

This first set of problems is based on Section 13.4 #33. A river is 40 m wide and flowing north. A person in a boat on the west bank wants to cross to the east bank. They can row at 5 m/s. We've done problems like this one already in this course. What's new here is that the speed of the current varies across space. Near the banks the speed is 0. At the center of the river, the speed is 3 m/s.

A. Let  $x$  be a coordinate running from  $x = 0$  at the west bank to  $x = 40$  at the east bank. Come up with a quadratic function (a parabola) that describes the speed of the current at  $x$ , for all  $x$  in the interval  $[0, 40]$ .

B. If the rower rows due east, then how long will they take to cross the river, and how far downstream will they land?

C. Actually, the rower doesn't want to land downstream or upstream. They want to land directly across the river from where they started. On what heading  $\theta$  should they row, to make this happen?

For this next set of problems, imagine a three-dimensional coordinate system centered on a star of mass  $M$ . A planet of mass  $m$ , which is much less than  $M$ , is orbiting the star. For simplicity, assume that the star is stationary. Let  $\vec{x}$  be the planet's trajectory. Newton's law of gravitation says that the force  $\vec{F}$  of gravity on the planet is of magnitude  $GMm/r^2$  toward the star, where  $G$  is a positive constant and  $r$  is the distance between the star and the planet. Newton's second law of motion says that the acceleration  $\vec{a}$  of the planet is related to the force by  $\vec{F} = m\vec{a}$ .

D. Prove that  $|\vec{x}|^3 \vec{x}'' = -GM\vec{x}$ . (This equation is a *differential equation* — an equation involving an unknown function  $\vec{x}$  and its derivatives  $\vec{x}'$ ,  $\vec{x}''$ , etc.)

E. For the differential equation given in problem D, is there a solution of the form

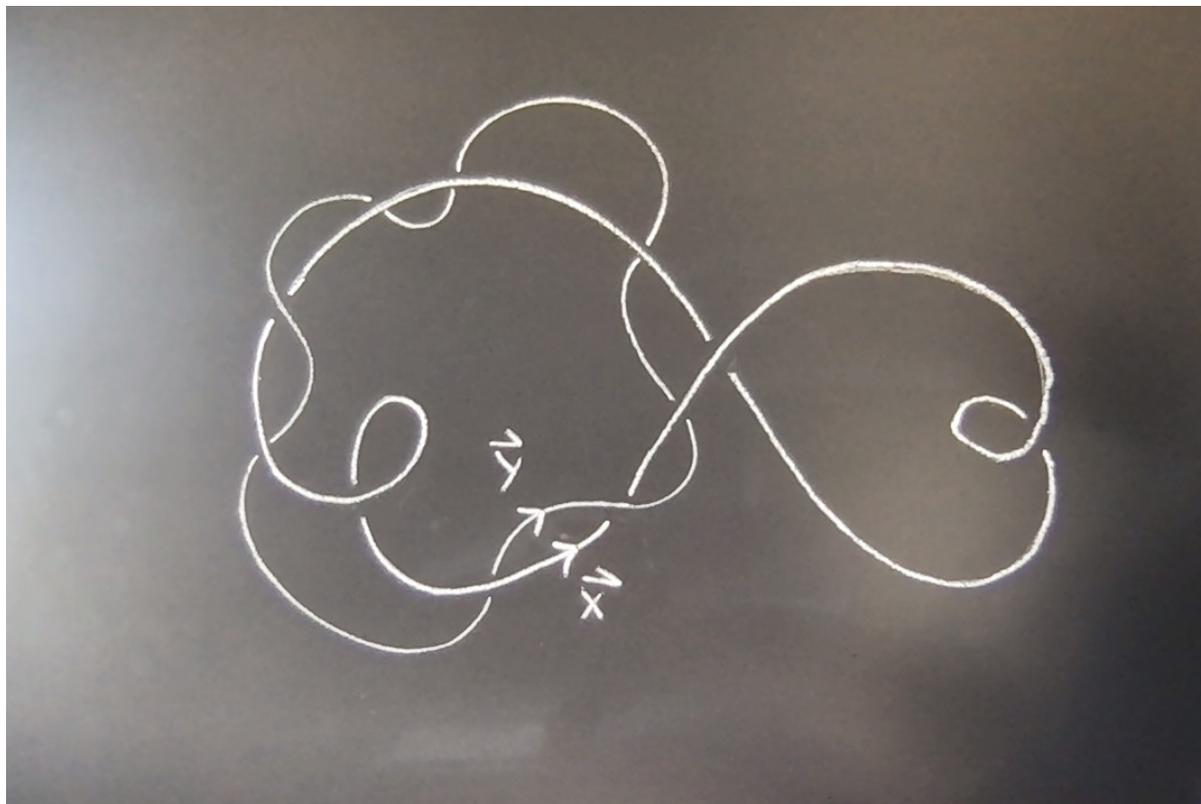
$$\vec{x}(t) = \langle R \cos \omega t, R \sin \omega t, 0 \rangle?$$

If so, how do  $R$  and  $\omega$  relate to the information given in the problem?

F. A year is the amount of time needed for the planet to revolve once about the star. Based on your answer to problem E, how does the length of the year depend on the distance to the star?

This last set of problems gives you a glimpse of how curves are used in the study of

DNA knotting. In the figure below,  $\vec{x}$  and  $\vec{y}$  are two parametrized curves in  $\mathbb{R}^3$ . They are defined on the same interval  $[a, b]$  of  $t$ -values. They are closed, meaning that  $\vec{x}(a) = \vec{x}(b)$  and  $\vec{y}(a) = \vec{y}(b)$ . There are three subtle concepts to be developed.



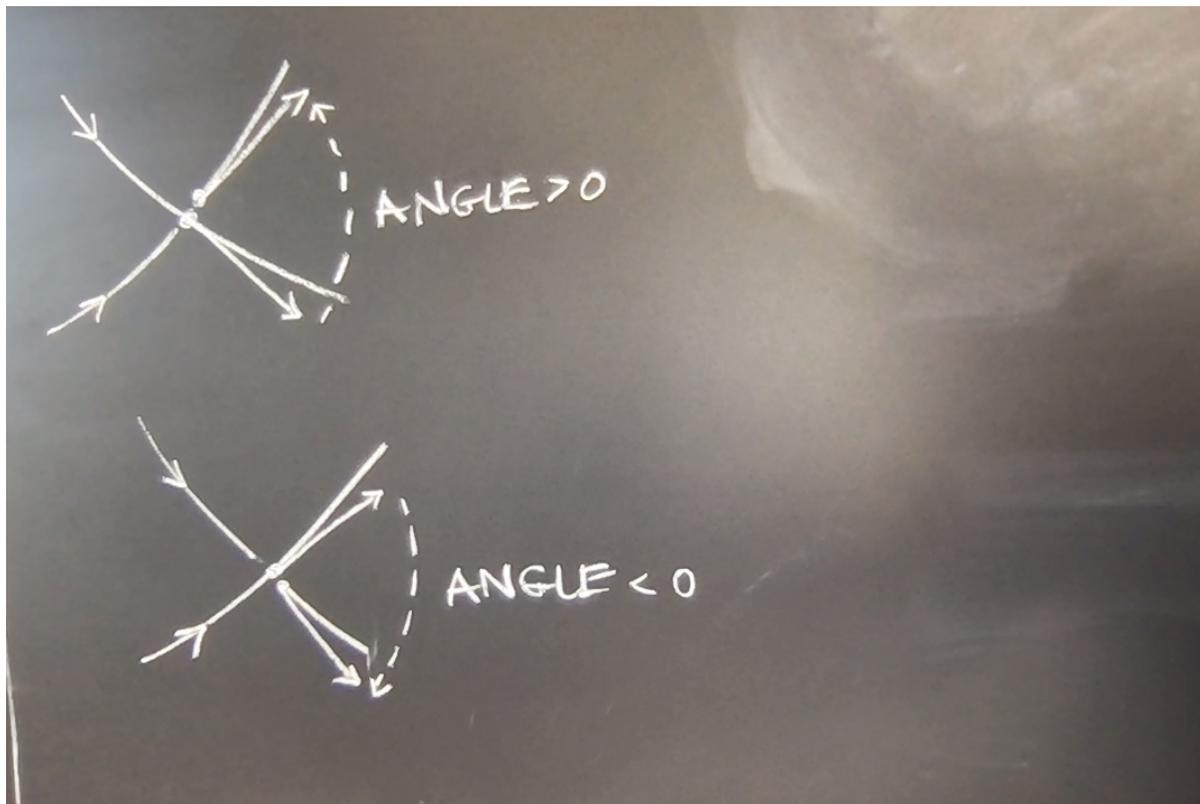
Here's the first concept. At any time  $t$  in  $[a, b]$ , let  $\vec{u}(t)$  be the unit vector pointing from  $\vec{x}(t)$  toward  $\vec{y}(t)$ , and let  $\vec{t} = \vec{x}'/|\vec{x}'|$  be the unit tangent vector of  $\vec{x}$ . (Draw a picture!) Define the *twist* as

$$\text{Tw}(\vec{x}, \vec{y}) = \frac{1}{2\pi} \int_a^b (\vec{t} \times \vec{u}) \cdot \frac{d\vec{u}}{dt} dt.$$

Intuitively, the twist measures how  $\vec{y}$  revolves about  $\vec{x}$ . Perhaps you agree that it seems difficult to compute. Or maybe it's easy to compute in some special cases, but any slight deviation from those cases might turn it into a big hassle. It is a delicate geometric concept.

For the second concept, focus on  $\vec{x}$  and ignore  $\vec{y}$ . Each point where  $\vec{x}$  appears to cross itself can be assigned a sign,  $\pm 1$ , as follows. Assign to each segment of the curve its unit tangent vector  $\vec{t}$  at the crossing point. Rotate the top vector until it aligns with the bottom vector. If the rotation angle is in  $(0, \pi)$ , then assign  $+1$ ; if it's in  $(-\pi, 0)$ , then assign  $-1$ . By summing over all of the crossing points, we get the *writhe* of  $\vec{x}$ , which is

denoted  $\text{Wr}(\vec{x})$ . See the diagram below. (Actually the writhe needs to be averaged over all possible viewpoints, but let's ignore that.)



G. For the example shown in the first figure above, compute the writhe.

The third concept is similar to the second. Now we ignore where  $\vec{x}$  crosses itself (and where  $\vec{y}$  crosses itself). Instead we focus on where  $\vec{x}$  and  $\vec{y}$  cross each other. Following the same idea as above, assign a  $\pm 1$  to each point where  $\vec{x}$  and  $\vec{y}$  cross. Sum these signs and divide by 2. The resulting integer is the *linking number*  $\text{Lk}(\vec{x}, \vec{y})$ .

H. For the example shown in the first figure above, compute the linking number.

Now here's something interesting. It can be proved — not just in this example, but in quite a general situation — that

$$\text{Lk}(\vec{x}, \vec{y}) = \text{Tw}(\vec{x}, \vec{y}) + \text{Wr}(\vec{x}).$$

This result is surprising in two ways. First, the linking number and the twist strongly depend on  $\vec{y}$ . However, their difference — the writhe — does not depend on  $\vec{y}$  at all. Second, the linking number and the writhe are *topological*, meaning that they aren't

affected by small perturbations of  $\vec{x}$  and  $\vec{y}$ , but rather depend only on the crude question of how the curves  $\vec{x}$  and  $\vec{y}$  are “knotted” in space. Therefore the difference — the twist — must also be topological, although nothing in its definition suggests so!

What does all of this have to do with DNA? Well, as it passes through its life, a DNA molecule might be coiled up sometimes (for storage and movement) and uncoiled sometimes (for replication). Biologists want to understand these processes, not just for the inherent value of scientific knowledge, but so that they can devise treatments for diseases caused by errors in these processes. In particular, when a DNA molecule needs to uncoil (or coil), it is aided by a class of enzymes called *topoisomerases*. Picture such an enzyme as a little machine that travels along the DNA molecule. Every so often, it comes to a point where its segment of the molecule crosses close by another segment. At that point, it can grab both segments, cut one of them, pass it around the other one, and reattach it. Doing so can help the DNA knot uncoil.

The enzyme doesn’t do this cut-and-reattach operation at every opportunity. Somehow it “decides” to do it in some circumstances and not in others. The question is: How does it decide? The answer is not obvious. One early hypothesis was that the decision process is random — basically, the enzyme flips a coin. But experimental data suggest that the enzyme is much more efficient at unknotting DNA than it would be, if it were deciding randomly. Somehow it has insight into the large-scale question of how the DNA molecule is knotted on itself. That’s surprising, because the enzyme, being small, can sense only a little neighborhood of where it is. There’s some subtle interaction between the small-scale geometry of the molecule and the large-scale topology.

Mathematically, a loop of DNA is a double helix floating in  $\mathbb{R}^3$ . Let  $\vec{y}$  be one of the strands of the double helix. Let  $\vec{x}$  be the imaginary center curve, about which the two strands mutually revolve. Then the linking number and the writhe get at something topological about how the DNA molecule is knotted, while the twist gets at something geometric about how much the strands curve about each other. Mathematical biologists use this theory to model how the topoisomerases employ geometric information to make topological changes in DNA. By the way, the linking number might be 500 or 5,000. So the problem is big.

For further reading, consult the chapter by White in the National Research Council’s *Calculating the Secrets of Life: Contributions of the Mathematical Sciences to Molecular Biology* (1995). See also Buck’s article “DNA Topology” in *Advanced School and Conference on Knot Theory and its Applications to Physics and Biology* (2009).