Math 670: Day 32

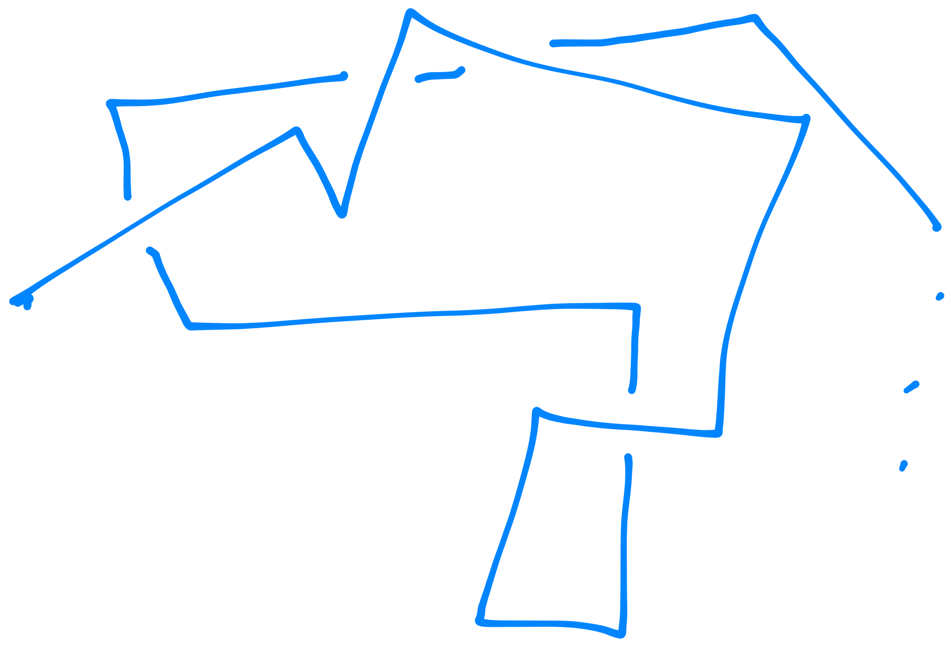
Remember from last time that Geodesics thru $\pi_1(Q) \in V_k\mathbb{R}^n$ are of the form $\pi_1(Q)\, e^{t\begin{bmatrix} 0 & -B^T \\ B & A \end{bmatrix}}$

& geodesics thru $\pi_2(Q) \in G_k\mathbb{R}^n$ are of the form $\pi_2(Q)\, e^{t\begin{bmatrix} 0 & -B^T \\ B & 0 \end{bmatrix}}$.

(Mathematica demo)

Now, let's apply all the knowledge we've developed this semester to understanding closed random walks.

Basic random walks are simple beasts: first, pick a starting point (in the plane or in $\mathbb{R}^3$ or in $\mathbb{R}^n$ or wherever you have a notion of distance & direction), a length, & a direction. Now, take a step of the chosen length in the chosen direction. Next, pick another direction & another length, then take a step of that length in that direction. Repeat for however many steps you desire.



There are various versions of this: lattice walks (when the steps are only allowed to be points on a lattice adjacent to the current point)

equilateral walks (when the steps are all the same length)

Gaussian walks (when the lengths are Gaussian)

Walks on graphs (like lattice walks, but on arbitrary graphs) $\rightsquigarrow$ relatedly, walks on groups

Brownian motion (the continuum limit of, say, equilateral walks)

Self-avoiding walk (the walk is constrained from self-intersecting)

Generally speaking, the direction of steps are chosen from the uniform distribution on the "unit sphere" (which could be just the collection of pts adjacent to the current step in the lattice & graph walks)

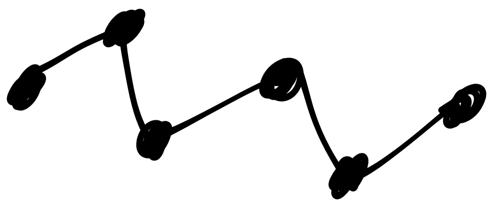
Provided the step lengths & step directions are all independent & identically distributed (i.i.d.), the random walk is a simple Markov chain & its behavior is reasonably well understood.

You can look at the Wiki article to see some of the many models that incorporate random walks (including everything from Black-Scholes to biodiffusion), but one in particular I want to mention is polymer modeling.

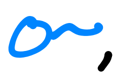
A polymer is a long molecule composed of a chain of identical (or at least similar) subunits called monomers.

For example, proteins (the monomers are the amino acids), RNA (the monomers are nucleotides: adenine, cytosine, guanine, uracil) DNA (slightly different since double-stranded, but still), starches (the monomers are glucose), plastics, rubber, etc.

Very roughly, one can think of a polymer as consisting of balls (the monomers) connected by sticks (the bonds b/w monomers)

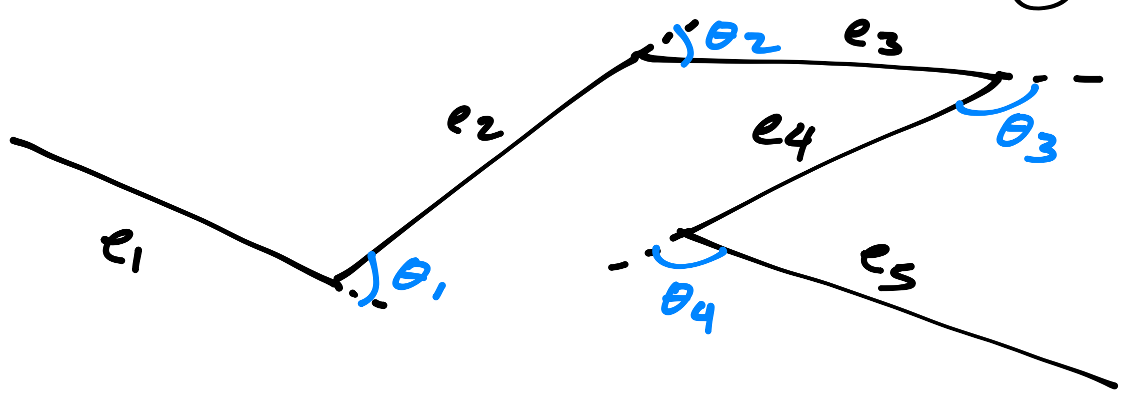


Now, the connection to random walks should be clear: if we let the monomers be vertices & the bonds be edges & we ignore thickness & any other physical constraint, we get something very like an equilateral random walk. This is called the ideal chain model & it turns out that the scaling behavior of random walks approximates that of polymers in solution (& best at a special temperature called the Θ-temperature) rather well.

However, not all polymers appear as open chains floating in solution. Biopolymers like proteins often do, but the likes of rubber form incredibly complicated networks & even many biopolymers (e.g. viral DNA) form closed loops, Θ curves, tadpole shapes , etc.

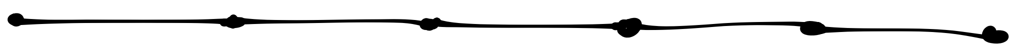
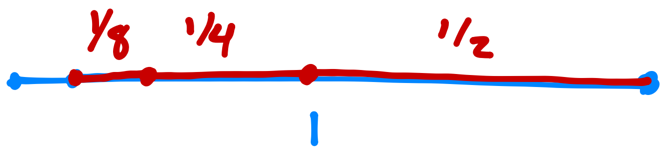
If you want to model a ring polymer (a polymer that forms a closed loop), then you need to put an extra global constraint on your random walk: now, you have to choose lengths & directions of steps subject to the constraint that you get back to the starting point after a fixed number of steps.

Ex: Consider an equilateral random walk in the plane. If we only care about the shape, we can mod out by translations & rotations... up to translation & rotation, such walks are completely determined by the list of turning angles



If the walk has n steps, then there are $n-1$ turning angles & we can parametrize the space of all n-step walks up to translation & rotation by the $(n-1)$-torus $T^{n-1} = (S^1)^{n-1}$, w/ coords given by the turning angles.

More generally, if the walk is not equilateral then you need two lists: the n edgelengths & the $n-1$ turning angles.

Now, the list of edgelengths & turning angles also determine a closed walk (though w/ the caveat has one more turning angle, b/w the last & first edges), but this isn't the whole story. After all, the list of turning angles $(0,0,0,0,\dots,0)$ can never give a closed walk (except in the stupid case when all edgelengths are 0)  , nor can the list of edgelengths $(1, \frac{1}{2}, \frac{1}{4}, \dots, \frac{1}{2^n})$ 

Obviously, more subtle things can also go wrong.

So the question becomes: how can we parametrize the space of closed random walks (in, say, the plane or in 3-space), preferably in a translation- & rotation-invariant way?