Complexity and Computation

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Preface

This book is about data structures and algorithms, intermediate programming in Python, computational modeling and the philosophy of science:

Data structures and algorithms: A data structure is a collection of data elements organized in a way that supports particular operations. For example, a Python dictionary organizes key-value pairs in a way that provides fast mapping from keys to values, but mapping from values to keys is slower.

An algorithm is a mechanical process for performing a computation. Designing efficient programs often involves the co-evolution of data structures and the algorithms that use them. For example, in the first few chapters I will present graphs, data structures that implement graphs, and graph algorithms based on those data structures.

Python programming: This book picks up where *Think Python* leaves off. I assume that you have read that book or have equivalent knowledge of Python. I try to emphasize fundamental ideas that apply to programming in many languages, but along the way you will learn some useful features that are specific to Python.

Computational modeling: A model of a system is a simplified description of a system used for simulation or analysis. Computational models are designed to take advantage of cheap, fast computation.

Philosophy of science: The models and results in this book raise questions relevant to the philosophy of science, including the nature of scientific laws, theory choice, realism and instrumentalism, holism and reductionism, and epistemology.

There are two kinds of computational models:

Continuous: Many computational models compute approximate solutions to equations that are continuous in space and time. For example, to compute the trajectory of a planet, you could describe planetary motion using differential equations and then compute the position of the planet at discrete points in time.

The fields of numerical methods and scientific computing tend to focus on these kinds of models.

Discrete: Discrete models include graphs, cellular automata, and agent-based models. They are often characterized by structure, rules and transitions rather than by equations. They tend to be more abstract than continuous models; in some cases there is no direct correspondence between the model and a physical system.

Complexity science is an interdisciplinary field—at the intersection of mathematics, computer science and natural science—that focuses on discrete models of physical systems.

And that's what this book is about.

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Contributor List

If you have a suggestion or correction, please send email to `downey@greenteapress.com`. If I make a change based on your feedback, I will add you to the contributor list (unless you ask to be omitted).

If you include at least part of the sentence the error appears in, that makes it easy for me to search. Page and section numbers are fine, too, but not quite as easy to work with. Thanks!

- Richard Hollands pointed out several typos.
- John Harley, Jeff Stanton, Colden Rouleau and Keerthik Omanakuttan are Computational Modeling students who pointed out typos.
- Muhammad Najmi bin Ahmad Zabidi caught some typos.
- Phillip Loh, Corey Dolphin, Noam Rubin and Julian Ceipek found typos and made helpful suggestions.
- Jose Oscar Mur-Miranda found several typos.

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Chapter 1

Graphs

1.1 What's a graph?

To most people a graph is a visual representation of a data set, like a bar chart or an EKG. That's not what this chapter is about.

In this chapter, a **graph** is an abstraction used to model a system that contains discrete, interconnected elements. The elements are represented by **nodes** (also called **vertices**) and the interconnections are represented by **edges**.

For example, you could represent a road map with one node for each city and one edge for each road between cities. Or you could represent a social network using one node for each person, with an edge between two people if they are "friends" and no edge otherwise.

In some graphs, edges have different lengths (sometimes called "weights" or "costs"). For example, in a road map, the length of an edge might represent the distance between two cities, or the travel time, or bus fare. In a social network there might be different kinds of edges to represent different kinds of relationships: friends, business associates, etc.

Edges may be **undirected**, if they represent a relationship that is symmetric, or **directed**. In a social network, friendship is usually symmetric: if A is friends with B then B is friends with A. So you would probably represent friendship with an undirected edge. In a road map, you would probably represent a one-way street with a directed edge.

Graphs have interesting mathematical properties, and there is a branch of mathematics called **graph theory** that studies them.

Graphs are also useful, because there are many real world problems that can be solved using **graph algorithms**. For example, Dijkstra's shortest path algorithm is an efficient way to find the shortest path from a node to all other nodes in a graph. A **path** is a sequence of nodes with an edge between each consecutive pair.

Sometimes the connection between a real world problem and a graph algorithm is obvious. In the road map example, it is not hard to imagine using a shortest path algorithm to find the route between two cities that minimizes distance (or time, or cost).

In other cases it takes more effort to represent a problem in a form that can be solved with a graph algorithm, and then interpret the solution.

For example, a complex system of radioactive decay can be represented by a graph with one node for each nuclide (type of atom) and an edge between two nuclides if one can decay into the other. A path in this graph represents a decay chain. See `wikipedia.org/wiki/Radioactive_decay`.

The rate of decay between two nuclides is characterized by a decay constant, λ, measured in becquerels (Bq) or decay events per second. You might be more familiar with half-life, $t_{1/2}$, which is the expected time until half of a sample decays. You can convert from one characterization to the other using the relation $t_{1/2} = \ln 2/\lambda$.

In our best current model of physics, nuclear decay is a fundamentally random process, so it is impossible to predict when an atom will decay. However, given λ, the probability that an atom will decay during a short time interval dt is λdt.

In a graph with multiple decay chains, the probability of a given path is the product of the probabilities of each decay process in the path.

Now suppose you want to find the decay chain with the highest probability. You could do it by assigning each edge a "length" of $-\log \lambda$ and using a shortest path algorithm. Why? Because the shortest path algorithm adds up the lengths of the edges, and adding up log-probabilities is the same as multiplying probabilities. Also, because the logarithms are negated, the smallest sum corresponds to the largest probability. So the shortest path corresponds to the most likely decay chain.

This is an example of a common and useful process in applying graph algorithms:

Reduce a real-world problem to an instance of a graph problem.

Apply a graph algorithm to compute the result efficiently.

Interpret the result of the computation in terms of a solution to the original problem.

We will see other examples of this process soon.

Exercise 1.1 Read the Wikipedia page about graphs at `http://en.wikipedia.org/wiki/Graph_(mathematics)` and answer the following questions:

1. What is a simple graph? In the rest of this section, we will be assuming that all graphs are simple graphs. This is a common assumption for many graph algorithms—so common it is often unstated.

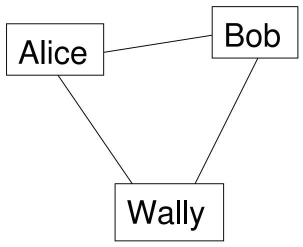
2. What is a regular graph? What is a complete graph? Prove that a complete graph is regular.

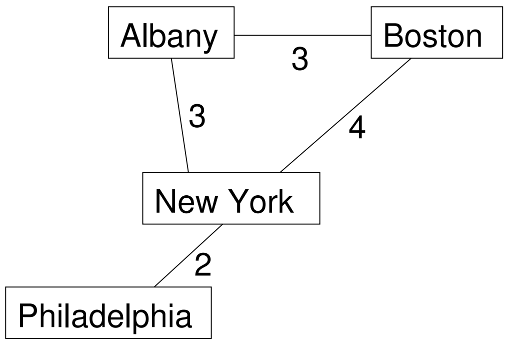
3. What is a path? What is a cycle?

4. What is a forest? What is a tree? Note: a graph is **connected** if there is a path from every node to every other node.

1.2 Representing graphs

Graphs are usually drawn with squares or circles for nodes and lines for edges. In the example below, the graph on the left represents a social network with three people.





In the graph on the right, the weights of the edges are the approximate travel times, in hours, between cities in the northeast United States. In this case the placement of the nodes corresponds roughly to the geography of the cities, but in general the layout of a graph is arbitrary.

To implement graph algorithms, you have to figure out how to represent a graph in the form of a data structure. But to choose the best data structure, you have to know which operations the graph should support.

To get out of this chicken-and-egg problem, I am going to present a data structure that is a good choice for many graph algorithms. Later we will come back and evaluate its pros and cons.

Here is an implementation of a graph as a dictionary of dictionaries:

```
class Graph(dict):
    def __init__(self, vs=[], es=[]):
        """create a new graph.  (vs) is a list of vertices;
        (es) is a list of edges."""
        for v in vs:
            self.add_vertex(v)

        for e in es:
            self.add_edge(e)

    def add_vertex(self, v):
        """add (v) to the graph"""
        self[v] = {}

    def add_edge(self, e):
        """add (e) to the graph by adding an entry in both directions.

        If there is already an edge connecting these Vertices, the
        new edge replaces it.
        """
        v, w = e
        self[v][w] = e
        self[w][v] = e
```

The first line declares that `Graph` inherits from the built-in type `dict`, so a Graph object has all the methods and operators of a dictionary.

More specifically, a Graph is a dictionary that maps from a Vertex v to an inner dictionary that maps from a Vertex w to an Edge that connects v and w. So if `g` is a graph, `g[v][w]` maps to an Edge if there is one and raises a `KeyError` otherwise.

`__init__` takes a list of vertices and a list of edges as optional parameters. If they are provided, it calls `add_vertex` and `add_edge` to add the vertices and edges to the graph.

Adding a vertex to a graph means making an entry for it in the outer dictionary. Adding an edge makes two entries, both pointing to the same Edge. So this implementation represents an undirected graph.

Here is the definition for `Vertex`:

```
class Vertex(object):
    def __init__(self, label=''):
        self.label = label

    def __repr__(self):
        return 'Vertex(%s)' % repr(self.label)

    __str__ = __repr__
```

A Vertex is just an object that has a label attribute. We can add attributes later, as needed.

`__repr__` is a special function that returns a string representation of an object. It is similar to `__str__` except that the return value from `__str__` is intended to be readable for people, and the return value from `__repr__` is supposed to be a legal Python expression.

The built-in function `str` invokes `__str__` on an object; similarly the built-in function `repr` invokes `__repr__`.

In this case `Vertex.__str__` and `Vertex.__repr__` refer to the same function, so we get the same string either way.

Here is the definition for `Edge`:

```
class Edge(tuple):
    def __new__(cls, *vs):
        return tuple.__new__(cls, vs)

    def __repr__(self):
        return 'Edge(%s, %s)' % (repr(self[0]), repr(self[1]))

    __str__ = __repr__
```

`Edge` inherits from the built-in type `tuple` and overrides the `__new__` method. When you invoke an object constructor, Python invokes `__new__` to create the object and then `__init__` to initialize the attributes.

For mutable objects it is most common to override `__init__` and use the default implementation of `__new__`, but because Edges inherit from `tuple`, they are immutable, which means that you can't modify the elements of the tuple in `__init__`.

By overriding `__new__`, we can use the `*` operator to gather the parameters and use them to initialize the elements of the tuple. A precondition of this method is that there should be exactly two arguments. A more careful implementation would check.

Here is an example that creates two vertices and an edge:

```
    v = Vertex('v')
    w = Vertex('w')
    e = Edge(v, w)
    print e
```

Inside `Edge.__str__` the term `self[0]` refers to `v` and `self[1]` refers to `w`. So the output when you print `e` is:

```
Edge(Vertex('v'), Vertex('w'))
```

Now we can assemble the edge and vertices into a graph:

```
    g = Graph([v, w], [e])
    print g
```

The output looks like this (with a little formatting):

```
{Vertex('w'): {Vertex('v'): Edge(Vertex('v'), Vertex('w'))},
 Vertex('v'): {Vertex('w'): Edge(Vertex('v'), Vertex('w'))}}
```

We didn't have to write `Graph.__str__`; it is inherited from `dict`.

Exercise 1.2 In this exercise you write methods that will be useful for many of the Graph algorithms that are coming up.

1. Download `thinkcomplex.com/GraphCode.py`, which contains the code in this chapter. Run it as a script and make sure the test code in `main` does what you expect.
2. Make a copy of `GraphCode.py` called `Graph.py`. Add the following methods to `Graph`, adding test code as you go.
3. Write a method named `get_edge` that takes two vertices and returns the edge between them if it exists and `None` otherwise. Hint: use a `try` statement.
4. Write a method named `remove_edge` that takes an edge and removes all references to it from the graph.
5. Write a method named `vertices` that returns a list of the vertices in a graph.
6. Write a method named `edges` that returns a list of edges in a graph. Note that in our representation of an undirected graph there are two references to each edge.
7. Write a method named `out_vertices` that takes a Vertex and returns a list of the adjacent vertices (the ones connected to the given node by an edge).

8. Write a method named `out_edges` that takes a Vertex and returns a list of edges connected to the given Vertex.
9. Write a method named `add_all_edges` that starts with an edgeless Graph and makes a complete graph by adding edges between all pairs of vertices.

Test your methods by writing test code and checking the output. Then download `thinkcomplex.com/GraphWorld.py`. GraphWorld is a simple tool for generating visual representations of graphs. It is based on the World class in Swampy, so you might have to install Swampy first: see `thinkpython.com/swampy`.

Read through `GraphWorld.py` to get a sense of how it works. Then run it. It should import your `Graph.py` and then display a complete graph with 10 vertices.

Exercise 1.3 Write a method named `add_regular_edges` that starts with an edgeless graph and adds edges so that every vertex has the same degree. The **degree** of a node is the number of edges it is connected to.

To create a regular graph with degree 2 you would do something like this:

```
vertices = [ ... list of Vertices ... ]
g = Graph(vertices, [])
g.add_regular_edges(2)
```

It is not always possible to create a regular graph with a given degree, so you should figure out and document the preconditions for this method.

To test your code, you might want to create a file named `GraphTest.py` that imports `Graph.py` and `GraphWorld.py`, then generates and displays the graphs you want to test.

1.3 Random graphs

A random graph is just what it sounds like: a graph with edges generated at random. Of course, there are many random processes that can generate graphs, so there are many kinds of random graphs. One interesting kind is the Erdős-Rényi model, denoted $G(n, p)$, which generates graphs with n nodes, where the probability is p that there is an edge between any two nodes. See `http://en.wikipedia.org/wiki/Erdos-Renyi_model`.

Exercise 1.4 Create a file named `RandomGraph.py` and define a class named `RandomGraph` that inherits from `Graph` and provides a method named `add_random_edges` that takes a probability `p` as a parameter and, starting with an edgeless graph, adds edges at random so that the probability is p that there is an edge between any two nodes.

1.4 Connected graphs

A graph is **connected** if there is a path from every node to every other node. See `wikipedia.org/wiki/Connectivity_(graph_theory)`.

There is a simple algorithm to check whether a graph is connected. Start at any vertex and conduct a search (usually a breadth-first-search or BFS), marking all the vertices you can reach. Then check to see whether all vertices are marked.

You can read about breadth-first-search at `wikipedia.org/wiki/Breadth-first_search`.

In general, when you process a node, we say that you are **visiting** it.

In a search, you visit a node by marking it (so you can tell later that it has been visited) then visiting any unmarked vertices it is connected to.

In a breadth-first-search, you visit nodes in the order they are discovered. You can use a queue or a "worklist" to keep them in order. Here's how it works:

1. Start with any vertex and add it to the queue.
2. Remove a vertex from the queue and mark it. If it is connected to any unmarked vertices, add them to the queue.
3. If the queue is not empty, go back to Step 2.

Exercise 1.5 Write a Graph method named `is_connected` that returns `True` if the Graph is connected and `False` otherwise.

1.5 Paul Erdős: peripatetic mathematician, speed freak

Paul Erdős was a Hungarian mathematician who spent most of his career (from 1934 until his death in 1992) living out of a suitcase, visiting colleagues at universities all over the world, and authoring papers with more than 500 collaborators.

He was a notorious caffeine addict and, for the last 20 years of his life, an enthusiastic user of amphetamines. He attributed at least some of his productivity to the use of these drugs; after giving them up for a month to win a bet, he complained that the only result was that mathematics had been set back by a month[1].

In the 1960s he and Afréd Rényi wrote a series of papers introducing the Erdős-Rényi model of random graphs and studying their properties.

One of their most surprising results is the existence of abrupt changes in the characteristics of random graphs as random edges are added. They showed that for a number of graph properties there is a threshold value of the probability p below which is the property is rare and above which it is almost certain. This transition is sometimes called a "phase change" by analogy with physical systems that change state at some critical value of temperature. See `wikipedia.org/wiki/Phase_transition`.

Exercise 1.6 One of the properties that displays this kind of transition is connectedness. For a given size n, there is a critical value, p^*, such that a random graph $G(n, p)$ is unlikely to be connected if $p < p^*$ and very likely to be connected if $p > p^*$.

Write a program that tests this result by generating random graphs for values of n and p and computes the fraction of them that are connected.

How does the abruptness of the transition depend on n?

You can download my solution from `thinkcomplex.com/RandomGraph.py`.

[1]Much of this biography follows `wikipedia.org/wiki/Paul_Erdos`

1.6 Iterators

If you have read the documentation of Python dictionaries, you might have noticed the methods `iterkeys`, `itervalues` and `iteritems`. These methods are similar to `keys`, `values` and `items`, except that instead of building a new list, they return iterators.

An **iterator** is an object that provides a method named `next` that returns the next element in a sequence. Here is an example that creates a dictionary and uses `iterkeys` to traverse the keys.

```
>>> d = dict(a=1, b=2)
>>> iter = d.iterkeys()
>>> print iter.next()
a
>>> print iter.next()
b
>>> print iter.next()
Traceback (most recent call last):
  File "<stdin>", line 1, in <module>
StopIteration
```

The first time `next` is invoked, it returns the first key from the dictionary (the order of the keys is arbitrary). The second time it is invoked, it returns the second element. The third time, and every time thereafter, it raises a `StopIteration` exception.

An iterator can be used in a `for` loop; for example, the following is a common idiom for traversing the key-value pairs in a dictionary:

```
    for k, v in d.iteritems():
        print k, v
```

In this context, `iteritems` is likely to be faster than `items` because it doesn't have to build the entire list of tuples; it reads them from the dictionary as it goes along.

But it is only safe to use the iterator methods if you do not add or remove dictionary keys inside the loop. Otherwise you get an exception:

```
>>> d = dict(a=1)
>>> for k in d.iterkeys():
...     d['b'] = 2
...
RuntimeError: dictionary changed size during iteration
```

Another limitation of iterators is that they do not support index operations.

```
>>> iter = d.iterkeys()
>>> print iter[1]
TypeError: 'dictionary-keyiterator' object is unsubscriptable
```

If you need indexed access, you should use `keys`. Alternatively, the Python module `itertools` provides many useful iterator functions.

A user-defined object can be used as an iterator if it provides methods named `next` and `__iter__`. The following example is an iterator that always returns `True`:

```
class AllTrue(object):
    def next(self):
        return True

    def __iter__(self):
        return self
```

The `__iter__` method for iterators returns the iterator itself. This protocol makes it possible to use iterators and sequences interchangeably in many contexts.

Iterators like `AllTrue` can represent an infinite sequence. They are useful as an argument to `zip`:

```
>>> print zip('abc', AllTrue())
[('a', True), ('b', True), ('c', True)]
```

1.7 Generators

For many purposes the easiest way to make an iterator is to write a **generator**, which is a function that contains a `yield` statement. `yield` is similar to `return`, except that the state of the running function is stored and can be resumed.

For example, here is a generator that yields successive letters of the alphabet:

```
def generate_letters():
    for letter in 'abc':
        yield letter
```

When you call this function, the return value is an iterator:

```
>>> iter = generate_letters()
>>> print iter
<generator object at 0xb7d4ce4c>
>>> print iter.next()
a
>>> print iter.next()
b
```

And you can use an iterator in a `for` loop:

```
>>> for letter in generate_letters():
...     print letter
...
a
b
c
```

A generator with an infinite loop returns an iterator that never terminates. For example, here's a generator that cycles through the letters of the alphabet:

```
def alphabet_cycle():
    while True:
        for c in string.lowercase:
            yield c
```

Exercise 1.7 Write a generator that yields an infinite sequence of alpha-numeric identifiers, starting with `a1` through `z1`, then `a2` through `z2`, and so on.

Chapter 2

Analysis of algorithms

Analysis of algorithms is the branch of computer science that studies the performance of algorithms, especially their run time and space requirements. See `wikipedia.org/wiki/Analysis_of_algorithms`.

The practical goal of algorithm analysis is to predict the performance of different algorithms in order to guide design decisions.

During the 2008 United States Presidential Campaign, candidate Barack Obama was asked to perform an impromptu analysis when he visited Google. Chief executive Eric Schmidt jokingly asked him for "the most efficient way to sort a million 32-bit integers." Obama had apparently been tipped off, because he quickly replied, "I think the bubble sort would be the wrong way to go." See `http://www.youtube.com/watch?v=k4RRi_ntQc8`.

This is true: bubble sort is conceptually simple but slow for large datasets. The answer Schmidt was probably looking for is "radix sort" (see `wikipedia.org/wiki/Radix_sort`)[1].

So the goal of algorithm analysis is to make meaningful comparisons between algorithms, but there are some problems:

- The relative performance of the algorithms might depend on characteristics of the hardware, so one algorithm might be faster on Machine A, another on Machine B. The general solution to this problem is to specify a **machine model** and analyze the number of steps, or operations, an algorithm requires under a given model.
- Relative performance might depend on the details of the dataset. For example, some sorting algorithms run faster if the data are already partially sorted; other algorithms run slower in this case. A common way to avoid this problem is to analyze the **worst case** scenario. It is also sometimes useful to analyze average case performance, but it is usually harder, and sometimes it is not clear what set of cases to average over.

[1]But if you get a question like this in an interview, I think a better answer is, "The fastest way to sort a million integers is to use whatever sort function is provided by the language I'm using. Its performance is good enough for the vast majority of applications, but if it turned out that my application was too slow, I would use a profiler to see where the time was being spent. If it looked like a faster sort algorithm would have a significant effect on performance, then I would look around for a good implementation of radix sort."

- Relative performance also depends on the size of the problem. A sorting algorithm that is fast for small lists might be slow for long lists. The usual solution to this problem is to express run time (or number of operations) as a function of problem size, and to compare the functions **asymptotically** as the problem size increases.

The good thing about this kind of comparison that it lends itself to simple classification of algorithms. For example, if I know that the run time of Algorithm A tends to be proportional to the size of the input, n, and Algorithm B tends to be proportional to n^2, then I expect A to be faster than B for large values of n.

This kind of analysis comes with some caveats, but we'll get to that later.

2.1 Order of growth

Suppose you have analyzed two algorithms and expressed their run times in terms of the size of the input: Algorithm A takes $100n + 1$ steps to solve a problem with size n; Algorithm B takes $n^2 + n + 1$ steps.

The following table shows the run time of these algorithms for different problem sizes:

Input size	Run time of Algorithm A	Run time of Algorithm B
10	1 001	111
100	10 001	10 101
1 000	100 001	1 001 001
10 000	1 000 001	$> 10^{10}$

At $n = 10$, Algorithm A looks pretty bad; it takes almost 10 times longer than Algorithm B. But for $n = 100$ they are about the same, and for larger values A is much better.

The fundamental reason is that for large values of n, any function that contains an n^2 term will grow faster than a function whose leading term is n. The **leading term** is the term with the highest exponent.

For Algorithm A, the leading term has a large coefficient, 100, which is why B does better than A for small n. But regardless of the coefficients, there will always be some value of n where $an^2 > bn$.

The same argument applies to the non-leading terms. Even if the run time of Algorithm A were $n + 1000000$, it would still be better than Algorithm B for sufficiently large n.

In general, we expect an algorithm with a smaller leading term to be a better algorithm for large problems, but for smaller problems, there may be a **crossover point** where another algorithm is better. The location of the crossover point depends on the details of the algorithms, the inputs, and the hardware, so it is usually ignored for purposes of algorithmic analysis. But that doesn't mean you can forget about it.

If two algorithms have the same leading order term, it is hard to say which is better; again, the answer depends on the details. So for algorithmic analysis, functions with the same leading term are considered equivalent, even if they have different coefficients.

An **order of growth** is a set of functions whose asymptotic growth behavior is considered equivalent. For example, $2n$, $100n$ and $n+1$ belong to the same order of growth, which is written $O(n)$ in **Big-Oh notation** and often called **linear** because every function in the set grows linearly with n.

All functions with the leading term n^2 belong to $O(n^2)$; they are **quadratic**, which is a fancy word for functions with the leading term n^2.

The following table shows some of the orders of growth that appear most commonly in algorithmic analysis, in increasing order of badness.

Order of growth	Name
$O(1)$	constant
$O(\log_b n)$	logarithmic (for any b)
$O(n)$	linear
$O(n \log_b n)$	"en log en"
$O(n^2)$	quadratic
$O(n^3)$	cubic
$O(c^n)$	exponential (for any c)

For the logarithmic terms, the base of the logarithm doesn't matter; changing bases is the equivalent of multiplying by a constant, which doesn't change the order of growth. Similarly, all exponential functions belong to the same order of growth regardless of the base of the exponent. Exponential functions grow very quickly, so exponential algorithms are only useful for small problems.

Exercise 2.1 Read the Wikipedia page on Big-Oh notation at `wikipedia.org/wiki/Big_O_notation` and answer the following questions:

1. What is the order of growth of $n^3 + n^2$? What about $1000000n^3 + n^2$? What about $n^3 + 1000000n^2$?
2. What is the order of growth of $(n^2 + n) \cdot (n + 1)$? Before you start multiplying, remember that you only need the leading term.
3. If f is in $O(g)$, for some unspecified function g, what can we say about $af + b$?
4. If f_1 and f_2 are in $O(g)$, what can we say about $f_1 + f_2$?
5. If f_1 is in $O(g)$ and f_2 is in $O(h)$, what can we say about $f_1 + f_2$?
6. If f_1 is in $O(g)$ and f_2 is $O(h)$, what can we say about $f_1 * f_2$?

Programmers who care about performance often find this kind of analysis hard to swallow. They have a point: sometimes the coefficients and the non-leading terms make a real difference. And sometimes the details of the hardware, the programming language, and the characteristics of the input make a big difference. And for small problems asymptotic behavior is irrelevant.

But if you keep those caveats in mind, algorithmic analysis is a useful tool. At least for large problems, the "better" algorithms is usually better, and sometimes it is *much* better. The difference between two algorithms with the same order of growth is usually a constant factor, but the difference between a good algorithm and a bad algorithm is unbounded!

2.2 Analysis of basic operations

Most arithmetic operations are constant time; multiplication usually takes longer than addition and subtraction, and division takes even longer, but these run times don't depend on the magnitude of the operands. Very large integers are an exception; in that case the run time increases linearly with the number of digits.

Indexing operations—reading or writing elements in a sequence or dictionary—are also constant time, regardless of the size of the data structure.

A `for` loop that traverses a sequence or dictionary is usually linear, as long as all of the operations in the body of the loop are constant time. For example, adding up the elements of a list is linear:

```
total = 0
for x in t:
    total += x
```

The built-in function `sum` is also linear because it does the same thing, but it tends to be faster because it is a more efficient implementation; in the language of algorithmic analysis, it has a smaller leading coefficient.

If you use the same loop to "add" a list of strings, the run time is quadratic because string concatenation is linear.

The string method `join` is usually faster because it is linear in the total length of the strings.

As a rule of thumb, if the body of a loop is in $O(n^a)$ then the whole loop is in $O(n^{a+1})$. The exception is if you can show that the loop exits after a constant number of iterations. If a loop runs k times regardless of n, then the loop is in $O(n^a)$, even for large k.

Multiplying by k doesn't change the order of growth, but neither does dividing. So if the body of a loop is in $O(n^a)$ and it runs n/k times, the loop is in $O(n^{a+1})$, even for large k.

Most string and tuple operations are linear, except indexing and `len`, which are constant time. The built-in functions `min` and `max` are linear. The run-time of a slice operation is proportional to the length of the output, but independent of the size of the input.

All string methods are linear, but if the lengths of the strings are bounded by a constant—for example, operations on single characters—they are considered constant time.

Most list methods are linear, but there are some exceptions:

- Adding an element to the end of a list is constant time on average; when it runs out of room it occasionally gets copied to a bigger location, but the total time for n operations is $O(n)$, so we say that the "amortized" time for one operation is $O(1)$.
- Removing an element from the end of a list is constant time.
- Sorting is $O(n \log n)$.

Most dictionary operations and methods are constant time, but there are some exceptions:

- The run time of `copy` is proportional to the number of elements, but not the size of the elements (it copies references, not the elements themselves).
- The run time of `update` is proportional to the size of the dictionary passed as a parameter, not the dictionary being updated.
- `keys`, `values` and `items` are linear because they return new lists; `iterkeys`, `itervalues` and `iteritems` are constant time because they return iterators. But if you loop through the iterators, the loop will be linear. Using the "iter" functions saves some overhead, but it doesn't change the order of growth unless the number of items you access is bounded.

The performance of dictionaries is one of the minor miracles of computer science. We will see how they work in Section 2.4.

Exercise 2.2 Read the Wikipedia page on sorting algorithms at `wikipedia.org/wiki/Sorting_algorithm` and answer the following questions:

1. What is a "comparison sort?" What is the best worst-case order of growth for a comparison sort? What is the best worst-case order of growth for any sort algorithm?
2. What is the order of growth of bubble sort, and why does Barack Obama think it is "the wrong way to go?"
3. What is the order of growth of radix sort? What preconditions do we need to use it?
4. What is a stable sort and why might it matter in practice?
5. What is the worst sorting algorithm (that has a name)?
6. What sort algorithm does the C library use? What sort algorithm does Python use? Are these algorithms stable? You might have to Google around to find these answers.
7. Many of the non-comparison sorts are linear, so why does does Python use an $O(n \log n)$ comparison sort?

2.3 Analysis of search algorithms

A **search** is an algorithm that takes a collection and a target item and determines whether the target is in the collection, often returning the index of the target.

The simplest search algorithm is a "linear search," which traverses the items of the collection in order, stopping if it finds the target. In the worst case it has to traverse the entire collection, so the run time is linear.

The `in` operator for sequences uses a linear search; so do string methods like `find` and `count`.

If the elements of the sequence are in order, you can use a **bisection search**, which is $O(\log n)$. Bisection search is similar to the algorithm you probably use to look a word up in a dictionary (the book, not the data structure). Instead of starting at the beginning and checking each item in order, you start with the item in the middle and check whether the word you are looking for comes before or after. If it comes before, then you search the first half of the sequence. Otherwise you search the second half. Either way, you cut the number of remaining items in half.

If the sequence has 1,000,000 items, it will take about 20 steps to find the word or conclude that it's not there. So that's about 50,000 times faster than a linear search.

Exercise 2.3 Write a function called `bisection` that takes a sorted list and a target value and returns the index of the value in the list, if it's there, or `None` if it's not.

Or you could read the documentation of the `bisect` module and use that!

Bisection search can be much faster than linear search, but it requires the sequence to be in order, which might require extra work.

There is another data structure, called a **hashtable** that is even faster—it can do a search in constant time—and it doesn't require the items to be sorted. Python dictionaries are implemented using hashtables, which is why most dictionary operations, including the `in` operator, are constant time.

2.4 Hashtables

To explain how hashtables work and why their performance is so good, I start with a simple implementation of a map and gradually improve it until it's a hashtable.

I use Python to demonstrate these implementations, but in real life you wouldn't write code like this in Python; you would just use a dictionary! So for the rest of this chapter, you have to imagine that dictionaries don't exist and you want to implement a data structure that maps from keys to values. The operations you have to implement are:

`add(k, v)`: Add a new item that maps from key `k` to value `v`. With a Python dictionary, `d`, this operation is written `d[k] = v`.

`get(target)`: Look up and return the value that corresponds to key `target`. With a Python dictionary, `d`, this operation is written `d[target]` or `d.get(target)`.

For now, I assume that each key only appears once. The simplest implementation of this interface uses a list of tuples, where each tuple is a key-value pair.

```
class LinearMap(object):

    def __init__(self):
        self.items = []

    def add(self, k, v):
        self.items.append((k, v))

    def get(self, k):
        for key, val in self.items:
            if key == k:
                return val
        raise KeyError
```

`add` appends a key-value tuple to the list of items, which takes constant time.

`get` uses a `for` loop to search the list: if it finds the target key it returns the corresponding value; otherwise it raises a `KeyError`. So `get` is linear.

An alternative is to keep the list sorted by key. Then `get` could use a bisection search, which is $O(\log n)$. But inserting a new item in the middle of a list is linear, so this might not be the best option. There are other data structures[2] that can implement `add` and `get` in log time, but that's still not as good as a hashtable, so let's move on.

One way to improve `LinearMap` is to break the list of key-value pairs into smaller lists. Here's an implementation called `BetterMap`, which is a list of 100 LinearMaps. As we'll see in a second, the order of growth for `get` is still linear, but `BetterMap` is a step on the path toward hashtables:

```
class BetterMap(object):

    def __init__(self, n=100):
        self.maps = []
        for i in range(n):
            self.maps.append(LinearMap())

    def find_map(self, k):
        index = hash(k) % len(self.maps)
        return self.maps[index]

    def add(self, k, v):
        m = self.find_map(k)
        m.add(k, v)

    def get(self, k):
        m = self.find_map(k)
        return m.get(k)
```

`__init__` makes a list of `n` `LinearMap`s.

`find_map` is used by `add` and `get` to figure out which map to put the new item in, or which map to search.

`find_map` uses the built-in function `hash`, which takes almost any Python object and returns an integer. A limitation of this implementation is that it only works with hashable keys. Mutable types like lists and dictionaries are unhashable.

Hashable objects that are considered equal return the same hash value, but the converse is not necessarily true: two different objects can return the same hash value.

[2]See `wikipedia.org/wiki/Red-black_tree`.

`find_map` uses the modulus operator to wrap the hash values into the range from 0 to `len(self.maps)`, so the result is a legal index into the list. Of course, this means that many different hash values will wrap onto the same index. But if the hash function spreads things out pretty evenly (which is what hash functions are designed to do), then we expect $n/100$ items per LinearMap.

Since the run time of `LinearMap.get` is proportional to the number of items, we expect BetterMap to be about 100 times faster than LinearMap. The order of growth is still linear, but the leading coefficient is smaller. That's nice, but still not as good as a hashtable.

Here (finally) is the crucial idea that makes hashtables fast: if you can keep the maximum length of the LinearMaps bounded, `LinearMap.get` is constant time. All you have to do is keep track of the number of items and when the number of items per LinearMap exceeds a threshold, resize the hashtable by adding more LinearMaps.

Here is an implementation of a hashtable:

```
class HashMap(object):

    def __init__(self):
        self.maps = BetterMap(2)
        self.num = 0

    def get(self, k):
        return self.maps.get(k)

    def add(self, k, v):
        if self.num == len(self.maps.maps):
            self.resize()

        self.maps.add(k, v)
        self.num += 1

    def resize(self):
        new_maps = BetterMap(self.num * 2)

        for m in self.maps.maps:
            for k, v in m.items:
                new_maps.add(k, v)
```

Each `HashMap` contains a `BetterMap`; `__init__` starts with just 2 LinearMaps and initializes `num`, which keeps track of the number of items.

`get` just dispatches to `BetterMap`. The real work happens in `add`, which checks the number of items and the size of the `BetterMap`: if they are equal, the average number of items per LinearMap is 1, so it calls `resize`.

`resize` make a new `BetterMap`, twice as big as the previous one, and then "rehashes" the items from the old map to the new.

Rehashing is necessary because changing the number of LinearMaps changes the denominator of the modulus operator in `find_map`. That means that some objects that used to wrap into the same LinearMap will get split up (which is what we wanted, right?).

Rehashing is linear, so `resize` is linear, which might seem bad, since I promised that `add` would be constant time. But remember that we don't have to resize every time, so `add` is usually constant time and only occasionally linear. The total amount of work to run `add` n times is proportional to n, so the average time of each `add` is constant time!

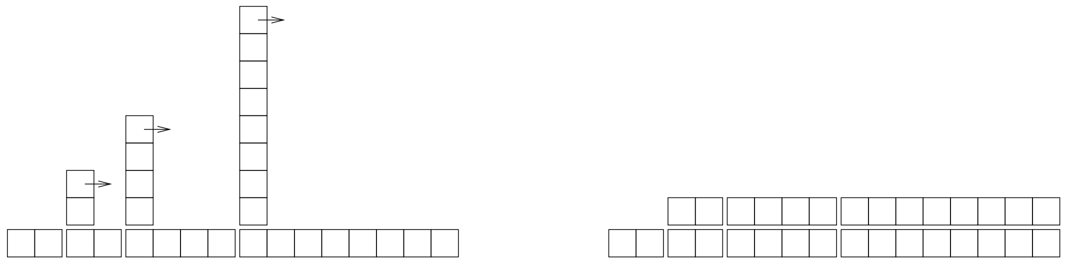
To see how this works, think about starting with an empty HashTable and adding a sequence of items. We start with 2 LinearMaps, so the first 2 adds are fast (no resizing required). Let's say that they take one unit of work each. The next add requires a resize, so we have to rehash the first two items (let's call that 2 more units of work) and then add the third item (one more unit). Adding the next item costs 1 unit, so the total so far is 6 units of work for 4 items.

The next `add` costs 5 units, but the next three are only one unit each, so the total is 14 units for the first 8 adds.

The next `add` costs 9 units, but then we can add 7 more before the next resize, so the total is 30 units for the first 16 adds.

After 32 adds, the total cost is 62 units, and I hope you are starting to see a pattern. After n adds, where n is a power of two, the total cost is $2n-2$ units, so the average work per add is a little less than 2 units. When n is a power of two, that's the best case; for other values of n the average work is a little higher, but that's not important. The important thing is that it is constant time!

The following figure shows how this works graphically. Each block represents a unit of work. The columns show the total work for each add in order from left to right: the first two `adds` cost 1 units, the third costs 3 units, etc.



The extra work of rehashing appears as a sequence of increasingly tall towers with increasing space between them. Now if you knock over the towers, amortizing the cost of resizing over all adds, you can see graphically that the total cost after n adds is $2n - 2$.

An important feature of this algorithm is that when we resize the HashTable it grows geometrically; that is, we multiply the size by a constant. If you increase the size arithmetically—adding a fixed number each time—the average time per `add` is linear.

You can download my implementation of HashMap from `thinkcomplex.com/Map.py`, but remember that there is no reason to use it; if you want a map, just use a Python dictionary.

Exercise 2.4 My implementation of `HashMap` accesses the attributes of `BetterMap` directly, which shows poor object-oriented design.

Improve it by:

1. The special method `__len__` is invoked by the built-in function `len`. Write a `__len__` method for `BetterMap` and use it in `add`.
2. Use a generator to write `BetterMap.iteritems`, and use it in `resize`.

Exercise 2.5 Write an implementation of the map interface called `TreeMap` that uses a red-black tree to perform `add` and `get` in log time.

2.5 Summing lists

Suppose you have a bunch of lists and you want to join them up into a single list. There are three ways you might do that in Python:

- You could use the `+=` operator:

  ```
  total = []
  for x in t:
      total += x
  ```

- Or the `extend` method:

  ```
  total = []
  for x in t:
      total.extend(x)
  ```

- Or the built-in function `sum`:

  ```
  total = sum(t, [])
  ```

  The second argument to `sum` is the initial value for the total.

Without knowing how `+=` and `extend` and `sum` are implemented, it is hard to analyze their performance. For example, if `total += x` creates a new list every time, the loop is quadratic; but if it modifies `total`, it's linear.

To find out, we could read the source code, but as an exercise, let's see if we can figure it out by measuring run times.

A simple way to measure the run time of a program is to use the function `times` in the `os` module, which returns a tuple of floats indicating the time your process has used (see the documentation for details). I use a function `etime`, which returns the sum of "user time" and "system time" which is usually what we care about for performance measurement:

```
import os

def etime():
    """See how much user and system time this process has used
    so far and return the sum."""

    user, sys, chuser, chsys, real = os.times()
    return user+sys
```

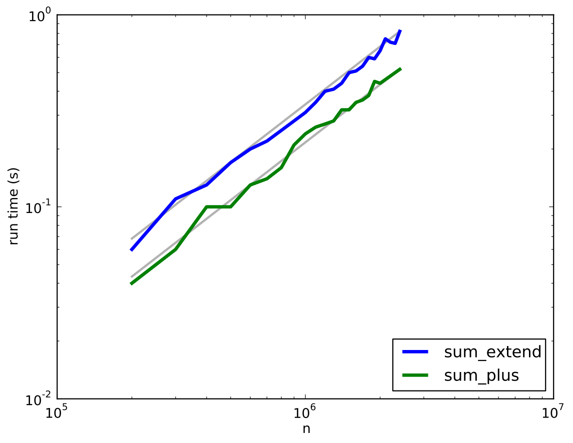


Figure 2.1: Runtime versus `n`. The gray lines have slope 1.

To measure the elapsed time of a function you can call `etime` twice and compute the difference:

```
start = etime()

# put the code you want to measure here

end = etime()
elapsed = end - start
```

Alternatively, if you use IPython, you can use the `timeit` command. See `ipython.scipy.org`.

If an algorithm is quadratic, we expect the run time, t as a function of input size, n, to look like this:

$$t = an^2 + bn + c$$

Where a, b and c are unknown coefficients. If you take the log of both sides you get:

$$\log t \sim \log a + 2 \log n$$

For large values of n, the non-leading terms are insignificant and this approximation is pretty good. So if we plot t versus n on a log-log scale, we expect a straight line with slope 2.

Similarly if the algorithm is linear, we expect a line with slope 1.

I wrote three functions that concatenate lists: `sum_plus` uses `+=`; `sum_extend` uses `list.extend`; and `sum_sum` uses `sum`. I timed them for a range of `n` and plotted the results on a log-log scale. Figures 2.1 and 2.2 show the results.

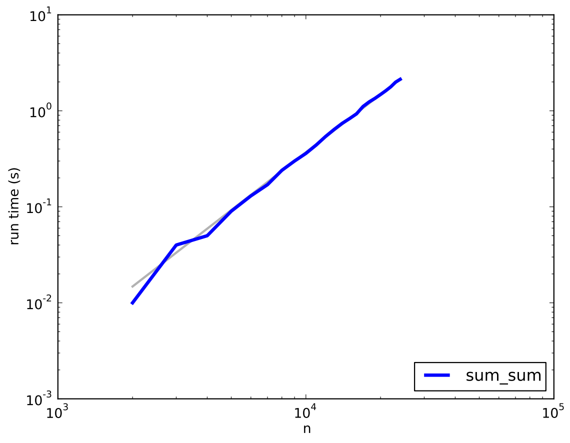


Figure 2.2: Runtime versus `n`. The gray line has slope 2.

In Figure 2.1 I fit a line with slope 1 to the curves. The data fit this line well, so we conclude that these implementations are linear. The implementation for `+=` is faster by a constant factor because it takes some time to look up the `extend` method each time through the loop.

In Figure 2.2 the data fit a line with slope 2, so the implementation of `sum` is quadratic.

2.6 pyplot

To make the figures in this section I used `pyplot`, which is part of `matplotlib`. If `matplotlib` is not part of your Python installation, you might have to install it, or you can use another library to make plots.

Here's an example that makes a simple plot:

```
import matplotlib.pyplot as pyplot

    pyplot.plot(xs, ys)
    scale = 'log'
    pyplot.xscale(scale)
    pyplot.yscale(scale)
    pyplot.title('')
    pyplot.xlabel('n')
    pyplot.ylabel('run time (s)')
    pyplot.show()
```

The import statement makes `matplotlib.pyplot` accessible with the shorter name `pyplot`.

`plot` takes a list of x-values and a list of y-values and plots them. The lists have to have the same length. `xscale` and `yscale` make the axes either linear or logarithmic.

`title`, `xlabel` and `ylabel` are self-explanatory. Finally, `show` displays the plot on the screen. You could also use `savefig` to save the plot in a file.

Documentation of `pyplot` is at `http://matplotlib.sourceforge.net/`.

Exercise 2.6 Test the performance of `LinearMap`, `BetterMap` and `HashMap`; see if you can characterize their order of growth.

You can download my map implementations from `thinkcomplex.com/Map.py`, and the code I used in this section from `thinkcomplex.com/listsum.py`.

You will have to find a range of `n` that is big enough to show asymptotic behavior, but small enough to run quickly.

2.7 List comprehensions

One of the most common programming patterns is to traverse a list while building a new list.

Here is an example that computes the square of each element in a list accumulates the results:

```
res = []
for x in t:
    res.append(x**2)
```

This pattern is so common that Python provides a more concise syntax for it, called a **list comprehension**. In this context, the sense of "comprehend" is something like "contain" rather than "understand." See `wikipedia.org/wiki/List_comprehension`.

Here's what it looks like:

```
res = [x**2 for x in t]
```

This expression yields the same result as the previous loop. List comprehensions tend to be fast because the loop is executed in C rather than Python. The drawback is that they are harder to debug.

List comprehensions can include an `if` clause that selects a subset of the items. The following example makes a list of the positive elements in `t`:

```
res = [x for x in t if x > 0]
```

The following is a common idiom for making a list of tuples, where each tuple is a value and a key from a dictionary:

```
res = [(v, k) for k, v in d.iteritems()]
```

In this case it is safe to use `iteritems`, rather than `items`, because the loop does not modify the dictionary; and it is likely to be faster because it doesn't have to make a list, just an iterator.

It is also possible to nest `for` loops inside a list comprehension. The following example builds a list of Edges between each pair of vertices in `vs`:

```
edges = [Edge(v, w) for v in vs for w in vs if v is not w]
```

That's pretty concise, but complicated comprehensions can be hard to read, so use them sparingly.

Exercise 2.7 Review the methods your wrote in `Graph.py` and see if any can be rewritten using list comprehensions.

Chapter 3

Small world graphs

3.1 Analysis of graph algorithms

The order of growth for a graph algorithm is usually expressed as a function of $|V|$, the number of vertices, and $|E|$, the number of edges.

The order of growth for BFS is $O(|V| + |E|)$, which is a convenient way to say that the run time grows in proportion to either $|V|$ or $|E|$, whichever is "bigger."

To see why, think about these four operations:

Adding a vertex to the queue: this happens once for each vertex, so the total cost is in $O(|V|)$.

Removing a vertex from the queue: this happens once for each vertex, so the total cost is in $O(|V|)$.

Marking a vertex "visited": this happens once for each vertex, so the total cost is in $O(|V|)$.

Checking whether a vertex is marked: this happens once each edge, so the total cost is in $O(|E|)$.

Adding them up, we get $O(|V| + |E|)$. If we know the relationship between $|V|$ and $|E|$, we can simplify this expression. For example, in a regular graph, the number of edges is in $O(|V|)$ so BFS is linear in $|V|$. In a complete graph, the number of edges is in $O(|V|^2)$ so BFS is quadratic in $|V|$.

Of course, this analysis is based on the assumption that all four operations—adding and removing vertices, marking and checking marks—are constant time.

Marking vertices is easy. You can add an attribute to the `Vertex` objects or put the marked ones in a set and use the `in` operator.

But making a first-in-first-out (FIFO) queue that can add and remove vertices in constant time turns out to be non-trivial.

3.2 FIFO implementation

A FIFO is a data structure that provides the following operations:

append: Add a new item to the end of the queue.

pop: Remove and return the item at the front of the queue.

There are several good implementations of this data structure. One is the **doubly-linked list**, which you can read about at `wikipedia.org/wiki/Doubly-linked_list`. Another is a circular buffer, which you can read about at `wikipedia.org/wiki/Circular_buffer`.

Exercise 3.1 Write an implementation of a FIFO using either a doubly-linked list or a circular buffer.

Yet another possibility is to use a Python dictionary and two indices: `nextin` keeps track of the back of the queue; `nextout` keeps track of the front. The dictionary maps from integer indices to values.

Here is an implementation based on Raymond Hettinger's recipe at `http://code.activestate.com/recipes/68436/`.

```
class DictFifo(object):

    def __init__(self):
        self.nextin = 0
        self.nextout = 0
        self.data = {}

    def append(self, value):
        self.data[self.nextin] = value
        self.nextin += 1

    def pop(self, n=-1):
        value = self.data.pop(self.nextout)
        self.nextout += 1
        return value
```

`append` stores the new item and increments `nextin`; both operations are constant time.

`pop` removes the last item and increments `nextout`. Again, both operations are constant time.

As yet another alternative, the Python `collections` module provides an object called a `deque`, which stands for "double-ended queue". It is supposed to be pronounced "deck," but many people say "deek." A Python deque can be adapted to implement a FIFO.

You can read about deques at `wikipedia.org/wiki/Deque` and get the details of the Python implementation at `docs.python.org/lib/deque-objects.html`.

Exercise 3.2 The following implementation of a BFS[1] contains two performance errors. What are they? What is the actual order of growth for this algorithm?

[1]This was the implementation at `wikipedia.org/wiki/Breadth-first_search` before I fixed it.

```
def bfs(top_node, visit):
    """Breadth-first search on a graph, starting at top_node."""
    visited = set()
    queue = [top_node]
    while len(queue):
        curr_node = queue.pop(0)    # Dequeue
        visit(curr_node)            # Visit the node
        visited.add(curr_node)

        # Enqueue non-visited and non-enqueued children
        queue.extend(c for c in curr_node.children
                     if c not in visited and c not in queue)
```

Test this code with a range of graph sizes and check your analysis. Then use a FIFO implementation to fix the errors and confirm that your algorithm is linear.

3.3 Stanley Milgram

Stanley Milgram was an American social psychologist who conducted two of the most famous experiments in social science, the Milgram experiment, which studied people's obedience to authority (`wikipedia.org/wiki/Milgram_experiment`) and the Small World Experiment `wikipedia.org/wiki/Small_world_phenomenon`, which studied the structure of social networks.

In the Small World Experiment, Milgram sent a package to several randomly-chosen people in Wichita, Kansas, with instructions asking them to forward an enclosed letter to a target person, identified by name and occupation, in Sharon, Massachusetts (which is the town near Boston where I grew up). The subjects were told that they could mail the letter directly to the target person only if they knew him personally; otherwise they were instructed to send it, and the same instructions, to a relative or friend they thought would be more likely to know the target person.

Many of the letters were never delivered, but of the ones that were it turned out that the average path length—the number of times the letters were forwarded—was about six. This result was taken to confirm previous observations (and speculations) that the typical distance between any two people in a social network is about “six degrees of separation.”

This conclusion is surprising because most people expect social networks to be localized—people tend to live near their friends—and in a graph with local connections, path lengths tend to increase in proportion to geographical distance. For example, most of my friends live nearby, so I would guess that the average distance between nodes in a social network is about 50 miles. Wichita is about 1600 miles from Boston, so if Milgram's letters traversed typical links in the social network, they should have taken 32 hops, not six.

3.4 Watts and Strogatz

In 1998 Duncan Watts and Steven Strogatz published a paper in *Nature*, “Collective dynamics of 'small-world' networks,” that proposed an explanation for the small world phenomenon.

Watts and Strogatz started with two kinds of graph that were well understood: random graphs and regular graphs. They looked at two properties of these graphs, clustering and path length.

Clustering is a measure of the "cliquishness" of the graph. In a graph, a **clique** is a subset of nodes that are all connected to each other; in a social network, a clique is a set of friends who all know each other. Watts and Strogatz defined a clustering coefficient that quantifies the likelihood that two nodes that are connected to the same node are also connected to each other.

Path length is a measure of the average distance between two nodes, which corresponds to the degrees of separation in a social network.

Their initial result was what you might expect: regular graphs have high clustering and high path lengths; random graphs with the same size tend to have low clustering and low path lengths. So neither of these is a good model of social networks, which seem to combine high clustering with short path lengths.

Their goal was to create a **generative model** of a social network. A generative model tries to explain a phenomenon by modeling the process that builds or leads to the phenomenon. In this case Watts and Strogatz proposed a process for building small-world graphs:

1. Start with a regular graph with n nodes and degree k. Watts and Strogatz start with a ring lattice, which is a kind of regular graph. You could replicate their experiment or try instead a graph that is regular but not a ring lattice.

2. Choose a subset of the edges in the graph and "rewire" them by replacing them with random edges. Again, you could replicate the procedure described in the paper or experiment with alternatives.

The proportion of edges that are rewired is a parameter, p, that controls how random the graph is. With $p = 0$, the graph is regular; with $p = 1$ it is random.

Watts and Strogatz found that small values of p yield graphs with high clustering, like a regular graph, and low path lengths, like a random graph.

Exercise 3.3 Read the Watts and Strogatz paper and answer the following questions:

1. What process do Watts and Strogatz use to rewire their graphs?

2. What is the definition of the clustering coefficient $C(p)$?

3. What is the definition of the average path length $L(p)$?

4. What real-world graphs did Watts and Strogatz look at? What evidence do they present that these graphs have the same structure as the graphs generated by their model?

Exercise 3.4 Create a file named `SmallWorldGraph.py` and define a class named `SmallWorldGraph` that inherits from `RandomGraph`.

If you did Exercise 1.4 you can use your own `RandomGraph.py`; otherwise you can download mine from `thinkcomplex.com/RandomGraph.py`.

1. Write a method called `rewire` that takes a probability `p` as a parameter and, starting with a regular graph, rewires the graph using Watts and Strogatz's algorithm.
2. Write a method called `clustering_coefficient` that computes and returns the clustering coefficient as defined in the paper.
3. Make a graph that replicates the line marked $C(p)/C(0)$ in Figure 2 of the paper. In other words, confirm that the clustering coefficient drops off slowly for small values of p.

Before we can replicate the other line, we have to learn about shortest path algorithms.

3.5 Dijkstra

Edsger W. Dijkstra was a Dutch computer scientist who invented an efficient shortest-path algorithm (see `wikipedia.org/wiki/Dijkstra's_algorithm`). He also invented the semaphore, which is a data structure used to coordinate programs that communicate with each other (see `wikipedia.org/wiki/Semaphore_(programming)` and Downey, *The Little Book of Semaphores*).

Dijkstra is famous (and notorious) as the author of a series of essays on computer science. Some, like "A Case against the GO TO Statement," have had a profound effect on programming practice. Others, like "On the Cruelty of Really Teaching Computing Science," are entertaining in their cantankerousness, but less effective.

Dijkstra's algorithm solves the "single source shortest path problem," which means that it finds the minimum distance from a given "source" node to every other node in the graph (or at least every connected node).

We start with a simplified version of the algorithm that considers all edges the same length. The more general version works with any non-negative edge lengths.

The simplified version is similar to the breadth-first search in Section 1.4 except that instead of marking visited nodes, we label them with their distance from the source. Initially all nodes are labeled with an infinite distance. Like a breadth-first search, Dijkstra's algorithm uses a queue of discovered unvisited nodes.

1. Give the source node distance 0 and add it to the queue. Give the other nodes infinite distance.
2. Remove a vertex from the queue and call its distance d. Find the vertices it is connected to. For each connected vertex with infinite distance, replace the distance with $d + 1$ and add it to the queue.
3. If the queue is not empty, go back to Step 2.

The first time you execute Step 2, the only node in the queue has distance 0. The second time, the queue contains all nodes with distance 1. Once those nodes are processed, the queue contains all nodes with distance 2, and so on.

So when a node is discovered for the first time, it is labeled with the distance $d + 1$, which is the shortest path to that node. It is not possible that you will discover a shorter path later, because if there were a shorter path, you would have discovered it sooner. That is not a proof of the correctness of the algorithm, but it sketches the structure of the proof by contradiction.

In the more general case, where the edges have different lengths, it is possible to discover a shorter path after you have discovered a longer path, so a little more work is needed.

Exercise 3.5 Write an implementation of Dijkstra's algorithm and use it to compute the average path length of a SmallWorldGraph.

Make a graph that replicates the line marked $L(p)/L(0)$ in Figure 2 of the Watts and Strogatz paper. Confirm that the average path length drops off quickly for small values of p. What is the range of values for p that yield graphs with high clustering and low path lengths?

Exercise 3.6 A natural question about the Watts and Strogatz paper is whether the small world phenomenon is specific to their generative model or whether other similar models yield the same qualitative result (high clustering and low path lengths).

To answer this question, choose a variation of the Watts and Strogatz model and replicate their Figure 2. There are two kinds of variation you might consider:

- Instead of starting with a regular graph, start with another graph with high clustering. One option is a locally-connected graph where vertices are placed at random locations in the plane and each vertex is connected to its nearest k neighbors.
- Experiment with different kinds of rewiring.

If a range of similar models yield similar behavior, we say that the results of the paper are **robust**.

Exercise 3.7 To compute the average path length in a SmallWorldGraph, you probably ran Dijkstra's single-source shortest path algorithm for each node in the graph. In effect, you solved the "all-pairs shortest path" problem, which finds the shortest path between all pairs of nodes.

1. Find an algorithm for the all-pairs shortest path problem and implement it. Compare the run time with your "all-source Dijkstra" algorithm.
2. Which algorithm gives better order-of-growth run time as a function of the number of vertices and edges? Why do you think Dijkstra's algorithm does better than the order-of-growth analysis suggests?

3.6 What kind of explanation is *that*?

If you ask me why planetary orbits are elliptical, I might start by modeling a planet and a star as point masses; I would look up the law of universal gravitation at `wikipedia.org/wiki/Newton's_law_of_universal_gravitation` and use it to write a differential equation for the motion of the planet. Then I would either derive the orbit equation or, more likely, look it up at `wikipedia.org/wiki/Orbit_equation`. With a little algebra, I could derive the conditions that yield an elliptical orbit. Then I would argue that the objects we consider planets satisfy these conditions.

People, or at least scientists, are generally satisfied with this kind of explanation. One of the reasons for its appeal is that the assumptions and approximations in the model seem reasonable. Planets and stars are not really point masses, but the distances between them are so big that their actual sizes are negligible. Planets in the same solar system can affect each others' orbits, but the effect is usually small. And we ignore relativistic effects, again on the assumption that they are small.

This explanation is also appealing because it is equation-based. We can express the orbit equation in a closed form, which means that we can compute orbits efficiently. It also means that we can derive general expressions for the orbital velocity, orbital period, and other quantities.

Finally, I think this kind of explanation is appealing because it has the form of a mathematical proof. It starts from a set of axioms and derives the result by logic and analysis. But it is important to remember that the proof pertains to the model and not the real world. That is, we can prove that an idealized model of a planet yields an elliptic orbit, but we can't prove that the model pertains to actual planets (in fact, it does not).

By comparison, Watts and Strogatz's explanation of the small world phenomenon may seem less satisfying. First, the model is more abstract, which is to say less realistic. Second, the results are generated by simulation, not by mathematical analysis. Finally, the results seem less like a proof and more like an example.

Many of the models in this book are like the Watts and Strogatz model: abstract, simulation-based and (at least superficially) less formal than conventional mathematical models. One of the goals of this book it to consider the questions these models raise:

- What kind of work can these models do: are they predictive, or explanatory, or both?
- Are the explanations these models offer less satisfying than explanations based on more traditional models? Why?
- How should we characterize the differences between these and more conventional models? Are they different in kind or only in degree?

Over the course of the book I will offer my answers to these questions, but they are tentative and sometimes speculative. I encourage you to consider them skeptically and reach your own conclusions.

Chapter 4

Scale-free networks

4.1 Zipf's Law

Zipf's law describes a relationship between the frequencies and ranks of words in natural languages; see `wikipedia.org/wiki/Zipf's_law`. The "frequency" of a word is the number of times it appears in a body of work. The "rank" of a word is its position in a list of words sorted by frequency: the most common word has rank 1, the second most common has rank 2, etc.

Specifically, Zipf's Law predicts that the frequency, f, of the word with rank r is:

$$f = cr^{-s}$$

where s and c are parameters that depend on the language and the text.

If you take the logarithm of both sides of this equation, you get:

$$\log f = \log c - s \log r$$

So if you plot $\log f$ versus $\log r$, you should get a straight line with slope $-s$ and intercept $\log c$.

Exercise 4.1 Write a program that reads a text from a file, counts word frequencies, and prints one line for each word, in descending order of frequency. You can test it by downloading an out-of-copyright book in plain text format from `gutenberg.net`. You might want to remove punctuation from the words.

If you need some help getting started, you can download `thinkcomplex.com/Pmf.py`, which provides an object named `Hist` that maps from value to frequencies.

Plot the results and check whether they form a straight line. For plotting suggestions, see Section 2.6. Can you estimate the value of s?

You can download my solution from `thinkcomplex.com/Zipf.py`

4.2 Cumulative distributions

A distribution is a statistical description of a set of values. For example, if you collect the population of every city and town in the U.S., you would have a set of about 14,000 integers.

The simplest description of this set is a list of numbers, which would be complete but not very informative. A more concise description is a statistical summary like the mean and variation, but that is not a complete description because there are many sets of values with the same summary statistics.

One alternative is a histogram, which divides the range of possible values into "bins" and counts the number of values that fall in each bin. Histograms are common, so they are easy to understand, but it is tricky to get the bin size right. If the bins are too small, the number of values in each bin is also small, so the histogram doesn't give much insight. If the bins are too large, they lump together a wide range of values, which obscures details that might be important.

A better alternative is a **cumulative distribution function** (CDF), which maps from a value, x, to the fraction of values less than or equal to x. If you choose a value at random, $CDF(x)$ is the probability that the value you get is less than or equal to x.

For a list of n values, the simplest way to compute CDF is to sort the values. Then the CDF of the ith value (starting from 1) is i/n.

I have written a class called `Cdf` that provides functions for creating and manipulating CDFs. You can download it from `thinkcomplex.com/Cdf.py`.

As an example, we'll compute the CDF for the values $\{1, 2, 2, 4, 5\}$:

```
import Cdf
cdf = Cdf.MakeCdfFromList([1,2,2,4,5])
```

`MakeCdfFromList` can take any sequence or iterator. Once you have the `Cdf`, you can find the probability, $CDF(x)$, for a given value:

```
prob = cdf.Prob(2)
```

The result is 0.6, because 3/5 of the values are less than or equal to 2. You can also compute the value for a given probability:

```
value = cdf.Value(0.5)
```

The value with probability 0.5 is the median, which in this example is 2.

To plot the `Cdf`, you can use `Render`, which returns a list of value-probability pairs.

```
    xs, ps = cdf.Render()
    for x, p in zip(xs, ps):
        print x, p
```

The result is:

```
1 0.0
1 0.2
2 0.2
2 0.6
```

```
4 0.6
4 0.8
5 0.8
5 1.0
```

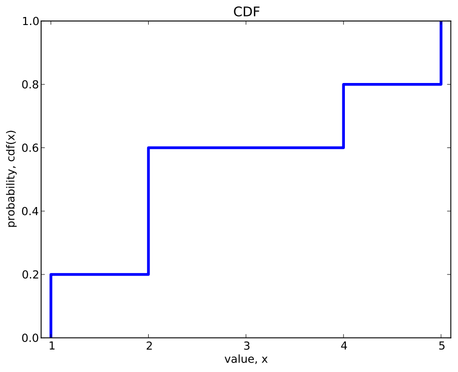
Each value appear twice. That way when we plot the CDF, we get a stair-step pattern.

```
import matplotlib.pyplot as pyplot

    xs, ps = cdf.Render()

    pyplot.plot(xs, ps, linewidth=3)
    pyplot.axis([0.9, 5.1, 0, 1])
    pyplot.title('CDF')
    pyplot.xlabel('value, x')
    pyplot.ylabel('probability, CDF(x)')
    pyplot.show()
```

The following figure shows the cumulative distribution function (CDF), for the values $(1, 2, 2, 4, 5)$.



I drew vertical lines at each of the values, which is not mathematically correct. To be more rigorous, I should draw a discontinuous function.

Exercise 4.2 Read the code in `Cdf.py`. What is the order of growth for `MakeCdfFromList` and the methods `Prob` and `Value`?

4.3 Continuous distributions

The distributions we have seen so far are sometimes called **empirical distributions** because they are based on a dataset that comes from some kind of empirical observation.

An alternative is a **continuous distribution**, which is characterized by a CDF that is a continuous function. Some of these distributions, like the Gaussian or normal distribution, are well known, at least to people who have studied statistics. Many real world phenomena can be approximated by continuous distributions, which is why they are useful.

For example, if you observe a mass of radioactive material with an instrument that can detect decay events, the distribution of times between events will most likely fit an exponential distribution. The same is true for any series where an event is equally likely at any time.

The CDF of the exponential distribution is:

$$CDF(x) = 1 - e^{-\lambda x}$$

The parameter, λ, determines the mean and variance of the distribution. This equation can be used to derive a simple visual test for whether a dataset can be well approximated by an exponential distribution. All you have to do is plot the **complementary distribution** on a log-y scale.

The complementary distribution (CCDF) is just $1 - CDF(x)$; if you plot the complementary distribution of a dataset that you think is exponential, you expect to see a function like:

$$y = 1 - CDF(x) \sim e^{-\lambda x}$$

If you take the log of both sides of this equation, you get:

$$\log y \sim -\lambda x$$

So on a log-y scale the CCDF should look like a straight line with slope $-\lambda$.

Exercise 4.3 Write a function called `plot_ccdf` that takes a list of values and the corresponding list of probabilities and plots the CCDF on a log-y scale.

To test your function, use `expovariate` from the `random` module to generate 100 values from an exponential distribution. Plot the CCDF on a log-y scale and see if it falls on a straight line.

4.4 Pareto distributions

The Pareto distribution is named after the economist Vilfredo Pareto, who used it to describe the distribution of wealth; see `wikipedia.org/wiki/Pareto_distribution`. Since then, people have used it to describe phenomena in the natural and social sciences including sizes of cities and towns, sand particles and meteorites, forest fires and earthquakes.

The Pareto distribution is characterized by a CDF with the following form:

$$1 - \left(\frac{x}{x_m}\right)^{-\alpha}$$

The parameters x_m and α determine the location and shape of the distribution. x_m is the minimum possible quantity.

Values from a Pareto distribution often have these properties:

Long tail: Pareto distributions contain many small values and a few very large ones.

80/20 rule: The large values in a Pareto distribution are so large that they make up a disproportionate share of the total. In the context of wealth, the 80/20 rule says that 20% of the people own 80% of the wealth.

Scale free: Short-tailed distributions are centered around a typical size, which is called a "scale." For example, the great majority of adult humans are between 100 and 200 cm in height, so we could say that the scale of human height is a few hundred centimeters. But for long-tailed distributions, there is no similar range (bounded by a factor of two) that contains the bulk of the distribution. So we say that these distributions are "scale-free."

To get a sense of the difference between the Pareto and Gaussian distributions, imagine what the world would be like if the distribution of human height were Pareto.

In Pareto World, the shortest person is 100 cm, and the median is 150 cm, so that part of the distribution is not very different from ours.

But if you generate 6 billion values from this distribution distribution, the tallest person might be 100 km—that's what it means to be scale-free!

There is a simple visual test that indicates whether an empirical distribution is well-characterized by a Pareto distribution: on a log-log scale, the CCDF looks like a straight line. The derivation is similar to what we saw in the previous section.

The equation for the CCDF is:

$$y = 1 - CDF(x) \sim \left(\frac{x}{x_m}\right)^{-\alpha}$$

Taking the log of both sides yields:

$$\log y \sim -\alpha(\log x - \log x_m)$$

So if you plot $\log y$ versus $\log x$, it should look like a straight line with slope $-\alpha$ and intercept $-\alpha \log x_m$.

Exercise 4.4 Write a version of `plot_ccdf` that plots the complementary CCDF on a log-log scale.

To test your function, use `paretovariate` from the `random` module to generate 100 values from an exponential distribution. Plot the CCDF on a log-y scale and see if it falls on a straight line. What happens to the curve as you increase the number of values?

Exercise 4.5 The distribution of populations for cities and towns has been proposed as an example of a real-world phenomenon that can be described with a Pareto distribution.

The U.S. Census Bureau publishes data on the population of every incorporated city and town in the United States. I wrote a small program that downloads this data and converts it into a convenient form. You can download it from `thinkcomplex.com/populations.py`.

Read over the program to make sure you know what it does and then write a program that computes and plots the distribution of populations for the 14593 cities and towns in the dataset.

Plot the CDF on linear and log-x scales so you can get a sense of the shape of the distribution. Then plot the CCDF on a log-log scale to see if it has the characteristic shape of a Pareto distribution.

What conclusion do you draw about the distribution of sizes for cities and towns?

4.5 Barabási and Albert

In 1999 Barabási and Albert published a paper in *Science*, "Emergence of Scaling in Random Networks," that characterizes the structure (also called "topology") of several real-world networks, including graphs that represent the interconnectivity of movie actors, world-wide web (WWW) pages, and elements in the electrical power grid in the western United States.

They measure the degree (number of connections) of each node and compute $P(k)$, the probability that a vertex has degree k; then they plot $P(k)$ versus k on a log-log scale. The tail of the plot fits a straight line, so they conclude that it obeys a **power law**; that is, as k gets large, $P(k)$ is asymptotic to $k^{-\gamma}$, where γ is a parameter that determines the rate of decay.

They also propose a model that generates random graphs with the same property. The essential features of the model, which distinguish it from the Erdős-Rényi model and the Watts-Strogatz model, are:

Growth: Instead of starting with a fixed number of vertices, Barabási and Albert start with a small graph and add vertices gradually.

Preferential attachment: When a new edge is created, it is more likely to connect to a vertex that already has a large number of edges. This "rich get richer" effect is characteristic of the growth patterns of some real-world networks.

Finally, they show that graphs generated by this model have a distribution of degrees that obeys a power law. Graphs that have this property are sometimes called **scale-free networks**; see `wikipedia.org/wiki/Scale-free_network`. That name can be confusing because it is the distribution of degrees that is scale-free, not the network.

In order to maximize confusion, distributions that obey the power law are sometimes called **scaling distributions** because they are invariant under a change of scale. That means that if you change the units the quantities are expressed in, the slope parameter, γ, doesn't change. You can read `wikipedia.org/wiki/Power_law` for the details, but it is not important for what we are doing here.

Exercise 4.6 This exercise asks you to make connections between the Watts-Strogatz (WS) and Barabási-Albert (BA) models:

1. Read Barabási and Albert's paper and implement their algorithm for generating graphs. See if you can replicate their Figure 2(A), which shows $P(k)$ versus k for a graph with 150 000 vertices.
2. Use the WS model to generate the largest graph you can in a reasonable amount of time. Plot $P(k)$ versus k and see if you can characterize the tail behavior.
3. Use the BA model to generate a graph with about 1000 vertices and compute the characteristic length and clustering coefficient as defined in the Watts and Strogatz paper. Do scale-free networks have the characteristics of a small-world graph?

4.6 Zipf, Pareto and power laws

At this point we have seen three phenomena that yield a straight line on a log-log plot:

Zipf plot: Frequency as a function of rank.

Pareto CCDF: The complementary CDF of a Pareto distribution.

Power law plot: A histogram of frequencies.

The similarity in these plots is not a coincidence; these visual tests are closely related.

Starting with a power-law distribution, we have:

$$P(k) \sim k^{-\gamma}$$

If we choose a random node in a scale free network, $P(k)$ is the probability that its degree equals k.

The cumulative distribution function, $CDF(k)$, is the probability that the degree is less than or equal to k, so we can get that by summation:

$$CDF(k) = \sum_{i=0}^{k} P(i)$$

For large values of k we can approximate the summation with an integral:

$$\sum_{i=0}^{k} i^{-\gamma} \sim \int_{i=0}^{k} i^{-\gamma} = \frac{1}{\gamma - 1}(1 - k^{-\gamma+1})$$

To make this a proper CDF we could normalize it so that it goes to 1 as k goes to infinity, but that's not necessary, because all we need to know is:

$$CDF(k) \sim 1 - k^{-\gamma+1}$$

Which shows that the distribution of k is asymptotic to a Pareto distribution with $\alpha = \gamma - 1$.

Similarly, if we start with a straight line on a Zipf plot, we have[1]

$$f = cr^{-s}$$

Where f is the frequency of the word with rank r. Inverting this relationship yields:

$$r = (f/c)^{-1/s}$$

Now subtracting 1 and dividing through by the number of different words, n, we get

$$\frac{r-1}{n} = \frac{(f/c)^{-1/s}}{n} - \frac{1}{n}$$

Which is only interesting because if r is the rank of a word, then $(r-1)/n$ is the fraction of words with lower ranks, which is the fraction of words with higher frequency, which is the CCDF of the distribution of frequencies:

$$CCDF(x) = \frac{(f/c)^{-1/s}}{n} - \frac{1}{n}$$

To characterize the asymptotic behavior for large n we can ignore c and $1/n$, which yields:

$$CCDF(x) \sim f^{-1/s}$$

Which shows that if a set of words obeys Zipf's law, the distribution of their frequencies is asymptotic to a Pareto distribution with $\alpha = 1/s$.

So the three visual tests are mathematically equivalent; a dataset that passes one test will pass all three. But as a practical matter, the power law plot is noisier than the other two, because it is the derivative of the CCDF.

The Zipf and CCDF plots are more robust, but Zipf's law is only applicable to discrete data (like words), not continuous quantities. CCDF plots work with both.

For these reasons—robustness and generality—I recommend using CCDFs.

Exercise 4.7 The Stanford Large Network Dataset Collection is a repository of datasets from a variety of networks, including social networks, communication and collaboration, Internet and road networks. See `http://snap.stanford.edu/data/index.html`.

Download one of these datasets and explore. Is there evidence of small-world behavior? Is the network scale-free? What else can you discover?

[1]This derivation follows Adamic, "Zipf, power law and Pareto—a ranking tutorial," available at `www.hpl.hp.com/research/idl/papers/ranking/ranking.html`

4.7 Explanatory models

We started the discussion of networks with Milgram's Small World Experiment, which shows that path lengths in social networks are surprisingly small; hence, "six degrees of separation".

When we see something surprising, it is natural to ask "Why?" but sometimes it's not clear what kind of answer we are looking for. One kind of answer is an **explanatory model**; the logical structure of an explanatory model is:

1. In a system, S, we see something observable, O, that warrants explanation.
2. We construct a model, M, that is analogous to the system; that is, there is a correspondence between the elements of the model and the elements of the system.
3. By simulation or mathematical derivation, we show that the model exhibits a behavior, B, that is analogous to O.
4. We conclude that S exhibits O *because* S is similar to M, M exhibits B, and B is similar to O.

At its core, this is an argument by analogy, which says that if two things are similar in some ways, they are likely to be similar in other ways.

Argument by analogy can be useful, and explanatory models can be satisfying, but they do not constitute a proof in the mathematical sense of the word.

First, remember that all models leave out, or "abstract away" details that we think are unimportant. But for any system there are many possible models that include or ignore different features. And there might be models that exhibit different behaviors, B, B' and B", that are similar to O in different ways.

In that case, which model explains O?

The small world phenomenon is a case in point: the Watts-Strogatz (WS) model and the Barabási-Albert (BA) model both exhibit small world behavior, but they offer different explanations:

- The WS model suggests that social networks are "small" because they include both strongly-connected clusters and "weak ties" that connect clusters[2].
- The BA model suggests that social networks are small because they include nodes with high degree that act as hubs, and that hubs grow, over time, due to preferential attachment.

As is often the case in young areas of science, the problem is not that we have no explanations, but too many.

[2]See `http://en.wikipedia.org/wiki/Mark_Granovetter`.

Exercise 4.8 Are these explanations compatible; that is, can they both be right?

Which do you find more satisfying as an explanation, and why?

Is there data you could collect, or experiments you could perform, that would provide evidence in favor of one model over the other?

Choosing among competing models is the topic of Thomas Kuhn's essay, "Objectivity, Value Judgment, and Theory Choice." Kuhn was a historian of science who wrote *The Structure of Scientific Revolutions* in 1962, and spent the rest of his life explaining what he meant to say.

What criteria does Kuhn propose for choosing among competing models? Do these criteria influence your opinion about the WS and BA models? Are there other criteria you think should be considered?

Chapter 5

Cellular Automata

A cellular automaton is a model of a world with very simple physics. “Cellular” means that the space is divided into discrete chunks, called cells. An “automaton” is a machine that performs computations—it could be a real machine, but more often the “machine” is a mathematical abstraction or a computer simulation.

Automata are governed by rules that determine how the system evolves in time. Time is divided into discrete steps, and the rules specify how to compute the state of the world during the next time step based on the current state.

As a trivial example, consider a cellular automaton (CA) with a single cell. The state of the cell is an integer represented with the variable x_i, where the subscript i indicates that x_i is the state of the system during timestep i. As an initial condition, $x_0 = 0$.

Now all we need is a rule. Arbitrarily, I'll pick $x_i = x_{i-1} + 1$, which says that after each time step, the state of the CA gets incremented by 1. So far, we have a simple CA that performs a simple calculation: it counts.

But this CA is atypical; normally the number of possible states is finite. To bring it into line, I'll choose the smallest interesting number of states, 2, and another simple rule, $x_i = (x_{i-1} + 1)\%2$, where % is the remainder (or modulus) operator.

This CA performs a simple calculation: it blinks. That is, the state of the cell switches between 0 and 1 after every timestep.

Most CAs are **deterministic**, which means that rules do not have any random elements; given the same initial state, they always produce the same result. There are also nondeterministic CAs, but I will not address them here.

5.1 Stephen Wolfram

The CA in the previous section was 0-dimensional and it wasn't very interesting. But 1-dimensional CAs turn out to be surprisingly interesting.

In the early 1980s Stephen Wolfram published a series of papers presenting a systematic study of 1-dimensional CAs. He identified four general categories of behavior, each more interesting than the last.

To say that a CA has dimensions is to say that the cells are arranged in a contiguous space so that some of them are considered "neighbors." In one dimension, there are three natural configurations:

Finite sequence: A finite number of cells arranged in a row. All cells except the first and last have two neighbors.

Ring: A finite number of cells arranged in a ring. All cells have two neighbors.

Infinite sequence: An infinite number of cells arranged in a row.

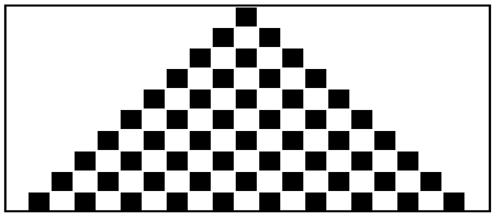
The rules that determine how the system evolves in time are based on the notion of a "neighborhood," which is the set of cells that determines the next state of a given cell. Wolfram's experiments use a 3-cell neighborhood: the cell itself and its left and right neighbors.

In these experiments, the cells have two states, denoted 0 and 1, so the rules can be summarized by a table that maps from the state of the neighborhood (a tuple of 3 states) to the next state for the center cell. The following table shows an example:

prev	111	110	101	100	011	010	001	000
next	0	0	1	1	0	0	1	0

The row first shows the eight states a neighborhood can be in. The second row shows the state of the center cell during the next timestep. As a concise encoding of this table, Wolfram suggested reading the bottom row as a binary number. Because 00110010 in binary is 50 in decimal, Wolfram calls this CA "Rule 50."

The following figure shows the effect of Rule 50 over 10 time steps:



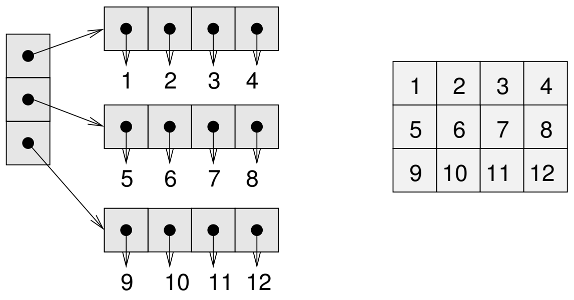
The first row shows the state of the system during the first timestep; it starts with one cell "on" and the rest "off". The second row shows the state of the system during the next time step, and so on.

The triangular shape in the figure is typical of these CAs; is it a consequence of the shape of the neighborhood. In one time step, each cell influences the state of one neighbor in either direction. During the next time step, that influence can propagate one more cell in each direction. So each cell in the past has a "triangle of influence" that includes all of the cells that can be affected by it.

5.2 Implementing CAs

To generate the previous figure, I wrote a Python program that implements and draws CAs. You can download my code from `thinkcomplex.com/CA.py`. and `thinkcomplex.com/CADrawer.py`.

To store the state of the CA, I use a NumPy array. An array is a multi-dimensional data structure whose elements are all the same type. It is similar to a nested list, but usually smaller and faster. The following figure shows why:



The diagram on the left shows a list of lists of integers; each dot represents a reference, which takes up 4–8 bytes. To access one of the integers, you have to follow two references.

The diagram on the right shows an array of the same integers. Because the elements are all the same size, they can be stored contiguously in memory. This arrangement saves space because it doesn't use references, and it saves time because the location of an element can be computed directly from the indices; there is no need to follow a series of references.

Here is a CA object that uses a NumPy array:

```
import numpy

class CA(object):

    def __init__(self, rule, n=100, ratio=2):
        self.table = make_table(rule)
        self.n = n
        self.m = ratio*n + 1
        self.array = numpy.zeros((n, self.m), dtype=numpy.int8)
        self.next = 0
```

`rule` is an integer in the range 0-255, which represents the CA rule table using Wolfram's encoding. `make_table` converts the rule to a dictionary that maps from neighborhood states to cell states. For example, in Rule 50 the table contains a map from $(1, 1, 1)$ to 0.

`n` is the number of rows in the array, which is the number of timesteps we will compute. `m` is the number of columns, which is the number of cells. At least to get started, we implement a finite array of cells.

`zeros` is provided by NumPy; it creates a new array with the given dimensions, `n` by `m`; `dtype` stands for "data type," and is specifies the type of the array elements. `int8` is an 8-bit integer, so we are limited to 256 states, but that's no problem: we only need two.

next is the index of the next timestep.

There are two common starting conditions for CAs: a single cell, or a row of random cells. start_single initializes the first row with a single cell and increments next:

```
    def start_single(self):
        """Starts with one cell in the middle of the top row."""
        self.array[0, self.m/2] = 1
        self.next += 1
```

Array indexing is similar to list and dictionary indexing. Array indexing is similar to list indexing.

step computes the next state of the CA:

```
    def step(self):
        i = self.next
        self.next += 1

        a = self.array
        t = self.table
        for j in xrange(1,self.m-1):
            a[i,j] = t[tuple(a[i-1, j-1:j+2])]
```

i is the timestep and the index of the row we are about to compute. j loops through the cells, skipping the first and last, which are always off.

Arrays support slice operations, so self.array[i-1, j-1:j+2] gets three elements from row i-1. Then we look up the neighborhood tuple in the table, get the next state, and store it in the array.

Array indexing is constant time, so step is linear in n. Filling in the whole array is $O(nm)$.

You can read more about NumPy and arrays at scipy.org/Tentative_NumPy_Tutorial.

5.3 CADrawer

An **abstract class** is a class definition that specifies the interface for a set of methods without providing an implementation. Child classes extend the abstract class and implement the incomplete methods. See http://en.wikipedia.org/wiki/Abstract_type.

As an example, I present an abstract class, CADrawer, that defines an interface for drawing CAs, and child classes that implement this interface.

Here's the definition for CADrawer:

```
class Drawer(object):
    """Drawer is an abstract class that should not be instantiated.
    It defines the interface for a CA drawer; child classes of Drawer
    should implement draw, show and save.

    If draw_array is not overridden, the child class should provide
    draw_cell.
    """
    def __init__(self):
        msg = 'CADrawer is an abstract type and should not be instantiated.'
        raise UnimplementedMethodException, msg

    def draw(self, ca):
        """Draws a representation of cellular automaton (CA).
        This function generally has no visible effect."""
        raise UnimplementedMethodException

    def draw_array(self, a):
        """Iterate through array (a) and draws any non-zero cells."""
        for i in xrange(self.rows):
            for j in xrange(self.cols):
                if a[i,j]:
                    self.draw_cell(j, self.rows-i-1)

    def draw_cell(self, ca):
        """Draws a single cell.
        Not required for all implementations."""
        raise UnimplementedMethodException

    def show(self):
        """Displays the representation on the screen, if possible."""
        raise UnimplementedMethodException

    def save(self, filename):
        """Saves the representation of the CA in filename."""
        raise UnimplementedMethodException
```

Abstract classes should not be instantiated; if you try, you get an `UnimplementedMethodException`, which is a simple extension of `Exception`:

```
class UnimplementedMethodException(Exception):
    """Used to indicate that a child class has not implemented an
    abstract method."""
```

To instantiate a `CADrawer` you have to define a child class that implements the methods, then instantiate the child.

`CADrawer.py` provides three implementations, one that uses `pyplot`, one that uses the Python Imaging Library (PIL), and one that generates Encapsulated Postscript (EPS).

Here is an example that uses `PyplotDrawer` to display a CA on the screen:

```
    ca = CA(rule, n)
    ca.start_single()
    ca.loop(n-1)

    drawer = CADrawer.PyplotDrawer()
    drawer.draw(ca)
    drawer.show()
```

Exercise 5.1 Download `thinkcomplex.com/CA.py` and `thinkcomplex.com/CADrawer.py` and confirm that they run on your system; you might have to install additional Python packages.

Create a new class called `CircularCA` that extends `CA` so that the cells are arranged in a ring.

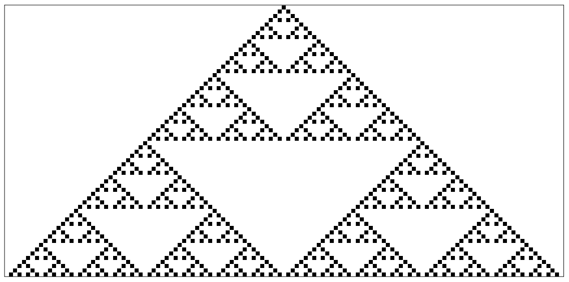
Hint: you might find it useful to add a column of "ghost cells" to the array.

You can download my solution from `thinkcomplex.com/CircularCA.py`

5.4 Classifying CAs

Wolfram proposes that the behavior of CAs can be grouped into four classes. Class 1 contains the simplest (and least interesting) CAs, the ones that evolve from almost any starting condition to the same uniform pattern. As a trivial example, Rule 0 always generates an empty pattern after one time step.

Rule 50 is an example of Class 2. It generates a simple pattern with nested structure; that is, the pattern contains many smaller versions of itself. Rule 18 makes the nested structure even clearer; here is what it looks like after 64 steps:

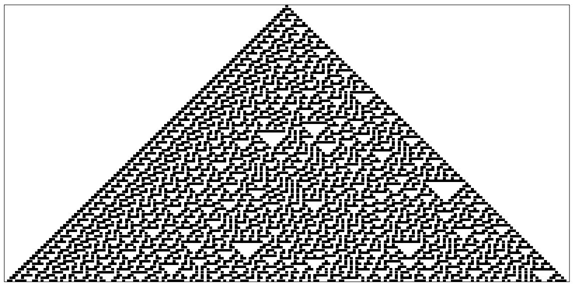


This pattern resembles the Sierpiński triangle, which you can read about at `wikipedia.org/wiki/Sierpinski_triangle`.

Some Class 2 CAs generate patterns that are intricate and aesthetic, but compared to Classes 3 and 4, they are relatively simple.

5.5 Randomness

Class 3 is a pattern that generate randomness. Rule 30 is an example; here is what it looks like after 100 timesteps:



Along the left side there is an apparent pattern, and on the right side there are triangles in various sizes, but the center seems quite random. In fact, if you take the center column and treat it as a sequence of bits, it is hard to distinguish from a truly random sequence. It passes many of the statistical tests people use to test whether a sequence of bits is random.

Programs that produce random-seeming numbers are called **pseudo-random number generators** (PRNGs). They are not considered truly random because

- Many of them produce sequences with regularities that can be detected statistically. For example, the original implementation of `rand` in the C library used a linear congruential generator that yielded sequences with easily detectable serial correlations.
- Any PRNG that uses a finite amount of state (that is, storage) will eventually repeat itself. One of the characteristics of a generator is the **period** of this repetition.
- The underlying process is fundamentally deterministic, unlike some physical processes, like radioactive decay and thermal noise, that are considered to be fundamentally random.

Modern PRNGs produce sequences that are statistically indistinguishable from random, and they can be implemented with with periods so long that the universe will collapse before they repeat. The existence of these generators raises the question of whether there is any real difference between a good quality pseudo-random sequence and a sequence generated by a "truly" random process. In *A New Kind of Science*, Wolfram argues that there is not (pages 315–326).

Exercise 5.2 This exercise asks you to implement and test several PRNGs.

1. Write a program that implements one of the linear congruential generators described at `wikipedia.org/wiki/Linear_congruential_generator`).
2. Download `DieHarder`, a random number test suite, from `phy.duke.edu/~rgb/General/rand_rate.php` and use it to test your PRNG. How does it do?
3. Read the documentation of Python's `random` module. What PRNG does it use? Test it using DieHarder.
4. Implement a Rule 30 CA on a ring with a few hundred cells, run it for as many time steps as you can in a reasonable amount of time, and output the center column as a sequence of bits. Test it using DieHarder.

5.6 Determinism

The existence of Class 3 CAs is surprising. To understand how surprising, it is useful to consider the philosophical stance called **determinism** (see `wikipedia.org/wiki/Determinism`). Most philosophical stances are hard to define precisely because they come in a variety of flavors. I often find it useful to define them with a list of statements ordered from weak to strong:

D1: Deterministic models can make accurate predictions for some physical systems.

D2: Many physical systems can be modeled by deterministic processes, but some are intrinsically random.

D3: All events are caused by prior events, but many physical systems are nevertheless fundamentally unpredictable.

D4: All events are caused by prior events, and can (at least in principle) be predicted.

My goal in constructing this range is to make D1 so weak that virtually everyone would accept it, D4 so strong that almost no one would accept it, with intermediate statements that some people accept.

The center of mass of world opinion swings along this range in response to historical developments and scientific discoveries. Prior to the scientific revolution, many people regarded the working of the universe as fundamentally unpredictable or controlled by supernatural forces. After the triumphs of Newtonian mechanics, some optimists came to believe something like D4; for example, in 1814 Pierre-Simon Laplace wrote

> We may regard the present state of the universe as the effect of its past and the cause of its future. An intellect which at a certain moment would know all forces that set nature in motion, and all positions of all items of which nature is composed, if this intellect were also vast enough to submit these data to analysis, it would embrace in a single formula the movements of the greatest bodies of the universe and those of the tiniest atom; for such an intellect nothing would be uncertain and the future just like the past would be present before its eyes.

This "intellect" came to be called "Laplace's Demon". See `wikipedia.org/wiki/Laplace's_demon`. The word "demon" in this context has the sense of "spirit," with no implication of evil.

Discoveries in the 19th and 20th centuries gradually dismantled this hope. The thermodynamic concept of entropy, radioactive decay, and quantum mechanics posed successive challenges to strong forms of determinism.

In the 1960s chaos theory showed that in some deterministic systems prediction is only possible over short time scales, limited by the precision of measurement of initial conditions.

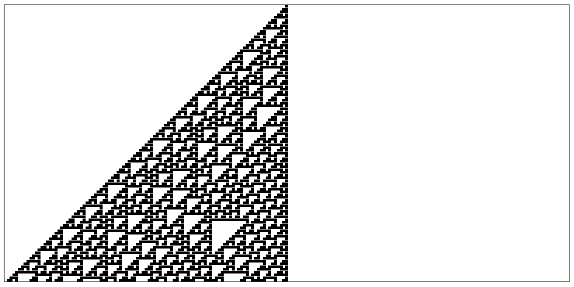
Most of these systems were continuous in space (if not time) and nonlinear, so the complexity of their behavior was not entirely surprising. Wolfram's demonstration of complex behavior in simple cellular automata is more surprising—and disturbing, at least to a deterministic world view.

So far I have focused on scientific challenges to determinism, but the longest-standing objection is the conflict between determinism and human free will. Complexity science provides an approach that may resolve this apparent conflict, but I will stop there for now.

5.7 Structures

The behavior of Class 4 CAs is even more surprising. Several 1-D CAs, most notably Rule 110, are **Turing complete**, which means that they can compute any computable function. This property, also called **universality**, was proved by Matthew Cook in 1998. See `http://en.wikipedia.org/wiki/Rule_110`.

Here is a what Rule 110 looks like with an initial condition of a single cell and 100 timesteps:



At this time scale it is not apparent that anything special is going on. There are some regular patterns but also some features that are hard to characterize.

Figure 5.7 shows a bigger picture, starting with a random initial condition and 600 timesteps:

After about 100 steps the background settles into a simple repeating pattern, but there are a number of persistent structures that appear as disturbances in the background. Some of these structures are stable, so they appear as vertical lines. Others translate in space, appearing as diagonals with different slopes, depending on how many time steps they take to shift by one column. These structures are sometimes called **spaceships**.

Collisions between spaceships yield different results depending on the types of the spaceships and the phase they are in when they collide. Some collisions annihilate both ships; others leave one ship unchanged; still others yield one or more ships of different types.

These collisions are the basis of computation in a Rule 110 CA. If you think of spaceships as signals that propagate on wires, and collisions as gates that compute logical operations like AND and OR, you can see what it means for a CA to perform a computation.

Exercise 5.3 This exercise asks you to experiment with Rule 110 and see how many spaceships you can find.

1. Modify your program from the previous exercises so it starts with an initial condition that yields the stable background pattern.

2. Modify the initial condition by adding different patterns in the center of the row and see which ones yield spaceships. You might want to enumerate all possible patterns

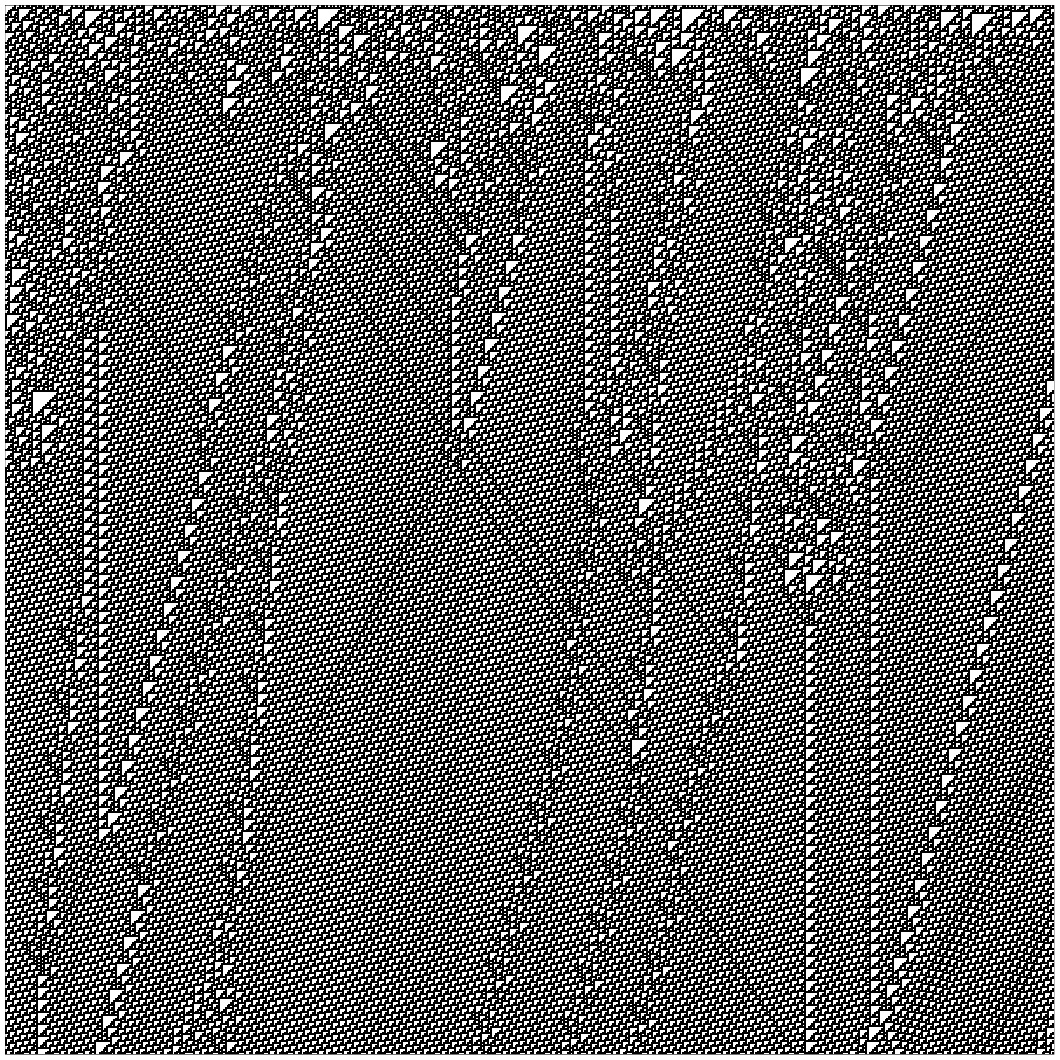


Figure 5.1: Rule 110 with random initial conditions and 600 timesteps.

of n bits, for some reasonable value of n. For each spaceship, can you find the period and rate of translation? What is the biggest spaceship you can find?

5.8 Universality

To understand universality, we have to understand computability theory, which is about models of computation and what they compute.

One of the most general models of computation is the Turing machine, which is an abstract computer proposed by Alan Turing in 1936. A Turing machine is a 1-D CA, infinite in both directions, augmented with a read-write head. At any time, the head is positioned over a single cell. It can read the state of that cell (usually there are only two states) and it can write a new value into the cell.

In addition, the machine has a register, which records which of a finite number of states the machine is in, and a table of rules. For each machine state and cell state, the table specifies an action. Actions include modifying the cell the head is over and moving one cell to the left or right.

A Turing machine is not a practical design for a computer, but it models common computer architectures. For a given program running on a real computer, it is possible (at least in principle) to construct a Turing machine that performs an equivalent computation.

The Turing machine is useful because it is possible to characterize the set of functions that can be computed by a Turing machine, which is what Turing did. Functions in this set are called Turing computable.

To say that a Turing machine can compute any Turing-computable function is a **tautology**: it true by definition. But Turing-computability is more interesting than that.

It turns out that just about every reasonable model of computation anyone has come up with is Turing complete; that is, it can compute exactly the same set of functions as the Turing machine. Some of these models, like lamdba calculus, are very different from a Turing machine, so their equivalence is surprising.

This observation led to the Church-Turing Thesis, which is essentially a definition of what it means to be computable. The "thesis" is that Turing-computability is the right, or at least natural, definition of computability, because it describes the power of such a diverse collection of models of computation.

The Rule 110 CA is yet another model of computation, and remarkable for its simplicity. That it, too, turns out to be universal lends support to the Church-Turing Thesis.

In *A New Kind of Science*, Wolfram states a variation of this thesis, which he calls the "principle of computational equivalence:"

> Almost all processes that are not obviously simple can be viewed as computations of equivalent sophistication.
>
> More specifically, the principle of computational equivalence says that systems found in the natural world can perform computations up to a maximal ("universal") level of computational power, and that most systems do in fact attain

this maximal level of computational power. Consequently, most systems are computationally equivalent[1].

Applying these definitions to CAs, Classes 1 and 2 are "obviously simple." It may be less obvious that Class 3 is simple, but in a way perfect randomness is as simple as perfect order; complexity happens in between. So Wolfram's claim is that Class 4 behavior is common in the natural world, and that almost all of the systems that manifest it are computationally equivalent.

Exercise 5.4 The goal of this exercise is to implement a Turing machine. See `http://en.wikipedia.org/wiki/Turing_machine`.

1. Start with a copy of `CA.py` named `TM.py`. Add attributes to represent the location of the head, the action table and the state register.
2. Override `step` to implement a Turing machine update.
3. For the action table, use the rules for a 3-state busy beaver.
4. Write a class named `TMDrawer` that generates an image that represents the state of the tape and the position and state of the head. For one example of what that might look like, see `http://mathworld.wolfram.com/TuringMachine.html`.

5.9 Falsifiability

Wolfram holds that his principle is a stronger claim than the Church-Turing Thesis because it is about the natural world rather than abstract models of computation. But saying that natural processes "can be viewed as computations" strikes me as a statement about theory choice more than a hypothesis about the natural world.

Also, with qualifications like "almost" and undefined terms like "obviously simple," his hypothesis may be **unfalsifiable**. Falsifiability is an idea from the philosophy of science, proposed by Karl Popper as a demarcation between scientific hypotheses and pseudoscience. A hypothesis is falsifiable if there is an experiment, at least in the realm of practicality, that would contradict the hypothesis if it were false.

For example, the claim that all life on earth is descended from a common ancestor is falsifiable because it makes specific predictions about similarities in the genetics of modern species (among other things). If we discovered a new species whose DNA was almost entirely different from ours, that would contradict (or at least bring into question) the theory of universal common descent.

On the other hand, "special creation," the claim that all species were created in their current form by a supernatural agent, is unfalsifiable because there is nothing that we could observe about the natural world that would contradict it. Any outcome of any experiment could be attributed to the will of the creator.

Unfalsifiable hypotheses can be appealing because they are impossible to refute. If your goal is never to be proved wrong, you should choose hypotheses that are as unfalsifiable as possible.

[1] See `mathworld.wolfram.com/PrincipleofComputationalEquivalence.html`.

But if your goal is to make reliable predictions about the world—and this is at least one of the goals of science—then unfalsifiable hypotheses are useless. The problem is that they have no consequences (if they had consequences, they would be falsifiable).

For example, if the theory of special creation were true, what good would it do me to know it? It wouldn't tell me anything about the creator except that he has an "inordinate fondness for beetles. [2]" And unlike the theory of common descent, which informs many areas of science and bioengineering, it would be of no use for understanding the world or acting in it.

Exercise 5.5 Falsifiability is an appealing and useful idea, but among philosophers of science it is not generally accepted as a solution to the demarcation problem, as Popper claimed.

Read `wikipedia.org/wiki/Falsifiability` and answer the following questions.

1. What is the demarcation problem?
2. How, according to Popper, does falsifiability solve the demarcation problem?
3. Give an example of two theories, one considered scientific and one considered unscientific, that are successfully distinguished by the criterion of falsifiability.
4. Can you summarize one or more of the objections that philosophers and historians of science have raised to Popper's claim?
5. Do you get the sense that practicing philosophers think highly of Popper's work?

5.10 What is this a model of?

Some cellular automata are primarily mathematical artifacts. They are interesting because they are surprising, or useful, or pretty, or because they provide tools for creating new mathematics (like the Church-Turing thesis).

But it is not clear that they are models of physical systems. And if they are, they are highly abstracted, which is to say that they are not very detailed or realistic. For example, some species of cone snail produce a pattern on their shells that resembles the patterns generated by cellular automata. See `en.wikipedia.org/wiki/Cone_snail`.

So it is natural to suppose that a CA is a model of the mechanism that produces patterns on shells as they grow. But, at least initially, it is not clear how the elements of the model (so-called cells, communication between neighbors, rules) correspond to the elements of a growing snail (real cells, chemical signals, protein interaction networks).

For conventional physical models, being realistic is a virtue, at least up to a point. If the elements of a model correspond to the elements of a physical system, there is an obvious analogy between the model and the system. In general, we expect a model that is more realistic to make better predictions and to provide more believable explanations.

[2] Attributed to J. B. S. Haldane.

Of course, this is only true up to a point. Models that are more detailed are harder to work with, and less likely to be amenable to analysis. At some point, a model can be so complex that it is easier to experiment with a real system.

At the other extreme, simple models can be compelling exactly because they are simple.

Simple models offer a different kind of explanation than detailed models. With a detailed model, the argument goes something like this: "We are interested in physical system S, so we construct a detailed model, M, and show by analysis and simulation that M exhibits a behavior, B, that is similar (qualitatively or quantitatively) to an observation of the real system, O. So why does O happen? Because S is similar to M, and B is similar to O, and we can prove that M leads to B."

With simple models we can't claim that S is similar to M, because it isn't. Instead, the argument goes like this: "There is a set of models, $M_0, M_1, ...$ that share a common set of features, $F_0, F_1, ...$.

Any model that has these features exhibits behavior B, and M_0 is the simplest. If we make an observation, O, that resembles B, one way to explain it is to show that the system, S, has the set of features in common with M_0 that produce B.

For this kind of argument, adding more features doesn't help. Making the model more realistic doesn't make the model more reliable; it only obscures the difference between the essential features that cause O and the incidental features that are particular to S.

Chapter 6

Game of Life

One of the first cellular automata to be studied, and probably the most popular of all time, is a 2-D CA called "The Game of Life," or GoL for short. It was developed by John H. Conway and popularized in 1970 in Martin Gardner's column in *Scientific American*. See `http://en.wikipedia.org/wiki/Conway_Game_of_Life`.

The cells in GoL are arranged in a 2-D **grid**, either infinite in both directions or wrapped around. A grid wrapped in both directions is called a **torus** because it is topographically equivalent to the surface of a doughnut. See `wikipedia.org/wiki/Torus`.

Each cell has two states—live and dead—and 8 neighbors—north, south, east, west, and the four diagonals. This set of neighbors is sometimes called a Moore neighborhood.

The rules of GoL are **totalistic**, which means that the next state of a cell depends on the number of live neighbors only, not on their arrangement. The following table summarizes the rules:

Number of neighbors	Current state	Next state
2–3	live	live
0–1,4–8	live	dead
3	dead	live
0–2,4–8	dead	dead

This behavior is loosely analogous to real cell growth: cells that are isolated or overcrowded die; at moderate densities they flourish.

GoL is popular because:

- There are simple initial conditions that yield surprisingly complex behavior.
- There are many interesting stable patterns: some oscillate (with various periods) and some move like the spaceships in Wolfram's Rule 110 CA.
- Like Rule 110, GoL is Turing complete.

- Conway posed an intriguing conjecture—that there is no initial condition that yields unbounded growth in the number of live cells—and offered $50 to anyone who could prove or disprove it.
- The increasing availability of computers made it possible to automate the computation and display the results graphically. That turns out to be more fun that Conway's original implementation using a checkerboard.

6.1 Implementing Life

To implement GoL efficiently, we can take advantage of the multi-dimensional convolution function in SciPy. SciPy is a Python package that provides functions related to scientific computing You can read about it at `http://www.scipy.org/`; if it is not already on your system, you might have to install it.

Convolution is an operation common in digital image processing, where an image is an array of pixels, and many operations involve computing a function of a pixel and its neighbors.

The neighborhood is described by a smaller array, called a **kernel** that specifies the location and **weight** of the neighbors. For example, this array:

```
    kernel = numpy.array([[1,1,1],
                          [1,0,1],
                          [1,1,1]])
```

represents a neighborhood with eight neighbors, all with weight 1.

Convolution computes the weighted sum of the neighbors for each element of the array. So this kernel computes the sum of the neighbors (not including the center element).

For example, if `array` represents a GoL grid with 1s for live cells and 0s for dead cells we can use convolution to compute the number of neighbors for each cell.

```
    import scipy.ndimage
    neighbors = scipy.ndimage.filters.convolve(array, kernel)
```

Here's an implementation of GoL using `convolve`:

```
import numpy
import scipy.ndimage

class Life(object):

    def __init__(self, n, mode='wrap'):
        self.n = n
        self.mode = mode
        self.array = numpy.random.random_integers(0, 1, (n, n))
        self.weights = numpy.array([[1,1,1],
                                    [1,10,1],
                                    [1,1,1]])

    def step(self):
        con = scipy.ndimage.filters.convolve(self.array,
                                             self.weights,
                                             mode=self.mode)

        boolean = (con==3) | (con==12) | (con==13)
        self.array = numpy.int8(boolean)
```

The attributes of the `Life` object are `n`, the number of rows and columns in the grid, `mode`, which controls the behaviors of the boundary cells, `array`, which represents the grid, and `weights` which is the kernel used to count the neighbors.

The weight of the center cell is 10, so the number of neighbors is 0-8 for dead cells and 10-18 for live cells.

In `step`, `boolean` is a boolean array with `True` for live cells; `numpy.int8` converts it to integers.

To display an animated sequence of grids, I use `pyplot`. Animation in `pyplot` is a little awkward, but here's a class that manages it:

```
import matplotlib
matplotlib.use('TkAgg')
import matplotlib.pyplot as pyplot


class LifeViewer(object):

    def __init__(self, life, cmap=matplotlib.cm.gray_r):
        self.life = life
        self.cmap = cmap

        self.fig = pyplot.figure()
        pyplot.axis([0, life.n, 0, life.n])
        pyplot.xticks([])
        pyplot.yticks([])

        self.pcolor = None
        self.update()
```

`life` is a `Life` object. `cmap` is a color map provided by `matplotlib`; you can see the other color maps at `http://www.scipy.org/Cookbook/Matplotlib/Show_colormaps`.

`self.fig` is a reference to the `matplotlib` figure, and `self.pcolor` is a reference to the **pseudocolor plot** created by `update`:

```
    def update(self):
        if self.pcolor:
            self.pcolor.remove()

        a = self.life.array
        self.pcolor = pyplot.pcolor(a, cmap=self.cmap)
        self.fig.canvas.draw()
```

If there is already a plot, we have to remove it; then we create a new one and invoke `draw` to update the display.

To run the animation, we need two methods:

```
    def animate(self, steps=10):
        self.steps = steps
        self.fig.canvas.manager.window.after(1000, self.animate_callback)
        pyplot.show()

    def animate_callback(self):
        for i in range(self.steps):
            self.life.step()
            self.update()
```

`animate` gets the animation started. It invokes `pyplot.show`, which sets up the GUI and waits for user events, but *first* it has to invoke `window.after` to set up a callback, so that `animate_callback` gets invoked after the window is set up. The first argument is the delay in milliseconds. The second argument is a bound method (see Chapter 19 of *Think Python*).

`animate_callback` invokes `step` to update the `Life` object and `update` to update the display.

Exercise 6.1 Download my implementation of GoL from `thinkcomplex.com/Life.py`.

Start the CA in a random state and run it until it stabilizes. What stable patterns can you identify?

6.2 Life patterns

If you run GoL from a random starting state, a number of stable patterns are likely to appear. Blocks, boats, beehives, blinkers and gliders are among the most common.

People have spent embarrassing amounts of time finding and naming these patterns. If you search the web, you will find many collections.

From most initial conditions, GoL quickly reaches a stable state where the number of live cells is nearly constant (usually with a small amount of oscillation).

But there are a some simple starting conditions that take a long time to settle down and yield a surprising number of live cells. These patterns are called "Methuselahs" because they are so long-lived.

One of the simplest is the r-pentomino, which has only five cells in the shape of a "r," hence the name. It runs for 1103 steps and yields 6 gliders, 8 blocks, 4 blinkers, 4 beehives, 1 boat, 1 ship, and 1 loaf. One of the longest-lived small patterns is rabbits, which starts with 9 live cells and takes 17 331 steps to stabilize.

Exercise 6.2 Start with an r-pentomino as an initial condition and confirm that the results are consistent with the description above. You might have to adjust the size of the grid and the boundary behavior.

6.3 Conway's conjecture

The existence of long-lived patterns bring us back to Conway's original question: are there initial patterns that never stabilize? Conway thought not, but he described two kinds of pattern that would prove him wrong, a "gun" and a "puffer train." A gun is a stable pattern that periodically produces a spaceship—as the stream of spaceships moves out from the source, the number of live cells grows indefinitely. A puffer train is a translating pattern that leaves live cells in its wake.

It turns out that both of these patterns exist. A team led by Bill Gosper discovered the first, a glider gun now called Gosper's Gun. Gosper also discovered the first puffer train. You can find descriptions and animations of these patterns in several places on the Web.

There are many patterns of both types, but they are not easy to design or find. That is not a coincidence. Conway chose the rules of GoL so that his conjecture would not be obviously true or false. Of all the possible rules for a 2-D CA, most yield simple behavior; most initial conditions stabilize quickly or grow unboundedly. By avoiding uninteresting CAs, Conway was also avoiding Wolfram's Class 1 and Class 2 behavior, and probably Class 3 as well.

If we believe Wolfram's Principle of Computational Equivalence, we expect GoL to be in Class 4. And it is. The Game of Life was proved Turing complete in 1982 (and again, independently, in 1983). Since then several people have constructed GoL patterns that implement a Turing machine or another machine known to be Turing complete.

Exercise 6.3 Many named patterns are available in portable file formats. Modify `Life.py` to parse one of these formats and initialize the grid.

6.4 Realism

Stable patterns in GoL are hard not to notice, especially the ones that move. It is natural to think of them as persistent entities, but remember that a CA is made of cells; there is no such thing as a toad or a loaf. Gliders and other spaceships are even less real because they are not even made up of the same cells over time. So these patterns are like constellations of stars. We perceive them because we are good at seeing patterns, or because we have active imaginations, but they are not real.

Right?

Well, not so fast. Many entities that we consider "real" are also persistent patterns of entities at a smaller scale. Hurricanes are just patterns of air flow, but we give them personal names. And people, like gliders, are not made up of the same cells over time. But even if you replace every cell in your body, we consider you the same person.

This is not a new observation—about 2500 years ago Heraclitus pointed out that you can't step in the same river twice—but the entities that appear in the Game of Life are a useful test case for thinking about **philosophical realism**.

In the context of philosophy, realism is the view that entities in the world exist independent of human perception and conception. By "perception" I mean the information that we get from our senses, and by "conception" I mean the mental model we form of the world. For example, our vision systems perceive something like a 2-D projection of a scene, and our brains use that image to construct a 3-D model of the objects in the scene.

Scientific realism pertains to scientific theories and the entities they postulate. A theory postulates an entity if it is expressed in terms of the properties and behavior of the entity. For example, Mendelian genetics postulated a "gene" as a unit that controls a heritable characteristic. Eventually we discovered that genes are encoded in DNA, but for about 50 years, a gene was just a postulated entity. See `http://en.wikipedia.org/wiki/Gene`.

Again, I find it useful to state philosophical positions in a range of strengths, where SR1 is a weak form of scientific realism and SR4 is a strong form:

SR1: Scientific theories are true or false to the degree that they approximate reality, but no theory is exactly true. Some postulated entities may be real, but there is no principled way to say which ones.

SR2: As science advances, our theories become better approximations of reality. At least some postulated entities are known to be real.

SR3: Some theories are exactly true; others are approximately true. Entities postulated by true theories, and some entities in approximate theories, are real.

SR4: A theory is true if it describes reality correctly, and false otherwise. The entities postulated by true theories are real; others are not.

SR4 is so strong that it is probably untenable; by such a strict criterion, almost all current theories are known to be false. Most realists would accept something in the space between SR1 and SR3.

6.5 Instrumentalism

But SR1 is so weak that it verges on **instrumentalism**, which is the view that we can't say whether a theory is true or false because we can't know whether a theory corresponds to reality. Theories are instruments that we use for our purposes; a theory is useful, or not, to the degree that it is fit for its purpose.

To see whether you are comfortable with instrumentalism, consider the following statements:

> "Entities in the Game of Life aren't real; they are just patterns of cells that people have given cute names."

> "A hurricane is just a pattern of air flow, but it is a useful description because it allows us to make predictions and communicate about the weather."

> "Freudian entities like the Id and the Superego aren't real, but they are useful tools for thinking and communicating about psychology (or at least some people think so)."

> "Electrons are postulated entities in our best theories of electro-magnetism, but they aren't real. We could construct other theories, without postulating electrons, that would be just as useful."
>
> "Many of the things in the world that we identify as objects are arbitrary collections like constellations. For example, a mushroom is just the fruiting body of a fungus, most of which grows underground as a barely-contiguous network of cells. We focus on mushrooms for practical reasons like visibility and edibility."
>
> "Some objects have sharp boundaries, but many are fuzzy. For example, which molecules are part of your body: Air in your lungs? Food in your stomach? Nutrients in your blood? Nutrients in a cell? Water in a cell? Structural parts of a cell? Hair? Dead skin? Dirt? Bacteria on your skin? Bacteria in your gut? Mitochondria? How many of those molecules do you include when you weigh yourself. Conceiving the world in terms of discrete objects is useful, but the entities we identify are not real."

Give yourself one point for each statement you agree with. If you score 4 or more, you might be an instrumentalist!

If you are more comfortable with some of these statements than with others, ask yourself why. What are the differences in these scenarios that influence your reaction? Can you make a principled distinction between them?

Exercise 6.4 Read `http://en.wikipedia.org/wiki/Instrumentalism` and construct a sequence of statements that characterize instrumentalism in a range of strengths.

6.6 Turmites

If you generalize the Turing machine to two dimensions, or add a read-write head to a 2-D CA, the result is a cellular automaton called a Turmite. It is named after a termite because of the way the read-write head moves, but spelled wrong as an homage to Turing.

The most famous Turmite is Langton's Ant, discovered by Chris Langton in 1986. See `http://en.wikipedia.org/wiki/Langton_ant`.

The ant is a read-write head with four states, which you can think of as facing north, south, east or west. The cells have two states, black and white.

The rules are simple. During each time step, the ant checks the color of the cell is it on. If it is black, the ant turns to the right, changes the cell to white, and moves forward one space. If the cell is white, the ant turns left, changes the cell to black, and moves forward.

Given a simple world, a simple set of rules, and only one moving part, you might expect to see simple behavior—but you should know better by now. Starting with all white cells, Langton's ant moves in a seemingly random pattern for more than 10 000 steps before it enters a cycle with a period of 104 steps. After each cycle, the ant is translated diagonally, so it leaves a trail called the "highway."

If you start with multiple Turmites, they interact with each other in seemingly complex ways. If one Turmite is on the highway, another can follow it, overtake it, and cause it to reverse its pattern, moving back up the highway and leaving only white cells behind.

Exercise 6.5 Write an implementation of Langton's Ant.

You can find a solution in `TurmiteWorld.py`, which is part of Swampy. See `http://thinkpython.com/swampy/`.

Chapter 7

Fractals

To understand fractals, we have to start with dimensions. The dimension of a space is the number of coordinates we need to specify a point in a space. A number line takes one coordinate, a Euclidean plane takes 2, a solid takes 3, etc. See `http://en.wikipedia.org/wiki/Dimension`.

For simple geometric objects, dimension is defined in terms of scaling behavior; that is, how "size" depends on length, l. For example, the area of a square is l^2; the exponent, 2, indicates that a square is 2-dimensional. Similarly, the volume of a cube is l^3 and a cube is 3-dimensional. A line has dimension 1 and, if we think of a point as infinitesimally small, it has dimension 0.

Fractal dimension is a more precise and more general extension of this definition. There are several versions; the one I find easiest to understand and apply is the **box-counting dimension**, which is defined for a set, S, of points in a d-dimensional space. See `http://en.wikipedia.org/wiki/Box-counting_dimension`.

To compute the box-counting dimension, we divide the space into a grid where the size of each cell is ε. Then we count $N(\varepsilon)$, the number of cells that contain at least one element of S. As ε gets smaller, $N(\varepsilon)$ gets bigger. For many objects the relationship has the form:

$$N(\varepsilon) \sim (1/\varepsilon)^D$$

The box counting dimension, D_{box}, is defined to be the exponent, D. Taking the log of both sides and rearranging yields:

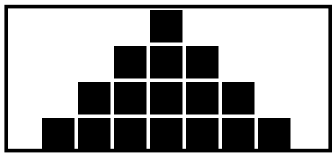
$$D_{box} = \frac{log N(\varepsilon)}{log\,(1/\varepsilon)}$$

More formally, D_{box} is the limit of this ratio as ε goes to zero.

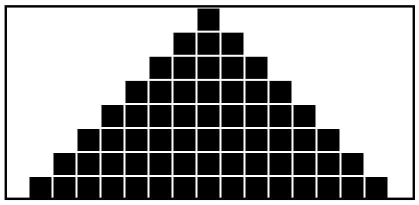
7.1 Fractal CAs

To investigate the behavior of fractal dimension, we'll apply it to cellular automata. Box-counting for CAs is simple; we just count the number of "on" cells.

As an example, consider Rule 254. Here's what it looks like after $t = 4$ time steps.



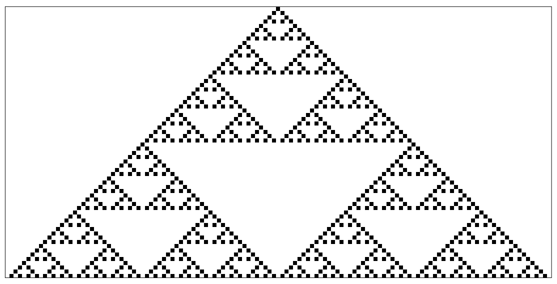
And here's what it looks like after $t = 8$ time steps:



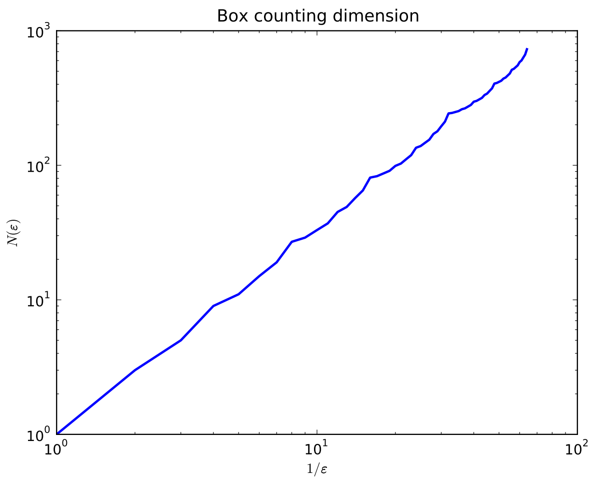
As t increases, we can imagine the triangle getting bigger, but for purposes of box-counting, it makes more sense to imagine the cells getting smaller. In that case the size of the cells, ε, is just $1/t$.

After 1 time step, there is 1 black cell. After 2 time steps, there are a total of 4, then 9, then 16, then 25. As expected, the area of the triangle goes up quadratically. More formally, $N(\varepsilon) = (1/\varepsilon)^2$, so $D_{box} = 2$. And we conclude that a triangle is 2-dimensional.

Rule 18 is more interesting. Here's what it looks like after 64 steps:



And here's $N(\varepsilon)$ versus $1/\varepsilon$ on a log-log scale:



To estimate D_{box} I fit a line to this curve; its slope is 1.56. D_{box} is a non-integer, which means that this set of points is a **fractal**. As t increases, the slope approaches $log3/log2$, which is the fractal dimension of Sierpiński's triangle. See `wikipedia.org/wiki/Sierpinski_triangle`.

Exercise 7.1 Write a function that takes a CA object, plots $N(\varepsilon)$ versus $1/\varepsilon$, where $\varepsilon = 1/t$, and estimates D_{box}.

Can you find other CAs with non-integer fractal dimensions? Be careful, you might have to run the CA for a while before D_{box} converges.

Here are some functions from `numpy` you might find useful: `cumsum`, `log`, and `polyfit`.

You can download my solution from `fractal.py`.

Exercise 7.2 In 1990 Bak, Chen and Tang proposed a cellular automaton that is an abstract model of a forest fire. Each cell is in one of three states: empty, occupied by a tree, or on fire.

The rules of the CA are:

1. An empty cell becomes occupied with probability p.
2. A cell with a tree burns if any of its neighbors is on fire.
3. A cell with a tree spontaneously burns, with probability f, even if none of its neighbors is on fire.
4. A cell with a burning tree becomes an empty cell in the next time step.

Read about this model at `http://en.wikipedia.org/wiki/Forest-fire_model` and write a program that implements it. You might want to start with a copy of `thinkcomplex.com/Life.py`.

Starting from a random initial condition, run the CA until it reaches a steady state where the number of trees no longer increases or decreases consistently. You might have to tune p and f.

In steady state, is the geometry of the forest fractal? What is its fractal dimension?

7.2 Percolation

The CAs we have seen so far are not physical models; that is, they are not intended to describe systems in the real world.

But some CAs are designed explicitly as physical models. In this section we consider a simple grid-based model of percolation; in the next chapter we see examples that model forest fires, avalanches, and earthquakes.

Percolation is a process in which a fluid flows through a semi-porous material. Examples include oil in rock formations, water in paper, and hydrogen gas in micropores. Percolation models are also used to study systems that are not literally percolation, including epidemics and networks of electrical resistors. See `http://en.wikipedia.org/wiki/Percolation_theory`.

Percolation processes often exhibit a phase change; that is, an abrupt transition from one behavior (low flow) to another (high flow) with a small change in a continuous parameter (like the porosity of the material). This transition is sometimes called a "tipping point."

There are two common models of these systems: bond percolation and site percolation. Bond percolation is based on a grid of sites, where each site is connected to four neighbors by a bond. Each bond is either porous or non-porous. A set of sites that are connected (directly or indirectly) by porous bonds is called a cluster. In the vocabulary of graphs, a site is a vertex, a bond is an edge, and a cluster is a connected subgraph.

Site percolation is based on a grid of cells, where each cell represents a porous segment of the material or a non-porous segment. If two porous cells are adjacent, they are considered connected; a set of connected cells is considered a cluster.

The rate of flow in a percolation system is primarily determined by whether or not the porous cells form a path all the way through the material, so it is useful to know whether a set of cells (or bonds) contains a "spanning cluster." There are several definitions of a spanning cluster; the choice depends on the system you are trying to model. The simplest choice is a cluster that reaches the top and bottom row of the grid.

To model the porosity of the material, it is common to define a parameter, p, which the probability that any cell (or bond) is porous. For a given value of p, you can estimate $R(p)$, which is the probability that there is a spanning cluster, by generating a large number of random grids and computing the fraction that contain a spanning cluster. This way of estimating probabilities is called a "Monte Carlo simulation" because it a similar to a game of chance.

Percolation models are often used to compute a critical value, p_c, which is the fraction of porous segments where the phase change occurs; that is, where the probability of a spanning cluster increases quickly from near 0 to near 1.

Exercise 7.3 The paper "Efficient Monte Carlo Algorithm and High-Precision Results for Percolation," by Newman and Ziff, presents an efficient algorithm for checking whether there is a path through a grid. Read this paper, implement their algorithm, and see if you can reproduce their Figure 2(a).

1. What is the difference between what Newman and Ziff call the "microcanonical ensemble" and the "canonical ensemble"[1]? Which one is easier to estimate by Monte Carlo simulation?

2. What algorithm do they use to merge two clusters efficiently?

3. What is the primary reason their algorithm is faster than the simpler alternative?

[1] You might find it useful to read about the use of these terms in statistical mechanics: `wikipedia.org/wiki/Statistical_mechanics`.

Chapter 8

Self-organized criticality

8.1 Sand piles

In 1987 Bak, Tang and Wiesenfeld published a paper in Physical Review Letters, "Self-organized criticality: an explanation of $1/f$ noise." The title takes some explaining. A system is "critical" if it is in transition between two phases; for example, water at its freezing point is a critical system.

A variety of critical systems demonstrate common behaviors:

- Long-tailed distributions of some physical quantities: for example, in freezing water the distribution of crystal sizes is characterized by a power law.
- Fractal geometries: freezing water tends to form fractal patterns—the canonical example is a snowflake. Fractals are characterized by self-similarity; that is, parts of the pattern resemble scaled copies of the whole.
- Variations in time that exhibit pink noise: what we call "noise" is a time series with many frequency components. In "white" noise, all of the components have equal power. In "pink" noise, low-frequency components have more power than high-frequency components. Specifically, the power at frequency f is proportional to $1/f$. Visible light with this power spectrum looks pink, hence the name.

Critical systems are usually unstable. For example, to keep water in a partially frozen state requires active control of the temperature. If the system is near the critical temperature, a small deviation tends to move the system into one phase or the other.

Many natural systems exhibit characteristic behaviors of criticality, but if critical points are unstable, they should not be common in nature. This is the puzzle Bak, Tang and Wiesenfeld address. Their solution is called self-organized criticality (SOC), where "self-organized" means that from any initial condition, the system tends to move toward a critical state, and stay there, without external control.

As an example, they propose a model of a sand pile. The model is not realistic, but it has become the standard example of self-organized criticality.

The model is a 2-D cellular automaton where the state of each cell, $z(i, j)$, represents the slope of a part of a sand pile. During each time step, each cell is checked to see whether it exceeds some critical value, K. If so, an "avalanche" occurs that transfers sand to neighboring cells; specifically, $z(i, j)$ is decreased by 4, and each of the 4 neighbors is increased by 1.

At the perimeter of the grid, all cells are kept at $z = 0$, so the excess spills over the edge. To initialize the system, Bak et al. start with all $z > K$ and evolve the system until it stabilizes. Then they observe the effect of small perturbations; they choose a cell at random, increment its value by 1, and evolve the system, again, until it stabilizes.

For each perturbation, they measure D, the total number of cells that are affected by the resulting avalanche. Most of the time, D is small, usually 1. But occasionally a large avalanche affects a substantial fraction of the grid. The distribution of D turns out to be long-tailed, which supports the claim that the system is in a critical state.

Exercise 8.1 Read the paper and write a program that implements their CA. You might want to start with a copy of `thinkcomplex.com/Life.py`.

See if you can reproduce their Figure 2(a), which shows the distribution of cluster sizes.

After the system has been running for a while, compute its fractal dimension.

8.2 Spectral density

To understand $1/f$ noise, we have to take a detour to understand spectral density. If $h(t)$ is a signal that varies in time, it can be described by its power spectral density, $P(f)$, which is a function that maps from a frequency, f, to the amount of power the signal contains at that frequency.

This analysis applies to any varying signal, but I use sound as an example. The note we call "middle A" corresponds to a frequency of 440 cycles per second, or Hertz (Hz). If you strike a middle A tuning fork, it produces a sound that is close to a pure sine wave at 440 Hz. But if you play the same note on a piano, what you hear is a complex sound that contains components at many different frequencies. The frequency with the most power is 440, which is why we perceive the sound as a middle A, but there are also components at 660, 880, and many higher frequencies. These components are called "harmonics."

What we identify as the pitch of a sound is usually the dominant frequency component. But if a sound contains many different components with roughly the same power, it has no particular pitch. To our ears, it sounds like noise.

Spectral analysis is the process of taking a signal and computing its spectral density[1]. The first step is to compute the Fourier transform of $h(t)$:

$$H(\omega) = \int_{-\infty}^{\infty} h(t) e^{i\omega t} dt$$

[1]The presentation here follows Press et al, *Numerical Recipes in C.*

where $\omega = 2\pi f$ is the angular frequency in radians per second (rather than cycles per second). The advantage of working with angular frequency is that it reduces the number of times the term 2π appears.

$H(\omega)$ is written with a capital letter because it is a complex number, which you can think of as a vector with a magnitude, $|H(\omega)|$, and an angle. The power spectral density is related to the Fourier transform by the following relation:

$$P(f) = |H(2\pi f)|^2$$

Depending on the application, we may not care about the difference between f and $-f$. In that case, we would use the one-sided power spectral density:

$$P(f) = |H(2\pi f)|^2 + |H(-2\pi f)|^2$$

So far we have assumed that $h(t)$ is a continuous function, but often it is a series of values at discrete times. In that case we can replace the continuous Fourier transform with the discrete Fourier transform (DFT). Suppose that we have N values h_k with k in the range from 0 to $N-1$. The DFT is written H_n, where n is an index related to frequency:

$$H_n = \sum_{k=0}^{N-1} h_k e^{2\pi ikn/N} \tag{8.1}$$

Each element of this sequence corresponds to a particular frequency. If the elements of h_k are equally spaced in time, with time step d, the frequency that corresponds to H_n is

$$f_n = \frac{n}{Nd}$$

To get the one-sided power spectral density, you can compute H_n with n in the range $-N/2$ to $N/2$, and

$$P_n = |H_n|^2 + |H_{-n}|^2$$

To avoid negative indices, it is conventional to compute H_n with n in the range 0 to $N-1$ and use the relation $H_{-n} = H_{N-n}$ to convert.

Exercise 8.2 Write a function named `dft` that takes h, a sequence of N values, and returns the sequence H_n with n in the range 0 to $N-1$.

Python provides support for complex numbers as a built-in type. The function `complex` takes two arguments, a real part and an imaginary part, and returns a complex number:

```
>>> complex(1, 1)
(1+1j)
```

The `cmath` module provides math functions that support complex numbers:

```
>>> import cmath
>>> i = complex(0, 1)
>>> N = 128
>>> cmath.exp(2 * math.pi * i / N)
(0.99879545620517241+0.049067674327418015j)
```

What is the order of growth run time of `dft`?

Hoisting is a way to speed up code by moving an expression that does not change out of a loop. See `http://en.wikipedia.org/wiki/Loop-invariant_code_motion`. You can make your code easier to read and more efficient by hoisting:

$$W = e^{2\pi i/N} \tag{8.2}$$

What effect does hoisting have on the order of growth?

8.3 Fast Fourier Transform

The Fast Fourier Transform (FFT) is an efficient algorithm for computing the DFT. It is often attributed to Cooley and Tukey, but it was independently discovered several times earlier. See `http://en.wikipedia.org/wiki/Fast_Fourier_transform`.

The first step toward the FFT is to rewrite Equation 8.1 with the substitution $W = e^{2\pi i/N}$:

$$H_n = \sum_{k=0}^{N-1} h_k W^{nk} \tag{8.3}$$

The second step is the Danielson-Lanczos Lemma which states

$$H_n = H_n^e + W^k H_n^o$$

where H^e is the DFT of the even-indexed elements of h, and H^o is the DFT of the odd-indexed elements. This lemma follows naturally from the definition of H_n; you can see a proof at `mathworld.wolfram.com/Danielson-LanczosLemma.html`.

This lemma suggests a recursive algorithm for evaluating the DFT of a sequence h. If h has only a single element, then $H = h$. Otherwise:

1. Split h into h^e and h^o.
2. Compute H^e and H^o by making two recursive calls.
3. Use the lemma to combine H^e and H^o to form H.

If H has $2N$ elements, H^e and H^o have only N. In order to merge them, you have to wrap around, but you can do that because $H^e_{n+N} = H^e_n$.

This recursive algorithm is the Fast Fourier Transform.

Exercise 8.3 Write a function called `fft` that implements the Fast Fourier Transform. To check your function, you can compare it to the function `fft` provided by the module `numpy.fft`.

What is the order of growth run time of your implementation? What is the order of growth for the space required?

Most FFT implementations use a clever indexing scheme to avoid copying the sequence; instead, they transform the elements in place. You can read `wikipedia.org/wiki/Butterfly_diagram` to get the details.

Once your `fft` is working, write a function named `psd` that takes a sequence, h, and returns its one-sided power spectral density, P.

You can download my solution from `thinkcomplex.com/Fourier.py`.

8.4 Pink noise

In a followup paper in 1988, Bak, Tang and Wiesenfeld looked at a time series $F(t)$, which is the number of cells that exceed the threshold during each time step. If I understand their model, they seed avalanches by incrementing the state of a random cell at random intervals; for example, there might be a fixed probability during each time step that a cell is incremented. In this model (unlike the previous one) there may be more than one avalanche at a time.

A plot of $F(t)$ shows that it is noisy, but not completely random, which is consistent with pink, or $1/f$ noise. As a stronger test, they plot the power spectral density of F on a log-log scale. If F is $1/f$ noise, then

$$P_n \sim 1/f_n = \frac{Nd}{n}$$

Since the units of time in this model are arbitrary, we can choose $d = 1$. Taking the log of both sides yields:

$$\log P_n \sim \log N - \log n$$

So on a log-log scale, the PSD of $1/f$ noise is a straight line with slope -1.

Exercise 8.4 Modify your implementation of the sand pile model to increment a random cell at random intervals and record the number of cells that exceed the threshold during each time step.

To estimate the average PSD, you can divide the time series into chunks of 128 to 256 values, compute the PSD of each chunk, and average together the PSDs. Plot the result on a log-log scale and estimate the slope.

Exercise 8.5 In a 1989 paper, "Self-organized criticality in the 'Game of Life'," Bak, Chen and Creutz present evidence that the Game of Life is a self-organized critical system.

To replicate their tests, run the GoL CA until it stabilizes, then choose a random cell and toggle it. Run the CA until it stabilizes again, keeping track of t, the number of timesteps it takes, and s, the number of cells affected. Repeat for a large number of trials and plot the distributions of t and s. Also, see if you can think of an effective experiment to test for $1/f$ noise.

Some later work has called the conclusions of this paper into question. You might want to read Blok, "Life without bounds," at `zoology.ubc.ca/~rikblok/lib/blok95b.html`.

8.5 Reductionism and Holism

The original paper by Bak, Tang and Wiesenfeld is one of the most frequently-cited papers in the last few decades. Many new systems have been shown to be self-organized critical, and the sand-pile model, in particular, has been studied in detail.

As it turns out, the sand-pile model is not a very good model of a sand pile. Sand is dense and not very sticky, so momentum has a non-negligible effect on the behavior of avalanches. As a result, there are fewer very large and very small avalanches than the model predicts, and the distribution is not long tailed.

Bak has suggested that this observation misses the point. The sand pile model is not meant to be a realistic model of a sand pile; it is meant to be a simple example of a broad category of models.

To understand this point, it is useful to think about two kinds of models, **reductionist** and **holistic**. A reductionist model describes a system by describing its parts and their interactions. When a reductionist model is used as an explanation, it depends on an analogy between the components of the model and the components of the system.

For example, to explain why the ideal gas law holds, we can model the molecules that make up a gas with point masses, and model their interactions as elastic collisions. If you simulate or analyze this model you find that it obeys the ideal gas law. This model is satisfactory to the degree that molecules in a gas behave like molecules in the model. The analogy is between the parts of the system and the parts of the model.

Holistic models are more focused on similarities between systems and less interested in analogous parts. A holistic approach to modeling often consists of two steps, not necessarily in this order:

- Identify a kind of behavior that appears in a variety of systems.
- Find the simplest model that demonstrates that behavior.

For example, in *The Selfish Gene*, Richard Dawkins suggests that genetic evolution is just one example of an evolutionary system. He identifies the essential elements of the category—discrete replicators, variability and differential reproduction—and proposes that any system that has these elements displays similar behavior, including complexity without design.

As another example of an evolutionary system, he proposes memes, which are thoughts or behaviors that are "replicated" by transmission from person to person. As memes compete for the resource of human attention, they evolve in ways that are similar to genetic evolution.

Critics of memetics have pointed out that memes are a poor analogy for genes. Memes differ from genes in many obvious ways. But Dawkins has argued that these differences are beside the point because memes are not *supposed* to be analogous to genes. Rather, memetics and genetics are examples of the same category—evolutionary systems. The differences between them emphasize the real point, which is that evolution is a general model that applies to many seemingly disparate systems.

Bak has made a similar argument that self-organized criticality is a general model for a broad category of systems. According to Wikipedia, "SOC is typically observed in slowly-driven non-equilibrium systems with extended degrees of freedom and a high level of nonlinearity."

Many natural systems demonstrate behaviors characteristic of critical systems. Bak's explanation for this prevalence is that these systems are examples of the broad category of self-organized criticality. There are two ways to support this argument. One is to build a realistic model of a particular system and show that the model exhibits SOC. The second is to show that SOC is a feature of many diverse models, and to identify the essential characteristics those models have in common.

The first approach, which I characterize as reductionist, can explain the behavior of a particular system. The second, holistic, approach, explains the prevalence of criticality in natural systems. They are different models with different purposes.

For reductionist models, realism is the primary virtue, and simplicity is secondary. For holistic models, it is the other way around.

Exercise 8.6 Read `wikipedia.org/wiki/Reductionism` and `wikipedia.org/wiki/Holism`.

Exercise 8.7 In a 1996 paper in Nature, Frette et al report the results of experiments with rice piles. They find that some kinds of rice yield evidence of critical behavior, but others do not.

Similarly, Pruessner and Jensen studied large-scale versions of the forest fire model (using an algorithm similar to Newman and Ziff's). In their 2004 paper, "Efficient algorithm for the forest fire model," they present evidence that the system is not critical after all.

How do these results bear on Bak's claim that SOC explains the prevalence of critical phenomena in nature?

Exercise 8.8 In *The Fractal Geometry of Nature*, Benoit Mandelbrot proposes an alternative explanation for the prevalence of long-tailed distributions in natural systems. It may not be, as Bak suggests, that many systems can generate this behavior in isolation. Instead there may be only a few, but there may be interactions between systems that cause the behavior to propagate.

To support this argument, Mandelbrot points out:

- Interactions between systems may be characterized by operations that are (at least approximately) like convolution. For example, if you choose value a from distribution

A, and independently choose value b from distribution B, the distribution of the sum is the convolution of A and B.

- Long-tailed distributions are stable under convolution; that is, if you convolve a long-tailed distribution with another distribution, the result is long-tailed.

Would you characterize Mandelbrot's argument as reductionist or holist?

8.6 SOC, causation and prediction

If a stock market index drops by a fraction of a percent in a day, there is no need for an explanation. But if it drops 10%, people want to know why. Pundits on television are willing to offer explanations, but the real answer may be that there is no explanation.

Day-to-day variability in the stock market shows evidence of criticality: the distribution of value changes is long-tailed and the time series exhibits $1/f$ noise. If the stock market is a self-organized critical system, we should expect occasional large changes as part of the ordinary behavior of the market.

The distribution of earthquake sizes is also long-tailed, and there are simple models of the dynamics of geological faults that might explain this behavior. If these models are right, they imply that large earthquakes are unexceptional; that is, they do not require explanation any more than small earthquakes do.

Similarly, Charles Perrow has suggested that failures in large engineered systems, like nuclear power plants, are like avalanches in the sand pile model. Most failures are small, isolated and harmless, but occasionally a coincidence of bad fortune yields a catastrophe. When big accidents occur, investigators go looking for the cause, but if Perrow's "normal accident theory" is correct, there may be no cause.

These conclusions are not comforting. Among other things, they imply that large earthquakes and some kinds of accidents are fundamentally unpredictable. It is impossible to look at the state of a critical system and say whether a large avalanche is "due." If the system is in a critical state, then a large avalanche is always possible. It just depends on the next grain of sand.

In a sand-pile model, what is the cause of a large avalanche? Philosophers sometimes distinguish the **proximate** cause, which is most immediately responsible, from the **ultimate** cause, which is, for whatever reason, considered the true cause.

In the sand-pile model, the proximate cause of an avalanche is a grain of sand, but the grain that causes a large avalanche is identical to any other grain, so it offers no special explanation. The ultimate cause of a large avalanche is the structure and dynamics of the systems as a whole: large avalanches occur because they are a property of the system.

Many social phenomena, including wars, revolutions, epidemics, inventions and terrorist attacks, are characterized by long-tailed distributions. If the reason for these distributions is that social systems are critical, that suggests that major historical events may be fundamentally unpredictable and unexplainable.

Exercise 8.9 Read about the "Great Man" theory of history at `wikipedia.org/wiki/Great_man_theory`. What implication does self-organized criticality have for this theory?

Chapter 9

Agent-based models

9.1 Thomas Schelling

In 1971 Thomas Schelling published "Dynamic Models of Segregation," which proposes a simple model of racial segregation. The Schelling model of the world is a grid; each cell represents a house. The houses are occupied by two kinds of "agents," which I label red and blue, in roughly equal numbers. About 10% of the houses are empty.

At any point in time, an agent might be happy or unhappy, depending on the other agents in the neighborhood. The neighborhood of each house is the set of eight adjacent cells. In one version of the model, agents are happy if they have at least two neighbors like themselves, and unhappy if they have one or zero.

The simulation proceeds by choosing an agent at random and checking to see whether it is happy. If so, then nothing happens; if not, the agent chooses one of the unoccupied cells at random and moves.

You might not be surprised to hear that this model leads to some segregation, but you might be surprised by the degree. Fairly quickly, clusters of similar agents appear. The clusters grow and coalesce over time until there are a small number of large clusters and most agents live in homogeneous neighborhoods.

If you did not know the process and only saw the result, you might assume that the agents were racist, but in fact all of them would be perfectly happy in a mixed neighborhood. Since they prefer not to be greatly outnumbered, they might be considered xenophobic at worst. Of course, these agents are a wild simplification of real people, so it may not be appropriate to apply these descriptions at all.

Racism is a complex human problem; it is hard to imagine that such a simple model could shed light on it. But in fact it provides a strong argument about the relationship between a system and its parts: if you observe segregation in a real city, you cannot conclude that individual racism is the immediate cause, or even that the people in the city are racists.

But we have to keep in mind the limitations of this argument: Schelling's model demonstrates a possible cause of segregation, but says nothing about actual causes.

Exercise 9.1 Implement Schelling's model in a grid. From random initial conditions, how does the system evolve?

Define a statistic that measures the degree of segregation, and plot this statistic over time.

Experiment with the parameters of the model. What happens as the agents become more tolerant? What happens if the agents are only happy in mixed neighborhoods; that is, if they are unhappy if too many of their neighbors are like themselves?

Exercise 9.2 In a recent book, *The Big Sort*, Bill Bishop argues that American society is increasingly segregated by political opinion, as people choose to live among like-minded neighbors.

The mechanism Bishop hypothesizes is not that people, like the agents in Schelling's model, are more likely to move if they are isolated, but that when they move for any reason, they are likely to choose a neighborhood with people like themselves.

Modify your implementation of Schelling's model to simulate this kind of behavior and see if it yields similar degrees of segregation.

9.2 Agent-based models

Schelling's model is one of the first, and one of the most famous, agent-based models. Since the 1970s, agent-based modeling has become an important tool in economics and other social sciences, and in some natural sciences.

The characteristics of agent-based models include:

- Agents that model intelligent behavior, usually with a simple set of rules.
- The agents are usually situated in space (or in a network), and interact with each other locally.
- They usually have imperfect, local information.
- Often there is variability between agents.
- Often there are random elements, either among the agents or in the world.

Agent-based models are useful for modeling the dynamics of systems that are not in equilibrium (although they are also used to study equilibrium). And they are particularly useful for understanding relationships between individual decisions and system behavior, or as in the title of Schelling's book, *Micromotives and Macrobehavior*.

For more about agent-based modeling, see `wikipedia.org/wiki/Agent-based_model`.

9.3 Traffic jams

What causes traffic jams? In some cases there is an obvious cause, like an accident, a speed trap, or something else that disturbs the flow of traffic. But other times traffic jams appear for no apparent reason.

Agent-based models can help explain spontaneous traffic jams. As an example, I implemented a simple highway simulation, based on a model in Resnick, *Turtles, Termites and Traffic Jams*.

You can download my program from `thinkcomplex.com/Highway.py`. It uses `TurtleWorld`, which is part of Swampy. See `thinkpython.com/swampy`.

This module defines two classes: `Highway`, which inherits from TurtleWorld, and `Driver`, which inherits from Turtle.

The Highway is a one-lane road that forms a circle, but it is displayed as a series of rows that spiral down the canvas.

Each driver starts with a random position and speed. At each time step, each Driver accelerates or brakes based on the distance between it and the Driver in front. Here is an example:

```
    def choose_acceleration(self, dist):
        if dist < self.safe_distance:
            return -1
        else:
            return 0.3
```

If the following distance is too short, the `Driver` brakes; otherwise it accelerates. In addition, if the current speed would cause a collision, the `Driver` comes to a complete stop. And there is a speed limit for each driver.

If you run `Highway.py` you will probably see a traffic jam, and the natural question is, "Why?" There is nothing about the `Highway` or `Driver` behavior that obviously causes traffic jams.

Exercise 9.3 Experiment with the parameters of the system to identify the factors that are necessary and sufficient to cause traffic jams. Some of the factors to explore are:

Density: What happens as the number of drivers increases (or the length of the highway)?

Acceleration and braking: What happens if drivers accelerate faster or brake more gently?

Safe distance: What happens as the safe distance between drivers changes?

Heterogeneity: What if all drivers are not the same; for example, if they have different speed limits or following distances?

9.4 Boids

In 1987 Craig Reynolds published an article, "Flocks, herds and schools: A distributed behavioral model," that describes an agent-based model of herd behavior. Agents in this models are called "boids," which is both a contraction of "bird-oid" and an accented pronunciation of "bird," (although boids are also used to model fish and herding land animals).

You can read an overview of the boid algorithm at `http://red3d.com/cwr/boids/`. Each agent simulates three behaviors:

Collision avoidance: avoid obstacles, including other birds.

Flock centering: move toward the center of the flock.

Velocity matching: align velocity with neighboring birds.

Boids make decisions based on local information only; each boid only sees (or pays attention to) other boids in its field of vision and range.

The `Visual` package, also known as VPython, is well-suited for implementing boids. It provides simple 3-D graphics as well as vector objects and operations that are useful for the computations.

You can download my implementation from `thinkcomplex.com/Boids.py`. It is based in part on the description of boids in Flake, *The Computational Beauty of Nature*.

The program defines two classes: `Boid`, which implements the boid algorithm, and `World`, which contains a list of Boids and a "carrot" the Boids are attracted to.

The boid algorithm uses `get_neighbors` to find other boids in the field of view:

```
    def get_neighbors(self, others, radius, angle):
        boids = []
        for other in others:
            if other is self:
               continue

            offset = other.pos - self.pos

            # if not in range, skip it
            if offset.mag > radius:
                continue

            # if not within viewing angle, skip it
            if self.vel.diff_angle(offset) > angle:
                continue

            # otherwise add it to the list
            boids.append(other)

        return boids
```

`get_neighbors` uses vector subtraction to compute the vector from `self` to `other`. The magnitude of this vector is the distance to the other boid. `diff_angle` computes the angle between the velocity of `self`, which is also the line of sight, and the other boid.

`center` finds the center of mass of the boids in the field of view and returns a vector pointing toward it:

```
    def center(self, others):
        close = self.get_neighbors(others, r_center, a_center)
        t = [other.pos for other in close]
        if t:
            center = sum(t)/len(t)
            toward = vector(center - self.pos)
            return limit_vector(toward)
        else:
            return null_vector
```

Similarly, `avoid` finds the center of mass of any obstacles in range and returns a vector pointing away from it, `copy` returns the difference between the current heading and the average heading of the neighbors, and `love` computes the heading toward the carrot.

`set_goal` computes the weighed sum of these goals and sets the overall goal:

```
    def set_goal(self, boids, carrot):
        self.goal = (w_avoid * self.avoid(boids, carrot) +
                     w_center * self.center(boids) +
                     w_copy * self.copy(boids) +
                     w_love * self.love(carrot))
```

Finally, `move` updates the velocity, position and attitude of the boid:

```
    def move(self, mu=0.1):
        self.vel = (1-mu) * self.vel + mu * self.goal
        self.vel.mag = 1

        self.pos += dt * self.vel
        self.axis = b_length * self.vel.norm()
```

The new velocity is the weighted sum of the old velocity and the goal. The parameter `mu` determines how quickly the birds can change speed and direction. The time step, `dt` determines how far the boids move.

Many parameters influence flock behavior, including the range, angle and weight for each behavior, and the maneuverability, `mu`.

These parameters determine the ability of the boids to form and maintain a flock and the patterns of motion and organization in the flock. For some settings, the boids resemble a flock of birds; other settings resemble a school of fish or a cloud flying insects.

Exercise 9.4 Run my implementation of the boid algorithm and experiment with different parameters. What happens if you "turn off" one of the behaviors by setting the weight to 0?

To generate more bird-like behavior, Flake suggests adding a fourth behavior to maintain a clear line of sight; in other words, if there is another bird nearly directly ahead, the boid should move away laterally. What effect do you expect this rule to have on the behavior of the flock? Implement it and see.

9.5 Prisoner's Dilemma

The Prisoner's Dilemma is a topic of study in game theory, so it's not the fun kind of game. Instead, it is the kind of game that sheds light on human motivation and behavior.

Here is the presentation of the dilemma from `http://en.wikipedia.org/wiki/Prisoner's_dilemma`.

> Two suspects [Alice and Bob] are arrested by the police. The police have insufficient evidence for a conviction, and, having separated the prisoners, visit each of them to offer the same deal. If one testifies for the prosecution against the other (defects) and the other remains silent (cooperates), the defector goes free and the silent accomplice receives the full one-year sentence. If both remain silent, both prisoners are sentenced to only one month in jail for a minor charge. If each betrays the other, each receives a three-month sentence. Each prisoner must choose to betray the other or to remain silent. Each one is assured that the other would not know about the betrayal before the end of the investigation. How should the prisoners act?

Notice that in this context, "cooperate" means to keep silent, not to cooperate with police.

It is tempting to say that the players should cooperate with each other, since they would both be better off. But neither player knows what the other will do. Looking at it from Bob's point of view:

- If Alice remains silent, Bob is better off defecting.
- If Alice defects, Bob is better off defecting.

Either way, Bob is better off defecting. And from her point of view, Alice reaches the same conclusion. So if both players do the math, and no other factors come into play, we expect them to defect and be worse off for it.

This result is saddening because it is an example of how good intentions can lead to bad outcomes, and, unfortunately, it applies to other scenarios in real life, not just hypothetical prisoners.

But in real life, the game is often iterated; that is, the same players face each other over and over, so they have the opportunity to learn, react and communicate, at least implicitly.

The iterated version of the game is not as easy to analyze; it is not obvious what the optimal strategy is or even whether one exists.

So in the late 1970s Robert Axelrod organized a tournament to compare strategies. He invited participants to submit strategies in the form of computer programs, then played the programs against each other and kept score.

I won't tell you the outcome, and if you don't know you should resist the temptation to look it up. Instead, I encourage you to run your own tournament. I'll provide the referee; you provide the players.

Exercise 9.5 Download `thinkcomplex.com/Referee.py`, which runs the tournament, and `thinkcomplex.com/PlayerFlipper.py`, which implements a simple player strategy.

Here is the code from `PlayerFlipper.py`:

```
def move(history):
    mine, theirs = history
    if len(mine) % 2 == 0:
        return 'C'
    else:
        return 'D'
```

Any file that matches the pattern `Player*.py` is recognized as a player. The file should contain a definition for `move`, which takes the history of the match so far and returns a string: `'D'` for defect and `'C'` for cooperate.

`history` is a pair of lists: the first list contains the player's previous responses in order; the second contains the opponent's responses.

`PlayerFlipper` checks whether the number of previous rounds is even or odd and returns `'C'` or `'D'` respectively.

Write a `move` function in a file like `PlayerFlipper.py`, but replace `Flipper` with a name that summarizes your strategy.

Run `Referee.py` and see how your strategy does.

9.6 Emergence

The examples in this chapter have something in common: emergence. An **emergent property** is a characteristic of a system that results from the interaction of its components, not from their properties.

For example, the agents in Schelling's model are not racist, but the outcome of their interactions is as if they were. Traffic jams move backward even though the cars in them are moving forward or standing still. The behavior of flocks and herds emerges from local interactions between their members. And as Axelrod says about the iterated prisoner's dilemma: "The emergence of cooperation can be explained as a consequence of individual[s] pursuing their own interests."

To clarify what emergence is, we can also consider what it isn't. For example, a brick wall is hard because bricks and mortar are hard, so that's not an emergent property. As another example, some rigid structures are built from flexible components, so that seems like a kind of emergence. But it is at best a weak kind, because structural properties follow from well-understood laws of mechanics.

Emergent properties are surprising: it is hard to predict the behavior of the system, even if we know all the rules. That difficulty is not an accident; it may be the defining characteristic of emergence.

As Wolfram discusses in *A New Kind of Science*, conventional science is based on the axiom that if you know the rules that govern a system, you can predict its behavior. What we call "laws" are often computational shortcuts that allow us to predict the outcome of a system without building or observing it.

But many cellular automata are **computationally irreducible**, which means that there are no shortcuts. The only way to get the outcome is to implement the system.

This result suggests that emergent properties are fundamentally unpredictable, and that studying complex systems requires different methods, what Wolfram calls a new kind of science.

You can read more about emergence at `http://en.wikipedia.org/wiki/Emergence`.

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