the only kinds of correlations that are ultimately important to our auditory system are those that lead to some form of repetition.

So in the end, any features of the behavior of a system that go beyond pure repetition will tend to seem to our ears essentially random.

## **Statistical Analysis**

When it comes to studying large volumes of data the method almost exclusively used in present-day science is statistical analysis. So what kinds of processes does such analysis involve? What is typically done in practice is to compute from raw data various fairly simple quantities whose values can then be used to assess models which could provide summaries of the data.

Most kinds of statistical analysis are fundamentally based on the assumption that such models must be probabilistic, in the sense that they give only probabilities for behavior, and do not specifically say what the behavior will be. In different situations the reasons for using such probabilistic models have been somewhat different, but before the discoveries in this book one of the key points was that it seemed inconceivable that there could be deterministic models that would reproduce the kinds of complexity and apparent randomness that were so often seen in practice.

If one has a deterministic model then it is at least in principle quite straightforward to find out whether the model is correct: for all one has to do is to compare whatever specific behavior the model predicts with behavior that one observes. But if one has a probabilistic model then it is a much more difficult matter to assess its validity—and indeed much of the technical development of the field of statistics, as well as many of its well-publicized problems, can be traced to this issue.

As one simple example, consider a model in which all possible sequences of black and white squares are supposed to occur with equal probability. By effectively enumerating all such sequences, it is easy to see that such a model predicts that in any particular sequence the fraction of black squares is most likely to be 1/2.

But what if a sequence one actually observes has 9 black squares out of 10? Even though this is not the most likely thing to see, one certainly cannot conclude from seeing it that the model is wrong. For the model does not say that such sequences are impossible—it merely says that they should occur only about 1% of the time.

And indeed there is no meaningful way without more information to deduce any kind of absolute probability for the model to be correct. So in practice what almost universally ends up being done is to consider not just an individual model, but rather a whole class of models, and then to try to identify which model from this class is the best one—as measured, say, by the criterion that its likelihood of generating the observed data is as large as possible.

For sequences of black and white squares a simple class of models to consider are those in which each square is taken to be black with some fixed independent probability p. Given a set of raw data the procedure for finding which model in this class is best—according, say, to the criterion of maximum likelihood—is extremely straightforward: all one does is to compute what fraction of squares in the data are black, and this value then immediately gives the value of p for the best model.

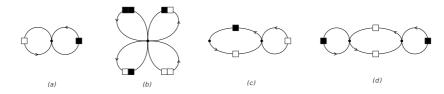
So what about more complicated models? Instead of taking each square to have a color that is chosen completely independently, one can for example take blocks of squares of some given length to have their colors chosen together. And in this case the best model is again straightforward to find: it simply takes the probabilities for different blocks to be equal to the frequencies with which these blocks occur in the data.

If one does not decide in advance how long the blocks are going to be, however, then things can become more complicated. For in such a case one can always just make up an extreme model in which only one very long block is allowed, with this block being precisely the sequence that is observed in the data.

Needless to say, such a model would for most purposes not be considered particularly useful—and certainly it does not succeed in providing any kind of short summary of the data. But to exclude models like this in a systematic way requires going beyond criteria such as maximum likelihood, and somehow explicitly taking into account the complexity of the model itself.

For specific types of models it is possible to come up with various criteria based for example on the number of separate numerical parameters that the models contain. But in general the problem of working out what model is most appropriate for any given set of data is an extremely difficult one. Indeed, as discussed at the beginning of Chapter 8, it is in some sense the core issue in any kind of empirical approach to science.

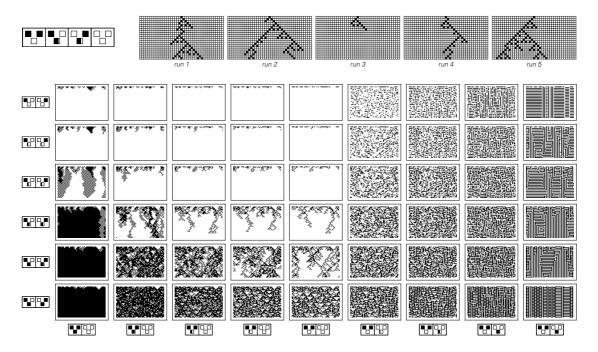
But traditional statistical analysis is usually far from having to confront such issues. For typically it restricts itself to very specific classes of models—and usually ones which even by the standards of this book are extremely simple. For sequences of black and white squares, for example, models that work as above by just assigning probabilities to fixed blocks of squares are by far the most common. An alternative, typically viewed as quite advanced, is to assign probabilities to sequences by looking at the paths that correspond to these sequences in networks of the kind shown below.



Networks defining probabilistic models. Each connection in each network has a certain probability associated with it, and the model takes sequences of black and white squares to be generated by tracing paths through the networks according to these probabilities. Cases (a) and (b) are so-called Markov models that in effect involve no memory and are equivalent to models discussed above. Cases (c) and (d) correspond to so-called hidden Markov models, with some short-term memory.

Networks (a) and (b) represent cases already discussed above. Network (a) specifies that the colors of successive squares should be chosen independently, while network (b) specifies that this should be done for successive pairs of squares. Network (c), however, specifies that different probabilities should be used depending on whether the path has reached the left or the right node in the network. But at least so long as the structure of the network is kept the same, it is fairly easy even in this case to deduce from a given set of data what probabilities in the network provide the best model for the data—for essentially all one need do is to follow the path corresponding to the data, and see with what frequency each connection from each node ends up being used.

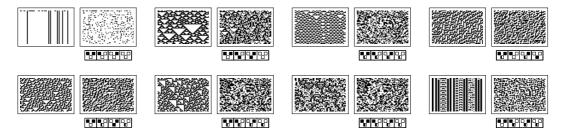
So what about two-dimensional data? From the discussion in Chapter 5 it follows that no straightforward analogs of the types of probabilistic models described above can be constructed in such a case. But as an alternative it turns out that one can use probabilistic versions of one-dimensional cellular automata, as in the pictures below.



Examples of probabilistic cellular automata, in which the rule specifies the probabilities for each color of cell to be generated given what the colors of its two neighbors were on the previous step. Because the rule is probabilistic a different detailed pattern of evolution will in general be obtained each time the cellular automaton is run—as in the top row of pictures above. Despite this, however, any particular probabilistic cellular automaton will typically exhibit some characteristic overall pattern of behavior, as illustrated in the array of pictures above. Note that it is fairly common for phase transitions to occur, in which continuous changes in underlying probabilistic sellular automata can be viewed as generalizations of so-called directed percolation models.

The rules for such cellular automata work by assigning to each possible neighborhood of cells a certain probability to generate a cell of each color. And for any particular form of neighborhood, it is once again quite straightforward to find the best model for any given set of data. For essentially all one need do is to work out with what frequency each color of cell appears below each possible neighborhood in the data.

But how good are the results one then gets? If one looks at quantities such as the overall density of black cells that were in effect used in finding the model in the first place then inevitably the results one gets seem quite good. But as soon as one looks at explicit pictures like the ones below, one immediately sees dramatic differences between the original data and what one gets from the model.



A comparison between data generated by ordinary cellular automata and the probabilistic cellular automata that are considered the best fit to it. While properties such as the density of black cells are typically set up to agree between the data and the model, the pictures make it clear that more detailed features do not.

In most cases, the typical behavior produced by the model looks considerably more random than the data. And indeed at some level this is hardly surprising: for by using a probabilistic model one is in a sense starting from an assumption of randomness.

The model can introduce certain regularities, but these almost never seem sufficient to force anything other than rather simple features of data to be correctly reproduced.

Needless to say, just as for most other forms of perception and analysis, it is typically not the goal of statistical analysis to find precise and complete representations of data. Rather, the purpose is usually just to extract certain features that are relevant for drawing specific conclusions about the data.

And a fundamental example is to try to determine whether a given sequence can be considered perfectly random—or whether instead it contains obvious regularities of some kind.

From the point of view of statistical analysis, a sequence is perfectly random if it is somehow consistent with a model in which all possible sequences occur with equal probability.

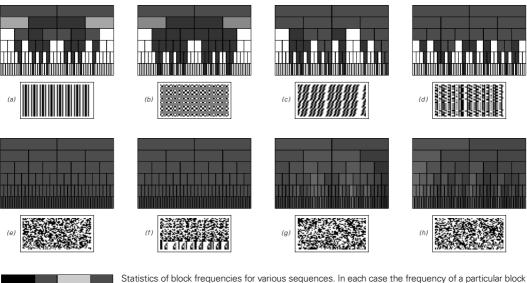
But how can one tell if this is so? What is typically done in practice is to take a sequence that is given and compute from it the values of various specific quantities, and then to compare these values with averages obtained by looking at all possible sequences.

Thus, for example, one might compute the fraction of squares in a given sequence that are black, and compare this to 1/2. Or one might compute the frequency with which more than two consecutive black squares occur together, and compare this with the value 1/4 obtained by averaging over all possible sequences.

And if one finds that a value computed from a particular sequence lies close to the average for all possible sequences then one can take this as evidence that the sequence is indeed random. But if one finds that the value lies far from the average then one can take this as evidence that the sequence is not random.

The pictures at the top of the next page show the results of computing the frequencies of different blocks in various sequences, and in each case each successive row shows results for all possible blocks of a given length. The gray levels on every row are set up so that the average of all possible sequences corresponds to the pattern of uniform gray shown below. So any deviation from such uniform gray potentially provides evidence for a deviation from randomness.

And what we see is that in the first three pictures, there are many obvious such deviations, while in the remaining pictures there are no obvious deviations. So from this it is fairly easy to conclude that the first three sequences are definitely not random, while the remaining sequences could still be random.



Statistics of block frequencies for various sequences. In each case the frequency of a particular block is represented by gray level, with results for blocks of successively greater lengths being shown on successive rows as indicated on the left. The original sequences are shown broken into lines and arranged in two dimensions. Sequences (b), (c) and (d) are generated by substitution systems with rules (b)  $\blacksquare \to \blacksquare, \square \to \blacksquare, \square \to \blacksquare, \square \to \square$  and (d)  $\blacksquare \to \blacksquare \blacksquare, \square \to \blacksquare$  respectively. (Note that these substitution systems are the simplest ones that yield equal frequencies of all blocks up to lengths 1,

2 and 3 respectively.) Sequence (e) is generated by a linear feedback shift register (essentially an additive cellular automaton) with tap positions {2, 11}. Sequence (f) is formed by concatenating base 2 digits of successive integers. Sequence (g) is the center column of the pattern generated by the rule 30 cellular automaton. Sequence (h) is the base 2 digits of  $\pi$ .

And indeed sequence (a) is certainly not random; in fact it is purely repetitive. And in general it is fairly easy to see that in any sequence that is purely repetitive there must beyond a certain length be many blocks whose frequencies are far from equal.

It turns out that the same is true for nested sequences. And in the picture above, sequences (b), (c) and (d) are all nested.

But what about the remaining sequences? Sequences (e) and (f) seem to yield frequencies that in every case correspond accurately to those obtained by averaging over all possible sequences. Sequences (g) and (h) yield results that are fairly similar, but exhibit some definite fluctuations.

So do these fluctuations represent evidence that sequences (g) and (h) are not in fact random? If one looks at the set of all possible sequences, one can fairly easily calculate the distribution of frequencies for any particular block. And from this distribution one can tell with what probability a given deviation from the average should occur for a sequence that is genuinely chosen at random.

The result turns out to be quite consistent with what we see in pictures (g) and (h). But it is far from what we see in pictures (e) and (f). So even though individual block frequencies seem to suggest that sequences (d) and (e) are random, the lack of any spread in these frequencies provides evidence that in fact they are not.

So are sequences (g) and (h) in the end truly random? Just like other sequences discussed in this chapter they are in some sense not, since they can both be generated by simple underlying rules. But what the picture on the facing page demonstrates is that if one just does statistical analysis by computing frequencies of blocks one will see no evidence of any such underlying simplicity.

One might imagine that if one were to compute other quantities one could immediately find such evidence. But it turns out that many of the obvious quantities one might consider computing are in the end equivalent to various combinations of block frequencies. And perhaps as a result of this, it has sometimes been thought that if one could just compute frequencies of blocks of all lengths one would have a kind of universal test for randomness. But sequences like (e) and (f) on the facing page make it clear that this is not the case.

So what kinds of quantities can one in the end use in doing statistical analysis? The answer is that at least in principle one can use any quantity whatsoever, and in particular one can use quantities that arise from any of the processes of perception and analysis that I have discussed so far in this chapter. For in each case all one has to do is to compute the value of a quantity from a particular sequence of data, and then compare this value with what would be obtained by averaging over all possible sequences. In practice, however, the kinds of quantities actually used in statistical analysis of sequences tend to be rather limited. Indeed, beyond block frequencies, the only other ones that are common are those based on correlations, spectra, and occasionally run lengths—all of which we already discussed earlier in this chapter.

Nevertheless, one can in general imagine taking absolutely any process and using it as the basis for statistical analysis. For given some

specific process one can apply it to a piece of raw data, and then see how the results compare with those obtained from all possible sequences.

If the process is sufficiently simple then by using traditional mathematics one can sometimes work out fairly completely what will happen with all possible sequences. But in the vast majority of cases this cannot be done, and so in practice one has no choice but just to compare with results obtained by sampling some fairly limited collection of possible sequences.

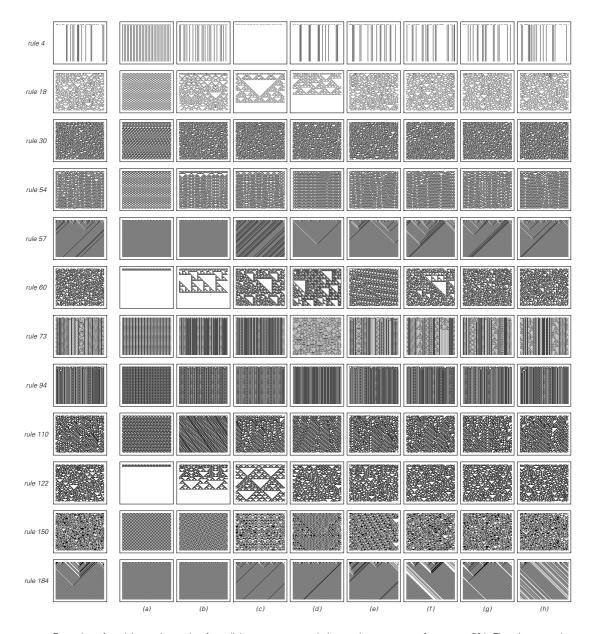
Under these circumstances therefore it becomes quite unrealistic to notice subtle deviations from average behavior. And indeed the only reliable strategy is usually just to look for cases in which there are huge differences between results for particular pieces of data and for typical sequences. For any such differences provide clear evidence that the data cannot in fact be considered random.

As an example of what can happen when simple processes are applied to data, the pictures on the facing page show the results of evolution according to various cellular automaton rules, with initial conditions given by the sequences from page 594. On each row the first picture illustrates the typical behavior of each cellular automaton. And the point is that if the sequences used as initial conditions for the other pictures are to be considered random then the behavior they yield should be similar.

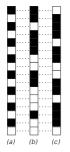
But what we see is that in many cases the behavior actually obtained is dramatically different. And what this means is that in such cases statistical analysis based on simple cellular automata succeeds in recognizing that the sequences are not in fact random.

But what about sequences like (g) and (h)? With these sequences none of the simple cellular automaton rules shown here yield behavior that can readily be distinguished from what is typical. And indeed this is what I have found for all simple cellular automata that I have searched.

So from this we must conclude that—just as with all the other methods of perception and analysis discussed in this chapter statistical analysis, even with some generalization, cannot readily recognize that sequences like (g) and (h) are anything but completely random—even though at an underlying level these sequences were generated by quite simple rules.



Examples of applying various rules for cellular automaton evolution to the sequences from page 594. The picture at the left-hand end of each row is chosen to show the typical behavior of each cellular automaton, given arbitrary initial conditions. Each cellular automaton rule in effect corresponds to a different statistical analysis procedure. Rule 4 picks out isolated black cells. Rule 60 essentially constructs a difference table for the sequence of elements. Rules 57 and 184 test for the overall density of black cells. (As indicated by page 136 the preponderance of white stripes with rule 184 in case (h) is a fluctuation.)



Example of a scheme for encryption. From the original message (a) an encrypted message (c) is generated by reversing the color of each square for which the corresponding square in the encrypting sequence (b) is black. This scheme is the basis for essentially all practical stream ciphers.

## Cryptography and Cryptanalysis

The purpose of cryptography is to hide the contents of messages by encrypting them so as to make them unrecognizable except by someone who has been given a special decryption key. The purpose of cryptanalysis is then to defeat this by finding ways to decrypt messages without being given the key.

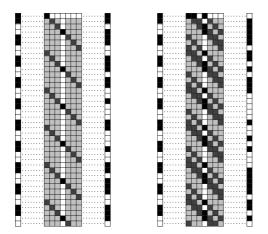
The picture on the left shows a standard method of encrypting messages represented by sequences of black and white squares. The basic idea is to have an encrypting sequence, shown as column (b) on the left, and from the original message (a) to get an encrypted version of the message (c) by reversing the color of every square for which the corresponding square in the encrypting sequence (b) is black.

So if one receives the encrypted message (c), how can one recover the original message (a)? If one knows the encrypting sequence (b) then it is straightforward. For all one need do is to repeat the process that was used for encryption, and reverse the color of every square in (c) for which the corresponding square in (b) is black.

But how can one arrange that only the intended recipient of the message knows the encrypting sequence (b)? In some situations it may be feasible to transmit the whole encrypting sequence in some secure way. But much more common is to be able to transmit only some short key in a secure way, and then to have to generate the encrypting sequence from this key.

So what kind of procedure might one use to get an encrypting sequence from a key? The picture at the top of the facing page shows an extremely simple approach that was widely used in practical cryptography until less than a century ago. The idea is just to form an encrypting sequence by repeatedly cycling through the elements in the key. And as the picture demonstrates, combining this with the original message leads to an encrypted message in which at least some of the structure in the original message is obscured.

But perhaps not surprisingly it is fairly easy to do cryptanalysis in such a case. For if one can find out what any sufficiently long segment in the encrypting sequence was, then this immediately gives the key,



A simple example of an encryption system in which the encrypting sequence is obtained by repetitively cycling through the elements of the key. Encryption with two different keys is shown. In each case the original message is on the left, the encrypted message is on the right, and the encrypting sequence corresponds to the highlighted column of cells. The system is essentially a Vigenère cipher of the kind widely used between the 1500s and the early 1900s.

and from the key the whole of the rest of the encrypting sequence can immediately be generated.

So what kind of analysis is needed to find a segment of the encrypting sequence? In an extreme but in practice common case one might happen to know what certain parts of the original message were perhaps standardized greetings or some such—and by comparing the original and encrypted forms of these parts one can immediately deduce what the corresponding parts of the encrypting sequence must have been.

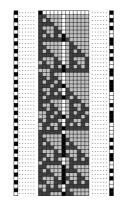
And even if all one knows is that the original message was in some definite language this is still typically good enough. For it means that there will be certain blocks—say corresponding to words like "the" in English—that occur much more often than others in the original message. And since such blocks must be encrypted in the same way whenever they occur at the same point in the repetition period of the encrypting sequence they will lead to occasional repeats in the encrypted message—with the spacing of such repeats always being some multiple of the repetition period. So this means that just by looking at the distribution of spacings between repeats one can expect to determine the repetition period of the encrypting sequence.

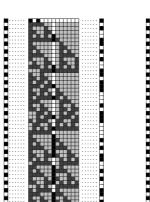
And once this is known, it is usually fairly straightforward to find the actual key. For one can pick out of the encrypted message all the squares that occur at a certain point in the repetition period of the encrypting sequence, and which are therefore encrypted using a particular element of the key. Then one can ask whether such squares are more often black or more often white, and one can compare this with the result obtained by looking at the frequencies of letters in the language of the original message. If these two results are the same, then it suggests that the corresponding element in the key is white, and if they are different then it suggests that it is black. And once one has found a candidate key it is easy to check whether the key is correct by trying to use it to recover some reasonably long part of the original message. For unless one has the correct key, the chance that what one recovers will be meaningful in the language of the original message is absolutely negligible.

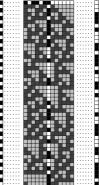
So what happens if one uses a more complicated rule for generating an encrypting sequence from a key? Methods like the ones above still turn out to allow features of the encrypting sequence to be found. And so to make cryptography work it must be the case that even if one knows certain features or parts of the encrypting sequence it is still difficult to deduce the original key or otherwise to generate the rest of the sequence.

The picture below shows one way of generating encrypting sequences that was widely used in the early years of electronic cryptography, and is still sometimes used today. The basic idea is to look at the evolution of an additive cellular automaton in a register of limited width. The key then gives the initial condition for the cellular automaton, and the encrypting sequence is extracted, for example, by sampling a particular cell on successive steps.

Encryption using the rule 60 additive cellular automaton. This is essentially equivalent to a linear feedback shift register.

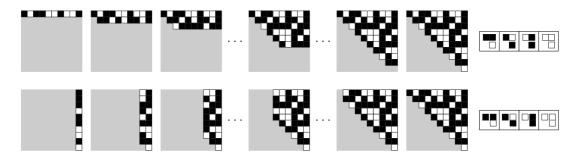






So given such an encrypting sequence, is there any easy way to do cryptanalysis and go backwards and work out the key?

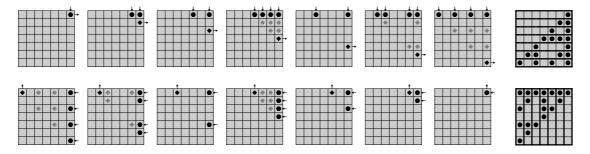
It turns out that there is. For as the picture below demonstrates, in an additive cellular automaton like the one considered here the underlying rule is such that it allows one not only to deduce the form of a particular row from the row above it, but also to deduce the form of a particular column from the column to its right. And what this means is that if one has some segment of the encrypting sequence, corresponding to part of a column, then one can immediately use this to deduce the forms of a sequence of other columns, and thus to find the form of a row in the cellular automaton—and hence the original key.



An example of the basis for cryptanalysis of an additive cellular automaton. The first set of pictures show the ordinary evolution of the rule 60 cellular automaton, in which each successive row is deduced from the one above. The second set of pictures show a kind of sideways evolution in which the rule is reinterpreted so as to allow a column of cells to be deduced from the column immediately to its right. Note that in both cases the colors of cells in the area on the lower right cannot be determined without knowing the colors of more initial cells than are shown.

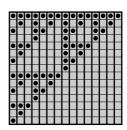
But what happens if the encrypting sequence does not include every single cell in a particular column? One cannot then immediately use the method described above. But it turns out that the additive nature of the underlying rule still makes comparatively straightforward cryptanalysis possible.

The picture on the next page shows how this works. Because of additivity it turns out that one can deduce whether or not some cell a certain number of steps down a given column is black just by seeing whether there are an odd or even number of black cells in certain specific positions in the row at the top. And one can then immediately



invert this to get a way to deduce the colors of cells on a given row from the colors of certain combinations of cells in a given column.

Another consequence of additivity: the correspondence between colors of cells on rows and columns in the rule 60 cellular automaton. In each case specifying the colors of the cells that are marked with dots immediately determines the colors of the cells that are marked with diamonds. The final diamond cell is black if an odd number of the dotted cells are black, and is white otherwise. The pictures on the right show which cells in the top row and which cells in the right-hand column determine the cells at successive positions in the right-hand column and in the top row respectively. These pictures can be thought of as matrices with 1's at the position of each black dot, and 0's elsewhere. Multiplying these matrices modulo 2 by vectors corresponding to a row of the cellular automaton gives a column, and vice versa. This means that the matrix on the second row of pictures is the inverse modulo 2 of the one on the first row.

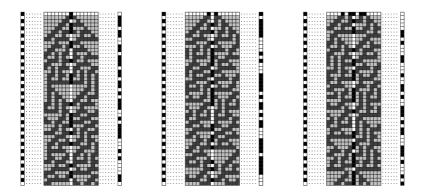


Which cells in a column are known will depend on how the encrypting sequence was formed. But with almost any scheme it will eventually be possible to determine the colors of cells at each of the positions across any register of limited width. So once again a fairly simple process is sufficient to allow the original key to be found.

So how then can one make a system that is not so vulnerable to cryptanalysis? One approach often used in practice is to form combinations of rules of the kind described above, and then to hope that the complexity of such rules will somehow have the effect of making cryptanalysis difficult.

But as we have seen many times in this book, more complicated rules do not necessarily produce behavior that is fundamentally any more complicated. And instead what we have discovered is that even among extremely simple rules there are ones which seem to yield behavior that is in a sense as complicated as anything. So can such rules be used for cryptography? I strongly suspect that they can, and that in fact they allow one to construct systems that are at least as secure to cryptanalysis as any that are known.

The picture below shows a simple example based on the rule 30 cellular automaton that I have discussed several times before in this book. The idea is to generate an encrypting sequence by sampling the evolution of the cellular automaton, starting from initial conditions that are defined by a key.



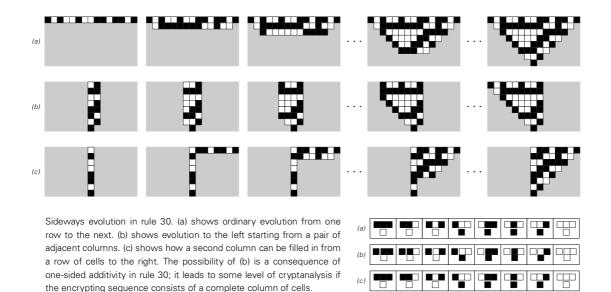
Encryption using a column of rule 30 as the encrypting sequence. I first suggested this method in 1985.

In the case of the additive cellular automaton shown on the previous page its nested structure makes it possible to recognize regularities using many of the methods of perception and analysis discussed in this chapter. But with rule 30 most sequences that are generated—even from simple initial conditions—appear completely random with respect to all of the methods of perception and analysis discussed so far.

So what about cryptanalysis? Does this also fail to find regularities, or does it provide some special way—at least within the context of a setup like the one shown above—to recognize whatever regularities are necessary for one to be able to deduce the initial condition and thus determine the key?

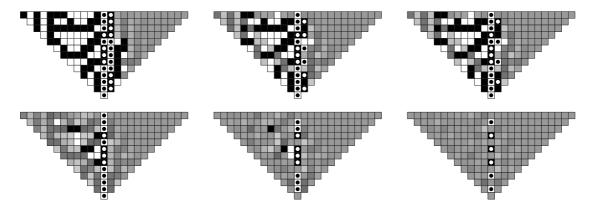
There is one approach that will always in principle work: one can just enumerate every possible initial condition, and then see which of them yields the sequence one wants. But as the width of the cellular automaton increases, the total number of possible initial conditions rapidly becomes astronomical, and to test all of them becomes completely infeasible.

So are there other approaches that can be used? It turns out that as illustrated in the picture below rule 30 has a property somewhat like the additive cellular automaton discussed two pages ago: in addition to allowing one row to be deduced from the row above, it allows columns to be deduced from columns to their right. But unlike for the additive cellular automaton, it takes not just one column but instead two adjacent columns to make this possible.



So if the encrypting sequence corresponds to a single column, how can one find an adjacent column? The last row of pictures above show a way to do this. One picks some sequence of cells for the right half of the top row, then evolves down the page. And somewhat surprisingly, it turns out that given the cells in one column, there are fairly few possibilities for what the neighboring column can be. So by sampling a limited number of sequences on the top row, one can often find a second column that then allows columns to the left to be determined, and thus for a candidate key to be found. But it is rather easy to foil this particular approach to cryptanalysis: all one need do is not sample every single cell in a given column in forming the encrypting sequence. For without every cell there does not appear to be enough information for any kind of local rule to be able to deduce one column from others.

The picture below shows evidence for this. The cells marked by dots have colors that are taken as given, and then the colors of other cells are filled in according to the average that is obtained by starting from all possible initial conditions.



Patterns generated by rule 30 after averaging over all possible initial conditions that reproduce the arrangements of colors in the cells indicated by dots. If a cell is completely black or completely white then this means that its color is uniquely determined by the constraints given. If the cell is shown as gray then this means that it has some probability of being black and some probability of being white. Note that when two complete adjacent columns are specified all the cells on the left-hand side are determined. But when fewer cells are specified, the number of cells that are determined decreases rapidly, indicating that cryptanalysis is likely to become difficult.

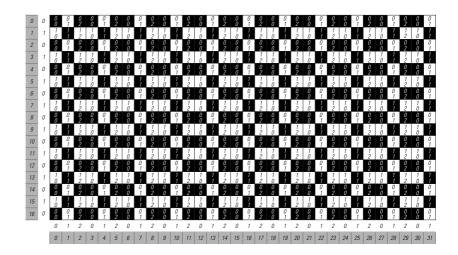
With two complete columns given, all cells to the left are determined to be either black or white. And with one complete column given, significant patches of cells still have determined colors. But if only every other cell in a column is given, almost nothing definite follows about the colors of other cells.

So what about the approach on page 602? Could this not be used here? It turns out that the approach relies crucially on the additivity of the underlying rules. And since rule 30 is not additive, it simply does not work. What happens is that the function that determines the color of a particular cell from the colors of cells in a nearby column rapidly becomes extremely complicated—so that the approach probably ends up essentially being no better than just enumerating possible initial conditions.

The conclusion therefore is that at least with standard methods of cryptanalysis—as well as a few others—there appears to be no easy way to deduce the key for rule 30 from any suitably chosen encrypting sequence. But how can one be sure that there really is absolutely no easy way to do this? In Chapter 12 I will discuss some fundamental approaches to such a question. But as a practical matter one can say that not only have direct attempts to find easy ways to deduce the key in rule 30 failed, but also—despite some considerable effort—little progress has been made in solving any of various problems that turn out to be equivalent to this one.

## **Traditional Mathematics and Mathematical Formulas**

Traditional mathematics has for a long time been the primary method of analysis used throughout the theoretical sciences. Its goal can usually be thought of as trying to find a mathematical formula that summarizes the behavior of a system. So in a simple case if one has an array of black and white squares, what one would typically look for is a formula that takes the numbers which specify the position of a particular square and from these tells one whether the square is black or white.



With a pattern that is purely repetitive, the formula is always straightforward, as the picture at the bottom of the facing page illustrates. For all one ever need do is to work out the remainder from dividing the position of a particular square by the size of the basic repeating block, and this then immediately tells one how to look up the color one wants.

So what about nested patterns? It turns out that in most of traditional mathematics such patterns are already viewed as quite advanced. But with the right approach, it is in the end still fairly straightforward to find formulas for them.

The crucial idea—much as in Chapter 4—is to think about numbers not in terms of their size but instead in terms of their digit sequences. And with this idea the picture on the next page shows an example of how what is in effect a formula can be constructed for a nested pattern.

What one does is to look at the digit sequences for the numbers that give the vertical and horizontal positions of a certain square. And then in the specific case shown one compares corresponding digits in these two sequences, and if these digits are ever respectively 0 and 1, then the square is white; otherwise it is black.

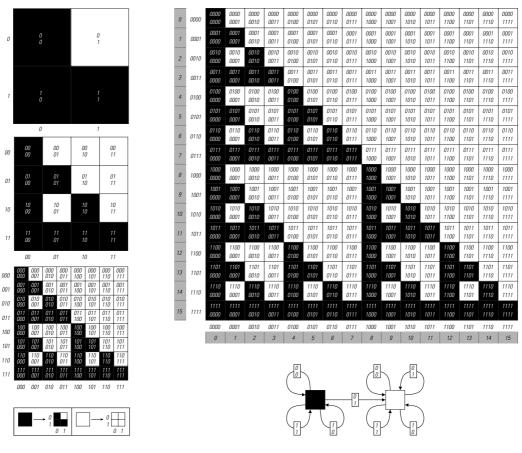
So why does this procedure work?

As we have discussed several times in this book, any nested pattern must—almost by definition—be able to be reproduced by a neighbor-independent substitution system. And in the case shown on the next page the rules for this system are such that they replace each square at each step by a  $2 \times 2$  block of new squares. So as the picture illustrates this means that new squares always have positions that involve numbers containing one extra digit. With the particular rules shown, the new squares always have the same color as the old one, except in one specific case: when a black square is replaced, the new square that appears in the upper right is always white. But this square

 $\blacktriangleleft$  An example of how the color of any square in a repetitive pattern can be found from its coordinates by a simple mathematical procedure. The procedure takes the *x* and *y* coordinates of the square, and computes their remainders after division by 3 and 2 respectively. Using these remainders—which are shown inside each square—the color of a particular square can be



determined by a simple lookup in the repeating block shown on the left. The whole procedure can be represented using a mathematical formula that involves either functions like *Mod* or more traditional functions like *Sin*.

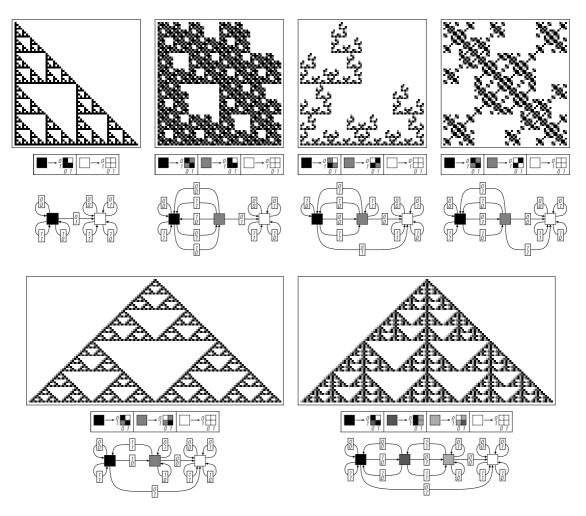


An example of how the color of any square in a nested pattern can be found from its coordinates by a fairly simple mathematical procedure. The procedure works by looking at the base 2 digit sequences of the coordinates. If any digit in the y coordinate of a particular square is 0 when the corresponding digit in the x coordinate is 1 then the square is white; otherwise it is black. The finite automaton at the bottom right gives a representation of this rule. Starting from the black square, one follows the sequence of connections that corresponds to the successive digits that one encounters in the y and x coordinates. Whatever square one lands up at in the finite automaton then gives the color one wants. Why this procedure works is illustrated by the pictures on the left. The nested pattern can be built up by a 2D substitution system with the rules shown. At each step in the evolution of this substitution system one gets a finer grid of squares, each specified in effect by one more digit in their coordinates.

has the property that its vertical position ends with a 0, and its horizontal position ends with a 1. So if the numbers that correspond to the position of a particular square contain this combination of digits at any point, it follows that the square must be white.

So what about other nested patterns? It turns out that using an extension of the argument above it is always possible to take the rules

for the substitution system that generates a particular nested pattern, and from these construct a procedure for finding the color of a square in the pattern given its position. The pictures below show several examples, and in all cases the procedures are fairly straightforward.



Procedures for determining the color of a square at a given position in various nested patterns. In each case the whole pattern can be generated by repeatedly applying the substitution system rule shown. The color of any particular square can also be found by feeding the digit sequences of its y and x coordinates to the finite automaton shown. The first example shown corresponds to cellular automaton rule 60; the last two examples correspond respectively to rules 90 and 150. In the top row of examples, the initial condition for the substitution system is a single black square, and the start state for the finite automaton is also its black state. In the second row of examples, the initial condition consists of a light gray square next to a black square. In these cases, the colors of squares to the left of the center can be found by starting from the light gray state in the finite automaton; the colors of squares to the right can be found by starting from the black state.

But while these procedures could easily be implemented as programs, they are in a sense not based on what are traditionally thought of as ordinary mathematical functions. So is it in fact possible to get formulas for the colors of squares that involve only such functions?

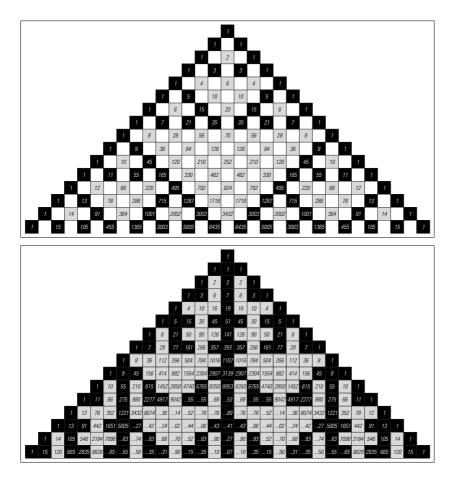
In the one specific case shown at the top of the facing page it turns out to be fairly easy. For it so happens that this particular pattern—which is equivalent to the patterns at the beginning of each row on the previous page—can be obtained just by adding together pairs of numbers in the format of Pascal's triangle and then putting a black square whenever there is an entry that is an odd number.

And as the table below illustrates, the entries in Pascal's triangle are simply the binomial coefficients that appear when one expands out the powers of 1 + x. So to determine whether a particular square in the pattern is black or white, all one need do is to compute the corresponding binomial coefficient, and see whether or not it is an odd number. And this means that if black is represented by 1 and white by 0, one can then give an explicit formula for the color of the square at position *x* on row *y*: it is simply  $(1 - (-1)^Binomial[y, x])/2$ .

1	1	1	1
1 + x	1 + x	$1 + x + x^2$	$1 + x + x^2$
$(1 + x)^2$	$1 + 2x + x^2$	$\left(1+x+x^2\right)^2$	$1 + 2x + 3x^2 + 2x^3 + x^4$
$(1 + x)^3$	$1 + 3x + 3x^2 + x^3$	$\left(1+x+x^2\right)^3$	$1 + 3x + 6x^2 + 7x^3 + 6x^4 + 3x^5 + x^6$
$(1 + x)^4$	$1 + 4x + 6x^2 + 4x^3 + x^4$	$\left(1+x+x^2\right)^4$	$1 + 4x + 10x^{2} + 16x^{3} + 19x^{4} + 16x^{5} + 10x^{6} + 4x^{7} + x^{8}$
$(1 + x)^5$	$1 + 5x + 10x^2 + 10x^3 + 5x^4 + x^5$	$\left(1+x+x^2\right)^5$	$1 + 5x + 15x^{2} + 30x^{3} + 45x^{4} + 51x^{5} + 45x^{6} + 30x^{7} + 15x^{8} + 5x^{9} + x^{10}$
Binomial[t, n]			GegenbauerC[n,-t,-1/2]

Algebraic representations of the patterns on the facing page. The coefficient of  $x^n$  on each row gives the value of each square. These coefficients can also be obtained from the formulas in terms of *Binomial* and *GegenbauerC* given. A particular square is colored black if its value *a* is odd. This can be determined either from Mod[a, 2] or equivalently from  $(1 - (-1)^a)/2$  or  $Sin[\pi a/2]^2$ . The succession of polynomials above can be obtained by expanding the generating functions 1/(1 - (1 + x)y) and  $1/(1 - (1 + x + x^2)y)$ . *Binomial[m, n]* is the ordinary binomial coefficient m!/(n! (m - n)!). *GegenbauerC* is a so-called orthogonal polynomial—a higher mathematical function.

So what about the bottom picture on the facing page? Much as in the top picture numbers can be assigned to each square, but now these numbers are computed by successively adding together triples rather



Nested patterns constructed using arithmetic operations. The example at the top is Pascal's triangle, formed by making each number be the sum of the numbers immediately to its left and right on the row above. The example at the bottom is a generalization of Pascal's triangle in which each number is the sum of the numbers above it and to its left and right on the row above. In both cases squares are colored black when the numbers that appear in them are odd. The limiting arrangements of colors correspond to nested patterns. For the top picture the pattern is what would be generated by an additive cellular automaton following rule 90; for the bottom picture it is what would be generated by one following rule 150. The numbers in the top picture are binomial coefficients; those in the bottom picture are particular trinomial coefficients.

than pairs. And once again the numbers appear as coefficients, but now in the expansion of powers of  $1 + x + x^2$  rather than of 1 + x.

So is there an explicit formula for these coefficients? If one restricts oneself to a fixed number of elementary mathematical

functions together with factorials and multinomial coefficients then it appears that there is not. But if one also allows higher mathematical functions then it turns out that such a formula can in fact be found: as indicated in the table above each coefficient is given by a particular value of a so-called Gegenbauer or ultraspherical function.

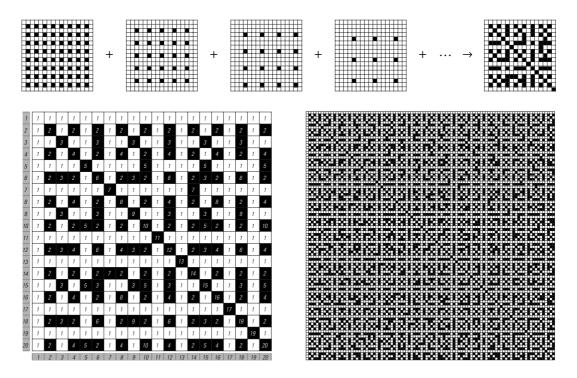
So what about other nested patterns? Both of the patterns shown on the previous page are rather special in that as well as being generated by substitution systems they can also be produced one row at a time by the evolution of one-dimensional cellular automata with simple additive rules. And in fact the approaches used above can be viewed as direct generalizations of such additive rules to the domain of ordinary numbers.

For a few other nested patterns there exist fairly simple connections with additive cellular automata and similar systems though usually in more dimensions or with more neighbors. But for most nested patterns there seems to be no obvious way to relate them to ordinary mathematical functions. Nevertheless, despite this, it is my guess that in the end it will in fact turn out to be possible to get a formula for any nested pattern in terms of suitably generalized hypergeometric functions, or perhaps other functions that are direct generalizations of ones used in traditional mathematics.

Yet given how simple and regular nested patterns tend to look it may come as something of a surprise that it should be so difficult to represent them as traditional mathematical formulas. And certainly if this example is anything to go by, it begins to seem unlikely that the more complex kinds of patterns that we have seen so many times in this book could ever realistically be represented by such formulas.

But it turns out that there are at least some cases where traditional mathematical formulas can be found even though to the eye or with respect to other methods of perception and analysis a pattern may seem highly complex.

The picture at the top of the facing page is one example. A pattern is built up by superimposing a sequence of repetitive grids, and to the eye this pattern seems highly complex. But in fact there is a simple formula for the color of each square: given the largest factor in common between the



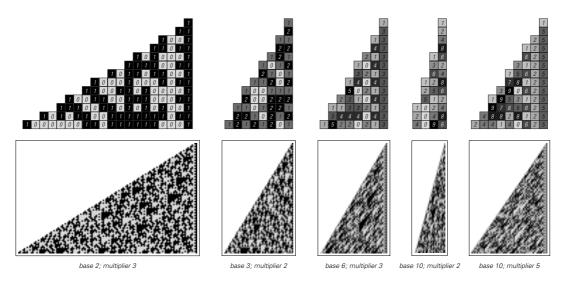
An example of a pattern that looks complex, but can nevertheless still be represented by a simple mathematical formula. Given the horizontal and vertical positions x and y a square is white when GCD[x, y] = 1 and is black otherwise. The condition GCD[x, y] = 1 is equivalent to the statement that x and y are relatively prime, or that no reduction is required to bring the fraction x/y to lowest terms. It can be shown that if the pattern is extended sufficiently far, then any possible local arrangement of black squares will eventually appear—though not necessarily with equal frequency.

numbers that specify the horizontal and vertical positions of the square, the square is white whenever this factor is 1, and is black otherwise.

So what about systems like cellular automata that have definite rules for evolution? Are there ever cases in which patterns generated by such systems seem complex to the eye but can in fact be described by simple mathematical formulas?

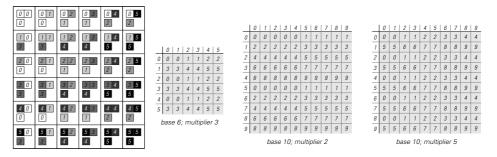
I know of one class of examples where this happens, illustrated in the pictures on the next page. The idea is to set up a row of cells corresponding to the digits of a number in a certain base, and then at each step to multiply this number by some fixed factor.

Such a system has many features immediately reminiscent of a cellular automaton. But at least in the case of multiplication by 3 in



Patterns of digits in various bases generated by successive multiplication by a fixed factor. Such systems were discussed on page 120. With multiplier m row t corresponds to the power  $m^t$ . The value of the cell at position n from the end of row t is thus the  $n^{th}$  digit of  $m^t$ , or  $Mod[Quotient[m^t, k^n], k]$ . Despite the apparent complexity of the patterns, a fairly simple mathematical formula thus exists for the color of each square they contain.

base 2, the presence of carry digits in the multiplication process makes the system not quite an ordinary cellular automaton. It turns out, however, that multiplication by 3 in base 6, or by 2 or 5 in base 10, never leads to carry digits, with the result that in such cases the system can be thought of as following a purely local cellular automaton rule of the kind illustrated below.



Cellular automaton rules equivalent to multiplication of digit sequences in various bases. The left part of the picture shows the explicit form of the rule for base 6 and multiplier 3. The arrays of numbers summarize the rule for this case and other cases. Note that only certain specific choices of base and multiplier lead to ordinary cellular automata; with other choices there are carries that propagate arbitrarily far. (See page 661.)

As the pictures at the top of the facing page demonstrate, the overall patterns produced in all cases tend to look complex, and in many respects random. But the crucial point is that because of the way the system was constructed there is nevertheless a simple formula for the color of each cell: it is given just by a particular digit in the number obtained by raising the multiplier to a power equal to the number of steps. So despite their apparent complexity, all the patterns on the facing page can in effect be described by simple traditional mathematical formulas.

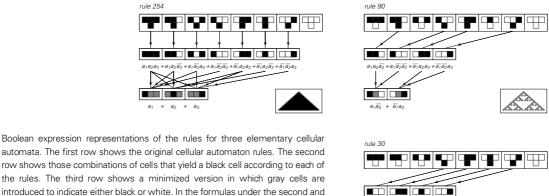
But if one thinks about actually using such formulas one might at first wonder what good they really are. For if one was to work out the value of a power  $m^t$  by explicitly performing t multiplications, this would be very similar to explicitly following t steps of cellular automaton evolution. But the point is that because of certain mathematical features of powers it turns out to be possible—as indicated in the table below—to find  $m^t$  with many fewer than toperations; indeed, one or two operations for every base 2 digit in t is always for example sufficient.

m1	т	т
m <sup>2</sup>	m x m	m <sup>2</sup>
m <sup>3</sup>	m x m x m	m <sup>2</sup> x m
m <sup>4</sup>	m x m x m x m	(m <sup>2</sup> ) <sup>2</sup>
m <sup>5</sup>	$m \times m \times m \times m \times m$	$(m^2)^2 \times m$
m <sup>6</sup>	$m \times m \times m \times m \times m \times m$	$(m^2 \times m)^2$
m <sup>7</sup>	$m \times m \times m \times m \times m \times m \times m$	(m <sup>2</sup> x m) <sup>2</sup> x m
m <sup>8</sup>	m x m x m x m x m x m x m x m	$((m^2)^2)^2$
m <sup>9</sup>	m x m x m x m x m x m x m x m x m	$((m^2)^2)^2 \times m$
m <sup>10</sup>	m x m x m x m x m x m x m x m x m x m	$((m^2)^2 \times m)^2$

Examples of how powers can be computed more efficiently than by successive multiplications. In the cases shown, the choice of whether to square or multiply by an additional factor of m at each step in computing  $m^t$  is made on the basis of the successive digits in the base 2 representation of the number t.

So what about other patterns produced by cellular automata and similar systems? Is it possible that in the end all such patterns could just be described by simple mathematical formulas? I do not think so. In fact, as I will argue in Chapter 12, my strong belief is that in the vast majority of cases it will be impossible for quite fundamental reasons to find any such simple formula. But even though no simple formula may exist, it is still always in principle possible to represent the outcome of any process of cellular automaton evolution by at least some kind of formula.

The picture below shows how this can be done for a single step in the evolution of three elementary cellular automata. The basic idea is to translate the rule for a given cellular automaton into a formula that depends on three variables  $a_1$ ,  $a_2$  and  $a_3$  whose values correspond to the colors of the three initial cells. The formula consists of a sum of terms, with each term being zero unless the colors of the three cells match a situation in which the rule yields a black cell.



automata. The first row shows the original cellular automaton rules. The second row shows those combinations of cells that yield a black cell according to each of the rules. The third row shows a minimized version in which gray cells are introduced to indicate either black or white. In the formulas under the second and third rows the variable  $a_i$  represents the color of the  $i^{th}$  cell.  $e_i e_i$  is analogous to  $e_i \wedge e_i$ ,  $e_i + e_i$  to  $e_i \vee e_i$ , and  $\overline{e_i}$  to  $\neg e_i$ . The formulas given are in so-called disjunctive normal form (DNF). They are set up so that only at most one term in each formula is ever relevant for any particular configuration of colors.

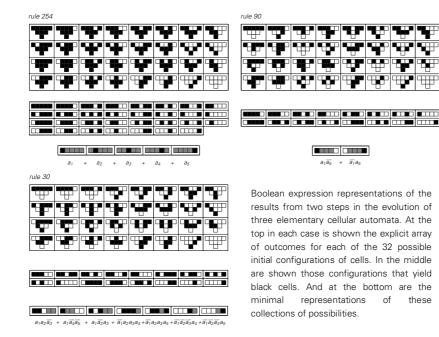
In the first instance, each term can be set up to correspond directly to one of the cases in the original rule. But in general this will lead to a more complicated formula than is necessary. For as the picture demonstrates, it is often possible to combine several cases into one term by ignoring the values of some of the variables.

a1222 + 21222 + 21222 + 21222

Æ

 $a_1\overline{a_2}\overline{a_3} + \overline{a_1}a_2 + \overline{a_1}a_3$ 

The picture at the top of the facing page shows what happens if one considers two steps of cellular automaton evolution. There are now altogether five variables, but at least for rules like rules 254 and 90 the individual terms end up not depending on most of these variables.



So what happens if one considers more steps? As the pictures on the next page demonstrate, rules like 254 and 90 that have fairly simple behavior lead to formulas that stay fairly simple. But for rule 30 the formulas rapidly get much more complicated.

So this strongly suggests that no simple formula exists—at least of the type used here—that can describe patterns generated by any significant number of steps of evolution in a system like rule 30.

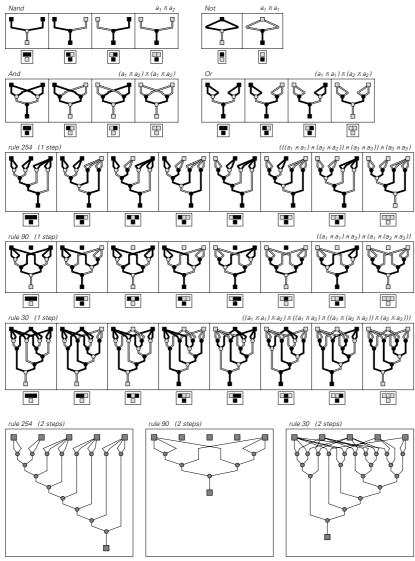
But what about formulas of other types? The formulas we have used so far can be thought of as always consisting of sums of products of variables. But what if we allow formulas with more general structure, not just two fixed levels of operations?

It turns out that any rule for blocks of black and white cells can be represented as some combination of just a single type of operation for example a so-called NAND function of the kind often used in digital electronics. And given this, one can imagine finding for any particular rule the formula that involves the smallest number of NAND functions.

rule 254 step 1:	a <sub>1</sub> + a <sub>2</sub> + a <sub>3</sub>
step 3:	<i>a</i> <sub>1</sub> + <i>a</i> <sub>2</sub> + <i>a</i> <sub>3</sub> + <i>a</i> <sub>4</sub> + <i>a</i> <sub>5</sub>
	$a_1 + a_2 + a_3 + a_4 + a_5 + a_6 + a_7$
	$a_1 + a_2 + a_3 + a_4 + a_5 + a_6 + a_7 + a_8 + a_9$
	a <sub>1</sub> + a <sub>2</sub> + a <sub>3</sub> + a <sub>4</sub> + a <sub>5</sub> + a <sub>6</sub> + a <sub>7</sub> + a <sub>8</sub> + a <sub>9</sub> + a <sub>10</sub> + a <sub>11</sub>
rule 90 step 1:	a <sub>1</sub> ā <sub>3</sub> + ā <sub>1</sub> a <sub>3</sub>
step 2:	$a_1\overline{a_5} + \overline{a_1}a_5$
	a1a3a5ā7 + a1a3ā5a7 + a1ā3a5a7 + a1ā3ā5ā7 + ā1a3a5a7 + ā1a3ā5ā7 + ā1ā3ā5ā7 + ā1ā3a5ā7 + ā1ā3ā5ā7
step 5:	$a_1\overline{a_9} + \overline{a_1}a_9$
	a1a3agāīi + a1a3āgā11 + a1ā3aga11 + a1ā3āgā11 + ā1a3aga11 + ā1a3āgāīi + ā1ā3agāīi + ā1ā3āgā11
rule 30 step 1:	$a_1\overline{a_2}\overline{a_3} + \overline{a_1}a_2 + \overline{a_1}a_3$
step 2:	$a_1a_2\overline{a_3} + a_1\overline{a_4}\overline{a_5} + a_1\overline{a_2}a_3 + \overline{a_1}a_2a_3a_4 + \overline{a_1}a_2a_3a_5 + \overline{a_1}\overline{a_2}\overline{a_3}\overline{a_4} + \overline{a_1}\overline{a_2}\overline{a_3}a_5$
	a1a2a3a4a5 + a1a2a3a5a6a7 + a1a2a4a5 + a1a2a3a4a5a8 + a1a2a3a4a5a7 + a1a2a3a4a6a7 + a1a2a3a4a6 + a1a2a3a4a7 + a1a2a3a4a6a7 + a1a2a4a5a6 + a1a2a4a5a7 + a1a2a4a5 + a1a3a4a5a6a7 + a1a3a4a6a7 + a1a3a4a6a7 + a1a3a4a6a7 + a1a3a a1a3a6a7 + a1a2a3a5 + a1a2a4a5
	$\begin{split} a_{12}a_{23}\overline{a_{4}a_{7}} + a_{12}\overline{a_{4}}\overline{a_{5}}a_{6} + a_{12}\overline{a_{2}}\overline{a_{3}}a_{4}a_{6}a_{7}a_{8} + a_{12}\overline{a_{2}}\overline{a_{3}}a_{4}a_{6}a_{7}a_{8} + a_{12}\overline{a_{2}}\overline{a_{4}}a_{6}a_{7}a_{8} + a_{12}\overline{a_{4}}a_{6}a_{7}a_{8}a_{7} + a_{12}\overline{a_{4}}a_{6}a_{7}a_{8}a_{8}a_{7}a_{8}a_{8}a_{8}a_{7}a_{8}a_{8}a_{8}a_{7}a_{8}a_{8}a_{8}a_{8}a_{8}a_{8}a_{8}a_{8$
	$\begin{aligned} a_{12}a_{23}a_{43}a_{5}\overline{a}\overline{b}\overline{b}\overline{c}\overline{c}\overline{c}\overline{c}\overline{c}\overline{c}\overline{c}\overline{c}\overline{c}c$

Minimal Boolean expression representations for the results of steps 1 through 5 in the evolution of three elementary cellular automata. Both rules 254 and 90 have fairly simple overall behavior, and yield comparatively small Boolean expressions. Rule 30 has much more complicated behavior and yields Boolean expressions whose size grows rapidly from one step to the next. (For steps 1 through 6, the expressions involve 3, 7, 17, 41, 102 and 261 terms respectively.) In each case the Boolean expressions given are the smallest possible in the disjunctive normal form (DNF) used.

The picture below shows some examples of the results. And once again what we see is that for rules with fairly simple behavior the formulas are usually fairly simple. But in cases like rule 30, the formulas one gets are already quite complicated even after just two steps.



Minimal representations in terms of NAND functions of the first two steps in the evolution of the same cellular automata as on the facing page. In each case, the network and formula shown are ones that involve absolute minimum the number of operations. Finding these effectively required searching through billions of possibilities. The picture at the top left shows the action of a single NAND function. The next three pictures show how the operations used in DNF formulas can be built up from NANDS.

(((((((a<sub>1</sub> ⊼ a<sub>1</sub>) ⊼ (a<sub>2</sub> ⊼ a<sub>2</sub>)) ⊼ (a<sub>3</sub> ⊼ a<sub>3</sub>)) ⊼ (a<sub>3</sub> ⊼ a<sub>3</sub>)) ⊼ (a<sub>4</sub> ⊼ a<sub>4</sub>)) ⊼ (a<sub>4</sub> ⊼ a<sub>4</sub>)) ⊼ (a<sub>5</sub> ⊼ a<sub>5</sub>)) ⊼ (a<sub>5</sub> ⊼ a<sub>5</sub>)

((a1 = a1) = a5) = (a1 = (a5 = a5))

 $\begin{array}{l} (((a_1 \ \pi \ a_2) \ \pi \ (a_1 \ \pi \ a_3)) \ \pi \ (a_2 \ \pi \ a_3)) \ \pi \ ((a_1 \ \pi \ a_5) \ \pi \ ((a_2 \ \pi \ a_3)) \ \pi \ ((a_2 \ \pi \ a_2) \ \pi \ ((a_1 \ \pi \ a_5)) \ \pi \ ((a_1 \ \pi \ a_5) \ \pi \ ((a_2 \ \pi \ a_5) \ \pi \ ((a_3 \ \pi \ a_5)) \ \pi \ ((a_1 \ \pi \ a_4) \ \pi \ (a_5 \ \pi \ a_5))))) \end{array}$ 

So even if one allows rather general structure, the evidence is that in the end there is no way to set up any simple formula that will describe the outcome of evolution for a system like rule 30.

And even if one settles for complicated formulas, just finding the least complicated one in a particular case rapidly becomes extremely difficult. Indeed, for formulas of the type shown on page 618 the difficulty can already perhaps double at each step. And for the more general formulas shown on the previous page it may increase by a factor that is itself almost exponential at each step.

So what this means is that just like for every other method of analysis that we have considered, we have little choice but to conclude that traditional mathematics and mathematical formulas cannot in the end realistically be expected to tell us very much about patterns generated by systems like rule 30.

### Human Thinking

When we are presented with new data one thing we can always do is just apply our general powers of human thinking to it. And certainly this allows us with rather modest effort to do quite well in handling all sorts of data that we choose to interact with in everyday life. But what about data generated by the kinds of systems that I have discussed in this book? How does general human thinking do with this?

There are definitely some limitations, since after all, if general human thinking could easily find simple descriptions of, for example, all the various pictures in this book, then we would never have considered any of them complex.

One might in the past have assumed that if a simple description existed of some piece of data, then with appropriate thinking and intelligence it would usually not be too difficult to find it. But what the results in this book establish is that in fact this is far from true. For in the course of this book we have seen a great many systems whose underlying rules are extremely simple, yet whose overall behavior is sufficiently complex that even by thinking quite hard we cannot recognize its simple origins. Usually a small amount of thinking allows us to identify at least some regularities. But typically these regularities are ones that can also be found quite easily by many of the standard methods of perception and analysis discussed earlier in this chapter.

So what then does human thinking in the end have to contribute? The most obvious way in which it stands out from other methods of perception and analysis is in its large-scale use of memory.

For all the other methods that we have discussed effectively operate by taking each new piece of data and separately applying some fixed procedure to it. But in human thinking we routinely make use of the huge amount of memory that we have built up from being exposed to billions of previous pieces of data.

And sometimes the results can be quite impressive. For it is quite common to find that even though no other method has much to say about a particular piece of data, we can immediately come up with a description for it by remembering some similar piece of data that we have encountered before.

And thus, for example, having myself seen thousands of pictures produced by cellular automata, I can recognize immediately from memory almost any pattern generated by any of the elementary rules even though none of the other methods of perception and analysis can get very far whenever such patterns are at all complex.

But insofar as there is sophistication in what can be done with human memory, does this sophistication come merely from the experiences that are stored in memory, or somehow from the actual mechanism of memory itself?

The idea of storing large amounts of data and retrieving it according to various criteria is certainly quite familiar from databases in practical computing. But there is at least one important difference between the way typical databases operate, and the way human memory operates. For in a standard database one tends to be able to find only data that meets some precise specification, such as containing an exact match to a particular string of text. Yet with human memory we routinely seem to be able to retrieve data on the basis of much more general notions of similarity. In general, if one wants to find a piece of data that has a certain property—either exact or approximate—then one way to do this is just to scan all the pieces of data that one has stored, and test each of them in turn. But even if one does all sorts of parallel processing this approach presumably in the end becomes quite impractical.

So what can one then do? In the case of exact matches there are a couple of approaches that are widely used in practice.

Probably the most familiar is what is done in typical dictionaries: all the entries are arranged in alphabetical order, so that when one looks something up one does not need to scan every single entry but instead one can quickly home in on just the entry one wants.

Practical database systems almost universally use a slightly more efficient scheme known as hashing. The basic idea is to have some definite procedure that takes any word or other piece of data and derives from it a so-called hash code which is used to determine where the data will be stored. And the point is that if one is looking for a particular piece of data, one can then apply this same procedure to that data, get the hash code for the data, and immediately determine where the data would have been stored.

But to make this work, does one need a complex hashing procedure that is carefully tuned to the particular kind of data one is dealing with? It turns out that one does not. And in fact, all that is really necessary is that the hashing procedure generate enough randomness that even though there may be regularities in the original data, the hash codes that are produced still end up being distributed roughly uniformly across all possibilities.

And as one might expect from the results in this book, it is easy to achieve this even with extremely simple programs—either based on numbers, as in most practical database systems, or based on systems like cellular automata.

So what this means is that regardless of what kind of data one is storing, it takes only a very simple program to set up a hashing scheme that lets one retrieve pieces of data very efficiently. And I suspect that at least some aspects of this kind of mechanism are involved in the operation of human memory. But what about the fact that we routinely retrieve from our memory not just data that matches exactly, but also data that is merely similar? Ordinary hashing would not let us do this. For a hashing procedure will normally put different pieces of data at quite different locations—even if the pieces of data happen in some sense to be similar.

So is it possible to set up forms of hashing that will in fact keep similar pieces of data together? In a sense what one needs is a hashing procedure in which the hash codes that are generated depend only on features of the data that really make a difference, and not on others.

One practical example where this is done is a simple procedure often used for looking up names by sound rather than spelling. In its typical form this procedure works by dropping all vowels and grouping together letters like "d" and "t" that sound similar, with the result that at least in some approximation the only features that are kept are ones that make a difference in the way a word sounds.

So how can one achieve this in general?

In many respects one of the primary goals of all forms of perception and analysis is precisely to pick out those features of data that are considered relevant, and to discard all others.

And so, as we discussed earlier in this chapter, the human visual system, for example, appears to be based on having nerve cells that respond only to certain specific features of images. And this means that if one looks only at the output from these nerve cells, then one gets a representation of visual images in which two images that differ only in certain kinds of details will be assigned the same representation.

So if it is a representation like this that is used as the basis for storing data in memory, the result is that one will readily be able to retrieve not only data that matches exactly, but also data that is merely similar enough to have the same representation.

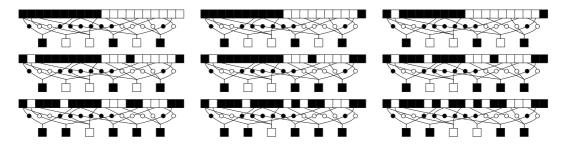
In actual brains it is fairly clear that input received by all the various sensory systems is first processed by assemblies of nerve cells that in effect extract certain specific features. And it seems likely that especially in lower organisms it is often representations formed quite directly from such features that are what is stored in memory. But at least in humans there is presumably more going on. For it is quite common that we can immediately recognize that we have encountered some particular object before even if it is superficially presented in a quite different way. And what this suggests is that quite different patterns of raw data from our sensory systems can at least in some cases still lead to essentially the same representation in memory.

So how might this be achieved? One possibility is that our brains might be set up to extract certain specific high-level features—such as, say, topological structure in three-dimensional space—that happen to successfully characterize particular kinds of objects that we traditionally deal with.

But my strong suspicion is that in fact there is some much simpler and more general mechanism at work, that operates essentially just at the level of arbitrary data elements, without any direct reference to the origin or meaning of these data elements.

And one can imagine quite a few ways that such a mechanism could potentially be set up with nerve cells.

One step in a particularly simple scheme is illustrated in the picture below. The basic idea is to have a sequence of layers of nerve cells—much as one knows exist in the brain—with each cell in each successive layer responding only if the inputs it gets from some fixed random set of cells in the layer above form some definite pattern.



One step in a very simple model of the way hash codes for arbitrary data might be generated by layers of nerve cells in the brain. The response of a single layer of idealized nerve cells to a sequence of progressively different inputs is shown. Each nerve cell fires and yields black output only if the inputs it gets from certain fixed positions match a particular template. The sequence of outputs from all the nerve cells can be used as a hash code, whose value tends to be the same for inputs that differ only by small changes.

In a sense this is a straightforward generalization of the scheme for visual perception that we discussed earlier in this chapter. But the point is that with such a setup detailed changes in the input to the first layer of cells only rarely end up having an effect on output from the last layer of cells.

It is not difficult to find systems in which different inputs often yield the same output. In fact, this is the essence of the very general phenomenon of attractors that we discussed in Chapter 6—and it is seen in the vast majority of cellular automata, and in fact in almost any kind of system that follows definite rules.

But what is somewhat special about the setup above is that inputs which yield the same output tend to be ones that might reasonably be considered similar, while inputs that yield different outputs tend to be significantly different.

And thus, for example, a change in a single input cell typically will not have a high probability of affecting the output, while a change in a large fraction of the input cells will.

So quite independent of precisely which features of the original data correspond to which input cells, this basic mechanism provides a simple way to get a representation—and thus a hash code—that will tend to be the same for pieces of data that somehow have enough features that are similar.

So how would such a representation in the end be used? In a scheme like the one above the output cells would presumably be connected to cells that actually perform actions of some kind—perhaps causing muscles to move, or perhaps just providing inputs to further nerve cells.

But so where in all of this would the actual content of our memory reside? Almost certainly at some level it is encoded in the details of connections between nerve cells.

But how then might such details get set up?

There is evidence that permanent changes can be produced in individual nerve cells as a result of the behavior of nerve cells around them. And as data gets received by the brain such changes presumably do occur at least in some cells. But if one looks, say, at nerve cells involved in the early stages of the visual system, then once the brain has matured past some point these never seem to change their properties much. And quite probably the same is true of many nerve cells involved in the general process of doing the analog of producing hash codes.

The reason for such a lack of change could conceivably be simply that at the relevant level the overall properties of the stream of data corresponding to typical experience remain fairly constant. But it might also be that if one expects to retrieve elements of memory reliably then there is no choice but to set things up so that the hashing procedure one uses always stays essentially the same.

And if there is a fixed such scheme, then this implies that while certain similarities between pieces of data will immediately be recognized, others will not.

So how does this compare to what we know of actual human memory? There are many kinds of similarities that we recognize quite effortlessly. But there are also ones that we do not. And thus, for example, given a somewhat complicated visual image—say of a face or a cellular automaton pattern—we can often not even immediately recognize similarity to the same image turned upside-down.

So are such limitations in the end intrinsic to the underlying mechanism of human memory, or do they somehow merely reflect characteristics of the memory that we happen to build up from our typical actual experience of the world?

My guess is that it is to some extent a mixture. But insofar as more important limitations tend to be the result of quite low-level aspects of our memory system it seems likely that even if these aspects could in principle be changed it would in practice be essentially impossible to do so. For the low levels of our memory system are exposed to an immense stream of data. And so to cause any substantial change one would presumably have to insert a comparable amount of data with the special properties one wants. But for a human interacting with anything like a normal environment this would in practice be absolutely impossible.

So in the end I strongly suspect that the basic rules by which human memory operates can almost always be viewed as being essentially fixed—and, I believe, fairly simple. But what about the whole process of human thinking? What does it ultimately involve? My strong suspicion is that the use of memory is what in fact underlies almost every major aspect of human thinking.

Capabilities like generalization, analogy and intuition immediately seem very closely related to the ability to retrieve data from memory on the basis of similarity. But what about capabilities like logical reasoning? Do these perhaps correspond to a higher-level type of human thinking?

In the past it was often thought that logic might be an appropriate idealization for all of human thinking. And largely as a result of this, practical computer systems have always treated logic as something quite fundamental. But it is my strong suspicion that in fact logic is very far from fundamental, particularly in human thinking.

For among other things, whereas in the process of thinking we routinely manage to retrieve remarkable connections almost instantaneously from memory, we tend to be able to carry out logical reasoning only by laboriously going from one step to the next. And my strong suspicion is that when we do this we are in effect again just using memory, and retrieving patterns of logical argument that we have learned from experience.

In modern times computer languages have often been thought of as providing precise ways to represent processes that might otherwise be carried out by human thinking. But it turns out that almost all of the major languages in use today are based on setting up procedures that are in essence direct analogs of step-by-step logical arguments.

As it happens, however, one notable exception is *Mathematica*. And indeed, in designing *Mathematica*, I specifically tried to imitate the way that humans seem to think about many kinds of computations. And the structure that I ended up coming up with for *Mathematica* can be viewed as being not unlike a precise idealization of the operation of human memory.

For at the core of *Mathematica* is the notion of storing collections of rules in which each rule specifies how to transform all pieces of data that are similar enough to match a single *Mathematica* pattern. And the success of *Mathematica* provides considerable evidence for the power of this kind of approach. But ultimately—like other computer languages—*Mathematica* tends to be concerned mostly with setting up fairly short specifications for quite definite computations. Yet in everyday human thinking we seem instead to use vast amounts of stored data to perform tasks whose definitions and objectives are often quite vague.

There has in the past been a great tendency to assume that given all its apparent complexity, human thinking must somehow be an altogether fundamentally complex process, not amenable at any level to simple explanation or meaningful theory.

But from the discoveries in this book we now know that highly complex behavior can in fact arise even from very simple basic rules. And from this it immediately becomes conceivable that there could in reality be quite simple mechanisms that underlie human thinking.

Certainly there are many complicated details to the construction of the brain, and no doubt there are specific aspects of human thinking that depend on some of these details. But I strongly suspect that there is a definite core to the phenomenon of human thinking that is largely independent of such details—and that will in the end turn out to be based on rules that are rather simple.

So how will we be able to tell if this is in fact the case? Detailed direct studies of the brain and its operation may give some clues. But my guess is that the only way that really convincing evidence will be obtained is if actual technological systems are constructed that can successfully be seen to emulate human thinking.

And indeed as of now our experience with practical computing provides rather little encouragement that this will ever be possible. There are certainly some tasks—such as playing chess or doing algebra—that at one time were considered indicative of human-like thinking, but which are now routinely done by computer. Yet when it comes to seemingly much more mundane and everyday types of thinking the computers and programs that exist at present tend to be almost farcically inadequate.

So why have we not done better? No doubt part of the answer has to do with various practicalities of computers and storage systems. But a more important part, I suspect, has to do with issues of methodology. For it has almost always been assumed that to emulate in any generality a process as sophisticated as human thinking would necessarily require an extremely complicated system. So what has mostly been done is to try to construct systems that perform only rather specific tasks.

But then in order to be sure that the appropriate tasks will actually be performed the systems tend to be set up—as in traditional engineering—so that their behavior can readily be foreseen, typically by standard mathematical or logical methods. And what this almost invariably means is that their behavior is forced to be fairly simple. Indeed, even when the systems are set up with some ability to learn they usually tend to act—much like the robots of classical fiction with far too much simplicity and predictability to correspond to realistic typical human thinking.

So on the basis of traditional intuition, one might then assume that the way to solve this problem must be to use systems with more complicated underlying rules, perhaps more closely based on details of human psychology or neurophysiology. But from the discoveries in this book we know that this is not the case, and that in fact very simple rules are quite sufficient to produce highly complex behavior.

Nevertheless, if one maintains the goal of performing specific well-defined tasks, there may still be a problem. For insofar as the behavior that one gets is complex, it will usually be difficult to direct it to specific tasks—an issue rather familiar from dealing with actual humans. So what this means is that most likely it will at some level be much easier to reproduce general human-like thinking than to set up some special version of human-like thinking only for specific tasks.

And it is in the end my strong suspicion that most of the core processes needed for general human-like thinking will be able to be implemented with rather simple rules.

But a crucial point is that on their own such processes will most likely not be sufficient to create a system that one would readily recognize as exhibiting human-like thinking. For in order to be able to relate in a meaningful way to actual humans, the system would almost certainly have to have built up a human-like base of experience. No doubt as a practical matter this could to some extent be done just by large-scale recording of experiences of actual humans. But it seems not unlikely that to get a sufficiently accurate experience base, the system would itself have to interact with the world in very much the same way as an actual human—and so would have to have elements that emulate many elaborate details of human biological and other structure.

Once one has an explicit system that successfully emulates human thinking, however, one can imagine progressively removing some of this complexity, and seeing just which features of human thinking end up being preserved.

So what about human language, for example? Is this purely learned from the details of human experience? Or are there features of it that reflect more fundamental aspects of human thinking?

When one learns a language—at least as a young child—one implicitly tends to deduce simple grammatical rules that are in effect specific generalizations of examples one has encountered. And I suspect that in doing this the types of generalizations that one makes are essentially those that correspond to the types of similarities that one readily recognizes in retrieving data from memory.

Actual human languages normally have many exceptions to any simple grammatical rules. And it seems that with sufficient effort we can in fact learn languages with almost any structure. But the fact that most modern computer languages are specifically set up to follow simple grammatical rules seems to make their structures particularly easy for us to learn—perhaps because they fit in well with low-level processes of human thinking.

But to what extent is the notion of a language even ultimately necessary in a system that does human-like thinking? Certainly in actual humans, languages seem to be crucial for communication. But one might imagine that if the underlying details of different individuals from some class of systems were sufficiently identical then communication could instead be achieved just by directly transferring low-level patterns of activity. My guess, however, is that as soon as the experiences of different individuals become different, this will not work, and that therefore some form of general intermediate representation or language will be required.

But does one really need a language that has the kind of sequential grammatical structure of ordinary human language? Graphical user interfaces for computer systems certainly often use somewhat different schemes. And in simple situations these can work well. But my uniform experience has been that if one wants to specify processes of any significant complexity in a fashion that can reasonably be understood then the only realistic way to do this is to use a language—like *Mathematica*—that has essentially an ordinary sequential grammatical structure.

Quite why this is I am not certain. Perhaps it is merely a consequence of our familiarity with traditional human languages. Or perhaps it is a consequence of our apparent ability to pay attention only to one thing at a time. But I would not be surprised if in the end it is a reflection of fairly fundamental features of human thinking.

And indeed our difficulty in thinking about many of the patterns produced by systems in this book may be not unrelated. For while ordinary human language has little trouble describing repetitive and even nested patterns, it seems to be able to do very little with more complex patterns—which is in a sense why this book, for example, depends so heavily on visual presentation.

At the outset, one might have imagined that human thinking must involve fundamentally special processes, utterly different from all other processes that we have discussed. But just as it has become clear over the past few centuries that the basic physical constituents of human beings are not particularly special, so also—especially after the discoveries in this book—I am quite certain that in the end there will turn out to be nothing particularly special about the basic processes that are involved in human thinking.

And indeed, my strong suspicion is that despite the apparent sophistication of human thinking most of the important processes that underlie it are actually very simple—much like the processes that seem to be involved in all the other kinds of perception and analysis that we have discussed in this chapter.

### **Higher Forms of Perception and Analysis**

In the course of this chapter we have discussed in turn each of the major methods of perception and analysis that we in practice use. And if our goal is to understand the actual experience that we get of the world then there is no reason to go further. But as a matter of principle one can ask whether the methods of perception and analysis that we have discussed in a sense cover what is ultimately possible—or whether instead there are higher and fundamentally more powerful forms of perception and analysis that for some reason we do not at present use.

As we discussed early in this chapter, any method of perception or analysis can at some level be viewed as a way of trying to find simple descriptions for pieces of data. And what we might have assumed in the past is that if a piece of data could be generated from a sufficiently simple description then the data itself would necessarily seem to us quite simple—and would therefore have many regularities that could be recognized by our standard methods of perception and analysis.

But one of the central discoveries of this book is that this is far from true—and that actually it is rather common for rules that have extremely simple descriptions to give rise to data that is highly complex, and that has no regularities that can be recognized by any of our standard methods.

But as we discussed earlier in this chapter the fact that a simple rule can ultimately be responsible for such data means that at some level the data must contain regularities. So the point is that these regularities are just not ones that can be detected by our standard methods of perception and analysis.

Yet the fact that there are in the end regularities means that at least in principle there could exist higher forms of perception and analysis that would succeed in recognizing them.

So might one day some new method of perception and analysis be invented that would in a sense manage to recognize all possible regularities, and thus be able to tell immediately if any particular piece of data could be generated from any kind of simple description? My strong belief—as I will argue in Chapter 12—is that at least in complete generality this will never be possible. But that does not mean that there cannot exist higher forms of perception and analysis that succeed in recognizing at least some regularities that our existing methods do not.

The results of this chapter, however, might seem to provide some circumstantial evidence that in practice even this might not be possible. For in the course of the chapter we have discussed a whole range of different kinds of perception and analysis, yet in essentially all cases we have found that the overall capabilities they exhibit are rather similar. Most of them, for example, recognize repetition, and some also recognize nesting. But almost none recognize anything more complex.

So what this perhaps suggests is that in the end there might be only certain specific capabilities that can be realized in practical methods of perception and analysis. And certainly it seems not inconceivable that there could be a fundamental result that the only kinds of regularities that both occur frequently in actual systems and can be recognized quickly enough to provide a basis for practical methods of perception and analysis are ones like repetition and nesting.

But there is another possible explanation for what we have seen in this chapter: perhaps it is just that we, as humans, are always very narrow in the methods of perception and analysis that we use. For certainly it is remarkable that none of the methods that we normally use ever in the end seem to manage to get much further than we can already get with our own built-in powers of perception. And what this perhaps suggests is that we choose the methods we use to be essentially those that pick out only regularities with which we are somehow already very familiar from our own built-in powers of perception.

For there is no difficulty in principle in constructing procedures that have capabilities very different from those of our standard methods of perception and analysis. Indeed, as one example, one could imagine just enumerating all possible simple descriptions of some particular type, and then testing in each case to see whether what one gets matches a piece of data that one has.

And in some specific cases, this might well succeed in finding extremely simple descriptions for the data. But to use such a method in

any generality almost inevitably requires computational resources far greater than one would normally consider reasonable in a practical method of perception or analysis.

And in fact there is really no reason to consider such a sophisticated procedure. For in a sense any program—including one that is very simple and runs very quickly—can be thought of as implementing a method of perception or analysis. For if one gives a piece of data as the input to the program, then the output one gets—whatever it may be—can be viewed as corresponding to some kind of description of the data.

But the problem is that under most circumstances this description will not be particularly useful. And indeed what typically seems to be necessary to make it useful is that somehow one is already familiar with similar descriptions, and knows their significance.

A description based on output from a cellular automaton rule that one has never seen before is thus for example not likely to be useful. But a description that picks out a feature like repetition that is already very familiar to us will typically be much more useful.

And potentially therefore our lack of higher forms of perception and analysis might in the end have nothing to do with any difficulty in implementing such forms, but instead may just be a reflection of the fact that we only have enough context to make descriptions of data useful when these descriptions are fairly close to the ones we get from our own built-in human methods of perception.

But why is it then that these methods themselves are not more powerful? After all, one might think that biological evolution would inevitably have made us as good as possible at handling data associated with any of the systems that we commonly encounter in nature.

Yet as we have seen in this book almost whenever there is significant complexity our powers of human perception end up being far from adequate to find any kind of minimal summaries of data.

And with the traditional view that biological evolution is somehow a process of infinite power this seems to leave one little choice but to conclude that there must be fundamental limitations on possible methods of perception that can be useful. One might imagine perhaps that while there could in principle be methods of perception that would recognize features beyond, say, repetition and nesting, any single such feature might never occur in a sufficiently wide range of systems to make its recognition generally useful to a biological organism.

But as of now I do not know of any fundamental reason why this might be so, and following my arguments in Chapter 8 I would not be at all surprised if the process of biological evolution had simply missed even methods of perception that are, in some sense, fairly obvious.

So what about an extraterrestrial intelligence? Free from any effects of terrestrial biological evolution might it have developed all sorts of higher forms of perception and analysis?

Of course we have no direct information on this. But the very fact that we have so far failed to discover any evidence for extraterrestrial intelligence may itself conceivably already be a sign that higher forms of perception and analysis may be in use.

For as I will discuss in Chapter 12 it seems far from inconceivable that some of the extraterrestrial radio and other signals that we pick up and assume to be random noise could in fact be meaningful messages but just encoded in a way that can be recognized only by higher forms of perception and analysis than those we have so far applied to them.

Yet whether or not this is so, the capabilities of extraterrestrial intelligence are not in the end directly relevant to an understanding of our own experience of the world. In the future we may well manage to use higher forms of perception and analysis, and as a result our experience of the world will change—no doubt along with certain aspects of our science and mathematics. But for now it is the kinds of methods of perception and analysis that we have discussed in most of this chapter that must form the basis for the conclusions we make about the world.

#### **NOTES FOR CHAPTER 10**

# Processes of Perception and Analysis

#### **Defining the Notion of Randomness**

■ Page 554 · Algorithmic information theory. A description of a piece of data can always be thought of as some kind of program for reproducing the data. So if one could find the shortest program that works then this must correspond to the shortest possible description of the data—and in algorithmic information theory if this is no shorter than the data itself then the data is considered to be algorithmically random.

How long the shortest program is for a given piece of data will in general depend on what system is supposed to run the program. But in a sense the program will on the whole be as short as possible if the system is universal (see page 642). And between any two universal systems programs can differ in length by at most a constant: for one can always just add a fixed interpreter program to the programs for one system in order to make them run on the other system.

As mentioned in the main text, any data generated by a simple program can by definition never be algorithmically random. And so even though algorithmic randomness is often considered in theoretical discussions (see note below) it cannot be directly relevant to the kind of randomness we see in so many systems in this book—or, I believe, in nature.

If one considers all  $2^n$  possible sequences (say of 0's and 1's) of length *n* then it is straightforward to see that most of them must be more or less algorithmically random. For in order to have enough programs to generate all  $2^n$  sequences most of the programs one uses must themselves be close to length *n*. (In practice there are subtleties associated with the encoding of programs that make this hold only for sufficiently large *n*.) But even though one knows that almost all long sequences must be algorithmically random, it turns out to be undecidable in general whether any particular sequence is algorithmically random. For in general one can give no upper limit to how much computational effort one might have to expend in order to find out whether any given short

program—after any number of steps—will generate the sequence one wants.

But even though one can never expect to construct them explicitly, one can still give formal descriptions of sequences that are algorithmically random. An example due to Gregory Chaitin is the digits of the fraction  $\Omega$  of initial conditions for which a universal system halts (essentially a compressed version—with various subtleties about limits—of the sequence from page 1127 giving the outcome for each initial condition). As emphasized by Chaitin, it is possible to ask questions purely in arithmetic (say about sequences of values of a parameter that yield infinite numbers of solutions to an integer equation) whose answers would correspond to algorithmically random sequences. (See page 786.)

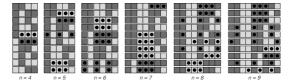
As a reduced analog of algorithmic information theory one can for example ask what the simplest cellular automaton rule is that will generate a given sequence if started from a single black cell. Page 1186 gives some results, and suggests that sequences which require more complicated cellular automaton rules do tend to look to us more complicated and more random.

• History. Randomness and unpredictability were discussed as general notions in antiquity in connection both with questions of free will (see page 1135) and games of chance. When probability theory emerged in the mid-1600s it implicitly assumed sequences random in the sense of having limiting frequencies following its predictions. By the 1800s there was extensive debate about this, but in the early 1900s with the advent of statistical mechanics and measure theory the use of ensembles (see page 1020) turned discussions of probability away from issues of randomness in individual sequences. With the development of statistical hypothesis testing in the early 1900s various tests for randomness were proposed (see page 1084). Sometimes these were claimed to have some kind of general significance, but mostly they were just viewed as simple practical methods. In many fields

outside of statistics, however, the idea persisted even to the 1990s that block frequencies (or flat frequency spectra) were somehow the only ultimate tests for randomness. In 1909 Emile Borel had formulated the notion of normal numbers (see page 912) whose infinite digit sequences contain all blocks with equal frequency. And in the 1920s Richard von Mises-attempting to capture the observed lack of systematically successful gambling schemes-suggested that randomness for individual infinite sequences could be defined in general by requiring that "collectives" consisting of elements appearing at positions specified by any procedure should show equal frequencies. To disallow procedures say specially set up to pick out all the infinite number of 1's in a sequence Alonzo Church in 1940 suggested that only procedures corresponding to finite computations be considered. (Compare page 1021 on coarsegraining in thermodynamics.) Starting in the late 1940s the development of information theory began to suggest connections between randomness and inability to compress data, but emphasis on pLog[p] measures of information content (see page 1071) reinforced the idea that block frequencies are the only real criterion for randomness. In the early 1960s, however, the notion of algorithmic randomness (see note above) was introduced by Gregory Chaitin, Andrei Kolmogorov and Ray Solomonoff. And unlike earlier proposals the consequences of this definition seemed to show remarkable consistency (in 1966 for example Per Martin-Löf proved that in effect it covered all possible statistical tests)so that by the early 1990s it had become generally accepted as the appropriate ultimate definition of randomness. In the 1980s, however, work on cryptography had led to the study of some slightly weaker definitions of randomness based on inability to do cryptanalysis or make predictions with polynomial-time computations (see page 1089). But quite what the relationship of any of these definitions might be to natural science or everyday experience was never much discussed. Note that definitions of randomness given in dictionaries tend to emphasize lack of aim or purpose, in effect following the common legal approach of looking at underlying intentions (or say at physical construction of dice) rather than trying to tell if things are random from their observed behavior.

• Inevitable regularities and Ramsey theory. One might have thought that there could be no meaningful type of regularity that would be present in all possible data of a given kind. But through the development since the late 1920s of Ramsey theory it has become clear that this is not the case. As one example, consider looking for runs of *m* equally spaced squares of the same color embedded in sequences of black

and white squares of length *n*. The pictures below show results with m = 3 for various *n*. For n < 9 there are always some sequences in which no runs of length 3 exist. But it turns out that for  $n \ge 9$  every single possible sequence contains at least one run of length 3. For any *m* the same is true for sufficiently large *n*; it is known that m = 4 requires  $n \ge 35$  and m = 5 requires  $n \ge 178$ . (In problems like this the analog of *n* often grows extremely rapidly with *m*.) If one has a sufficiently long sequence, therefore, just knowing that a run of equally spaced identical elements exists in it does not narrow down at all what the sequence actually is, and can so cannot ultimately be considered a useful regularity.



(Compare pattern-avoiding sequences on page 944.)

#### **Defining Complexity**

Page 557 · History. There have been terms for complexity in everyday language since antiquity. But the idea of treating complexity as a coherent scientific concept potentially amenable to explicit definition is quite new: indeed this became popular only in the late 1980s-in part as a result of my own efforts. That what one would usually call complexity can be present in mathematical systems was for example already noted in the 1890s by Henri Poincaré in connection with the three-body problem (see page 972). And in the 1920s the issue of quantifying the complexity of simple mathematical formulas had come up in work on assessing statistical models (compare page 1083). By the 1940s general comments about biological, social and occasionally other systems being characterized by high complexity were common, particularly in connection with the cybernetics movement. Most often complexity seems to have been thought of as associated with the presence of large numbers of components with different types or behavior, and typically also with the presence of extensive interconnections or interdependencies. But occasionally-especially in some areas of social science-complexity was instead thought of as being characterized by somehow going beyond what human minds can handle. In the 1950s there was some discussion in pure mathematics of notions of complexity associated variously with sizes of axioms for logical theories, and with numbers of ways to satisfy such axioms. The development of information theory in the late 1940s-followed by the discovery of the structure of DNA in 1953-led to the idea that perhaps complexity might be related to information content. And when the notion of algorithmic information content as the length of a shortest program (see page 1067) emerged in the 1960s it was suggested that this might be an appropriate definition for complexity. Several other definitions used in specific fields in the 1960s and 1970s were also based on sizes of descriptions: examples were optimal orders of models in systems theory, lengths of logic expressions for circuit and program design, and numbers of factors in Krohn-Rhodes decompositions of semigroups. Beginning in the 1970s computational complexity theory took a somewhat different direction, defining what it called complexity in terms of resources needed to perform computational tasks. Starting in the 1980s with the rise of complex systems research (see page 862) it was considered important by many physicists to find a definition that would provide some kind of numerical measure of complexity. It was noted that both very ordered and very disordered systems normally seem to be of low complexity, and much was made of the observation that systems on the border between these extremes-particularly class 4 cellular automata-seem to have higher complexity. In addition, the presence of some kind of hierarchy was often taken to indicate higher complexity, as was evidence of computational capabilities. It was also usually assumed that living systems should have the highest complexity-perhaps as a result of their long evolutionary history. And this made informal definitions of complexity often include all sorts of detailed features of life (see page 1178). One attempt at an abstract definition was what Charles Bennett called logical depth: the number of computational steps needed to reproduce something from its shortest description. Many simpler definitions of complexity were proposed in the 1980s. Quite a few were based just on changing  $p_i Log[p_i]$  in the definition of entropy to a quantity vanishing for both ordered and disordered  $p_i$ . Many others were based on looking at correlations and mutual information measures-and using the fact that in a system with many interdependent and potentially hierarchical parts this should go on changing as one looks at more and more. Some were based purely on fractal dimensions or dimensions associated with strange attractors. Following my 1984 study of minimal sizes of finite automata capable of reproducing states in cellular automaton evolution (see page 276) a whole series of definitions were developed based on minimal sizes of descriptions in terms of deterministic and probabilistic finite automata (see page 1084). In general it is possible to imagine setting up all sorts of definitions for quantities that one chooses to call complexity. But what is most relevant for my purposes in this

book is instead to find ways to capture everyday notions of complexity—and then to see how systems can produce these. (Note that since the 1980s there has been interest in finding measures of complexity that instead for example allow maintainability and robustness of software and management systems to be assessed. Sometimes these have been based on observations of humans trying to understand or verify systems, but more often they have just been based for example on simple properties of networks that define the flow of control or data—or in some cases on the length of documentation needed.) (The kind of complexity discussed here has nothing directly to do with complex numbers such as  $\sqrt{-7}$  introduced into mathematics since the 1600s.)

#### Data Compression

• **Practicalities.** Data compression is important in making maximal use of limited information storage and transmission capabilities. One might think that as such capabilities increase, data compression would become less relevant. But so far this has not been the case, since the volume of data always seems to increase more rapidly than capabilities for storing and transmitting it. In the future, compression is always likely to remain relevant when there are physical constraints—such as transmission by electromagnetic radiation that is not spatially localized.

History. Morse code, invented in 1838 for use in telegraphy, is an early example of data compression based on using shorter codewords for letters such as "e" and "t" that are more common in English. Modern work on data compression began in the late 1940s with the development of information theory. In 1949 Claude Shannon and Robert Fano devised a systematic way to assign codewords based on probabilities of blocks. An optimal method for doing this was then found by David Huffman in 1951. Early implementations were typically done in hardware, with specific choices of codewords being made as compromises between compression and error correction. In the mid-1970s, the idea emerged of dynamically updating codewords for Huffman encoding, based on the actual data encountered. And in the late 1970s, with online storage of text files becoming common, software compression programs began to be developed, almost all based on adaptive Huffman coding. In 1977 Abraham Lempel and Jacob Ziv suggested the basic idea of pointer-based encoding. In the mid-1980s, following work by Terry Welch, the so-called LZW algorithm rapidly became the method of choice for most general-purpose compression systems. It was used in programs such as PKZIP, as well as in hardware devices such as modems. In the late 1980s, digital images became more common, and standards for compressing them emerged. In the early 1990s, lossy compression methods (to be discussed in the next section) also began to be widely used. Current image compression standards include: FAX CCITT 3 (run-length encoding, with codewords determined by Huffman coding from a definite distribution of run lengths); GIF (LZW); JPEG (lossy discrete cosine transform, then Huffman or arithmetic coding); BMP (run-length encoding, etc.); TIFF (FAX, JPEG, GIF, etc.). Typical compression ratios currently achieved for text are around 3:1, for line diagrams and text images around 3:1, and for photographic images around 2:1 lossless, and 20:1 lossy. (For sound compression see page 1080.)

**Page 560 · Number representations.** The sequence of 1's and 0's representing a number *n* are obtained as follows:

(a) Unary. Table[0, {n}]. (Not self-delimited.)

(b) Ordinary base 2. IntegerDigits[n, 2]. (Not self-delimited.)

(c) *Length prefixed*. Starting with an ordinary base 2 digit sequence, one prepends a unary specification of its length, then a specification of that length specification, and so on:

(Flatten[{Sign[-Range[1 - Length[#], 0]], #}] &)[ Map[Rest, IntegerDigits[Rest[Reverse[NestWhileList[ Floor[Log[2, #]] &, n + 1, # > 1 &]]], 2]]]

(d) *Binary-coded base 3*. One takes base 3 representation, then converts each digit to a pair of base 2 digits, handling the beginning and end of the sequence in a special way.

Flatten[IntegerDigits[ Append[2 - With[{w = Floor[Log[3, 2 n]]}, IntegerDigits[n - (3<sup>w+1</sup> - 1)/2, 3, w]], 3], 2, 2]]

(e) *Fibonacci encoding*. Instead of decomposing a number into a sum of powers of an integer base, one decomposes it into a sum of Fibonacci numbers (see page 902). This decomposition becomes unique when one requires that no pair of 1's appear together.

Apply[Take, RealDigits[(N[#, N[Log[10, #] + 3]] &)[  $n\sqrt{5}$  /GoldenRatio<sup>2</sup> + 1/2], GoldenRatio]]

The representations of all the first *Fibonacci*[*n*]-1 numbers can be obtained from (the version in the main text has *Rest*[*RotateLeft*[*Join*[#, {0, 1}]]] & applied)

Apply[Join, Map[Last, NestList[{#[[2]], Join[Map[Join[{1, 0}, Rest[#]] &, #[[2]]], Map[Join[{1, 0}, #] &, #[[1]]]]} &, {{}, {{1}}}, n-3]]]

 Lengths of representations. (a) n, (b) Floor[Log[2, n] + 1], (c) Tr[FixedPointList[Max[0, Ceiling[Log[2, #]]] &, n + 2]] - n - 3, (d) 2 Ceiling[Log[3, 2n + 1]], (e)

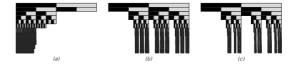
*Floor*[Log[GoldenRatio,  $\sqrt{5}$  (n + 1/2)]]. Large *n* approximations:

(a) n, (b) Log[2, n], (c) Log[2, n] + Log[2, Log[2, n]] + ..., (d) 2 Log[3, n], (e) Log[GoldenRatio, n].

Shown on a logarithmic scale, representations (b) through (e) (given here for numbers 1 through 500) all grow roughly linearly:



• **Completeness.** If one successively reads 0's and 1's from an infinite sequence then the representations (c), (d) and (e) have the property that eventually one will always accumulate a valid representation for some number or another. The pictures below show which sequences of 0's and 1's correspond to complete numbers in these representations. Every vertical column is a possible sequence of 0's and 1's, and the column is shown to terminate when a complete number is obtained.



With an infinite random sequence of 0's and 1's, different number representations yield different distributions of sizes of numbers. Representation (b), for example, is more weighted towards large numbers, while (c) is more weighted towards small numbers. Maximal compression for a sequence of numbers with a particular distribution of sizes is obtained by choosing a representation that yields a matching such distribution. (See also page 949.)

• **Practical computing.** Numbers used for arithmetic in practical computing are usually assumed to have a fixed length of, say, 32 bits, and thus do not need to be self-delimiting. In *Mathematica*, where integers can be of essentially any size, a representation closer to (b) above is used.

• Page 561 · Run-length encoding. Data can be converted to run lengths by *Map[Length, Split[data]]*. Each number is then replaced by its representation.

With completely random input, the output will on average be longer by a factor  $Sum[2^{-(n+1)} r[n], \{n, 1, \infty\}]$  where r[n] is the length of the representation for *n*. For the Fibonacci encoding used in the main text, this factor is approximately 1.41028. (In base 2 this number has 1's essentially at positions *Fibonacci[n]*; as discussed on page 914, the number is transcendental.) ■ **Page 563** • **Huffman coding.** From a list *p* of probabilities for blocks, the list of codewords can be generated using

Map[Drop[Last[#], -1] &, Sort[ Flatten[MapIndexed[Rule, FixedPoint[Replace[Sort[#], {{p0\_, i0\_}, {p1\_, i1\_}, pi\_\_\_} → {{p0 + p1, {i0, i1}}, pi]] &, MapIndexed[List, p]][[1, 2]], {-1}]]]] - 1

Given the list of codewords c, the sequence of blocks that occur in encoded data d can be uniquely reconstructed using

First[{{}, d}//. MapIndexed[

{{r\_\_\_}, Flatten[{#1, s\_\_\_}]} → {{r, #2[[1]]}, {s}} &, c]]

Note that the encoded data can consist of any sequence of 0's and 1's. If all  $2^b$  possible blocks of length *b* occur with equal probability, then the Huffman codewords will consist of blocks equivalent to the original ones. In an opposite extreme, blocks with probabilities 1/2, 1/4, 1/8, ... will yield codewords of lengths 1, 2, 3, ...

In practical applications, Huffman coding is sometimes extended to allow the choice of codewords to be updated dynamically as more data is read.

Maximal block compression. If one has data that consists of a long sequence of blocks, each of length b, and each independently chosen with probability p[i] to be of type *i*, then as argued by Claude Shannon in the late 1940s, it turns out that the minimum number of base 2 bits needed on average to represent each block in such a sequence is  $h = -Sum[p[i]Log[2, p[i]], \{i, 2^b\}]$ . If all blocks occur with an equal probability of  $2^{-b}$ , then *h* takes on its maximum possible value of *b*. If only one block occurs with nonzero probability then h = 0. Following Shannon, the quantity h (whose form is analogous to entropy in physics, as discussed on page 1020) is often referred to as "information content". This name, however, is very misleading. For certainly *h* does not in general give the length of the shortest possible description of the data; all it does is to give the shortest length of description that is obtained by treating successive blocks as if they occur with independent probabilities. With this assumption one then finds that maximal compression occurs if a block of probability p[i] is represented by a codeword of length -Log[2, p[i]]. Huffman coding with a large number of codewords will approach this if all the p[i] are powers of 1/2. (The self-delimiting of codewords leads to deviations for small numbers of codewords.) For *p[i]* that are not powers of 1/2, non-integer length codewords would be required. The method of arithmetic coding provides an alternative in which the output does not consist of separate codewords concatenated together. (Compare algorithmic information content discussed on pages 554 and 1067.)

• Arithmetic coding. Consider dividing the interval from 0 to 1 into a succession of bins, with each bin having a width equal to the probability for some sequence of blocks to occur.

The idea of arithmetic coding is to represent each such bin by the digit sequence of the shortest number within the bin after trailing zeros have been dropped. For any sequence *s* this can be done using

Module[{c, m = 0}, Map[c[#] = {m, m += Count[s, #]/Length[s]} &, Union[s]]; Function[x, (First[RealDigits[2<sup>#</sup> Ceiling[2<sup>-#</sup> Min[x]], 2, -#, -1]] &)[Floor[Log[2, Max[x] - Min[x]]]][ Fold[(Max[#1] - Min[#1])c[#2] + Min[#1] &, {0, 1}, s]]]

Huffman coding of a sequence containing a single 0 block together with n 1 blocks will yield output of length about n; arithmetic coding will yield length about Log[n]. Compression in arithmetic coding still relies, however, on unequal block probabilities, just like in Huffman coding. Originally suggested in the early 1960s, arithmetic coding reemerged in the late 1980s when high-speed floating-point computation became common, and is occasionally used in practice.

■ **Page 565** · **Pointer-based encoding.** One can encode a list of data *d* by generating pointers to the longest and most recent copies of each subsequence of length at least *b* using

$$\begin{split} & PEncode[d_, b_: 4] := Module[\{i, a, u, v\}, \\ & i = 2; a = \{First[d]\}; While[i \leq Length[d], \{u, v\} = \\ & Last[Sort[Table]{MatchLength[d, i, j], j}, \{j, i - 1\}]]]; \\ & If[u \geq b, AppendTo[a, p[i - v, u]]; i + = u, \\ & AppendTo[a, d[[i]]]; i + 1]; a] \\ & MatchLength[d_, i_, j_] := With[\{m = Length[d] - i\}, Catch[ \\ & Do[If[d[[i + k]] = != d[[j + k]], Throw[k]], \{k, 0, m\}]; m + 1]] \end{split}$$

The process of encoding can be made considerably faster by keeping a dictionary of previously encountered subsequences. One can reproduce the original data using

PDecode[a\_] := Module[{d = Flatten[ a /. p[j\_, r\_] :→ Table[p[j], {r}]]}, Flatten[MapIndexed[ If[Head[#1] === p, d[[#2]] = d[[#2 - First[#1]]], #1] &, d]]]

To get a representation purely in terms of 0 and 1, one can use a self-delimiting representation for each integer that appears. (Knowing the explicit representation one could then determine whether each block would be shorter if encoded literally or using a pointer.) The encoded version of a purely repetitive sequence of length *n* has a length that grows like Log[n]. The encoded version of a purely nested sequence grows like  $Log[n]^2$ . The encoded version of a sufficiently random sequence grows like *n* (with the specific encoding used in the text, the length is about 2n). Note that any sequence of 0's and 1's corresponds to the beginning of the encoding for some sequence or another.

It is possible to construct sequences whose encoded versions grow roughly like fractional powers of *n*. An example is the sequence *Table[Append[Table[0, {r}]], 1], {r, s}]* whose encoded version grows like  $\sqrt{n} Log[n]$ . Cyclic tag systems often seem to produce sequences whose encoded versions grow like fractional

powers of *n*. Sequences produced by concatenation sequences are not typically compressed by pointer encoding.

With completely random input, the probability that the length *b* subsequence which begins at element *n* is a repeat of a previous subsequence is roughly  $1 - (1 - 2^{-b})^{n-1}$ . The overall fraction of a length *n* input that consists of repeats of length at least *b* is greater than  $1 - 2^{b}/n$  and is essentially



• LZW algorithms. Practical implementations of pointerbased encoding can maintain only a limited dictionary of possible repeats. Various schemes exist for optimizing the construction, storage and rewriting of such dictionaries.

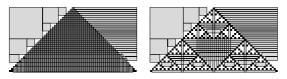
Page 568 · Recursive subdivision. In one dimension, encoding can be done using Subdivide[a\_] := Flatten[

If[Length[a] == 2, a, If[Apply[SameQ, a], {1, First[a]}, {0, Map[Subdivide, Partition[a, Length[a]/2]]}]]]

In *n* dimensions, it can be done using

Subdivide[a\_, n\_] := With[{s = Table[1, {n}]}, Flatten[
 If[Dimensions[a] == 2 s, a, If[Apply[SameQ, Flatten[a]],
 {1, First[Flatten[a]]}, {0, Map[Subdivide[#, n] &,
 Partition[a, 1/2 Length[a] s], {n}]}]]]

• 2D run-length encoding. A simple way to generalize runlength encoding to two dimensions is to scan data one row after another, always finding the largest rectangle of uniform color that starts at each particular point. The pictures below show regions with an area of more than 10 cells found in this way. The presence of so many thin and overlapping regions prevents good compression.



2D run-length encoding can also be done by scanning the data according to a more complicated space-filling curve, of the kind discussed on page 893.

#### Irreversible Data Compression

• History. The idea of creating sounds by adding together pure tones goes back to antiquity. At a mathematical level,

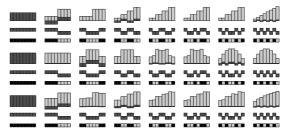
following work by Joseph Fourier around 1810 it became clear by the mid-1800s how any sufficiently smooth function could be decomposed into sums of sine waves with frequencies corresponding to successive integers. Early telephony and sound recording in the late 1800s already used the idea of compressing sounds by dropping high- and lowfrequency components. From the early days of television in the 1950s, some attempts were made to do similar kinds of compression for images. Serious efforts in this direction were not made, however, until digital storage and processing of images became common in the late 1980s.

• Orthogonal bases. The defining feature of a set of basic forms is that it is complete, in the sense that any piece of data can be built up by adding the basic forms with appropriate weights. Most sets of basic forms used in practice also have the feature of being orthogonal, which turns out to make it particularly easy to work out the weights for a given piece of data. In 1D, a basic form a[[i]] is just a list. Orthogonality is then the property that  $a[[i]] \cdot a[[j]] = 0$  for all  $i \neq j$ . And when this property holds, the weights are given essentially just by *data*. a.

The concept of orthogonal bases was historically worked out first in the considerably more difficult case of continuous functions. Here a typical orthogonality property is *Integrate*[*f*[*r*, *x*]*f*[*s*, *x*], {*x*, 0, 1}] == *KroneckerDelta*[*r*, *s*]. As discovered by Joseph Fourier around 1810, this is satisfied for basis functions such as  $Sin[2n\pi x]/\sqrt{2}$ .

■ Page 573 · Walsh transforms. The basic forms shown in the main text are 2D Walsh functions—represented as ±1 matrices. Each collection of such functions can be obtained from lists of vectors representing 1D Walsh functions by using Outer[Outer[Times, ##] &, b, b, 1, 1], or equivalently Map[Transpose, Map[# b &, b, [2]]].

The pictures below show how 1D arrays of data values can be built up by adding together 1D Walsh functions. At each step the Walsh function used is given underneath the array of values obtained so far.



The components of the vectors for 1D Walsh functions can be ordered in many ways. The pictures below show the

complete matrices of basis vectors obtained with three common orderings.



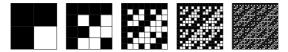
The matrices for size  $n = 2^s$  can be obtained from

Nest[Apply[Join, f[{Map[Flatten[Map[{#, #}] &, #]], Map[Flatten[Map[{#, -#} &, #]] &, g[#]]]] &, {{1}}, s]
with (a) f = Identity, g = Reverse, (b) f = Transpose, g = Identity, and (c) f = g = Identity. (a) is used in the main text. Known as sequency order, it has the property that each row involves one more change of color than the previous row. (b) is known as natural or Hadamard order. It exhibits a nested structure, and can be obtained as in the pictures below from the evolution of a 2D substitution system, or equivalently from a Kronecker product as in

 $Nest[Flatten2D[Map[\# \{ \{1, 1\}, \{1, -1\} \} \&, \#, \{2\} ]] \&, \{ \{1\} \}, s]$  with

Flatten2D[a\_] :=

Apply[Join, Apply[Join, Map[Transpose, a], {2}]]



(c) is known as dyadic or Paley order. It is related to (a) by Gray code reordering of the rows, and to (b) by reordering according to (see page 905)

BitReverseOrder[a\_] :=

With[{n = Length[a]}, a[[Map[FromDigits[Reverse[#], 2] &, IntegerDigits[Range[0, n - 1], 2, Log[2, n]]] + 1]]]

It is also given by

Array[Apply[Times, (-1)^(IntegerDigits[#1, 2, s] Reverse[IntegerDigits[#2, 2, s]])] &, 2^{(s, s), 0] where (b) is obtained simply by dropping the Reverse.

Walsh functions can correspond to nested sequences. The function at position  $2/3(1+4^{(-(F|oor[s/2]+1/2)))2^s}$  in basis (a), for example, is exactly the Thue-Morse sequence (with 0 replaced by -1) from page 83.

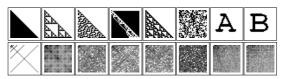
Given the matrix *m* of basis vectors, the Walsh transform is simply *data* . *m*. Direct evaluation of this for length *n* takes  $n^2$  steps. However, the nested structure of *m* in natural order allows evaluation in only about nLog[n] steps using

Nest[Flatten[Transpose[Partition[#, 2]. {{1, 1}, {1, -1}}]] &, data, Log[2, Length[data]]]

This procedure is similar to the fast Fourier transform discussed below. Transforms of 2D data are equivalent to 1D transforms of flattened data.

Walsh functions were used by electrical engineers such as Frank Fowle in the 1890s to find transpositions of wires that minimized crosstalk; they were introduced into mathematics by Joseph Walsh in 1923. Raymond Paley introduced the dyadic basis in 1932. Mathematical connections with harmonic analysis of discrete groups were investigated from the late 1940s. In the 1960s, Walsh transforms became fairly widespread in discrete signal and image processing.

**Page 575 · Walsh spectra.** The arrays of absolute values of weights of basic forms for successive images are as follows:

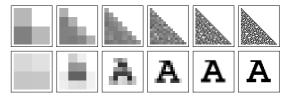


• **Hadamard matrices.** Hadamard matrices are  $n \times n$  matrices with elements -1 and +1, whose rows are orthogonal, so that *m*. *Transpose*[*m*] == *nIdentity*/*Matrix*[*n*]. The matrices used in Walsh transforms are special cases with  $n = 2^s$ . There are thought to be Hadamard matrices with every size n = 4k (and for n > 2 no other sizes are possible); the number of distinct such matrices for each *k* up to 7 is 1, 1, 1, 5, 3, 60, 487. The so-called Paley family of Hadamard matrices for n = 4k = p + 1 with *p* prime are given by

PadLeft[Array[JacobiSymbol[#2 - #1, n - 1] &, {n, n} - 1] -IdentityMatrix[n - 1], {n, n}, 1]

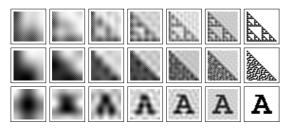
Originally introduced by Jacques Hadamard in 1893 as the matrices with elements  $Abs[a] \le 1$  which attain the maximal possible determinant  $\pm n^{n/2}$ , Hadamard matrices appear in various combinatorial problems, particularly design of exhaustive combinations of experiments and Reed-Muller error-correcting codes.

• **Image averaging.** Walsh functions yield significantly better compression than simple successive averaging of 2×2 blocks of cells, as shown below.



• **Practical image compression.** Two basic phenomena contribute to our ability to compress images in practice. First, that typical images of relevance tend to be far from random—indeed they often involve quite limited numbers of distinct objects. And second, that many fine details of images go unnoticed by the human visual system (see the next section).

• Fourier transforms. In a typical Fourier transform, one uses basic forms such as  $Exp[i \pi r x/n]$  with r running from 1 to n. The weights associated with these forms can be found using *Fourier*, and given these weights the original data can also be reconstructed using *InverseFourier*. The pictures below show what happens in such a so-called discrete cosine transform when different fractions of the weights are kept, and others are effectively set to zero. High-frequency wiggles associated with the so-called Gibbs phenomenon are typical near edges.



*Fourier[data]* can be thought of as multiplication by the  $n \times n$  matrix  $Array[Exp[2 \pi i \# 1 \# 2/n] \&, \{n, n\}, 0]$ . Applying *BitReverseOrder* to this matrix yields a matrix which has an essentially nested form, and for size  $n = 2^s$  can be obtained from

```
Nest[With[{c = BitReverseOrder[Range[0, Length[#]-1]/
Length[#]]}, Flatten2D[MapIndexed[#1 {{1, 1},
{1, -1}(-1)^c[[Last[#2]]] &, #, {2}]]] &, {{1}}, s]
```

Using this structure, one obtains the so-called fast Fourier transform which operates in n Log[n] steps and is given by

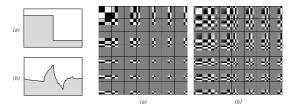
With[{n = Length[data]}, Fold[Flatten[Map[With[ {k = Length[#]/2}, {{1, 1}, {1, -1}}. {Take[#, k], Drop[ #, k](-1)^(Range[0, k - 1]/k)]] &, Partition[##]]] &, BitReverseOrder[data], 2^Range[Log[2, n]]]/\n]

(See also page 1080.)

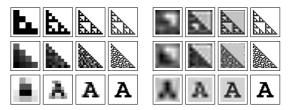
• JPEG compression. In common use since the early 1990s JPEG compression works by first assigning color values to definite bins, then applying a discrete Fourier cosine transform, then applying Huffman encoding to the resulting weights. The "quality" of the image is determined by how many weights are kept; a typical default quality factor, used say by *Export* in *Mathematica*, is 75.

• Wavelets. Each basic form in an ordinary Walsh or Fourier transform has nonzero elements spread throughout. With wavelets the elements are more localized. As noted in the late

1980s basic forms can be set up by scaling and translating just a single appropriately chosen underlying shape. The (a) Haar and (b) Daubechies wavelets  $\psi[x]$  shown below both have the property that the basic forms  $2^{m2} \psi[2^m x - n]$  (whose 2D analogs are shown as on page 573) are orthogonal for every different *m* and *n*.



The pictures below show images built up by keeping successively more of these basic forms. Sharp edges have fewer wiggles than with Fourier transforms.



Sound compression. See page 1080.

#### Visual Perception

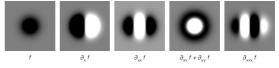
• **Color vision.** The three types of color-sensitive cone cells on the human retina each have definite response curves as a function of wavelength. The perceived color of light with a given wavelength distribution is basically determined by the three numbers obtained by integrating these responses. For any wavelength distribution it turns out that if one scales these numbers to add up to one, then the chromaticity values obtained must lie within a certain region. Mixing *n* specific colors in different proportions allows one to reach any point in an *n*-cornered polytope. For n = 3 this polytope comes close to filling the region of all possible colors, but for no *n* can it completely fill it—which is why practical displays and printing processes can produce only limited ranges of colors.

An important observation, related to the fact that limitations in color ranges are usually not too troublesome, is that the perceived colors of objects stay more or less constant even when viewed in very different lighting, corresponding to very different wavelength distributions. In recent years it has become clear that the origin of this phenomenon is that beyond the original cone cells, most color-sensitive cells in our visual system respond not to absolute color levels, but instead to differences in color levels at slightly different positions. (Responses to nearby relative values rather than absolute values seem to be common in many forms of human perception.)

The fact that white light is a mixture of colors was noticed by Isaac Newton in 1704, and it became clear in the course of the 1700s that three primaries could reproduce most colors. Thomas Young suggested in 1802 that there might be three types of color receptors in the eye, but it was not until 1959 that these were actually identified—though on the basis of perceptual experiments, parametrizations of color space were already well established by the 1930s. While humans and primates normally have three types of cone cells, it has been found that other mammals normally have two, while birds, reptiles and fishes typically have between 3 and 5.

Nerve cells. In the retina and the brain, nerve cells typically have an irregular tree-like structure, with between a few and a few thousand dendrites carrying input signals, and one or more axons carrying output signals. Nerve cells can respond on timescales of order milliseconds to changes in their inputs by changing their rate of generating output electrical spikes. As has been believed since the 1940s, most often nerve cells seem to operate at least roughly by effectively adding up their inputs with various positive or negative weights, then going into an excited state if the result exceeds some threshold. The weights seem to be determined by detailed properties of the synapses between nerve cells. Their values can presumably change to reflect certain aspects of the activity of the cell, thus forming a basis for memory (see page 1102). In organisms with a total of only a few thousand nerve cells, each individual cell typically has definite connections and a definite function. But in humans with perhaps 100 billion nerve cells, the physical connections seem quite haphazard, and most nerve cells probably develop their function as a result of building up weights associated with their actual pattern of behavior, either spontaneous or in response to external stimuli.

• The visual system. Connected to the 100 million or so lightsensitive photoreceptor cells on the retina are roughly two layers of nerve cells, with various kinds of cross-connections, out of which come the million fibers that form the optic nerve. After essentially one stop, most of these go to the primary visual cortex at the back of the brain, which itself contains more than 100 million nerve cells. Physical connections between nerve cells have usually been difficult to map. But starting in the 1950s it became possible to record electrical activity in single cells, and from this the discovery was made that many cells respond to rather specific visual stimuli. In the retina, most common are center-surround cells, which respond when there is a higher level of light in the center of a roughly circular region and a lower level outside, or vice versa. In the first few layers of the visual cortex about half the cells respond to elongated versions of similar stimuli, while others seem sensitive to various forms of change or motion. In the fovea at the center of the retina, a single center-surround cell seems to get input from just a few nearby photoreceptors. In successive layers of the visual cortex cells seem to get input from progressively larger regions. There is a very direct mapping of positions on the retina to regions in the visual cortex. But within each region there are different cells responding to stimuli at different angles, as well as to stimuli from different eyes. Cells with particular kinds of responses are usually found to be arranged in labyrinthine patterns very much like those shown on page 427. And no doubt the processes which produce these patterns during the development of the organism can be idealized by simple 2D cellular automata. Quite what determines the pattern of illumination to which a given cell will respond is not yet clear, although there is some evidence that it is the result of adaptation associated with various kinds of test inputs. Since the late 1970s, it has been common to assume that the response of a cell can be modelled by derivatives of Gaussians such as those shown below, or perhaps by Gabor functions given by products of trigonometric functions and Gaussians. Experiments have determined responses to these and other specific stimuli, but inevitably no experiment can find all the stimuli to which a cell is sensitive.



The visual systems of a number of specific higher and lower organisms have now been studied, and despite a few differences (such as cross-connections being behind the photoreceptors on the retinas of octopuses and squids, but in front in most higher animals), the same general features are usually seen. In lower organisms, there tend to be fewer layers of cells, with individual cells more specialized to particular visual stimuli of relevance to the organism.

• Feedback. Most of the lowest levels of visual processing seem to involve only signals going successively from one layer in the eye or brain to the next. But presumably there is at least some feedback to previous layers, yielding in effect iteration of rules like the ones used in the main text. The resulting evolution process is likely to have attractors, potentially explaining the fact that in images such as "Magic Eye" random dot stereograms features can pop out after several seconds or minutes of scrutiny, even without any conscious effort.

• Scale invariance. In a first approximation our recognition of objects does not seem to be much affected by overall size or overall light level. For light level-as with color constancythis is presumably achieved by responding only to differences between levels at different positions. Probably the same effect contributes to scale invariance by emphasizing only edges and corners. And if one is looking at objects like letters, it helps that one has learned them at many different sizes. But also similar cells most likely receive inputs from regions with a range of different sizes on the retina-making even unfamiliar textures seem the same over at least a certain range of scales. When viewed at a normal reading distance of 12 inches each square in the picture on page 578 covers a region about 5 cells across on the retina. With good lighting and good eyesight the textures in the picture can still be distinguished at a distance of 5 feet, where each square covers only one cell. But if the picture is enlarged by a factor of 3 or more then at normal reading distance it can become difficult to distinguish the textures-perhaps because the squares cover regions larger than the templates used at the lowest levels in our visual system.

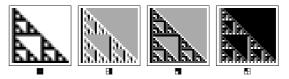
• **History.** Ever since antiquity the visual arts have yielded practical schemes and sometimes also fairly abstract frameworks for determining what features of images will have what impact. In fact, even in prehistoric times it seems to have been known, for example, that edges are often sufficient to communicate visual forms, as in the pictures below.

Visual perception has been used for centuries as an example in philosophical discussions about the nature of experience. Traditional mathematical methods began to be applied to it in the second half of the 1800s, particularly through the development of psychophysics. Studies of visual illusions around the end of the 1800s raised many questions that were not readily amenable to numerical measurement or traditional mathematical analysis, and this led in part to the Gestalt approach to psychology which attempted to formulate various global principles of visual perception. In the 1940s and 1950s, the idea emerged that visual images might be processed using arrays of simple elements. At a largely theoretical level, this led to the perceptron model of the visual system as a network of idealized neurons. And at a practical level it also led to many systems for image processing (see below), based essentially on simple cellular automata (see page 928). Such systems were widely used by the end of the 1960s, especially in aerial reconnaissance and biomedical applications.

Attempts to characterize human abilities to perceive texture appear to have started in earnest with the work of Bela Julesz around 1962. At first it was thought that the visual system might be sensitive only to the overall autocorrelation of an image, given by the probability that randomly selected points have the same color. But within a few years it became clear that images could be constructed—notably with systems equivalent to additive cellular automata (see below)—that had the same autocorrelations but looked completely different. Julesz then suggested that discrimination between textures might be based on the presence of "textons", loosely defined as localized regions like those shown below with some set of distinct geometrical or topological properties.

## =========================

In the 1970s, two approaches to vision developed. One was largely an outgrowth of work in artificial intelligence, and concentrated mostly on trying to use traditional mathematics to characterize fairly high-level perception of objects and their geometrical properties. The other, emphasized particularly by David Marr, concentrated on lower-level processes, mostly based on simple models of the responses of single nerve cells, and very often effectively applying *ListConvolve* with simple kernels, as in the pictures below.



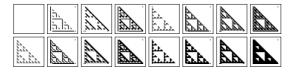
In the 1980s, approaches based on neural networks capable of learning became popular, and attempts were made in the context of computational neuroscience to create models combining higher- and lower-level aspects of visual perception.

The basic idea that early stages of visual perception involve extraction of local features has been fairly clear since the 1950s, and researchers from a variety of fields have invented and reinvented implementations of this idea many times. But mainly through a desire to use traditional mathematics, these implementations have tended to be implicitly restricted to using elements with various linearity properties—typically leading to rather unconvincing results. My model is closer to what is often done in practical image processing, and apparently to how actual nerve cells work, and in effect assumes highly nonlinear elements.

Page 581 · Implementation. The exact matches for a template σ in data containing elements 0 and 1 can be obtained from Sign[ListCorrelate[2 σ - 1, data] - Count[σ, 1, 2]] + 1

• Testing the model. Although it is difficult to get good systematic data, the many examples I have tried indicate that the levels of discrimination between textures that we achieve with our visual system agree remarkably well with those suggested by my simple model. A practical issue that arises is that if one repeatedly tries experiments with the same set of textures, then after a while one learns to discriminate these particular textures better. Shifting successive rows or even just making an overall rotation seems, however, to avoid this effect.

• **Related models.** Rather than requiring particular templates to be matched, one can consider applying arbitrary cellular automaton rules. The pictures below show results from a single step of the 16 even-numbered totalistic 5-neighbor rules. The results are surprisingly easy to interpret in terms of feature extraction.



• Image processing. The release of programs like Photoshop in the late 1980s made image processing operations such as smoothing, sharpening and edge detection widely available on general-purpose computers. Most of these operations are just done by applying ListConvolve with simple kernels. (Even before computers, such convolutions could be done using the fact that diffraction of light effectively performs Fourier transforms.) Ever since the 1960s all sorts of schemes for nonlinear processing of images have been discussed and used in particular communities. An example originally popular in the earth and environmental sciences is so-called mathematical morphology, based on "dilation" of data consisting of 0's and 1's with a "structuring element"  $\sigma$ according to Sign[ListConvolve[ $\sigma$ , data, 1, 0]] (as well as the dual operation of "erosion"). Most schemes like this can ultimately be thought of as picking out templates or applying simple cellular automaton rules.

• Real textures. The textures I consider in the main text are all based on arrays of discrete black and white squares. One can also consider textures associated, say, with surface roughness of physical objects. Models of these are often needed for realistic computer graphics. Common approaches are to assume that the surfaces are random with some frequency spectrum, or can be generated as fractals using substitution systems with random parameters. In recent times, models based on wavelets have also been used.

• Statistical methods. Even though they do not appear to correspond to how the human visual system works, statistical methods are often used in trying to discriminate textures automatically. Correlations, conditional entropies and fractal dimensions are commonly computed. Often it is assumed that different parts of a texture are statistically independent, so that the texture can be characterized by probabilities for local patterns, as in a so-called Markov random field or generalized autoregressive moving average (ARMA) process.

• **Camouflage.** On both animals and military vehicles it is often important to have patterns that cannot be distinguished from a background by the visual systems of predators. And in most cases this is presumably best achieved by avoiding differences in densities of certain local features. Note that in a related situation almost any fairly random overlaid pattern containing many local features can successfully be used to mask the contents of a paper envelope.

• **Halftoning.** In printed books like this one, gray levels are usually obtained by printing small dots of black with varying sizes. On displays consisting of fixed arrays of pixels, gray levels must be obtained by having only a certain density of pixels be black. One way to achieve this is to break the array into  $2^n \times 2^n$  blocks, then successively to fill in pixels in each block until the appropriate gray level is reached, as in the pictures below, in an order given for example by *Nestl* 

Flatten2D[{{4#+0,4#+2}, {4#+3,4#+1}}] &, {{0}}, n]

## 

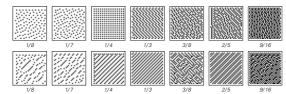
An alternative to this so-called ordered dither approach is the Floyd-Steinberg or error-diffusion method invented in 1976. This scans sequentially, accumulating and spreading total gray level in the data, then generating a black pixel whenever a threshold is exceeded. The method can be implemented using

```
Module[{a = Flatten[data], r, s},
```

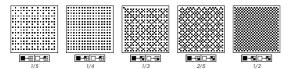
{r, s} = Dimensions[data]; Partition[Do[

$$\begin{split} a[[i + \{1, s - 1, s, s + 1\}]] +&= m (a[[i]] - If[a[[i]] < 1/2, 0, 1]), \\ \{i, rs - s - 1\}]; Map[If[\# < 1/2, 0, 1] \&, a], s]] \end{split}$$

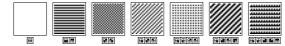
In its original version  $m = \{7, 3, 5, 1\}/16$ , as in the first row of pictures below. But even with  $m = \{1, 0, 1, 0\}/2$  the method generates fairly random patterns, as in the second row below. (Note that significantly different results can be obtained if different boundary conditions are used for each row.)



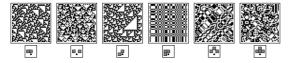
To give the best impression of uniform gray, one must in general minimize features detected by the human visual system. One simple way to do this appears to be to use nested patterns like the ones below.



• Generating textures. As discussed on page 217, it is in general difficult to find 2D patterns which at all points match some definite set of templates. With 2×2 templates, there turn out to be just 7 minimal such patterns, shown below. Constructing patterns in which templates occur with definite densities is also difficult, although randomized iterative schemes allow some approximation to be obtained.



One-dimensional cellular automata are especially convenient generators of distinctive textures. Indeed, as was noticed around 1980, generalizations of additive rules involving cells in different relative locations can produce textures with similar statistics, but different visual appearance, as shown below. (All the examples shown turn out to correspond to ordinary, sequential and reversible cellular automata seen elsewhere in this book.) (See also page 1018.)

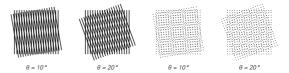


• **Moire patterns.** The pictures below show moire patterns formed by superimposing grids of points at different angles. Our visual system does not immediately perceive the grids,

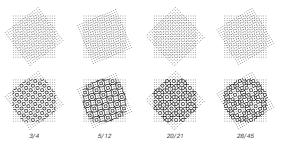
but instead mainly picks up features formed from local arrangements of dots. The second picture below is similar to patterns of halftone screens visible in 4-color printing under a magnifying glass.



In the first two pictures below, bands with spacing  $1/2 Csc[\theta/2]$  are visible wherever lines cross. In the second two pictures there is also an apparent repetitive pattern with approximately the same repetition period.

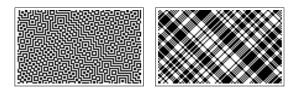


The patterns are exactly repetitive only when  $Tan[\theta] = u/v$ , where *u* and *v* are elements of a primitive Pythagorean triple (so that *u*, *v* and  $Sqrt[u^2 + v^2]$  are all integers, and GCD[u, v] = 1). This occurs when  $u = r^2 - s^2$ , v = 2rs (see page 945), and in this case the minimum displacement that leaves the whole pattern unchanged is {*s*, *r*}.



The second row of pictures illustrates what happens if points closer than distance  $1/\sqrt{2}$  are joined. The results appear to capture at least some of the features picked out by our visual system.

• Perception and presentation. In writing this book it has been a great challenge to find graphical representations that make the behavior of systems as clear as possible for the purposes of human visual perception. Even small changes in representation can greatly affect what properties are noticed. As a simple example, the pictures below are identical, except for the fact that the colors of cells on alternate rows have been reversed.



#### **Auditory Perception**

**Sounds.** The human auditory system is sensitive to sound at frequencies between about 20 Hz and 20 kHz. Middle A on a piano typically corresponds to a frequency of 440 Hz. Each octave represents a change in frequency by a factor of two. In western music there are normally 12 notes identified within an octave. These differ in frequency by successive factors of roughly 2<sup>1/12</sup>—with different temperament schemes using different rational approximations to powers of this quantity.

The perceived character of a sound seems to depend most on the frequencies it contains, but also to be somewhat affected by the way its intensity ramps up with time, as well as the way frequencies change during this ramp up. Many musical instruments produce sound by vibrating strings or air in cylindrical or conical tubes, and in these cases, there is one main frequency, together with roughly equally spaced overtones. In percussion instruments, the spectrum of frequencies is usually much more complicated. In speech, vowels and voiced consonants tend to be characterized by the lowest two or three frequencies of the mouth. In nature, processes such as fluid turbulence and fracture yield a broad spectrum of frequencies. In speech, letters like "s" also yield broad spectra, presumably because they involve fluid turbulence.

Any sound can be specified by giving its amplitude or waveform as a function of time.  $Sin[\omega t]$  corresponds to a pure tone. Other simple mathematical functions can also yield distinctive sounds. FM synthesis functions such as  $Sin[\omega (t + a Sin[b t])]$  can be made to sound somewhat like various musical instruments, and indeed were widely used in early synthesizers.

• Auditory system. Sound is detected by the motion it causes in hair cells in the cochlea of the inner ear. When vibrations of a particular frequency enter the cochlea an active process involving hair cells causes the vibrations to be concentrated at a certain distance down the cochlea. To a good approximation this distance is proportional to the logarithm of the frequency, and going up one octave in frequency corresponds to moving roughly 3.5 mm. Of the 12,000 or so hair cells in the cochlea most seem to be involved mainly with mechanical issues; about 3500 seem to produce outgoing signals. These are collected by about 30,000 nerve fibers which go down the auditory nerve and after several stops reach the auditory cortex. Different nerve cells seem to have rates of firing which are set up to reflect both sound intensity, and below perhaps 300 Hz, actual amplitude peaks in the sound waveform. Much as in both the visual and tactile systems, there seems to be a fairly direct mapping from position on the cochlea to position in the auditory cortex. In animals such as bats it is known that specific nerve cells respond to particular kinds of frequency changes. But in primates, for example, little is known about exactly what features are extracted in the auditory cortex.

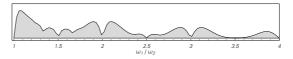
The fact that there are a million nerve fibers going from the eye to the brain, but only about 30,000 going from the ear to the brain means that while it takes several million bits per second to transmit video of acceptable quality, a few tens of thousands of bits are adequate for audio (NTSC television is 5 MHz; audio CDs 22 kHz; telephone 8 kHz). Presumably related is also the fact that it is typically much easier to make realistic sound effects than realistic visual ones.

Chords. Two pure tones played together exhibit beats at the difference of their frequencies—a consequence of the fact that Sin(w, t) + Sin(w, t) ==

$$2 \sin[1/2(\omega_1 + \omega_2)t] \cos[1/2(\omega_1 - \omega_2)t]$$

With  $\omega \approx 500 \text{ Hz}$ , one can explicitly hear the time variation of the beats if their frequency is below about 15 Hz, and the result is quite pleasant. But between 15 Hz and about 60 Hz, the sound tends to be rather grating—possibly because this frequency range conflicts with that used for signals in the auditory nerve.

In music it is usually thought that chords consisting of tones with frequencies whose ratios have small denominators (such as 3/2, corresponding to a perfect fifth) yield the most pleasing sounds. The mechanics of the ear imply that if two tones of reasonable amplitude are played together, progressively smaller additional signals will effectively be generated at frequencies  $Abs[n_1 \omega_1 \pm n_2 \omega_2]$ . The picture below shows the extent to which such frequencies tend to be in the range that yield grating effects. The minima at values of  $\omega_2/\omega_1$  corresponding to rationals with small denominators may explain why such chords seem more pleasing. (See also page 917.)



• **History.** The notion of musical notes and of concepts such as octaves goes back at least five thousand years. Around 550 BC the Pythagoreans identified various potential connections between numbers and the perception of sounds. And over the course of time a wide range of mathematical and aesthetic principles were suggested. But it was not until the 1800s, particularly with the work of Hermann Helmholtz, that the physical basis for the perception of sound began to be seriously investigated. Work on speech sounds by Alexander Graham Bell and others was related to the development of the telephone in the late 1800s. In the past few decades, with better experiments, particularly on the emission of sound by the ear, and with ideas and analysis from electrical engineers and physicists the basic behavior of at least the cochlea is becoming largely understood.

• Sonification. Sound has occasionally been used as a means of understanding scientific data. In the 1950s and 1960s analog computers (and sometimes digital computers) routinely had sound output. And in the 1970s some discoveries about chaos in differential equations were made using such output. In experimental neuroscience sounds are also routinely used to monitor impulses in nerve cells.

• Implementation. *ListPlay[data]* in *Mathematica* generates sound output by treating the elements of *data* as successive samples in the waveform of the sound, typically with a default sample rate of 8000 Hz.

• Time variation. Many systems discussed in this book produce sounds with distinctive and sometimes pleasing time variation. Particularly dramatic are the concatenation systems discussed on page 913, as well as successive rows in nested patterns such as *Flatten[IntegerDigits[NestList[BitXor[#, 2 #] &, 1, 500], 2]]* and sequences based on numbers such as *Flatten[Table[If[GCD[i, j] == 0, 1, 0], {i, 1000}, {j, i, j]]* (see page 613). The recursive sequences on page 130 yield sounds reminiscent of many natural systems.

• **Musical scores.** Instead of taking a sequence to correspond directly to the waveform of a sound, one can consider it to give a musical score in which each element represents a note of a certain frequency, played for some specific short time. (One can avoid clicks by arranging the waveform to cross zero at both the beginning and end of each note.) With this setup my experience is that both repetitive and random sequences tend to seem quite monotonous and dull. But nested sequences I have found can quite often generate rather pleasing tunes. (One can either determine frequencies of notes directly from the values of elements, or, say, from cumulative sums of such values, or from heights in paths like those on page 892.) (See also page 869.)

• **Recognizing repetition.** The curve of the function  $Sin[x] + Sin[\sqrt{2} x]$  shown on page 146 looks complicated to the eye. But a sound with a corresponding waveform is recognized by the ear as consisting simply of two pure tones. However, if one uses the function to generate a score—say playing a note at the position of each peak—then no such simplicity can be recognized. And this fact is presumably why musical scores normally have notes only at integer multiples of some fixed time interval.

• Sound compression. Sound compression has in practice mostly been applied to human speech. In typical voice coders (vocoders) 64k bits per second of digital data are obtained by sampling the original sound waveform 8000 times per second, and assigning one of 256 possible levels to each sample. (Since the 1960s, so-called mu-law companding has often been used, in which these levels are distributed exponentially in amplitude.) Encoding only differences between successive samples leads to perhaps a factor of 2 compression. Much more dramatic compression can be achieved by making an explicit model for speech sounds. Most common is to assume that within each phoneme-length chunk of a few tens of milliseconds the vocal tract acts like a linear filter excited either by pure tones or randomness. In socalled linear predictive coding (LPC) optimal parameters are found to make each sound sample be a linear combination of, say, 8 preceding samples. The residue from this procedure is then often fitted to a code book of possible forms, and the result is that intelligible speech can be obtained with as little as 3 kbps of data. Hardware implementations of LPC and related methods have been widespread since before the 1980s; software implementations are now becoming common. Music has in the past rarely been compressed, except insofar as it can be specified by a score. But recently the MP3 format associated with MPEG and largely based on LPC methods has begun to be used for compression of arbitrary sounds, and is increasingly applied to music.

• **Page 586** • **Spectra.** The spectra shown are given by *Abs[Fourier[data]]*, where the symmetrical second half of this list is dropped in the pictures. Also of relevance are intensity or power spectra, obtained as the square of these spectra. These are related to the autocorrelation function according to

Fourier[list]<sup>2</sup> ==

Fourier[ListConvolve[list, list, {1, 1}]]/Sqrt[Length[list]]
(See also page 1074.)

• Spectra of substitution systems. Questions that turn out to be related to spectra of substitution systems have arisen in various areas of pure mathematics since the late 1800s. In the 1980s, particularly following discoveries in iterated maps and quasicrystals, studies of such spectra were made in the context of number theory and dynamical systems theory. Some general principles were proposed, but a great many exceptions were always eventually found.

As suggested by the pictures in the main text, spectra such as (b) and (d) in the limit consist purely of discrete Dirac delta function peaks, while spectra such as (a) and (c) also contain essentially continuous parts. There seems to be no simple criterion for deciding from the rule what type of spectrum will be obtained. (In some cases it works to look at whether the limiting ratio of lengths on successive steps is a Pisot number.) One general result, however, is that all so-called Sturmian sequences Round[(n + 1)a + b] - Round[na + b] with *a* an irrational number must yield discrete spectra. And as discussed on page 903, if *a* is a quadratic irrational, then such sequences can be generated by substitution systems.

For any substitution system the spectrum  $\phi[i][t, \omega]$  at step t from initial condition i is given by a linear recurrence relation in terms of the  $\phi[j][t-1, \omega]$ . With k colors each giving a string of the same length s the recurrence relation is

Thread  $[Map[\phi[\#][t + 1, \omega] \&, Range[k] - 1] == Apply[Plus, MapIndexed[Exp[i \omega (Last[#2] - 1) s<sup>t</sup>]$  $<math>\phi[#1][t, \omega] \&, Range[k] - 1/. rules, [-1]], [1]]/\sqrt{s}$ 

Some specific properties of the examples shown include:

(a) (Thue-Morse sequence) The spectrum is essentially Nest[Range[2Length[#]]Join[#, Reverse[#]] &, {1}, t]. The main peak is at position 1/3, and in the power spectrum this peak contains half of the total. The generating function for the sequence (with 0 replaced by -1) satisfies  $f[z] = (1 - z) f[z^2]$ , so that  $f[z] = Product[1 - z^{2^n}, \{n, 0, \infty\}]$ . (Z transform or generating function methods can be applied directly only for substitution systems with rules such as  $\{1 \rightarrow list, 0 \rightarrow 1 - list\}$ .) After *t* steps a continuous approximation to the spectrum is *Product*[1 - *Exp*[ $2^{s}i\omega$ ], {*s*, *t*}], which is an example of a type of product studied by Frigyes Riesz in 1918 in connection with questions about the convergence of trigonometric series. It is related to the product of sawtooth functions given by *Product*[*Abs*[*Mod*[ $2^{s} \omega$ , 2, -1]], {s, t}]. Peaks occur for values of  $\omega$  such as 1/3 that are not well approximated by numbers of the form  $a/2^b$  with small a and b.

(b) (*Fibonacci-related sequence*) This sequence is a Sturmian one. The maximum of the spectrum is at *Fibonacci[t]*. The spectrum is roughly like the markings on a ruler that is recursively divided into {GoldenRatio, 1} pieces.

(c) (*Cantor set*) In the limit, no single peak contains a nonzero fraction of the power spectrum. After *t* steps a continuous approximation to the spectrum is  $Product[1 + Exp[3^{s} 2i\omega], \{s, t\}]$ .

(d) (*Period-doubling sequence*) The spectrum is  $(2^{\#} - (-1)^{\#} \&)[1 + IntegerExponent[n, 2]]$ , almost like the markings on a base 2 ruler.

(See also page 917.)

• Flat spectra. Any impulse sequence Join[{1}, Table[0, {n}]] will yield a flat spectrum. With odd *n* the same turns out to be true for sequences  $Exp[2\pi i Mod[Range[n]^2, n]/n]$ —a fact used in the design of acoustic diffusers (see page 1183). For sequences involving only two distinct integers flat spectra are rare; with  $\pm 1$  those equivalent to  $\{1, 1, 1, -1\}$  seem to be the only examples. ( $\{r^2, rs, s^2, -rs\}$  works for any r and s, as do all lists obtained working modulo  $x^n - 1$  from p[x]/p[1/x]where p[x] is any invertible polynomial.) If one ignores the first component of the spectrum the remainder is flat for a constant sequence, or for a random sequence in the limit of infinite length. It is also flat for maximal length LFSR (see page 1084) and for sequences sequences JacobiSymbol[Range[0, p-1], p] with prime p (see page 870). By adding a suitable constant to each element one can then arrange in such cases for the whole spectrum to be flat. If Mod[p, 4] == 1 JacobiSymbol sequences also satisfy Fourier[list] == list. Sequences of 0's and 1's that have the same property are {1, 0, 1, 0}, {1, 0, 0, 1, 0, 0, 1, 0, 0} or in general Flatten[Table[{1, Table[0, {n - 1}]}, {n}]]. If -1 is allowed, additional sequences such as {0, 1, 0, -1, 0, -1, 0, 1} are also possible. (See also pages 911.)

• Nested vibrations. With an assembly of springs arranged in a nested pattern simple initial excitations can yield motion that shows nested behavior in time. If the standard methodology of mechanics is followed, and the system is analyzed in terms of normal modes, then the spectrum of possible frequencies can look complicated, just as in the examples on page 586. (Similar considerations apply to the motion of quantum mechanical electrons in nested potentials.)

■ Page 587 · Random block sequences. Analytical forms for all but the last spectrum are: 1,  $u^2/(1+8u^2)$ ,  $1/(1+8u^2)$ ,  $u^2$ ,  $(1-4u^2)^2/(1-5u^2+8u^4)$ ,  $u^2/(1-5u^2+8u^4)$ ,

 $u^2 + 1/36 \text{ DiracDelta}[\omega - 1/3]$ , where  $u = \cos[\pi \omega]$ , and  $\omega$  runs from 0 to 1/2 in each plot. Given a list of blocks such as  $\{\{1, 1\}, \{0\}\}$  each element of *Flatten*[*list*] can be thought of as a state in a finite automaton or a Markov process (see page 1084). The transitions between these states have probabilities given by *m*[*Map*[*Length*, *list*]] where

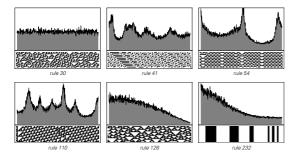
m[s\_] := With[{q = FoldList[Plus, 0, s]}, ReplacePart[ RotateRight[IdentityMatrix[Last[q]], {0, 1}], 1/Length[s], Flatten[Outer[List, Rest[q], Drop[q, -1] + 1], 1]]] The average spectrum of sequences generated according to these probabilities can be obtained by computing the correlation function for elements a distance r apart

#### & {[list\_, r\_] := With[{w = (# - Apply[Plus, #]/Length[#] &)[ Flatten[list]]}, w . MatrixPower[ m[Map[Length, list]], r] . w/Length[w]]

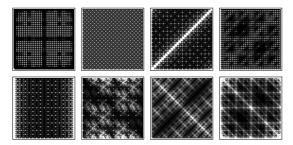
then forming  $Sum[\xi[Abs[r]]Cos[2 \pi r \omega], \{r, -n/2, n/2\}]$  and taking the limit  $n \to \infty$ . If  $\xi[r] = \lambda^r$  then the spectrum is  $(1 - \lambda^2)/(\lambda^2 - 2\lambda \cos[2 \pi \omega] + 1) - 1$ . For a random walk (see page 977) in which  $\pm 1$  occur with equal probability the spectrum is  $Csc[\pi \omega]^2/2$ , or roughly  $1/\omega^2$ .

The same basic setup also applies to spectra associated with linear filters and ARMA time series processes (see page 1083), in which elements in a sequence are generated from external random noise by forming linear combinations of the noise with definite configurations of elements in the sequence.

• Spectra of cellular automata. When cellular automata have non-trivial attractors as discussed in Chapter 6 the spectra of sequences obtained at particular steps can exhibit a variety of features, as shown below.



**2D spectra.** The pictures below give the 2D Fourier transforms of the nested patterns shown on page 583.



• Diffraction patterns. X-ray diffraction patterns give Fourier transforms of the spatial arrangement of atoms in a material. For an ordinary crystal with atoms on a repetitive lattice, the

patterns consist of a few isolated peaks. For quasicrystals with generalized Penrose tiling structures the patterns also contain a few large peaks, though as in example (b) on page 586 there are also a hierarchy of smaller peaks present. In general, materials with nested structures do not necessarily yield discrete diffraction patterns. In the early 1990s, experiments were done in which layers a few atoms thick of two different materials were deposited in a Thue-Morse sequence. The resulting object was found to yield X-ray diffraction patterns just like example (a) on page 586.

#### Statistical Analysis

• History. Some computations of odds for games of chance were already made in antiquity. Beginning around the 1200s increasingly elaborate results based on the combinatorial enumeration of possibilities were obtained by mystics and mathematicians, with systematically correct methods being developed in the mid-1600s and early 1700s. The idea of making inferences from sampled data arose in the mid-1600s in connection with estimating populations and developing precursors of life insurance. The method of averaging to correct for what were assumed to be random errors of observation began to be used, primarily in astronomy, in the mid-1700s, while least squares fitting and the notion of probability distributions became established around 1800. Probabilistic models based on random variations between individuals began to be used in biology in the mid-1800s, and many of the classical methods now used for statistical analysis were developed in the late 1800s and early 1900s in the context of agricultural research. In physics fundamentally probabilistic models were central to the introduction of statistical mechanics in the late 1800s and quantum mechanics in the early 1900s. Beginning as early as the 1700s, the foundations of statistical analysis have been vigorously debated, with a succession of fairly specific approaches being claimed as the only ones capable of drawing unbiased conclusions from data. The practical use of statistical analysis began to increase rapidly in the 1960s and 1970s, particularly among biological and social scientists, as computers became more widespread. All too often, however, inadequate amounts of data have ended up being subjected to elaborate statistical analyses whose results are then blindly assumed to represent definitive scientific conclusions. In the 1980s, at least in some fields, traditional statistical analysis began to become less popular, being replaced by more direct examination of data presented graphically by computer. In addition, in the 1990s, particularly in the context of consumer electronics devices, there has been an increasing emphasis on using statistical analysis to make decisions from data, and methods such as fuzzy logic and neural networks have become popular.

• **Practical statistics.** The vast majority of statistical analysis is in practice done on continuous numerical data. And with surprising regularity it is assumed that random variations in such data follow a Gaussian distribution (see page 976). But while this may sometimes be true—perhaps as a consequence of the Central Limit Theorem—it is rarely checked, making it likely that many detailed inferences are wrong. So-called robust statistics uses for example medians rather than means as an attempt to downplay outlying data that does not follow a Gaussian distribution.

Classical statistical analysis mostly involves trying to use data to estimate parameters in specific probabilistic models. Non-parametric statistics and related methods often claim to derive conclusions without assuming particular models for data. But insofar as a conclusion relies on extrapolation beyond actual measured data it must inevitably in some way use a model for data that has not been measured.

• Time series. Sequences of continuous numerical data are often known as time series, and starting in the 1960s standard models for them have consisted of linear recurrence relations or linear differential equations with random noise continually being added. The linearity of such models has allowed efficient methods for estimating their parameters to be developed, and these are widely used, under slightly different names, in control engineering and in business analysis. In recent years nonlinear models have also sometimes been considered, but typically their parameters are very difficult to estimate reliably. As discussed on page 919 it was already realized in the 1970s that even without external random noise nonlinear models could produce time series with seemingly random features. But confusion about the importance of sensitivity to initial conditions caused the kind of discoveries made in this book to be missed.

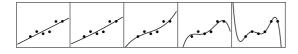
• Page 588 · Origin of probabilities. Probabilities are normally assumed to enter for at least two reasons: (a) because of random variation between individuals, and (b) because of random errors in measurement. (a) is particularly common in the biological and social sciences; (b) in the physical sciences. In physics effects of statistical mechanics and quantum mechanics are also assumed to introduce probabilities. Probabilistic models for abstract mathematical systems have in the past been rare, though the results about randomness in this book may make them more common in the future.

• **Probabilistic models.** A probabilistic model must associate with every sequence a probability that is a number between 0 and 1. This can be done either by giving an explicit procedure for taking sequences and finding probabilities, or by defining a process in which sequences are generated with appropriate probabilities. A typical example of the first approach is the Ising model for spin systems in which relative probabilities of sequences are found by multiplying together the results of applying a simple function to blocks of nearby elements in the sequence. Monte Carlo methods and probabilistic cellular automata provide examples of the second approach.

■ **Page 588** • **Binomial distribution.** If black squares appear independently with probability *p* then the probability that *m* squares out of *n* are black is *Binomial*[*n*, *m*] $p^m$  (1 – *p*)<sup>*n*-m</sup>.

■ Page 589 · Estimation of parameters. One way to estimate parameters in simple probabilistic models is to compute the mean and other moments of the data and then to work out what values of the parameters will reproduce these. More general is the maximum likelihood method in which one finds the values of the parameters which maximize the probability of generating the observed data from the model. (Least squares fits do this for models in which the data exhibits independent Gaussian variations.) Various modifications can be made involving for example weighting with a risk function before maximizing. If one starts with a priori probability distributions for all parameters, then Bayes's Theorem on conditional probabilities allows one to avoid the arbitrariness of methods such as maximum likelihood and explicitly to work out from the observed data what the probability is for each possible choice of parameters in the model. It is rare in practice, however, to be able to get convincing a priori probability distributions, although when there are physical or other reasons to expect entropy to be maximized the so-called maximum entropy method may be useful.

• **Complexity of models.** The pictures at the top of the next page show least squares fits (found using *Fit* in *Mathematica*) to polynomials with progressively higher degrees and therefore progressively more parameters. Which fit should be considered best in any particular case must ultimately depend on external considerations. But since the 1980s there have been attempts to find general criteria, typically based on maximizing quantities such as -Log[p]-d (the Akaike information criterion), where *p* is the probability that the observed data would be generated from a given model (-Log[p] is proportional to variance in a least squares fit), and *d* is the number of parameters in the model.



■ Page 590 · Markov processes. The networks in the main text can be viewed as representing finite automata (see page 957) with probabilities associated with transitions between nodes or states. Given a vector of probabilities to be in each state, the evolution of the system corresponds to multiplication by the matrix of probabilities for each transition. (Compare the calculation of properties of substitution systems on page 890.) Markov processes first arose in the early 1900s and have been widely studied since the 1950s. In their first uses as models it was typically assumed that each state transition could explicitly be observed. But by the 1980s hidden Markov models were being studied, in which only some of the states or transitions could be distinguished by outside observations. Practical applications were made in speech understanding and text compression. And in the late 1980s, building on work of mine from 1984 (described on page 276), James Crutchfield made a study of such models in which he defined the complexity of a model to be equal to -*pLog[p]* summed over all connections in the network. He argued that the best scientific model is one that minimizes this complexity-which with probabilities 0 and 1 is equivalent to minimizing the number of nodes in the network.

• Non-local processes. It follows from the fact that any path in a finite network must always eventually return to a node where it has been before that any Markov process must be fundamentally local, in the sense that the probabilities it implies for what happens at a given point in a sequence must be independent of those for points sufficiently far away. But probabilistic models based on other underlying systems can yield sequences with long-range correlations. As an example, probabilistic neighbor-independent substitution systems can yield sequences with hierarchical structures that have approximate nesting. And since the mid-1990s such systems (usually characterized as random trees or random contextfree languages) have sometimes been used in analyzing data that is expected to have grammatical structure of some kind.

• **Page 594** • **Block frequencies.** In any repetitive sequence the number of distinct blocks of length m must become constant with m for sufficiently large m. In a nested sequence the number must always continue increasing roughly linearly, and must be greater than m for every m. (The differences of successive numbers themselves form a nested sequence.) If exactly m+1 distinct blocks occur for every m, then the sequence must be of the so-called Sturmian type discussed

on page 916, and the  $n^{\text{th}}$  element must be given by Round[(n + 1)a + b] - Round[na + b], where *a* is an irrational number. Up to limited *m* nested sequences can contain all  $k^m$  possible blocks, and can do so with asymptotically equal frequencies. Pictures (b), (c) and (d) show the simplest cases where this occurs (for length 3 {1 → {1, 1, 1, 0, 0, 0}, 0 → {1, 0}}} also works). Linear feedback shift registers of the type used in picture (e) are discussed below. Concatenation sequences of the type used in picture (f) are discussed on page 913. In both cases equal frequencies of blocks are obtained only for sequences of length exactly  $2^j$ .

• LFSR sequences. Often referred to as pseudonoise or PN sequences, maximal length linear feedback shift register sequences have repetition period  $2^n - 1$  and are generated by shift registers that go through all their possible states except the one consisting of all 0's, as discussed on page 974. Blocks in such sequences obtained from Partition[list, n, 1] must all be distinct since they correspond to successive complete states of the shift register. This means that every block with length up to n (except all 0's) must occur with equal frequency. (Note that only a small fraction of all possible sequences with this property can be generated by LFSRs.) The regularity of PN sequences is revealed by looking at the autocorrelation RotateLeft[(-1)<sup>list</sup>, m]. (-1)<sup>list</sup>. This quantity is -1 for all nonzero m for PN sequences (so that all but the first component in Abs[Fourier[(-1)<sup>list</sup>]]<sup>2</sup> are equal), but has mean 0 for truly random sequences. (Related sequences can be generated from *RealDigits[1/p, 2]* as discussed on page 912.)

• Entropy estimates. Fitting the number of distinct blocks of length *b* to the form  $k^{hb}$  for large *b* the quantity *h* gives the so-called topological entropy of the system. The so-called measure entropy is given as discussed on page 959 by the limit of  $-Sum[p_i Log[k, p_i], \{i, k^b\}]/b$  where the  $p_i$  are the probabilities for the blocks. Actually getting accurate estimates of such entropies is however often rather difficult, and typically upper bounds are ultimately all that can realistically be given. Note also that as discussed in the main text having maximal entropy does not by any means imply perfect randomness.

• Tests of randomness. Statistical analysis has in practice been much more concerned with finding regularities in data than in testing for randomness. But over the course of the past century a variety of tests of randomness have been proposed, especially in the context of games of chance and their government regulation. Most often the tests are applied not directly to sequences of 0's and 1's, but instead say to numbers obtained from blocks of 8 elements. A typical collection of tests described by Donald Knuth in 1968 includes: (1) frequency or equidistribution test (possible elements should occur with equal frequency); (2) serial test (pairs of elements should be equally likely to be in descending and ascending order); (3) gap test (runs of elements all greater or less than some fixed value should have lengths that follow a binomial distribution); (4) poker test (blocks corresponding to possible poker hands should occur with appropriate frequencies); (5) coupon collector's test (runs before complete sets of values are found should have lengths that follow a definite distribution); (6) permutation test (in blocks of elements possible orderings of values should occur equally often); (7) runs up test (runs of monotonically increasing elements should have lengths that follow a definite distribution); (8) maximum-of-t test (maximum values in blocks of elements should follow a power-law distribution). With appropriate values of parameters, these tests in practice tend to be at least somewhat independent, although in principle, if sufficient data were available, they could all be subsumed into basic block frequency and run-length tests. Of the sequences on page 594, (a) through (d) as well as (f) fail every single one of the tests, (e) fails only the serial test, while (g) and (h) pass all the tests. (Failure is defined as a value that is as large or small as that obtained from the data occurring below a specified probability in the set of all possible sequences.) Widespread use of tests like these on pseudorandom generators (see page 974) began in the late 1970s, with discoveries of defects in common generators being announced every few years.

In the 1980s simulations in physics had begun to use pseudorandom generators to produce sequences with billions of elements, and by the late 1980s evidence had developed that a few common generators gave incorrect results in such cases as phase transition properties of the 3D Ising model and shapes of diffusion-limited aggregates. (These difficulties provided yet more support for my contention that models with intrinsic randomness are more reliable than those with external randomness.) In the 1990s various idealizations of physics simulations—based on random walks, correlation functions, localization of eigenstates, and so on—were used as tests of pseudorandom generators. These tests mostly seem simpler than those shown on page 597 obtained by running a cellular automaton rule on the data.

Over the years, essentially every proposed statistical test of randomness has been applied to the center column of rule 30. And occasionally people have told me that their tests have found deviations from randomness. But in every single case further investigation showed that the results were somehow incorrect. So as of now, the center column of rule 30 appears to pass every single proposed statistical test of randomness.

### Difference tables. See page 1091.

• Randomized algorithms. Whether a randomized algorithm gives correct answers can be viewed as a test of randomness for whatever supposedly random sequence is provided to it. But in most practical cases such tests are not particularly stringent; linear congruential generators, for example, almost always pass. (There are perhaps exceptions in VLSI testing.) And this is basically why it has so often proved possible to replace randomized algorithms by deterministic ones that are at least as efficient (see page 1192). An example is Monte Carlo integration, where what ultimately matters is uniform sampling of the integrand—which can usually be achieved better by quasi-random irrational number multiple (see page 903) or digit reversal (see page 905) sequences than by sequences one might consider more random.

### Cryptography and Cryptanalysis

• History. Cryptography has been in use since antiquity, and has been a decisive factor in a remarkably large number of military and other campaigns. Typical of early systems was the substitution cipher of Julius Caesar, in which every letter was cyclically shifted in the alphabet by three positions, with A being replaced by D, B by E, and so on. Systems based on more arbitrary substitutions were in use by the 1300s. And while methods for their cryptanalysis were developed in the 1400s, such systems continued to see occasional serious use until the early 1900s. Ciphers of the type shown on page 599 were introduced in the 1500s, notably by Blaise de Vigenère; systematic methods for their cryptanalysis were developed in the mid-1800s and early 1900s. By the mid-1800s, however, codes based on books of translations for whole phrases were much more common than ciphers, probably because more sophisticated algorithms for ciphers were difficult to implement by hand. But in the 1920s electromechanical technology led to the development of rotor machines, in which an encrypting sequence with an extremely long period was generated by rotating a sequence of noncommensurate rotors. A notable achievement of cryptanalysis was the 1940 breaking of the German Enigma rotor machine using a mixture of statistical analysis and automatic enumeration of keys. Starting in the 1950s, electronic devices were the primary ones used for cryptography. Linear feedback shift registers and perhaps nonlinear ones seem to have been common, though little is publicly known about military cryptographic systems after World War II. In 1977 the U.S. government introduced the DES data encryption standard, and in the 1980s this became the dominant force in the growing field of commercial cryptography. DES takes 64-bit

blocks of data and a 56-bit key, and applies 16 rounds of substitutions and permutations. The S-box that implements each substitution works much like a single step of a cellular automaton. No fast method of cryptanalysis for DES is publicly known, although by now for a single DES system an exhaustive search of keys has become feasible. Two major changes occurred in cryptography in the 1980s. First, cryptographic systems routinely began to be implemented in software rather than in special-purpose hardware, and thus became much more widely available. And second, following the introduction of public-key cryptography in 1975, the idea emerged of basing cryptography not on systems with complicated and seemingly arbitrary construction, but instead on systems derived from well-known mathematical problems. Initially several different problems were considered, but after a while the only ones to survive were those such as the RSA system discussed below based essentially on the problem of factoring integers. Present-day publicly available cryptographic systems are almost all based on variants of either DES (such as the IDEA system of PGP), linear feedback shift registers or RSA. My cellular automaton cryptographic system is one of the very few fundamentally different systems to have been introduced in recent years.

• **Basic theory.** As was recognized in the 1920s the only way to make a completely secure cryptographic system is to use a so-called one-time pad and to have a key that is as long as the message, and is chosen completely at random separately for each message. As soon as there are a limited number of possible keys then in principle one can always try each of them in turn, looking in each case to see whether they imply an original message that is meaningful in the language in which the message is written. And as Claude Shannon argued in the 1940s, the length of message needed to be reasonably certain that only one key will satisfy this criterion is equal to the length of the key divided by the redundancy of the language in which the message is written—equal to about 0.5 for English (see below).

In a cryptographic system with keys of length *n* there will typically be a total of  $k^n$  possible keys. If one guesses a key it will normally take a time polynomial in *n* to check whether the key is correct, and thus the problem of cryptanalysis is in the class known in theoretical computer science as NP or non-deterministic polynomial time (see page 1142). It is suspected but not established that there exist at least some problems in NP that cannot be solved in polynomial time, potentially indicating that for an appropriate system it might be impossible to do cryptanalysis in any time polynomial in *n*. (See page 1089.)

• Text. As the picture below illustrates, English text typically remains intelligible until about half its characters have been deleted, indicating that it has a redundancy of around 0.5. Most other languages have slightly higher redundancies, making documents in those languages slightly longer than their counterparts in English.

									redundant.
About	half	the	letter-	in	typical	Engsh	text	are	redun-ant.
									redunnt.
Abou-	half	the	-e-t	i -	ty-ical	Engsh	text	are	redunnt.
									red-nnt.
Abou-	h - 1 -	t-e	-e		ty-ical	Engsh	text	ar-	r-d-nnt.
									d-nnt.
									d-nnt.
Abou-	h		-e		tya-	- ng h	te	- r -	d-nnt.
									dn
									n
			- e		t		- 0		

Redundancy can in principle be estimated by breaking text into blocks of length *b*, then looking for the limit of the entropy as  $b \rightarrow \infty$  (see page 1084). Statistically uniform samples of text do not in practice, however, tend to be large enough to allow more than about b = 6 to be reached, and the presence of correlations (even though exponentially damped) between far-separated letters means that computed entropies usually decrease continually with *b*, making it difficult to estimate their limit (see page 1084). Note that particularly in computer languages higher redundancy is found if one takes account of grammatical structure.

• Page 599 · Cryptanalysis. The so-called Vigenère cipher was thought for several centuries to be unbreakable. The idea of looking for repeats was introduced by Friedrich Kasiski in 1863. A statistical approach based on the fact that frequencies tend to be closer to uniform for longer keys was introduced by William Friedman in the 1920s. The methods described in the main text are fairly characteristic of the mixture between generality and detail that is typical in practical cryptanalysis.

■ Page 600 · Linear feedback shift registers. See notes on pages 974 and 1084. LFSR sequences are widely used in radio technology, particularly in the context of spread spectrum applications. Their purpose is usually to provide a way to distinguish or synchronize signals, and sometimes to provide a level of cryptographic security. In CDMA technology for cellular telephones, for example, data is overlaid on LFSR sequences, and sequences other than the one intended for a particular receiver seem like noise which can be ignored. As another example, the Global Positioning System (GPS) works by having 24 satellites each transmit maximal length sequences from different length 10 LFSRs. Position is deduced from the arrival times of signals, as determined by the relative phases of the LFSR sequences received. (GPS Pcode apparently uses much longer LFSR sequences and repeats only every 267 days. Before May 2000 it was used to add unpredictable timing errors to ordinary GPS signals.)

**LFSR cryptanalysis.** Given a sequence obtained from a length *n* LFSR (see page 975)

*Nest[Mod[Append[#, Take[#, -n] . vec], 2] &, list, t]* the vector of taps *vec* can be deduced from

LinearSolve[Table[Take[seq, {i, i + n - 1}], {i, n}], Take[seq, {n + 1, 2n}], Modulus  $\rightarrow$  2]

(An iterative algorithm in *n* taking about  $n^2$  rather than  $n^3$  steps was given by Elwyn Berlekamp and James Massey in 1968.) The same basic approach can be used to deduce the rule for an additive cellular automaton from vertical sequences.

■ Page 603 · Rule 30 cryptography. Rule 30 is known to have many of the properties desirable for practical cryptography. It does not repeat with any short period or show any obvious structure for almost all keys. Small changes in keys typically leads to large changes in the encrypting sequence. The Boolean expressions which determine the encrypting sequence from the key rapidly become highly complex (see page 618). And furthermore the system can be implemented very efficiently, particularly in parallel hardware.

I originally studied rule 30 in the context of basic science, but I soon realized that it could serve as the basis for practical random sequence generation and cryptography, and I analyzed this extensively in 1985. (Most but not all of the results from my original paper are included in this book, together with various new results.) In 1985 and soon thereafter a number of people (notably Richard and Carl Feynman) tried to cryptanalyze rule 30, but without success. From the beginning, computations of spacetime entropies for rule 30 (see page 960) gave indications that for strong cryptography one should not sample all cells in a column, and in 1991 Willi Meier and Othmar Staffelbach described essentially the explicit cryptanalysis approach shown on page 601. Rule 30 has been widely used for random sequence generation, but for a variety of reasons I have not in the past much emphasized its applications in cryptography.

■ **Properties of rule 30.** Rule 30 can be written in the form  $p \space{alpha}(q \lor r)$  (see page 869) and thus exhibits a kind of one-sided additivity on the left. This leads to some features that are desirable for cryptography (such as long repetition periods) and to some that are not (such as the sideways evolution of page 601). It implies that every block of length *m* that occurs at a particular step has exactly 4 immediate predecessor blocks of length m + 2 (see page 960). It also implies that all  $2^t$  possible single columns of *t* cells can be generated from some initial condition. Not all  $4^t$  pairs of adjacent columns can occur, however. There seems to be no simple

characterization, say in terms of paths through networks, of which can, but for successive t the total numbers are

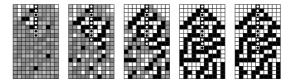
 {4, 12, 32, 80, 200, 496, 1208, 2916, 6964, 16476, 38616, 89844, 207544, 476596, 1089000, 2477236, 5615036}
 or roughly 2.25<sup>t</sup>.

Given two complete adjacent columns page 601 shows how all columns any distance to the left can be found. It turns out that this can be done even if the right-hand one of the two adjacent columns is not complete. So for example whenever there is a black cell in the left column it is irrelevant what appears in the right column. Note that the configuration of relevant cells can be repetitive only if the initial conditions were repetitive (see page 871).

In a cellular automaton of limited size *n*, any column must eventually repeat. There could be  $2^n$  distinct possible columns; in practice, for successive *n* there are  $\{2, 3, 7, 14, 30, 60, 101, 245, 497, 972, 1997, 3997\}$ —within  $2^n$  of  $2^n$  already for n = 12. This means that for the initial conditions to be determined uniquely, the number of cells that must be given in a column is almost exactly *n*, as illustrated in the pictures below. Many distinct columns correspond to starting at different points on a single cycle of states. The length of the longest cycle grows roughly like  $2^{0.63n}$  (see page 260). The complete cycle structure is illustrated on page 962. Most of the  $2^n$  possible states have unique predecessors; for large *n*, about  $2^{0.76n}$  or  $Root[\#^3 - \#^2 - 2 & , 1]^n$  instead have 0 or 2 predecessors. The predecessors of a given state can be found from

Cases[Map[Fold[Prepend[#1, If[#2 == 1 ⊻

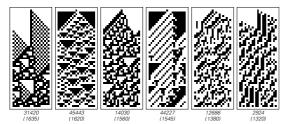
 $Take[#1, 2] == \{0, 0\}, 0, 1]\} \&, #, Reverse[list]\} \&, \{\{0, 0\}, \{0, 1\}, \{1, 0\}, \{1, 1\}\}\}, \{a_{-}, b_{-}, c_{--}, a_{-}, b_{-}\} \rightarrow \{b, c, a\}]$ 



• Directional sampling. One can consider sampling cells not in a vertical column but on lines at any angle. In a rule 30 system of infinite size, it turns out that at 45 ° clockwise from vertical all possible sequences can occur on any two adjacent lines, probably making cryptanalysis more difficult in this case. (Note that directional sampling is always equivalent to looking at a vertical column in the evolution of a cellular automaton whose basic rule has been composed with an appropriate shift rule.)

 Alternative rules. Among elementary rules, rule 45 is the only plausible alternative to rule 30. It usually yields longer repetition periods (see page 260), but shows slightly slower responses to changes in the key. (Changes expand about 1.24 cells per step in rule 30, and about 1.17 in rule 45.) Rule 45 shares with rule 30 the property of one-sided additivity. With the occasional exception of the additive rule 60, elementary rules not equivalent to 30 or 45 tend to exhibit vastly shorter repetition periods. (The completely non-additive rule with largest typical repetition period is rule 110.) (See page 951.)

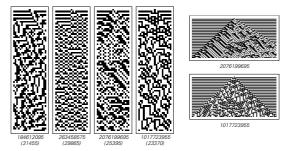
If one considers rules that depend on 4 rather than 3 cells, then the results turn out to be surprisingly similar: out of all 65536 possible such rules the ones with longest periods essentially always seem to be variants of rules 45, 30 or 60. In a region of size 15, for example, the longest period is 20460, and this is achieved by rule 13251, which is just rule 45 applied to the first three cells in the neighborhood. (Rule 45 itself has period 6820 in this case.) After a few rules with long periods, the periods obtained drop off rapidly. (In general the number of rules with a given period seems to decrease roughly exponentially with period.) For size 15, the 33 rules with the longest periods are all additive with respect to one position. The pictures below show the first rules that are not additive with respect to any position.



Among the 4,294,967,296 r = 2 rules which depend on 5 cells, there are again just a few that give long periods, but now only a small fraction of these seem directly related to rules 45 and 30, and perhaps half are not additive with respect to any position. The pictures below show the rules with longest periods for size 15; these same rules also yield the longest periods for many other sizes. The first two are additive with respect to one position, but do not appear to be directly related to rules 45 or 30; the last two are not additive with respect to any position. Formulas for the rules are respectively:

 $p \succeq (\neg q \lor r \lor s \land \neg t)$   $r \succeq (\neg p \lor q \lor s \land \neg t)$   $u = \neg p \land \neg q \lor q \land t; \neg r \land u \lor q \land \neg s \land (p \lor \neg r) \lor r \land s \land \neg u$   $s \land (q \land \neg r \lor p \land \neg q \land t) \lor \neg (s \lor (p \lor q) \land (r \succeq (q \lor t)))$ 

Note that for size 15 the maximum possible period is 32730 (see page 950).



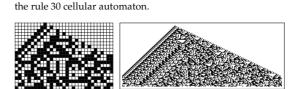
• **Nonlinear feedback shift registers.** Linear feedback shift registers of the kind discussed on page 974 can be generalized to allow any function *f* (note the slight analogy with cyclic tag systems):

NLFSRStep[f\_, taps\_, list\_] := Append[Rest[list], f[list[[taps]]]]

With the choice  $f = IntegerDigits[s, 2, 8][[8 - #. {4, 2, 1}]] \&$ and  $taps = \{1, 2, 3\}$  this is essentially a rule *s* elementary cellular automaton. With a list of length *n*, *Nest*[*NLFSRStep*[*f*, *taps*, #] &, *list*, *n*] gives one step in the evolution of the cellular automaton in a register of width *n*, with a certain kind of spiral boundary condition. The case analogous to rule 30 yields some of the longest repetition periods—usually remarkably close to the absolute maximum of  $2^n - 1$  (for n = 21 the result is 1999864, 95% of the maximum).

Nonlinear feedback shift registers were apparently studied in the context of military cryptography in the 1950s, but very little about them has made its way into the open literature (see page 878). An empirical investigation of repetition periods in such systems was made by Solomon Golomb in 1959. The main conclusion drawn from extensive data was that nothing like the linear theory applies. One set of computations concerned functions

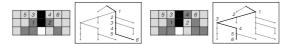
```
f[\{w_{-}, x_{-}, y_{-}, z_{-}\}] := Mod[w + y + z + xy + xz + yz, 2]
(apparently chosen to have balance between 0's and 1's that
would minimize correlations). Tap positions {1, 2, 3, 4} were
among those studied, but nothing like the pictures below
were apparently ever explicitly generated—and nearly three
```



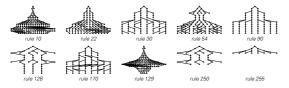
decades passed before I noticed the remarkable behavior of

Sequences of states in any shift register must correspond to paths through a network of the kind shown on page 941. And as noted by Nicolaas de Bruijn in 1946 there are  $2^{2^{n-1}-n}$  such paths with length  $2^n$ , and thus this number of functions f out of the  $2^{2^n}$  possible must yield sequences of maximal length. (For k colors, the number of paths is  $k l^{k^{n-1}}/k^n$ .)

**Backtracking.** If one wants to find out which of the  $2^n$  possible initial conditions of width *n* evolve to yield a specific column of colors in a system like an elementary cellular automaton one can usually do somewhat better than just testing all possibilities. The picture below illustrates a typical approach, applied to 3 steps of rule 30. The idea is successively to look at each numbered cell, and to make a tree of possibilities representing what happens if one tries to fill in each possible color for each cell. A branch in the resulting tree continues only if it corresponds to a configuration of cell colors whose evolution is consistent with the specified column of colors.

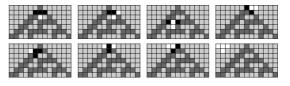


The picture below shows trees obtained for the column in various elementary cellular automata. In cases like rules 250 and 254 no initial condition gives the specified column, so all branches eventually die out. In class 2 examples like rule 10 many intermediate configurations are possible. Rules like 90 and to some extent 30 that allow sideways evolution yield comparatively simple trees.



If one wants to find just a single initial condition that works then one can set up a recursive algorithm that in effect does a depth-first traversal of the tree. No doubt in many cases the number of nodes that have to be visited eventually increases like  $2^t$ , but many branches usually die off quickly, greatly reducing the typical effort required in practice.

• Deducing cellular automaton rules. Given a complete cellular automaton pattern it is easy to deduce the rule which produced it just by identifying examples of places where each element in the rule was used, as in the picture at the top of the next column. Given an incomplete pattern, deducing the rule in effect requires solving Boolean equations.



• Linear congruential generators. Cryptanalysis of linear congruential generators is fairly straightforward. Given only an output list *NestList[Mod[a#, m] &, x, n]* parameters *(a, m)* that generate the list can be found for sufficiently large *n* from

With[{α = Apply[#2 . Rest[list]/#1 &, Apply[ ExtendedGCD, Drop[list, -1]]]}, ({Mod[α, #], #} &)[ Fold[GCD[#1, If[#1 == 0, #2, Mod[#2, #1]]] &, 0, ListCorrelate[{α, -1}, list]]]]

With slightly more effort both *x* and *{a, m}* can be found just from *First[IntegerDigits[list, 2, p]]*.

Digit sequence encryption. One can consider using as encrypting sequences the digit sequences of numbers obtained from standard mathematical functions. As discussed on page 139 such digit sequences often seem locally very random. But in many cases one can immediately tell how a sequence was made just by globally applying appropriate mathematical functions. Thus, for example, given the digit sequence of  $\sqrt{s}$  one can retrieve the key s just by squaring the number obtained from early digits in the sequence. Whenever a number x is known to satisfy  $Sum[a[i]f[i][x], \{i, n\}] = 0$  with fixed f[i] one can take the early digits of x and use LatticeReduce to find integer solutions for the a[i]. With  $f[i_{-}] = \#^{i} \&$  this method allows algebraic numbers to be recognized. If no linear equation is satisfied by any combination of known functions of x, however, the method fails, and it seems quite likely that in such cases secure encrypting sequences can be generated, albeit less efficiently than with systems like cellular automata.

• Problem-based cryptography. Particularly following the work of Whitfield Diffie and Martin Hellman in 1976 it became popular to consider cryptography systems based on mathematical problems that are easy to state but have been found difficult to solve. It was at first hoped that the problems could be NP-complete ones, which are universal in the sense that their solution can be used to provide a solution to any problem in the class NP (see page 1086). To date, however, no system has been devised whose cryptanalysis is known to be NP-complete. Indeed, essentially the only problem on which cryptography systems have so far successfully been based is factoring of integers (see below). And while this problem has resisted a fair number of

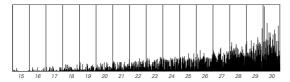
attempts at solution, it is not known to be NP-complete (and indeed its ability to be solved in polynomial time on a formal quantum computer may suggest that it is not).

My cellular automaton cryptography system follows the principle of being based on a problem that is easy to state. And indeed the general problem of finding initial conditions for a cellular automaton is NP-complete (see page 767). But the problem is not known to be NP-complete for the specific case of, say, rule 30. Significantly less work has been done on the problem of finding initial conditions for rule 30 than on the problem of factoring integers. But the greater simplicity of rule 30 might make one already have almost as much confidence in the difficulty of solving this problem as of factoring integers.

• Factoring integers. The difficulty of factoring is presumably related to the irregularity of the pattern of divisors shown on page 909. One approach to factoring a number *n* is just to try dividing it by each of the numbers up to  $\sqrt{n}$ . A sequence of much faster methods have however been developed over the past few decades, one simple example that works for most *n* being the so-called rho method of John Pollard (compare the quadratic residue sequences discussed below):

 $\begin{aligned} & Module[\{f = Mod[\#^2 + 1, n] \&, a = 2, b = 5, c\}, \\ & While[(c = GCD[n, a - b]) == 1, \{a, b\} = \{f[a], f[f[b]]\}]; c] \end{aligned}$ 

Most existing methods depend on facts in number theory that are fairly easy to state, though implementing them for maximum efficiency tends to lead to complex programs. Typical running times for *FactorInteger[n]* in *Mathematica* 4 are shown below for the first 1000 numbers with each of 15 through 30 digits. Different current methods asymptotically require slightly different numbers of steps—but all typically at least *Exp[Sqrt[Log[n]]]*. Nevertheless, to test whether a number is prime (*PrimeQ*) it is known that only a few more than *Log[n]* steps suffice.

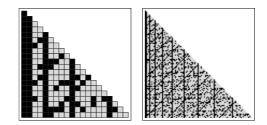


• **RSA cryptography.** Widely used in practice, the idea is to encode messages using a public key specified by a number *n*, but to make it so that to decode the messages requires a private key based on the factors of *n*. An element *m* in a message is encoded as *c* = *PowerMod*[*m*, *d*, *n*]. It can then be decoded as *PowerMod*[*c*, *e*, *n*], where *e* = *PowerMod*[*d*, -1, *EulerPhi*[*n*]]. But to find *EulerPhi*[*n*] (see page 1093) is equivalent in difficulty to finding the factors of *n*.

• Quadratic residue sequences. As an outgrowth of ideas related to RSA cryptography it was shown in 1982 by Lenore Blum, Manuel Blum and Michael Shub that the sequence

Mod[NestList[Mod[#<sup>2</sup>, m] &, x0, n], 2]

discussed on page 975 has the property that if m = pq with p and q primes (congruent to 3 modulo 4) then any systematic regularities detected in the sequence can eventually be used to discover factors of m. What is behind this is that each of the numbers in the basic sequence here must be a so-called quadratic residue of the form  $Mod[v^2, m]$ , and given any such quadratic residue x the expression  $GCD[x + Mod[x^2, m], m]$ turns out always to be a factor of *m*—and at least sometimes a non-trivial one. So if one could reconstruct sufficiently many complete numbers x from the sequence of Mod[x, 2] values then this would provide a way to factor m (compare the Pollard rho method above). But in practice it is difficult to do this, because without knowing the factors of m one cannot even readily tell whether a given x is a quadratic residue modulo m. The pictures below show as black squares all the quadratic residues for each successive *m* going down the page (the ordinary squares 1, 4, 9, 16, ... show up as vertical black stripes). If m is a prime p, then the simple tests JacobiSymbol[x, p] == 1 (see page 1081) or  $Mod[x^{(p-1)/2}, p] == 1$ determine whether x is a quadratic residue. But with m = pq, one has to factor m and find p and q in order to carry out similar tests. The condition Mod[p, 4] == Mod[q, 4] == 3 ensures that only one of the solutions +v and -v to  $x = Mod[v^2, m]$  is ever a quadratic residue, with the result that the iterated mapping  $x \rightarrow Mod[x^2, m]$  always has a unique inverse. But unlike in a cellular automaton even given a complete x (the analog of a complete cellular automaton state) it is difficult to invert the mapping and solve for the *x* on the previous step.

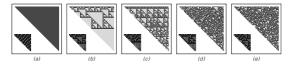


**Traditional Mathematics and Mathematical Formulas** 

• **Practical empirical mathematics.** In looking for formulas to describe behavior seen in this book I have in practice typically taken associated sequences of numbers and then

tested whether obvious regularities are revealed by combinations of such operations as: computing successive differences (see note below), computing running totals, looking for repeated blocks, picking out running maxima, picking out numbers with particular modular residues, and looking at positions of particular values, and at the forms of the digit sequences of these positions.

• Difference tables and polynomials. A common mathematical approach to analyzing sequences is to form a difference table by repeatedly evaluating  $d[list_-] := Drop[list, 1] - Drop[list, -1]$ . If the elements of *list* correspond to values of a polynomial of degree *n* at successive integers, then *Nest[d, list, n + 1]* will contain only zeros. If the differences are computed modulo *k* then the difference table corresponds essentially to the evolution of an additive cellular automaton (see page 597). The pictures below show the results with *k* = 2 (rule 60) for (a) *Fibonacci[n]*, (b) Thue-Morse sequence, (c) Fibonacci substitution system, (d) (*Prime[n] - 1)/2*, (e) digits of  $\pi$ . (See also page 956.)



■ **Page 607** • **Implementation**. The color of a cell at position {*x*, *y*} in the pattern shown is given by *Extract* [{{1, 0, 1}, {0, 1, 0}}, *Mod*[{*y*, *x*}, {2, 3}] + 1].

■ Page 608 · Nested patterns and numbers. See page 931.

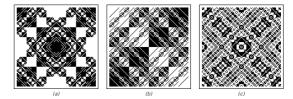
• **Page 609** • **Implementation.** Given the rules for a substitution system in the form used on page 931 a finite automaton (as on page 957) which yields the color of each cell from the digit sequences of its position is

 $\begin{array}{l} Map[Flatten[MapIndexed[\#2-1 \rightarrow Position[rules, \#1 \rightarrow \_]][\\ 1, 1]] \&, \ Last[\#], \ \{-1\}]] \&, \ rules] \end{array}$ 

This works in any number of dimensions so long as each replacement yields a block of the same cuboidal form.

• Arbitrary digit operations. If the operation on digit sequences that determines whether a square will be black can be performed by a finite automaton (see page 957) then the pattern generated must always be either repetitive or nested. The pictures below show examples with more general operations. Picture (a) in effect shows which words in a simple context-free language of parenthesis matching (see page 939) are syntactically correct. Scanning the digit sequences from the left, one starts with 0 open parentheses, then adds 1 whenever corresponding digits in the *x* and *y* coordinates differ, and subtracts 1 whenever they are the

same. A square is black if no negative number ever appears. Picture (b) has a black square wherever digits at more than half the possible positions differ between the x and y coordinates. Picture (c) has a black square wherever the maximum run of either identical or different digits has a length which is an odd number. All the patterns shown have the kind of intricate substructure typical of nesting. But none of the patterns are purely nested.



■ Page 610 · Generating functions. A convenient algebraic way to describe a sequence of numbers a[n] is to give a generating function  $Sum[a[n]x^n, \{n, 0, \infty\}]$ . 1/(1-x) thus corresponds to the constant sequence and  $1/(1-x-x^2)$  to the Fibonacci sequence (see page 890). A 2D array can be described by  $Sum[a[t, n]x^ny^t, \{n, -\infty, \infty\}]$ . The array for rule 60 is then 1/(1-(1+x)y), for rule 90 1/(1-(1/x+x)y), for rule 150 1/(1-(1/x+1+x)y) and for second-order reversible rule 150 (see page 439)  $1/(1-(1/x+1+x)y-y^2)$ . Any rational function is the generating function for some additive cellular automaton.

- Page 611 · Pascal's triangle. See notes on page 870.
- Nesting in bitwise functions. See page 871.

**Trinomial coefficients.** The coefficient of  $x^n$  in the expansion of  $(1 + x + x^2)^t$  is

Sum[Binomial[n + t - 1 - 3k, n - 3k] Binomial[t, k](-1)<sup>k</sup>, {k, 0, t}]

which can be evaluated as

Binomial[2 t, n] Hypergeometric2F1[-n, n-2 t, 1/2-t, 1/4]

or finally GegenbauerC[n, -t, -1/2]. This result follows directly from the generating function formula

 $(1-2xz+x^2)^{-m} == Sum[GegenbauerC[n, m, z]x^n, \{n, 0, \infty\}]$ 

• **Gegenbauer functions.** Introduced by Leopold Gegenbauer in 1893 *GegenbauerC[n, m, z]* is a polynomial in *z* with integer coefficients for all integer *n* and *m*. It is a special case of *Hypergeometric2F1* and *JacobiP* and satisfies a secondorder ordinary differential equation in *z*. The *GegenbauerC[n, d/2 - 1, z]* form a set of orthogonal functions on a *d*-dimensional sphere. The *GegenbauerC[n, 1/2, z]* obtained for d = 3 are *LegendreP[n, z]*.

• Standard mathematical functions. There are an infinite number of possible functions with integer or continuous

arguments. But in practice there is a definite set of standard named mathematical functions that are considered reasonable to include as primitives in formulas, and that are implemented as built-in functions in Mathematica. The socalled elementary functions (logarithms, exponentials, trigonometric and hyperbolic functions, and their inverses) were mostly introduced before about 1700. In the 1700s and 1800s another several hundred so-called special functions were introduced. Most arose first as solutions to specific differential equations, typically in physics and astronomy; some arose as products, sums of series or inverses of other functions. In the mid-1800s it became clear that despite their different origins most of these functions could be viewed as special cases of Hypergeometric2F1[a, b, c, z], and that the functions covered the solutions to all linear differential equations of a certain type. (Zeta and PolyLog are parametric derivatives of Hypergeometric2F1; elliptic modular functions are inverses.) Rather few new special functions have been introduced over the past century. The main reason has been that the obvious generalizations seem to yield classes of functions whose properties cannot be worked out with much completeness. So, for example, if there are more parameters it becomes difficult to find continuous definitions that work for all complex values of these parameters. (Typically one needs to generalize formulas that are initially set up with integer numbers of terms; examples include taking Power[x, y] to be Exp[Log[x]y] and x! to be Gamma[x+1].) And if one hypergeometric modifies the usual equation y''[x] = f[y[x], y'[x]] by making f nonlinear then solutions typically become hard to find, and vary greatly in character with the form of f. (For rational f Paul Painlevé in the 1890s identified just 6 additional types of functions that are needed, but even now series expansions are not known for all of them.) Generalizations of special functions can in principle be used to represent the results of many kinds of computations. Thus, for example, generalized elliptic theta functions represent solutions to arbitrary polynomial equations, while multivariate hypergeometric functions represent arbitrary conformal mappings. In Mathematica, however, functions like Root provide more convenient ways to access such results.

A variety of standard mathematical functions with integer arguments were introduced in the late 1800s and early 1900s in connection with number theory. A few functions that involve manipulation of digits have also become standard since the use of computers became widespread.

• **1D** sequences. Generating functions that are rational always lead to sequences which after reduction modulo 2 are purely

repetitive. Algebraic generating functions can also lead to nested sequences. (Note that to get only integer sequences such generating functions have to be specially chosen.) Sqrt[1-4x]/2 yields a sequence with 1's at positions  $2^m$ , as essentially obtained from the substitution system  $\{2 \rightarrow \{2, 1\}, 1 \rightarrow \{1, 0\}, 0 \rightarrow \{0, 0\}\}$ . Sqrt[(1-3x)/(1+x)]/2 yields sequence (a) on page 84. (1 + Sqrt[(1-3x)/(1+x)])/(2(1+x)) (see page 890) yields the Thue-Morse sequence. (This particular generating function satisfies the equation  $(1+x)^3 f^2 - (1+x)^2 f + x = 0.) (1-9x)^{1/3}$  yields almost the Cantor set sequence from page 83. *EllipticTheta[3, π, x]/2* gives a sequence with 1's at positions  $m^2$ .

For any sequence with an algebraic generating function and thus for any nested sequence the  $n^{\text{th}}$  element can always be expressed in terms of hypergeometric functions. For the Thue-Morse sequence the result is

1/2 (-1)<sup>n</sup> + (-3)<sup>n</sup> √π Hypergeometric2F1[3/2, -n, 3/2 - n, -1/3]/(4 n! Gamma[3/2 - n])

• **Multidimensional additive rules.** The 2D analog of rule 90 yields the patterns shown below. The colors of cells are given essentially by *Mod*[*Multinomial*[*t*, *x*, *y*], *2*]. In *d* dimensions (*2d*)^*DigitCount*[*t*, *2*, *1*] cells are black at step *t*. The fractal dimension of the (*d*+1)-dimensional structure formed from all black cells is *Log*[*2*, *1* + *2d*].

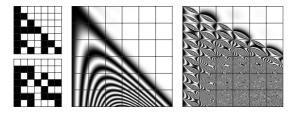
	٠	÷	۲	÷	***	$\diamond$	۲
· · ·	• • •	* * * *	**		••••••		

The 2D analog of rule 150 yields the patterns below; the fractal dimension of the structure in this case is Log[2, (1 + Sqrt[1 + 4/d])d].

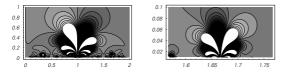
	•	÷	¢	·÷·	÷	¢	۲
	• • •	$\overset{+}{\overset{+}{\overset{+}{\overset{+}{\overset{+}{\overset{+}{\overset{+}{\overset{+}$	\$ \$ \$		÷		

• **Continuous generalizations.** Functions such as *Binomial[t, n]* and *GegenbauerC[n, -t, -1/2]* can immediately be evaluated for continuous *t* and *n*. The pictures on the right below show  $Sin[1/2 \pi a[t, n]]^2$  for these functions (equivalent to Mod[a[t, n], 2] for integer a[t, n]). The discrete results on the left can be obtained by sampling only where integer grid lines cross. Note that without further conditions the continuous forms cannot be considered unique extensions of the discrete ones. The presence of poles in quantities such as

*GegenbauerC*[1/2, -t, -1/2] leads to essential singularities in the rightmost picture below. (Compare page 922.)



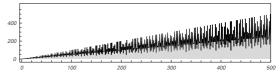
■ Nested continuous functions. Most standard continuous mathematical functions never show any kind of nested behavior. Elliptic theta and elliptic modular functions are exceptions. Each of these functions has definite finite values only in a limited region of the complex plane, and on the boundary of this region they exhibit singularities at every single rational point. The picture below shows *Im*[*ModularLambda*[x + *i*y]]. Like other elliptic modular functions, *ModularLambda* satisfies f[z] = f[(a + bz)/(c + dz)] with *a*, *b*, *c*, *d* integers such that ac - bd = 1. The function can be obtained as the solution to a second-order nonlinear ordinary differential equation. Nested behavior is also found for example in *EllipticTheta*[3, 0, *z*], which is given essentially by  $Sum[z^{n^2}, \{n, \infty\}]$ .



■ **Page 613** • **GCD array.** (See also page 950.) There are various deviations from perfect randomness. The density of white squares is asymptotically  $6/\pi^2 \simeq 0.61$ . (The probability for *s* randomly chosen integers to be relatively prime is 1/Zeta[s].) No 2×2 or larger block of white squares can ever occur. An arrangement of black squares with any list of relative offsets will always eventually occur. (This follows from the Chinese Remainder Theorem.) The first 2×2 block of black squares occurs at {14, 20}, the first 3×3 block at {1274, 1308} and the first 4×4 block at {7247643, 10199370}. The densities of such blocks are respectively about 0.002, 2×10<sup>-6</sup> and 10<sup>-14</sup>. In general the density for an arrangement of white squares with offsets *v* is given in *s* dimensions by (no simple closed formula seems to exist except for the 1×1 case)

 $\begin{aligned} & Product[With[{p = Prime[n]}, \\ & 1 - Length[Union[Mod[v, p]]]/p^{s}], \{n, \infty\}] \end{aligned}$ 

White squares correspond to lattice points that are directly visible from the origin at the top left of the picture, so that lines to them do not pass through any other integer points. On row n the number of white squares encountered before reaching the leading diagonal is *EulerPhi[n]*. This function is shown below. Its computation is known in general to be equivalent in difficulty to factoring n (see page 1090). *GCD* can be computed using Euclid's algorithm as discussed on page 915.



• **Power cellular automata.** Multiplication by *m* in base *k* corresponds to a local cellular automaton operation on digit sequences when every prime that divides *m* also divides *k*. The first non-trivial cases for which this is so are k = 6,  $m = 2^i 3^j$  and k = 10,  $m = 2^i 5^j$ . When *m* itself divides *k*, the cellular automaton rule is  $\{., b_-, c_-\} \rightarrow mMod[b, k/m] + Quotient[c, k/m];$  in other cases the rule can be obtained by composition. A similar result holds for rational *m*, obtained for example by allowing *i* and *j* above to be negative. In all cases the cellular automaton rule, like the original operation on numbers, is invertible. The inverse rule, corresponding to multiplication by 1/m, can be obtained by applying the rule for multiplication by the integer  $k^q/m$ , then shifting right by *q* positions. (See page 903.)

The condition for locality in negative bases (see page 902) is more stringent. The first non-trivial example is k = -6, m = 8, corresponding to a rule that depends on four neighboring cells.

Non-trivial examples of multiplication by m in base k all appear to be class 3 systems (see page 250), with small changes in initial conditions growing at a roughly fixed rate.

■ **Page 615** · **Computing powers**. The method of repeated squaring (also known as the binary power method, Russian peasant method and Pingala's method) computes the quantity *m<sup>t</sup>* by performing about *Log[t]* multiplications and building up the sequence

FoldList[#1<sup>2</sup> m<sup>#2</sup> &, 1, IntegerDigits[t, 2]]

(related to the Horner form for the base 2 representation of t). Given two numbers x and y their product can be computed in base k by (*FromDigits* does the carries)

FromDigits[ListConvolve[IntegerDigits[x, k], IntegerDigits[y, k], {1, -1}, 0], k]

For numbers with *n* digits direct evaluation of the convolution would take about  $n^2$  steps. But FFT-related methods reduce this to about nLog[n] steps (see also page 1142). And this implies that to find a particular digit of  $m^t$  in base *k* will take altogether about  $tLog[t]^2$  steps.

One might think that a more efficient approach would be to start with the trivial length *t* digit sequence for  $c^t$  in base *c*, then to find a particular base *k* digit just by converting to base *k*. However, the straightforward method for converting a *t*-digit number *x* to base *k* takes about *t* divisions, though this can be reduced to around *Log[t]* by using a recursive method such as

FixedPoint[Flatten[Map[If[# < k, #, With[ {e = Ceiling[Log[k, #]/2]}, {Ouotient[#, k<sup>e</sup>], With[ {s = Mod[#, k<sup>e</sup>]}, If[s == 0, Table[0, {e}], {Table[0, {e - Floor[Log[k, s]] - 1}], s}]]]] &, #]] &, {x}]

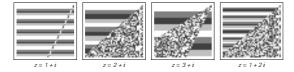
The pictures below show stages in the computation of  $3^{20}$  (a) by a power tree in base 2 and (b) by conversion from base 3. Both approaches seem to require about the same number of underlying steps. Note that even though one may only want to find a single digit in  $m^t$ , I know of no way to do this without essentially computing all the other digits in  $m^t$  as well.



• **Complex powers.** The pictures below show successive powers of complex numbers *z* with digits extracted according to

(2 d[Re[#], w] + d[Im[#], w] &)[z<sup>t</sup>] d[x\_, w\_] := If[x < 0, 1 - d[-x, w], IntegerDigits[x, 2, w]]

Non-trivial cases of complex number multiplication never correspond to local cellular automaton operations. (Compare page 933.)



• Additive cellular automata. As discussed on page 951 a step in the evolution of an additive cellular automaton can be thought of as multiplication by a polynomial modulo *k*. After *t* steps, therefore, the configuration of such a system is given by *PolynomialMod[poly<sup>t</sup>*, *k]*. This quantity can be computed using power tree methods (see below), though as discussed on page 609, even more efficient methods are also available. (A similar formalism can be set up for any of the cellular automata with generalized additivity discussed on page 952; see also page 886.)

• The more general case. One can think of a single step in the evolution of any system as taking a rule r and state s, and producing a new state h[r, s]. Usually the representations that are used for r and s will be quite different, and the

function *h* will have no special properties. But for both multiplication rules and additive cellular automata it turns out that rules and states can be represented in the same way, and the evolution functions *h* have the property of being associative, so that h[a, h[b, c]] == h[h[a, b], c]. This means that in effect one can always choose to evolve the rule rather than a state. A consequence is that for example 4 steps of evolution can be computed not only as h[r, h[r, h[r, h[r, s]]]] but also as h[h[h[r, r], h[r, r]], s] or u = h[r, r]; h[h[u, u], s]—which requires only 3 applications of *h*. And in general if *h* is associative the result Nest[h[r, #] &, s, t] of *t* steps of evolution can be rewritten for example using the repeated squaring method as

h[Fold[If[#2 == 0, h[#1, #1], h[r, h[#1, #1]]] &,

r, Rest[IntegerDigits[t, 2]]], s]

which requires only about Log[t] rather than t applications of h.

As a very simple example, consider a system which starts with the integer 1, then at each step just adds 1. One can compute the result of 9 steps of evolution as 1 + 1 + 1 + 1 + 1 + 1 + 1 + 1 + 1 + 1, but a better scheme is to use partial results and compute successively 1 + 1; 2 + 2; 1 + 4; 5 + 5—which is what the repeated squaring method above does when h = Plus, r = s = 1. This same basic scheme can be used with any associative function h—*Max*, *GCD*, *And*, *Dot*, *Join* or whatever—so long as suitable forms for r and s are used.

For the multiplication rules discussed in the main text both states and rules can immediately be represented by integers, with h = Times, and r = m giving the multiplier. For additive cellular automata, states and rules can be represented as polynomials (see page 951), with  $h[a_{-}, b_{-}] := PolynomialMod[a b, k]$  and for example r = 1 + x for elementary rule 60. The correspondence between multiplication rules and additive cellular automata can be seen even more directly if one represents all states by integers and computes h in terms of base k digits. In both cases it then turns out that h can be obtained from (see note above)

## *h*[*a*\_, *b*\_] := FromDigits[g[ListConvolve[

IntegerDigits[a, k], IntegerDigits[b, k], {1, -1}, 0]], k] where for multiplication rules g = Identity and for additive cellular automata g = Mod[#, k] &. For multiplication rules, there are normally carries (handled by *FromDigits*), but for power cellular automata, these have only limited range, so that  $g = Mod[\#, k^{\sigma}] \&$  can be used.

For any associative function h the repeated squaring method allows the result of t steps of evolution to be computed with only about Log[t] applications of h. But to be able to do this some of the arguments given to h inevitably need to be larger. So whether a speedup is in the end achieved will depend on how fast *h* can be evaluated for arguments of various sizes. Typically the issue is whether h[a, b] for large *a* and *b* can be found with much less effort than it would take to evaluate h[r, b] about *a* times. If h = Times, then as discussed in the note above, the most obvious procedure for evaluating h[a, b] would involve about mn operations, where m and nare the numbers of digits in *a* and *b*. But when  $m \simeq n$  FFTrelated methods allow this to be reduced to about nLog[n]operations. And in fact whenever *h* is commutative (*Orderless*) it turns out that such methods can be used, and substantial speedups obtained. But whether anything like this will work in other cases is not clear.

# (See also page 886.)

• Evaluation chains. The idea of building up computations like 1 + 1 + 1 + ... from partial results has existed since Egyptian times. Since the late 1800s there have been efforts to find schemes that require the absolute minimum number of steps. The method based on *IntegerDigits* in the previous two notes can be improved (notably by power tree methods), but apparently about Log[t] steps are always needed. (Finding the optimal addition chain for given *t* may be NP-complete.)

One can also consider building up lists of non-identical elements, say by successively using *Join*. In general a length n list can require about n steps. But if the list contains a nested sequence, say generated using a substitution system, then about *Log[n]* steps should be sufficient. (Compare page 566.)

**Boolean formulas.** A Boolean function of *n* variables can always be specified by an explicit table giving values for all  $2^n$ possible inputs. (Any cellular automaton rule with an n-cell neighborhood corresponds to such a function; digit sequences in rule numbers correspond to explicit tables of values.) Like ordinary algebraic functions, Boolean functions can also be represented by a variety of kinds of formulas. Those on pages 616 and 618 use so-called disjunctive normal form (DNF) And[...] v And[...] v ..., which is common in practice in programmable logic arrays (PLAs). (The addition and multiplication operators in the main text should be interpreted as Or and And respectively.) In general any given function will allow many DNF representations; minimal ones can be found as described below. Writing a Boolean function in DNF is the rough analog of applying Expand to a polynomial. Conjunctive normal form (CNF) Or[...] ^ Or[...] ^ ... is the rough analog of applying Factor . DNF and CNF both involve Boolean formulas of depth 2. As in the note on multilevel formulas below, one can also in effect introduce intermediate

variables to get recursive formulas of larger depth, somewhat analogous to results from *Collect*. (Unbalanced depths in different parts of a formula lead to latencies in a circuit, reducing practical utility.)

DNF minimization. From a table of values for a Boolean function one can immediately get a DNF representation just by listing cases where the value is 1. For one step in rule 30, for example, this yields {{1, 0, 0}, {0, 1, 1}, {0, 1, 0}, {0, 0, 1}}, as shown on page 616. One can think of this as specifying corners that should be colored on an n-dimensional Boolean hypercube. To reduce the representation, one must introduce "don't care" elements \_; in this example the final minimal form consists of the list of 3 so-called implicants {{1, 0, 0}, {0, 1, \_}, {0, \_, 1}}. In general, an implicant with *m* \_'s can be thought of as corresponding to an *m*-dimensional hyperplane on the Boolean hypercube. The problem of minimization is then to find the minimal set of hyperplanes that will cover the corners for a particular Boolean function. The first step is to work out so-called prime implicants corresponding to hyperplanes that cannot be contained in higher-dimensional ones. Given an original DNF list s, this can be done using *PI*[*s*, *n*]:

 $\begin{array}{l} PI[s_{-}, n_{-}] := Union[Flatten[ \\ FixedPointList[f[Last[#], n] \&, \{\{\}, s\}][[All, 1]], 1]] \\ g[a_{-}, b_{-}] := With[\{i = Position[Transpose[\{a, b\}], \{0, 1\}]\}, \\ If[Length[i] == 1 \&\& Delete[a, i] === Delete[b, i], \\ \{ReplacePart[a, _, i]\}, \{\}]] \\ f[s_{-}, n_{-}] := With[ \\ \{w = Flatten[Apply[Outer[g, #1, #2, 1] \&, Partition[Table[ \\ Select[s, Count[#, 1] == i \&], (i, 0, n]], 2, 1], \{1\}], \\ 3]\}, \{Complement[s, w, SameTest \rightarrow MatchQ], w\}] \end{array}$ 

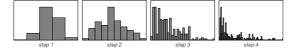
The minimal DNF then consists of a collection of these prime implicants. Sometimes it is all of them, but increasingly often when  $n \ge 3$  it is only some. (For example, in {{0, 0, \_}, {0, \_, 1}, {\_-, 0, 0}} the first prime implicant is covered by the others, and can therefore be dropped.) Given the original list *s* and the complete prime implicant list *p* the so-called Quine-McCluskey procedure can be used to find a minimal list of prime implicants, and thus a minimal DNF:

The number of steps required in this procedure can increase exponentially with the length of p. Other procedures work slightly more efficiently, but in general the problem of finding the minimal DNF for a Boolean function of n

variables is NP-complete (see page 768) and is thus expected to grow in difficulty faster than any polynomial in *n*. In practice, however, cases up to about n = 12 are nevertheless currently handled quite routinely.

• **Formula sizes.** There are a total of  $2^{2^n}$  possible Boolean functions of *n* variables. The maximum number of terms needed to represent any of these functions in DNF is  $2^{n-1}$ . The actual numbers of functions which require 0, 1, 2, ... terms is for n = 2: {1, 9, 6}; for n = 3: {1, 27, 130, 88, 10}, and for n = 4: {1, 81, 1804, 13472, 28904, 17032, 3704, 512, 26}. The maximal length turns out always to be realized for the simple parity function *Xor*, as well as its negation. The reason for this is essentially that these functions are the ones that make the coloring of the Boolean hypercube maximally fragmented. (Other functions with maximal length are never additive, at least for  $n \le 4$ .)

• **Cellular automaton formulas.** See page 869. The maximum length DNF for elementary rules after 1 step is 4, and this is achieved by rules 105, 107, 109, 121, 150, 151, 158, 182, 214 and 233. These rules have behavior of quite varying complexity. Rules 150 and 105 are additive, and correspond to *Xor* and its negation. After *t* steps the maximum conceivable DNF would be of length  $2^{2t}$ . In practice, after 2 steps, the maximum length is 9, achieved by rules 107, 121 and 182; after 3 steps, it is 33 achieved by rule 182; after 4 steps, 78 achieved by rule 129; after 5 steps 256 achieved by rules 105 and 150. The distributions of lengths for all elementary rules are shown below.



Note that the length of a minimal DNF representation cannot be considered a reliable measure of the complexity of a function, since among other things, just exchanging the role of black and white can substantially change this length (as in the case of rule 126 versus rule 129).

• **Primitive functions.** There are several possible choices of primitive functions that can be combined to represent any Boolean function. In DNF *And*, *Or* and *Not* are used. *Nand* = *Not*[*And*[##]] & alone is also sufficient, as shown on page 619 and further discussed on page 807. (It is indicated by  $\bar{\pi}$  in the main text.) The functions *And*, *Xor* and *Not* are equivalent to *Times*, *Plus* and 1-# & for variables modulo 2, and in this case algebraic functions like *PolynomialReduce* can be used for minimization. (See also page 1102.)

• Multilevel formulas. DNF formulas always have depth 2. By allowing larger depths one can potentially find smaller formulas

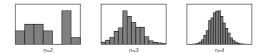
for functions. A major result from the 1980s is that it requires a formula with depth at least Log[n]/(c + Log[Log[n]]) to make it possible to represent an *Xor* of *n* variables using a polynomial number of *And*, *Or* and *Not* operations. If one chooses an *n*-variable Boolean function at random out of the  $2^{2^n}$  possibilities, it is typical that regardless of depth a formula involving at least  $2^n/n$  operations will be needed to represent it. A formula of polynomial size and logarithmic depth exists only when a function is the computational complexity class NC discussed on page 1149.

Little is known about systematic minimization of Boolean formulas with depths above 2. Nevertheless, some programs for circuit design such as SIS do include a few heuristics. And this for example allows SIS to generate higher depth formulas somewhat smaller than the minimal DNF for the first three steps of rule 30 evolution.

$b_1 = a_2 + a_3; \overline{a}_1 b_1 + a_1 \overline{b}_1$	
$b_1 = \overline{a}_2  a_3 + a_2  \overline{a}_3;  b_2 = a_4 + a_5;  a_1  b_1 + a_1  \overline{b}_2 + \overline{a}_1  \overline{b}_1  b_2$	
$b_1 = a_6 + a_7; b_2 = a_4 + a_5; b_3 = \overline{a}_5 b_1 + a_4 \overline{b}_1; b_4 = \overline{b}_1 + b_2; \overline{a}_1 \overline{a}_3 b_3 + \overline{a}_1 a_2 \overline{b}_2 + b_4 \overline{b}_1; b_4 = \overline{b}_1 + b_2; \overline{a}_1 \overline{a}_3 b_3 + \overline{a}_1 a_2 \overline{b}_2 + b_4 \overline{b}_1; b_4 = \overline{b}_1 + b_2; \overline{a}_1 \overline{a}_3 b_3 + \overline{a}_1 a_2 \overline{b}_2 + b_4 \overline{b}_1; b_4 = \overline{b}_1 + b_2; \overline{a}_1 \overline{a}_3 b_3 + \overline{a}_1 a_2 \overline{b}_2 + b_4 \overline{b}_1; b_4 = \overline{b}_1 + b_2; \overline{a}_1 \overline{a}_3 b_3 + \overline{a}_1 a_2 \overline{b}_2 + b_4 \overline{b}_1; b_4 = \overline{b}_1 + b_2; \overline{a}_1 \overline{a}_3 b_3 + \overline{a}_1 a_2 \overline{b}_2 + b_4 \overline{b}_1; b_4 = \overline{b}_1 + b_2; \overline{a}_1 \overline{a}_3 b_3 + \overline{a}_1 a_2 \overline{b}_2 + b_4 \overline{b}_1; b_4 = \overline{b}_1 + b_2; \overline{a}_1 \overline{a}_3 b_3 + \overline{a}_1 a_2 \overline{b}_2 + b_4 \overline{b}_1; b_4 = \overline{b}_1 + b_2; \overline{a}_1 \overline{a}_3 b_3 + \overline{a}_1 a_2 \overline{b}_2 + b_4 \overline{b}_1; b_4 = \overline{b}_1 + b_2; \overline{a}_1 \overline{a}_3 b_3 + \overline{a}_1 a_2 \overline{b}_2 + b_4 \overline{b}_1; b_4 = \overline{b}_1 + b_4 \overline{b}_1; b_4 = \overline{b}_1 + b_4 \overline{b}_2; \overline{a}_1 \overline{a}_3 b_3 + \overline{a}_1 a_2 \overline{b}_2 + b_4 \overline{b}_2; \overline{b}_2 + b_4 \overline{b}_2; \overline{b}_3 = \overline{b}_1 + b_4 \overline{b}_2; \overline{b}_2 + b_4 \overline{b}_2; \overline{b}_2 + b_4 \overline{b}_2; \overline{b}_3 = \overline{b}_1 + b_4 \overline{b}_2; \overline{b}_2 + b_4 \overline{b}_2; \overline{b}_2 + b_4 \overline{b}_2; \overline{b}_3 = \overline{b}_1 + b_4 \overline{b}_2; \overline{b}_3 = \overline{b}_1 + b_4 \overline{b}_2; \overline{b}_2 + b_4 \overline{b}_2; \overline{b}_2 + b_4 \overline{b}_2; \overline{b}_3 = \overline{b}_1 + b_4 \overline{b}_2; \overline{b}_3 = \overline{b}_1 + b_4 \overline{b}_2; \overline{b}_2 = \overline{b}_2 $	
$a_1 \overline{a}_2 \overline{a}_3 \overline{b}_3 + \overline{a}_1 a_2 a_4 \overline{b}_3 + a_1 a_2 \overline{a}_4 b_2 + \overline{a}_1 \overline{a}_2 a_3 b_4 + a_1 \overline{a}_2 a_3 \overline{b}_4 + a_1 a_2 a_3 b_3 b_4$	

• Page 619 • NAND expressions. If one allows a depth of at most 2 n any n-input Boolean function can be obtained just by combining 2-input Nand functions. (See page 807.) (Note that unless one introduces an explicit copy operation—or adds variables as in the previous note—there is no way to use the same intermediate result multiple times without recomputing it.)

The pictures below show the distributions of numbers of *Nand* operations needed for all  $2^{2^n}$  *n*-input Boolean functions. For *n* = 2, the largest number of such operations is 6, achieved by *Nor*; for *n* = 3, it is 14, achieved by *Xor* (rule 150); for *n* = 4, it is 27, achieved by rule 5737, which is *Not*[*Xor*[##]] & except when all inputs are *True*. The average number of operations needed when *n* = 2, 3, 4 is about {2.875, 6.09, 12.23}.

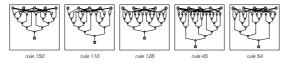


The maximum depths for the expressions of minimal size are respectively 4, 6 and 7, always achieved among others for the function taking the most *Nand* operations. The total numbers of functions involving successive depths are: n = 2: {2, 3, 5, 6}, n = 3: {3, 6, 22, 99, 72, 54}, n = 4: {4, 10, 64, 923, 9663, 54622, 250}, corresponding to averages {2.9, 4.5, 5.8}.

The following generates explicit lists of *n*-input Boolean functions requiring successively larger numbers of *Nand* operations:

Map[FromDigits[#, 2] &, NestWhile[Append[#, Complement[Flatten[Table[Outer[1 - Times[##]] &, #[[i]], #[[-i]], 1], (i, Length[#]]), [J, Flatten[#, 1]]] &, {1 - Transpose[IntegerDigits[Range[2<sup>n</sup>] - 1, 2, n]]}, Length[Flatten[#, 1]] < 2<sup>n</sup> &], [2]

The results for 2-step cellular automaton evolution in the main text were found by a recursive procedure. First, expressions containing progressively more *Nand* operations were enumerated, and those for functions that had not been seen before were kept. It then turned out that this made it possible to get to expressions at least half as large as any needed, so that it could be assumed that remaining expressions could be decomposed as  $f[##] \pi g[##] \&$ , where *f* had already been found. The pictures below show some more results obtained in this way.



• **Cellular automaton formulas.** For 1 step, the elementary cellular automaton rules are exactly the 256 n = 3 Boolean functions. For 2 steps, they represent a small subset of the  $2^{32}$  n = 5 functions. They require an average of about 11.6 *Nand* operations, and a maximum of 27 (achieved by rules 107 and 121).

For rule 254 the result after t steps (which is always asymmetric, even though the rule is symmetric) is

Nest[{{#, #[[2]] + 1}, #[[2]] + 1} &, {{1, 1}, {2, 2}}, t-2]

If explicit copy operations were allowed, then the number of *Nand* operations after *t* steps could not increase faster than  $t^2$  for any rule. But without copy (fanout) operations no corresponding result is immediately clear.

■ **Binary decision diagrams.** One can specify a Boolean function of *n* variables by giving a finite automaton (and thus a network) in which paths exist only for those lists of values for which the function yields *True*. The resulting so-called binary decision diagram (BDD) can be minimized using the methods of page 957. Out of all possible Boolean functions the number that require BDDs of sizes 1, 2, ... is for *n* = 2: {1, 0, 6, 9} and for *n* = 3: {1, 0, 0, 27, 36, 132, 60}; the absolute maximum grows roughly like 2<sup>*n*</sup>. For cellular automata with simple behavior, the minimal BDD typically grows linearly on successive steps. For rule 254, for example, it is 8 *t* + 2, while for rule 90 it is 4 *t* + 2. For cellular automata with more complex behavior, it typically grows roughly exponentially.

Thus for rule 30 it is {7, 14, 29, 60, 129} and for rule 110 {7, 15, 27, 52, 88}. The size of the minimal BDD can depend on the order in which variables are specified; thus for example, just reflecting rule 30 to give rule 86 yields {6, 11, 20, 36, 63}.

In practical system design BDDs have become fairly popular in the past ten years, and by maintaining minimality when logical combinations of functions are formed, cases with millions of nodes have been studied. (Some practical systems are found to yield fairly small BDDs, while others are not.)

 History. Logic has been used as an abstraction of arguments in ordinary language since antiquity. Its serious mathematical formulation began with the work of George Boole in the mid-1800s. (See page 1151.) Concepts of Boolean algebra were applied to electronic switching circuits by Claude Shannon in 1937, and became a standard part of electronic design methodology by the 1950s. DNF had been introduced as part of the development of mathematical logic in the early 1900s, but became particularly popular in the 1970s with the advent of programmable logic arrays (PLAs) used in applicationspecific integrated circuits (ASICs). Diagrammatic and mechanical methods for minimizing simple logic expressions have existed since at least medieval times. More systematic methods for minimizing complex expressions began to be developed in the early 1950s, but until well into the 1980s a diagrammatic method known as a Karnaugh map was the most commonly used in practice. In the late 1970s there began to be computer programs for large-scale Boolean minimization-the best known being Espresso. Only in the 1990s, however, did exact minimization of complex DNF expressions become common. Minimization of Boolean expressions with depth larger than 2 has been considered off and on since the late 1950s, and became popular in the 1990s in connection with the BDDs discussed above. Various forms of Boolean minimization have routinely been used in chip and circuit design since the late 1980s, though often physical and geometrical constraints are now more important than pure logical ones. In addition, theoretical studies of minimal Boolean circuits became increasingly popular starting in the 1980s, as discussed on page 1148.

• **Reversible logic.** In an ordinary Boolean function with n inputs there is no unique way to tell from its output which of the  $2^n$  possible sets of inputs was given. But as noted in the 1970s, it is possible to set up systems that evaluate Boolean functions, yet operate reversibly. The basic idea is to have m outputs as well as m inputs—with every one of the  $2^m$  possible sets of inputs mapping to a unique set of outputs. Normally one specifies the first n inputs, taking the others to be fixed, and then looks say at the first output, ignoring all others. One can represent the inside of such a system much

like a sorting network from page 1142-but with s-input soutput gates instead of pair comparisons. If each such gate is itself reversible, then overall reversibility is guaranteed. With gates that in effect implement  $\{p, q\} \rightarrow \{p \ \overline{n} \ q\}$  and  $\{p\} \rightarrow \{p, p\}$ (with other inputs constant, and other outputs ignored) one can set up a direct translation of Boolean functions given in the form shown on page 619. Of the 24 possible reversible s = 2 gates, none can yield anything other than additive Boolean functions (as formed from Xor and Not). But of the 40,320 (8!) reversible s = 3 gates (in 52 distinct classes) it turns out that 38,976 (in 23 classes) can be used to reproduce any possible Boolean function. A simple example of such a universal gate is  $\{p_{-}, q_{-}, 1\} \rightarrow \{q, p, 1\}$ —and not allowing permutations of gate inputs (or in effect wire crossings) a simple example is  $\{p_{-}, q_{-}, q_{-}\} \rightarrow \{q, 1-p, 1-p\}$ . (Compare pages 1147 and 1173.)

• **Continuous systems.** The systems I discuss in the main text of this section are mostly discrete. But from experience with traditional mathematics one might have the impression that it would at some basic level be easier to get formulas for continuous systems. I believe, however, that this is not the case, and that the reason for the impression is just that it is usually so much more difficult even to represent the states of continuous systems that one normally tends to work only with ones that have comparatively simple overall behavior—and are therefore more readily described by formulas. (See also pages 167 and 729.)

As an example of what can happen in continuous systems consider iterated mappings  $x \rightarrow a x (1-x)$  from page 920. Each successive step in such a mapping can in principle be represented by an algebraic formula. But the table below gives for example the actual algebraic formulas obtained in the case a = 4 after applying *FullSimplify*—and shows that these increase quite rapidly in complexity.

X
4 (1 - x) x
16 (1 – 2 x) <sup>2</sup> (1 – x) x
$64(1-2x)^2(1-x)x(8(x-1)x+1)^2$
$256 (1 - 2x)^2 (1 - x) x (8 (x - 1) x + 1)^2 (32 (x - 1) x (1 - 2x)^2 + 1)^2$
$1024(1-2x)^{2}(1-x)x(8(x-1)x+1)^{2}(32(x-1)x(1-2x)^{2}+1)^{2}$
$(128(1-2x)^{2}(x-1)x(8(x-1)x+1)^{2}+1)^{2}$

In the specific case a = 4, however, it turns out that by allowing more sophisticated mathematical functions one can get a complete formula: the result after any number of steps *t* can be written in any of the forms

 $Sin[2^t ArcSin[\sqrt{x}]]^2$ 

 $(1 - Cos[2^t ArcCos[1 - 2x]])/2$ 

 $(1 - ChebyshevT[2^t, 1 - 2x])/2$ 

where these follow from functional relations such as Sin[2x]<sup>2</sup> == 4 Sin[x]<sup>2</sup> (1 - Sin[x]<sup>2</sup>) ChebyshevT[mn, x] == ChebyshevT[m, ChebyshevT[n, x]]

For a = 2 it also turns out that there is a complete formula:  $(1 - (1 - 2x)^{2^{t}})/2$ 

And the same is true for a = -2:  $1/2 - Cos[1/3(\pi - (-2)^{t}(\pi - 3ArcCos[1/2 - x]))]$ 

In all these examples t enters essentially only in  $a^t$ . And if one assumes that this is a general feature then one can formally derive for any a the result

$$1/2(1-g[a^t InverseFunction[g][1-2x]]$$

where *g* is a function that satisfies the functional equation  $g[ax] = 1 + 1/2 a (g[x]^2 - 1)$ 

When a = 4, g[x] is Cosh[Sqrt[2x]]. When a = 2 it is Exp[x] and when a = -2 it is  $2 Cos[1/3(\pi - \sqrt{3} x)]$ . But in general for arbitrary *a* there is no standard mathematical function that seems to satisfy the functional equation. (It has long been known that only elliptic functions such as *JacobiSN* satisfy polynomial addition formulas—but there is no immediate analog of this for replication formulas.) Given the functional equation one can find a power series for g[x] for any *a*. The series has an accumulation of poles on the circle  $Abs[a]^2 = 1$ ; the coefficient of  $x^m$  turns out to have denominator

```
2^(m-DigitCount[m, 2, 1]) Apply[Times,
```

Table[Cyclotomic[s, a] ^ Floor[(m - 1)/s], {s, m - 1}]]

For other iterated maps general formulas also seem rare. But for example  $x \rightarrow ax + b$  and  $x \rightarrow 1/(a+bx)$  both give results just involving powers, while  $x \rightarrow Sqrt[ax+b]$  sometimes yields trigonometric functions, as on page 915. In addition, from a known replication formula for an elliptic or other function one can often construct an iterated map whose behavior can be expressed in terms of that function. (See also page 919.)

### Human Thinking

• The brain. There are a total of about 100 billion neurons in a human brain (see page 1075), each with an average of a few thousand synapses connecting it to other cells. On a small scale the arrangement of neurons seems quite haphazard. But on a larger scale the brain seems to be organized into areas with very definite functions. This organization is sometimes revealed by explicitly following nerve fibers. More often it has been deduced by looking at what happens if parts of the brain are disabled or stimulated. In recent times it has also begun to be possible to image local electrical and metabolic activity while the brain is in normal operation. From all these methods it is known that each kind of sensory input is first

processed in its own specific area of the brain. Inputs from different senses are integrated in an area that effectively maintains a map of the body; a similar area initiates output to muscles. Certain higher mental functions are known to be localized in definite areas of the brain, though within these areas there is often variability between individuals. Areas are currently known for specific aspects of language, memory (see below) and various cognitive tasks. There is some evidence that thinking about seemingly rather similar things can lead to significantly different patterns of activity.

Most of the action of the brain seems to be associated with local electrical connections between neurons. Some collective electrical activity is however revealed by EEG. In addition, levels of chemicals such as hormones, drugs and neurotransmitters can have significant global effects on the brain.

• History. Ever since antiquity immense amounts have been written about human thinking. Until recent centuries most of it was in the tradition of philosophy, and indeed one of the major themes of philosophy throughout its history has been the elucidation of principles of human thinking. However, almost all the relevant ideas generated have remained forever controversial, and almost none have become concrete enough to be applied in science or technology. An exception is logic, which was introduced in earnest by Aristotle in the 4<sup>th</sup> century BC as a way to model certain patterns of human reasoning. Logic developed somewhat in medieval times, and in the late 1600s Gottfried Leibniz tried to use it as the foundation for a universal language to capture all systematic thinking. Beginning with the work of George Boole in the mid-1800s most of logic began to become more closely integrated with mathematics and even less convincingly relevant as a model for general human thinking.

The notion of applying scientific methods to the study of human thinking developed largely with the rise of the field of psychology in the mid-1800s. Two somewhat different approaches were taken. The first concentrated on doing fairly controlled experiments on humans or animals and looking at responses to specific stimuli. The second concentrated on trying to formulate fairly general theories based on observations of overall human behavior, initially in adults and later especially in children. Both approaches achieved some success, but by the 1930s many of their positions had become quite extreme, and the identification of phenomena to contradict every simple conclusion reached led increasingly to the view that human thinking would allow no simple explanations.

The idea that it might be possible to construct machines or other inanimate objects that could emulate human thinking existed already in antiquity, and became increasingly popular starting in the 1600s. It began to appear widely in fiction in the 1800s, and has remained a standard fixture in portrayals of the future ever since.

In the early 1900s it became clear that the brain consists of neurons which operate electrically, and by the 1940s analogies between brains and electrical machines were widely discussed, particularly in the context of the cybernetics movement. In 1943 Warren McCulloch and Walter Pitts formulated a simple idealized model of networks of neurons and tried to analyze it using methods of mathematical logic. In 1949 Donald Hebb then argued that simple underlying neural mechanisms could explain observed psychological phenomena such as learning. Computer simulations of neural networks were done starting in the mid-1950s, but the networks were too small to have any chance to exhibit behavior that could reasonably be identified with thinking. (Ironically enough, as mentioned on page 879, the phenomenon central to this book of complex behavior with simple underlying rules was in effect seen in some of these experiments, but it was considered a distraction and ignored.) And in the 1960s, particularly after Frank Rosenblatt's introduction of perceptrons, neural networks were increasingly used only as systems for specific visual and other tasks (see page 1076).

The idea that computers could be made to exhibit human-like thinking was discussed by Alan Turing in 1950 using many of the same arguments that one would give today. Turing made the prediction that by 2000 a computer would exist that could pass the so-called Turing test and be able to imitate a human in a conversation. (René Descartes had discussed a similar test for machines in 1637, but concluded that it would never be passed.) When electronic computers were first becoming widespread in the 1950s they were often popularly referred to as "electronic brains". And when early efforts to make computers perform tasks such as playing games were fairly successful, the expectation developed that general humanlike thinking was not far away. In the 1960s, with extensive support from the U.S. government, great effort was put into the field of artificial intelligence. Many programs were written to perform specific tasks. Sometimes the programs were set up to follow general models of the high-level processes of thinking. But by the 1970s it was becoming clear that in almost all cases where programs were successful (notable examples being chess, algebra and autonomous control), they typically worked by following definite algorithms not closely related to general human thinking.

Occasional work on neural networks had continued through the 1960s and 1970s, with a few definite results being obtained using methods from physics. Then in the early 1980s, particularly following work by John Hopfield, computer simulations of neural networks became widespread. Early applications, particularly by Terrence Sejnowski and Geoffrey Hinton, demonstrated that simple neural networks could be made to learn tasks of at least some sophistication. But by the mid-1990s it was becoming clear that—probably in large part as a consequence of reliance on methods from traditional mathematics—typical neural network models were mostly being successful only in situations where what was needed was a fairly straightforward extension of standard continuous probabilistic models of data.

• The future. To achieve human-like thinking with computers will no doubt require advances in both basic science and technology. I strongly suspect that a key element is to be able to store a collection of experiences comparable to those of a human. Indeed, to succeed even with specific tasks such as speech recognition or language translation seems to require human-like amounts of background knowledge. Present-day computers are beginning to have storage capacities that are probably comparable to those of the brain. From looking at the brain one might guess that parallel or other non-standard hardware might be required to achieve efficient human-like thinking. But I rather suspect that-much as in the analogy between birds and airplanes-it will in the end be possible to set up algorithms that achieve the same basic functions but work satisfactorily even on standard sequential-processing computers.

• Sleep. A common feature of higher organisms is the existence of distinct behavioral states of sleep and wakefulness. There are various theories that sleep is somehow fundamental to the process of thinking. But my guess is that its most important function is quite mundane: just as muscles build up lactic acid waste products, so also I suspect synapses in the brain build up waste products, and these can only safely be cleared out when the brain is not in normal use.

■ Page 621 · Pointer encoding. The pointer encoding compression method discussed on page 571 implements a very simple form of memory based on literal repetitions, and already leads to fairly good compression of many kinds of data.

**Page 622 · Hashing.** Given data in the form of sequences of numbers between 0 and k - 1, a very simple hashing scheme is just to compute *FromDigits*[*Take*[*list*, *n*], *k*]. But for data corresponding, say, to English words this scheme yields a very nonuniform distribution of hash codes, since, for example, there are many words beginning with "ba", but

none beginning with "bb". The slightly modified but still very simple scheme Mod[FromDigits[list, k], m], where *m* is usually chosen to be a prime, is what is most often used in practice. For a fair fraction of values of *m*, the hash codes obtained from this scheme change whenever any element of *list* is changed. If  $m = k^s - 1$  then it turns out that interchanging a pair of adjacent length *s* blocks in *list* never affects the result. Out of the many hundreds of times that I have used hashing in practice, I recall only a couple of cases where schemes like the one just described were not adequate, and in these cases the data always turned out to have quite dramatic regularities.

In typical applications hash codes give locations in computer memory, from which actual data is found either by following a chain of pointers, or by probing successive locations until an empty one is reached. In the internals of *Mathematica* the most common way that hashing is used is for recognizing data and finding unique stored versions of it. There are several subtleties associated with setting up hash codes that appropriately handle approximate real numbers and *Mathematica* patterns.

Hashing is a sufficiently simple idea that it has been invented independently many times since at least the 1950s. The main alternative to hashing is to store data with successive elements corresponding to successive levels in a tree. In the past decade, hashing has become widely used not only for searching but also for authentication. The basic idea in this case is to take a document and to compute from it a small hash code that changes when almost any change is made in the document, and for which it is a difficult problem of cryptanalysis to work out what changes in the document will lead to no change in the hash code. Schemes for such hash codes can fairly easily be constructed using rule 30 and other cellular automata.

• Page 623 · Similar words. The soundex system for hashing names according to sound was first used on 1880 U.S. census data, and is still today widely used by telephone information services. The system works essentially by dropping vowels and assigning consonants to six possible groups. More sophisticated systems along the same lines can be set up using finite automata.

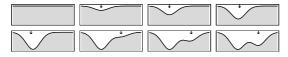
Natural language query systems usually work by stripping words to their linguistic roots (e.g. "stripping"  $\rightarrow$  "strip") before looking them up. Spell-checking systems typically find suggested corrections by doing a succession of lookups after applying transformations based on common errors.

Even given two specific words it can be difficult to find out whether they should be considered similar. Fairly efficient algorithms are known for cases such as genetic sequences where small numbers of insertions, deletions and substitutions are expected. But if more complicated transformations are allowed—say corresponding to rules in a multiway system—the problem rapidly becomes intractable (see page 765).

• Numerical data. In situations where pieces of data can be thought of as points in space similarity can often be defined in terms of spatial distance. And this means that around every point corresponding to a piece of data in memory there is a region of points that can be considered more similar to that point than to any other. Picture (a) shows a so-called Voronoi diagram (see page 1038) obtained in this way in two dimensions. Particularly in higher dimensions, it becomes rather difficult in practice to determine for certain which existing point is closest to some new point. But to do it approximately is considerably easier. One approach, illustrated in picture (b), is to use a ddimensional tree. Another approach, illustrated in picture (c), is to set up a continuous function with minima at the existing points, and then to search for the closest minimum. In most cases, this search will be done using some iterative scheme such as Newton's method; the result is that the boundaries between regions typically take on an intricate nested form. (The case shown corresponds to iteration of the map  $z \rightarrow z - (z^3 - 1)/(3z^2)$  corresponding to Newton's method for finding the complex roots of  $z^3 = 1$ .)



The pictures below show how one can build up a kind of memory landscape by successively adding points. In a first approximation, the regions considered similar to a particular minimum are delimited by sharp watersheds corresponding to local maxima in the landscape. But if an iterative scheme for minimization is used, these watersheds are typically no longer sharp, but take on a local nested structure, much as in picture (c) above.



In numbers earlier digits are traditionally considered more important than later ones, and this allows numbers to be arranged in a simple one-dimensional sequence. But in strings where each element is considered equally important, no such layout is possible. A vague approximation, perhaps useful for some applications, is nevertheless to use a spacefilling curve (see page 893).

• Error-correcting codes. In many information transmission and storage applications one needs to be able to recover data even if some errors are introduced into it. The standard way to do this is to set up an error-correcting code in which blocks of m original data elements are represented by a codeword of length *n* that in effect includes some redundant elements. Then-somewhat in analogy to retrieving closest memories—one can take a sequence of length n that one receives and find the codeword that differs from it in the fewest elements. If the codewords are chosen so that every pair differs by at least r elements (or equivalently, have socalled Hamming distance at least r), then this means that errors in up to Floor[(r - 1)/2] elements can be corrected, and finding suitable codewords is like finding packings of spheres in n-dimensional space. It is common in practice to use so-called linear codes which can be analyzed using algebraic methods, and for which the spheres are arranged in a repetitive array. The Hamming codes with  $n = 2^s - 1$ , m = n - s, r = 3 are an example, invented by Marcel Golay in 1949 and Richard Hamming in 1950. Defining

 $PM[s_] := IntegerDigits[Range[2^{s} - 1], 2, s]$ blocks of data of length *m* can be encoded with

Join[data, Mod[data. Select[PM[s], Count[#, 1] > 1 &], 2]] while blocks of length n (and at most one error) can be decoded with

Drop[(If[# == 0, data, MapAt[1 - # &, data, #]] &)[ FromDigits[Mod[data . PM[s], 2], 2]], -s]

A number of families of linear codes are known, together with a few nonlinear ones. But in all cases they tend to be based on rather special mathematical structures which do not seem likely to occur in any system like the brain.

• Matrix memories. Many times since the 1950s it has been noted that methods from linear algebra suggest ways to construct associative memories in which data can potentially be retrieved on the basis of some form of similarity. Typically one starts from some list of vectors to be stored, then forms a matrix such as m = PseudoInverse[list]. Given a new piece of data corresponding to a vector v, its decomposition in terms of stored vectors can be found by computing  $v \cdot m$ . And by applying various forms of thresholding one can often pick out at least approximately the stored vector closest to the piece of data given. But such schemes tend to be inefficient in practice, as well as presumably being unrealistic as actual models of the brain.

Neural network models. The basic rule used in essentially all neural network models is extremely simple. Each neuron is assumed to have a value between -1 and 1 corresponding roughly to a firing rate. Then given a list *s*[*i*] of the values of one set of neurons, one finds the values of another set using  $s[i+1] = u[w \cdot s[i]]$ , where in early models u = Sign was usually chosen, and now u = Tanh is more common, and w is a rectangular matrix which gives weights-normally assumed to be continuous numbers, often between -1 and +1-for the synaptic connections between the neurons in each set. In the simplest case, studied especially in the context of perceptrons in the 1960s, one has only two sets of neurons: an input layer and an output layer. But with suitable weights one can reproduce many functions. For example, with three inputs and one output,  $w = \{\{-1, +1, -1\}\}$  yields essentially the rule for the rule 178 elementary cellular automaton. But out of the  $2^{2^n}$  possible Boolean functions of ninputs, only 14 (out of 16) can be obtained for n = 2, 104 (out of 256) for *n* = 3, 1882 for *n* = 4, and 94304 for *n* = 5. (The VC dimension is n+1 for such systems.) The key idea that became popular in the early 1980s was to consider neural networks with an additional layer of "hidden units". By introducing enough hidden units it is then possible-just as in the formulas discussed on page 616-to reproduce essentially any function. Suitable weights (which are typically far from unique) are in practice usually found by gradient descent methods based either on minimization of deviations from desired outputs given particular inputs (supervised learning) or on maximization of some discrimination or other criterion (unsupervised learning).

Particularly in early investigations of neural networks, it was common to consider systems more like very simple cellular automata, in which the s[i] corresponded not to states of successive layers of neurons, but rather to states of the same set of neurons at successive times. For most choices of weights, such a system exhibits typical class 3 behavior and never settles down to give an obvious definite output. But in special circumstances probably not of great biological relevance it can yield class 2 behavior. An example studied by John Hopfield in 1981 is a symmetric matrix w with neuron values being updated sequentially in a random order rather than in parallel.

• Memory. Since the early 1900s it has been suspected that long-term memory is somehow encoded in the strengths of synaptic connections between nerve cells. It is known that at least in specific cases such strengths can remain unchanged for at least hours or more, but can immediately change if connected nerve cells have various patterns of simultaneous excitation. The changes that occur appear to be associated changes in ionic channels in cell membranes and sometimes with the addition of new synapses between cells.

Observations suggest that in humans there are several different types of memory, with somewhat different characteristics. (Examples include memory for facts and for motor skills.) Usually there is a short-term or so-called working component, lasting perhaps 30 seconds, and typically holding perhaps seven items, and a long-term component that can apparently last a lifetime. Specific parts of the brain (such as the hippocampus) appear necessary for the long-term component to form. In at least some cases there is evidence for specialized areas that handle particular types of memories. When new data is first presented, many parts of the brain are often active in processing it. But once the data has somehow been learned, only parts directly associated with handling it usually appear to be active.

Memories often seem at some level to be built up incrementally, as reflected in smooth learning curves for motor skills. It is not clear whether this is due to actual incremental changes in nerve cells or just to the filling in of progressively more cases that differ in detail.

Experiments on human learning suggest that a particular memory typically involves an association between components from several sensory systems, as well as emotional state.

When several incomplete examples of data are presented, there appears to be some commonality in the character of generalizations that we make. One mathematically convenient but probably unrealistic model studied in recent years in the context of computational learning theory involves building up minimal Boolean formulas consistent with the examples seen.

• Child development. As children get older their thinking becomes progressively more sophisticated, advancing through a series of fairly definite stages that appear to be associated with an increasing ability to handle generalization and abstraction. It is not clear whether this development is primarily associated with physiological changes or with the accumulation of more experiences (or, in effect, with the addition of more layers of software). Nor is it clear how it relates to the fact that the number of items that can be stored in short-term memory seems steadily to increase.

• **Computer interfaces.** The earliest computer interfaces were essentially just numerical. By the 1960s text-based interfaces were common, and in the decade following the introduction of the Macintosh in 1984 graphical interfaces based on menus and dialogs came to largely dominate consumer software. Such interfaces work well if what one wants is basically to take a

single object and apply operations to it. And they can be extended somewhat by using visual block diagrams or flowcharts. But whenever there is neither just a single active data element nor an obvious sequence of independent execution steps—as for many of the programs in this book—my experience has always been that the only viable choice of interface is a computer language like *Mathematica*, based essentially on one-dimensional sequences of word-like constructs. The rule diagrams in this book represent a possible new method for specifying some simpler programs, but it remains to be seen whether such diagrams can readily both be created incrementally by humans and interpreted by computer.

■ Page 627 · Structure of *Mathematica*. Beneath all the sophisticated capabilities of *Mathematica* lies a remarkably simple basic structure. The key idea is to represent data of any kind by a symbolic expression of the general form  $head[arg_1, arg_2, ...]$ .  $(a + b^2$  is thus Plus[a, Power[b, 2]],  $\{a, b, c\}$  is *List[a, b, c]* and a = b + 1 is Set[a, Plus[b, 1]].) The basic action of *Mathematica* is then to transform such expressions according to whatever rules it knows. Most often these rules are specified in terms of *Mathematica* patterns— expressions in which \_ can stand for any expression.

• **Context-free languages.** The set of valid expressions in a context-free language can be defined recursively by rules such as " $e" \rightarrow "e + e"$  and " $e" \rightarrow "(e)$ " that specify how one expression can be built up from sequences of literal objects or "tokens" and other expressions. (As discussed on page 939, the fact that the left-hand side contains nothing more than "e" is what makes the language context free.) To interpret or parse an expression in a context-free language one has to go backwards and find out which rules could be used to generate that expression. (For the built-in syntax of *Mathematica* this is achieved using *ToExpression*.)

It is convenient to think of expressions in a language as having forms such as s["(", "(", ")", ")"] with *Attributes*[*s*] = *Flat*. Then the rules for the language consisting of balanced runs of parentheses (see page 939) can be written as

 $\{s[e] \rightarrow s[e, e], s[e] \rightarrow s["(", e, ")"], s[e] \rightarrow s["(", ")"]\}$ Different expressions in the language can be obtained by applying different sequences of these rules, say using (this gives so-called leftmost derivations)

Fold[#1 /. rules[[#2]] &, s[e], list]

Given an expression, one can then use the following to find a list of rules that will generate it—if this exists:

 $\begin{array}{l} Parse[rules_, expr_] := Catch[Block[{t = {}}, NestWhile[ \\ ReplaceList[\#, MapIndexed[ReverseRule, rules]] \&, \\ { {expr, {}}, {} / {. {s[e], u_} } \rightarrow Throw[u]; \# =! = { } {. {s[;]}} \\ ReverseRule[a_ \rightarrow b_-, {i_-}] := { ____, {s[x_..., b, y_...], {u_...}}, \\ ____ } := { s[x, a, y], {i, u} ] /; FreeQ[s[x], s[a]] \\ \end{array}$ 

In general, there will in principle be more than one such list, and to pick the appropriate list in a practical situation one normally takes the rules of the language to apply with a certain precedence—which is how, for example, x + yz comes to be interpreted in *Mathematica* as Plus[x, Times[y, z]] rather than *Times[Plus[x, y], z]*. (Note that in practice the output from a parser for a context-free language is usually represented as a tree—as in *Mathematica FullForm*—with each node corresponding to one rule application.)

Given only the rules for a context-free language, it is often very difficult to find out the properties of the language (compare page 944). Indeed, determining even whether two sets of rules ultimately yield the same set of expressions is in general undecidable (see page 1138).

Languages. There are about 140 human languages and 15 full-fledged computer languages currently in use by a million people or more. Human languages typically have perhaps 50,000 reasonably common words; computer languages usually have a few hundred at most (Mathematica, however, has at least nominally somewhat over 1000). In expressing general human issues, different human languages tend to be largely equivalent-though they often differ when it comes to matters of special cultural or environmental interest to their users. Computer languages are also mostly equivalent in their handling of general programming issues-and indeed among widespread languages the only substantial exception is Mathematica, which supports symbolic, functional and pattern-based as well as procedural programming. Human languages have mostly evolved quite haphazardly over the course of many centuries, becoming sometimes simpler, sometimes more complicated. Computer languages are almost always specifically designed once and for all, usually by a single person. New human languages have sometimes been developed-a notable example being Esperanto in the 1890s-but for reasons largely of political history none have in practice become widely used.

Human languages always seem to have fairly definite rules for what is grammatically correct. And in a first approximation these rules can usually be thought of as specifying that every sentence must be constructed from various independent nested phrases, much as in a contextfree grammar (see above). But in any given language there are always many exceptions, and in the end it has proved essentially impossible to identify specific detailed features beyond for example the existence of nouns and verbs—that are convincingly universal across more than just languages with clear historical connections (such as the Indo-European ones). (One obvious general deviation from the context-free model is that in practice subordinate clauses can never be nested too deep if a sentence is expected to be understood.)

All the computer languages that are in widespread use today are based quite explicitly on context-free grammars. And even though the original motivation for this was typically ease of specification or implementation, I strongly suspect that it has also been critical in making it readily possible for people to learn such languages. For in my observation, exceptions to the context-free model are often what confuse users of computer languages the most-even when those users have never been exposed to computer languages before. And indeed the same seems to be true for traditional mathematical notation, where occasional deviations from the context-free model in fields like logic seem to make material particularly hard to read. (A notable feature that I was surprised to discover in designing Mathematica 3 is that users of mathematical notation seem to have a remarkably universal view of the precedence of different mathematical operators.)

The idea of describing languages by grammars dates back to antiquity (see page 875). And starting in the 1800s extensive studies were made of the comparative grammars of different languages. But the notion that grammars could be thought of like programs for generating languages did not emerge with clarity until the work of Noam Chomsky beginning in 1956. And following this, there were for a while many efforts to formulate precise models for human languages, and to relate these to properties of the brain. But by the 1980s it became clear—notably through the failure of attempts to automate natural language understanding and translation—that language cannot in most cases (with the possible exception of grammar-checking software) meaningfully be isolated from other aspects of human thinking.

Computer languages emerged in the early 1950s as higherlevel alternatives to programming directly in machine code. FORTRAN was developed in 1954 with a syntax intended as a simple idealization of mathematical notation. And in 1958, as part of the ALGOL project, John Backus used the idea of production systems from mathematical logic (see page 1150) to set up a recursive specification equivalent to a context-free grammar. A few deviations from this approach were tried notably in LISP and APL—but by the 1970s, following the development of automated compiler generators such as yacc, so-called Backus-Naur context-free specifications for computer languages had become quite standard. (A practical enhancement to this was the introduction of twodimensional grammar in *Mathematica* 3 in 1996.)

• Page 631 · Computer language fluency. It is common that when one knows a human language sufficiently well, one

feels that one can readily "think in that language". In my experience the same is eventually true with computer languages. In particular, after many years of using *Mathematica*, I have now got to the point where I can effectively think directly in *Mathematica*, so that I can start entering a *Mathematica* program even though I may be a long way from being able to explain in English what I want to do.

• **Brainteasers.** In many puzzles and IQ tests the setup is to give a few elements in some sequence of numbers, strings or pictures, then to ask what the next element would be. The correct answer is normally assumed to be the one that in a sense allows the simplest description of all the data. But despite attempts to remove cultural and other biases such questions in practice seem almost always to rely on being able to retrieve from memory various specific forms and transformations. And I strongly suspect that if one were, for example, to construct similar questions using outputs from many of the simple programs I discuss in this book then unless one had studied almost exactly the cases of such programs used one would never manage to work out the answers.

• Human generation of randomness. If asked to type a random sequence of 0's and 1's, most people will at first produce a sequence with too many alternations between 0 and 1. But with modest learning time my experience is that one can generate sequences with quite good randomness.

Game theory. Remarkably simple models are often believed to capture features of what might seem like sophisticated decision making by humans, animals and human organizations. A particular case on which many studies have been done is the so-called iterated Prisoner's Dilemma, in which two players make a sequence of choices a and b to "cooperate" (1) or "defect" (2), each trying to maximize their score m[[a, b]] with  $m = \{\{1, -1\}, \{2, 0\}\}$ . At a single step, standard static game theory from the 1940s implies that a player should always defect, but in the 1960s a folk theorem emerged that if a whole sequence of steps is considered then a possible strategy for perfectly rational players is always to cooperate-in apparent agreement with some observations on human and animal behavior. In 1979 Robert Axelrod tried setting up computer programs as players and found that in tournaments between them the winner was often a simple "tit-for-tat" program that cooperates on the first step, then on subsequent steps just does whatever its opponent did on the previous step. The same winner was also often obtained by natural selectiona fact widely taken to explain cooperation phenomena in evolutionary biology and the social sciences. In the late 1980s similar studies were done on processes such as auctions (cf page 1015), and in the late 1990s on games such as Rock, Paper, Scissors (RoShamBo) (with  $m = \{\{0, -1, 1\}, \{1, 0, -1\}, \{-1, 1, 0\}\}$  (A simpler game certainly played since antiquity-is Penny Matching or Evens and Odds, with  $m = \{\{1, -1\}, \{-1, 1\}\}\}$ .) But even though they seemed to capture or better actual human behavior, the programs considered in all these cases typically just used standard statistical or Markov model methods, or matching of specific sequences-making them far too weak to make predictions about the kinds of complex behavior shown in this book. (Note that a program can always win the games above if it can in effect successfully predict each move its opponent will make. In a game between two arbitrary programs it can be undecidable which will win more often over the course of an infinite number of moves.)

• Games between programs. One can set up a game between two programs generating single bits of output by for example taking the input at each step to be the concatenation of the historical sequences of outputs from the two programs. The pictures below show what happens if the programs operate by applying elementary cellular automaton rules t times to 2t + 1 inputs. The plots on the left show cumulative scores in the Evens and Odds game; the array on the right indicates for each of the 256 possible rules the average number of wins it gets against each of the 256 rules. At some level considerable complexity is evident. But the rules that win most often typically seem to do so in rather simple ways.

					)	rules	255
30 vs. 90	30 vs. 91	30 vs. 92	30 vs. 93	0			
31 vs. 90	31 vs. 91	31 vs. 92	31 vs. 93				
32 vs. 90	32 vs. 91	32 vs. 92	32 vs. 93				
<u>33 vs. 90</u>	33 vs. 91	33 vs. 92	33 vs. 93				C.R.
34 vs. 90	34 vs. 91	_34 vs. 92	_34 vs. 93				
35 vs. 90	35 vs. 91	35 vs. 92	35 vs. 93		-		
36 vs. 90	36 vs. 91	36 vs. 92	36 vs. 93				

#### Higher Forms of Perception and Analysis

• Biological perception. Animals can process data not only from visual or auditory sources (as discussed on pages 577 and 585), but also from mechanical, thermal, chemical and other sources. Usually special receptors for each type of data convert it into electrical impulses in nerve cells. Mechanical and thermal data are often mapped onto an array of nerve cells in the brain, from which features are extracted similar to those in visual perception. Taste involves data from solids

and liquids; smell data from gases. The human tongue has millions of taste buds scattered on its surface, each with many tens of nerve cells. Rather little is currently known about how taste data is processed, and it is not even clear whether the traditional notion that there are just four or so primary tastes is correct. The human nose has several tens of millions of receptors, apparently broken into a few hundred distinct types. Each of these types probably has proteins that form pockets with definite shapes, making it respond to molecules whose shapes fit into these pockets. People typically distinguish a few thousand odors, presumably by comparing responses of different receptor types. (Foods usually contain tens of distinct odors; manufactured scents hundreds.) There is evidence that at the first level of processing in the brain all receptors of a given type excite nerve cells that lie in the same spatial region. But just how different regions are laid out is not clear, and may well differ between individuals. Polymers whose lengths differ by more than one or two repeating units often seem to smell different, and it is conceivable that elaborate general features of shapes of molecules can be perceived. But more likely there is no way to build up sophisticated taste or smell data-and no analog of any properties such as repetition or nesting.

■ Page 634 · Evolving to predict. If one thinks that biological evolution is infinitely powerful one might imagine that by emulating it one would always be able to find ways to predict any sequence of data. But in practice methods based, for example, on genetic programming seem to do at best only about as well as all sorts of other methods discussed in this chapter. And typically what limits them seems to be much the same as I argue in Chapter 8 limits actual biological evolution: that incremental changes are difficult to make except when the behavior is fairly simple. (See also page 985.)

It is common for animals to move in apparently random ways when they are trying to avoid predators. Yet I suspect that the randomness they use is often generated by quite simple rules (see page 1011)—so that in principle it could be predictable. So it is then notable that biological evolution has apparently never made predators able to catch their prey by predicting anything that looks to us particularly random; instead strategies tend to be based on tricks that do not require predicting more than at most repetition.

Page 635 · Familiar features. What makes features familiar to us is that they are common in our typical environment and are readily recognized by our built-in human powers of perception. In the distant past humans were presumably exposed only to features generated by ordinary natural

processes. But ever since the dawn of civilization humans have increasingly been exposed to things that were explicitly constructed through engineering, architecture, art, mathematics and other human activities. And indeed as human knowledge and culture have progressed, humans have ended up being exposed to new kinds of features. For example, while repetition has been much emphasized for several millennia, it is only in the past couple of decades that precise nesting has had much emphasis. So this may make one wonder what features will be emphasized in the future. The vast majority of forms created by humans in the past say in art or architecture—have had basic features that are either directly copied from systems in nature, or are in effect built up by using extremely simple kinds of rules. On the basis of the discoveries in this book I thus tend to suspect that almost any feature that might end up becoming emphasized in the future will already be present—and probably even be fairly common—in the behavior of the kinds of simple programs that I have discussed in this book. (When future technology is routinely able to interact with individual atoms there will presumably quickly be a new class of quantum and other features that become familiar.)

• Relativism and postmodernism. See pages 1131 and 1196.