

Networks, random walks and statistical optimality

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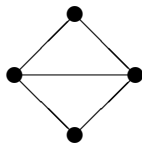
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From some points of view, a network is the same as a graph, although the different names indicate different emphasis in their study.

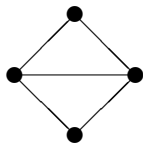
What is a graph?

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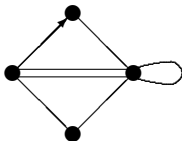


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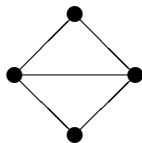


More elaborate graphs could have **loops** joining vertices to themselves; **multiple edges** joining the same pairs of vertices, or **directed edges** like one-way streets:

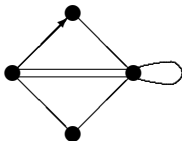


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We can also add further structure such as weights or colours to vertices or edges.

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Another example is in ecology, where the vertices may be species inhabiting the same environment; two species can be in various relations such as predator/prey, symbiotic, parasitic,

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- ▶ Networks may have some associated dynamics.

This may refer to the network itself (e.g. the Web is constantly growing and changing; what processes are involved?), or to the flow of some commodity such as traffic or information in the network.

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Similarly the effect of one gene on another can be quite complicated.

But I will give another example, which involves giving some extra structure to the nodes rather than the edges, namely **network coding**.

Information flow

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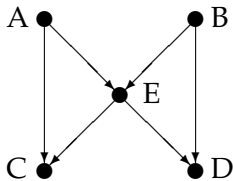
The usual way to deal with this is to decide which aspects of the data are really important and just export these. But people also look at ways of speeding up data transmission. Network coding is one of these.

Network coding

Network coding can be illustrated with a very simple example, the **butterfly network**.

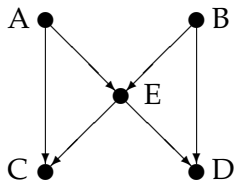
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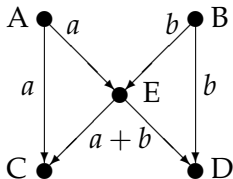
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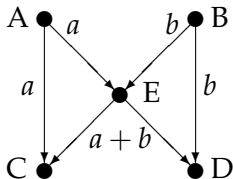
Nodes A and B possess some information in the form of bitstrings a and b . The task is for A to send a to D, and B to send b to C. If it were physical commodities rather than information, it would take two time units to send each bit because of the bottleneck at E.

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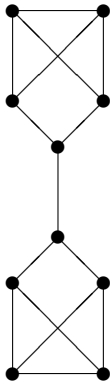
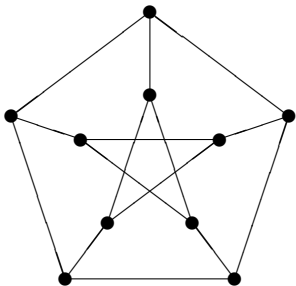


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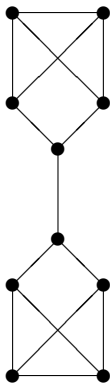
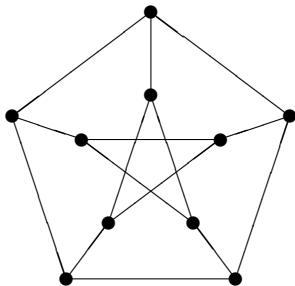


Node A transmits its information a to both C and E, and node B sends b to D and E. Now E adds its two inputs to give $a + b$, which it sends on to C and D. Now C possesses a and $a + b$, and can find b by subtraction; similarly D can find a .

What makes a good network?



What makes a good network?



Suppose you wanted to build a network connecting ten nodes. You could afford to construct fifteen edges. You want the network to be well connected and resilient. Which one of the two shown above would you choose?

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- ▶ A **spanning tree** in a graph is a collection of edges forming a connected subgraph with no cycles (a “minimal connector”). The more spanning trees, the better connected. The first graph has 2000 spanning trees, the second 576.
- ▶ Regarding the graph as an electrical network with each edge being a 1-ohm resistor, we can measure the **effective resistance** between two nodes by connecting a battery and measuring the current that flows. We can sum these over all pairs of vertices. The lower sum the better. For the first graph, the sum is 33; for the second, it is $206/3 = 68.66\dots$, more than twice as large.

- ▶ In a good network there will be many edges out of any set of nodes. The **isoperimetric number** is the smallest ratio of number of edges from S to its complement to number of vertices in S , for $|S| \leq n/2$. The larger, the better. For the first graph it is 1, and for the second, only 0.2.

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The intuition is that, if the isoperimetric number is large, you will not get trapped in a small set of vertices (for example if you walk randomly on the graph).

The isoperimetric number is related to other important properties of a good network such as expansion (where **Ramanujan graphs** are optimal) and rapid convergence of the random walk on the graph.

All three measures are related to the **Laplacian matrix** of the network, which I will define shortly. (Note to topologists: networks can be used as discrete approximations to manifolds; the Laplacian matrix is an approximation to the classical Laplacian operator on the manifold.)

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We will also see that the three measures suggested correspond exactly to three popular **optimality criteria** in experimental design in statistics.

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In a more general form, there are positive weights on the edges, and the next step in the random walk is chosen with probability proportional to the weight on the edge.

An example: permutation groups

Here is an example chosen from my own field, permutation groups. We are given a group G which acts on a set X in some way. The set will be partitioned into **orbits** of the group, an orbit consisting of all points which can be reached from a given one by applying elements of the group.

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This was answered by Mark Jerrum, as follows. Form a bipartite graph with $G \cup X$ as vertex set. Put an edge from $g \in G$ to $x \in X$ if the permutation g fixes the element x . Then the limiting distribution of the random walk of even length starting in X is uniform on orbits.

Another example: Latin squares

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Jacobson and Mathews gave a method for choosing a random Latin square, based in an ingenious way on a set a bit larger than the set of all Latin squares of given order.

Rate of convergence

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How do we find good networks?

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There are two places we might look.

- ▶ **Naturally occurring networks** such as gene networks, which have been refined by the pressure of millions of years of evolution, are likely to have good properties. But of course, the “selfish gene” might have a view of what makes a good network which is rather different from ours.

- ▶ The other place we can look is algebra, specifically **group theory**. Groups were invented to measure symmetry, but they can be used to construct networks which have good properties, and also provide techniques to analyse and quantify these properties, based on the symmetry of the networks.

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Before looking at this, I will describe one more network which has captured the interest of mathematicians.

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Jerry Grossman at Oakland University in the USA keeps the data for this. There are roughly 400000 authors of mathematics papers on MathSciNet (so the network has 400000 nodes). Of these, about 268000 lie in a single large connected component; 84000 are isolated nodes (mathematicians who have never written a joint paper), and the remainder, about 50000, lie in small components with between 2 and 23 vertices. (These figures date from 2004 so the picture is probably different now.)

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I am going to propose a possible answer to this question in the rest of this lecture.

Resistance distance

Take a network, and suppose (to start) that the vertices are terminals in an electrical network, and each edge is a 1-ohm resistor. As we saw earlier, we can measure the effective resistance between any pair of terminals by connecting a battery to those terminals and measuring the current that flows; or we can calculate the effective resistance using Kirchhoff's and Ohm's Laws.

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Theorem

Effective resistance is a metric on the network.

This means that it is positive, symmetric (doesn't depend on the order of the terminals), and satisfies the **triangle inequality**:

$$R(i,j) + R(j,k) \geq R(i,k).$$

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If we connect a battery between two terminals of a network, the potential at any other terminal will be between the potentials of the two terminals connected to the battery.

The other fact needed in the proof is that the equations for the network (Kirchhoff's and Ohm's laws) are linear, so if we have two solutions, we can superimpose them to get another solution by adding the currents.

Conductance

It is convenient to use conductance instead of resistance for the network elements. Conductance is just the reciprocal of resistance; its units are mhos. By the law for parallel connection, if several edges connect the same pair of terminals, we can replace them by a single edge by adding the conductances.

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As far as I know, nobody has ever computed resistance distances in this network.

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Form the **Laplacian matrix** L of the network, an $n \times n$ matrix with rows and columns indexed by network nodes, as follows. For $i \neq j$, the (i, j) entry is $-s_{ij}$, while the (i, i) diagonal entry is the sum of all conductances between i and other vertices.

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This matrix has all row and column sums zero; such a matrix has the property that all order $n - 1$ cofactors (determinants obtained by deleting the i th row and j th column, with a change of sign if $i + j$ is odd) are equal. This common value A counts the spanning trees in the network, if all conductances are 0 or 1. In general, it counts spanning trees by weight, where the **weight** of a tree is the product of the conductances of its edges.

Connected components and random walks

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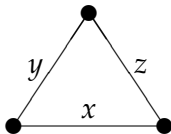
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This shows up in various ways. For a regular graph of valency k , the smallest non-trivial eigenvalue is at most $k - 2\sqrt{k-1}$; equality implies that the graph is a **Ramanujan graph**. In general, a large value of the smallest eigenvalue is associated with a large isoperimetric number, and with rapid convergence of the random walk on the graph.

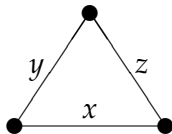
Furthermore, if we delete the i th and j th row and the i th and j th column, then the value is not independent of i and j ; it counts spanning **2-forests** (forests with two connected components) in which the nodes i and j lie in different components. If this value is B_{ij} , then the effective resistance between i and j is B_{ij}/A .

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I would be very interested in a calculation of the resistance distances in the mathematicians' collaboration graph!

Statistics

I spoke earlier about three ways of deciding which network is “good”, according to three different criteria. These correspond precisely to three **optimality conditions** in experimental design in statistics, which I now briefly mention.

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The situation is that we have a number n of “treatments” to compare, and a number of “experimental units” to apply them to. What is the best way to do this? For the most accurate experimental result, we want to minimize the variances between the estimators of treatment differences; but this is a multidimensional problem, so we cannot minimize all variances simultaneously!

If all experimental units are exactly alike, then we simply apply each treatment to the same number of experimental units (as near as possible). But a more usual situation is that the experimental units are grouped into **blocks**, so that units in a block are alike but differ systematically from those in a different block.

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In this situation, we form the **concurrence graph** of the design, where the vertices are the treatments, and we put an edge between treatments i and j each time there is a block containing both. So the graph can have multiple edges. It is important to realise that the graph can be chosen by the experimenter as part of the design, subject to constraints about the numbers and sizes of blocks.

Optimal designs

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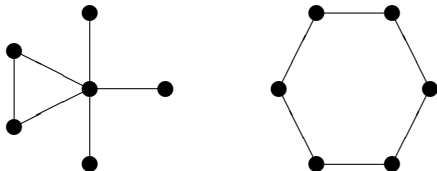
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- ▶ If we minimize the largest variance, and hence the largest resistance (this is roughly the same as maximizing the isoperimetric number), the design is **E-optimal** (E for “extreme”).
- ▶ Minimizing the volume of a confidence ellipsoid containing the estimated values is equivalent to maximizing the count of spanning trees by weight; such a design is **D-optimal** (D for “determinant”).

An example

Suppose that we have n treatments to compare, and $2n$ experimental units divided into n blocks of size 2. What is the best design?

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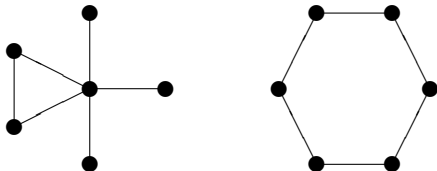
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The cycle has n spanning trees, the design on the left just three, so the cycle wins on the D-criterion. However, it can be shown that the design on the left (the “queen bee design”) is A-optimal if $n \geq 12$ and E-optimal if $n \geq 7$, a result which came as a surprise to some statisticians.

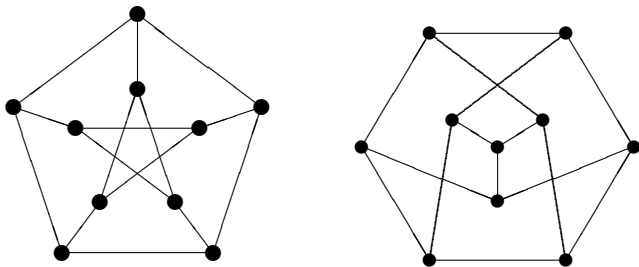
Graph isomorphism

Two graphs or networks are **isomorphic** if the vertices of the first can be matched up with those of the second so that corresponding pairs of vertices are either both joined or both not joined (and if the edges are weighted, these edges should have the same weight).

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For example, these two graphs are isomorphic:



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It is easy to find negative tests. For example, if the graphs have different numbers of vertices or of edges, or if the lists of vertex degrees are different, then they cannot be isomorphic.

One of the first serious attacks on this problem was the **Weisfeiler–Leman algorithm**. It is based on a refinement of the ideas above, refining the graph by adding purely combinatorial labels to the vertices and edges to distinguish them. The end result is an object known as a **coherent configuration**; if the two coherent configurations are not isomorphic then the graphs are not isomorphic.

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The algorithm does not always succeed; but using these ideas, László Babai has recently given a **quasi-polynomial** algorithm for graph isomorphism (running in time $\exp(O((\log n)^c))$ for some c (here $c = 1$ would be polynomial-time).

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This is currently being investigated. Because it is global, it usually takes many fewer steps than the WL algorithm. We think that the stable configurations are **Jordan schemes**, related to coherent configurations as Jordan algebras are to associative algebras.

Jordan algebras

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The operation is commutative but not associative. Jordan algebras are not much used in physics now but have found a place in statistics and in algebraic combinatorics.



... for your attention.