Intermediate Magnet Play:

As you read and saw, TMV is a filamentous virus. Most viruses have a roughly spherical appearance at low resolution. In 1956, three years after describing the structure of DNA (based on some good guesses and some purloined data), Crick and Watson predicted what shape viruses would take based on purely theoretical considerations.

The problem can be summed up like this: the "box" made of protein must be large enough to accommodate the physical size of the DNA or RNA that encodes the virus. Based on some rules for how DNA encodes protein (which we will learn more about later), the protein that forms the box has to be very small. Thus, the box must be made out of many copies of the same subunit. There must be some repeating pattern that can make a box big enough to hold the DNA or RNA. You have already seen one solution to this problem: a cylindar. Crick and Watson proposed a different one. To get the ideas they needed to solve the problem, they had to read Plato (yes…that Plato).

Plato defined "regular solids," also known as Platonic solids, in which three-dimensional objects could be built with repeating identical shapes meeting at each edge and identical angles at all vertices. There are 5 and they are shown below:

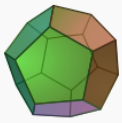
Polyhedron		Vertices	Edges	Faces
tetrahedron		4	6	4
octahedron		6	12	8
icosahedron		12	30	20
hexahedron (cube)		8	12	6
dodecahedron		20	30	12

Figure 1: Platonic Solids

You are probably familiar with the tetrahedron (4 triangles) and certainly with the cube (6 squares). Making some assumptions about how large the repeating protein component could be, Crick and Watson proposed that only the Icosahedron (20 triangles) and Dodecahedron (12 pentagons) would work in order for a small enough protein subunit to form a large enough box to house the DNA or RNA. Thus, they confidently proposed, "spherical" viruses would really be icosahedral or dodecahedral in shape. It turns out that choosing between them is not necessary. They are mathematical duals of each other: they have the same number of edges (30) and

either 12 vertices and 20 faces (icosahedron) or 20 vertices and 12 faces (dodecahedron). You can model the virus either as 12 pentagons or 20 triangles. You'll get to see this close up.

We will build both versions. The beads will each represent entire proteins, which will then form 4° structures, either 12 pentagons each comprising 15 spheres or 20 triangles each comprising 9 spheres. Hmmm…180 beads in each case. These intermediate subunits will then form the complete structure.

Dodecahedron

Here is a pentagon and a video on how to form it.

You need to make 12 of them, as shown at the left. You should make all 12 starting from the same end of the chain, so that the polarities are all correct. All the edges will be antiparallel to each other, resulting in the "Bead-on-Bead" appearance where they meet. If you goof and they don't line up correctly, there is an easy way to fix them. I'll show you. Once you get all 12, it will be hard to keep them apart. Watch this video. Start nudging them toward each other.

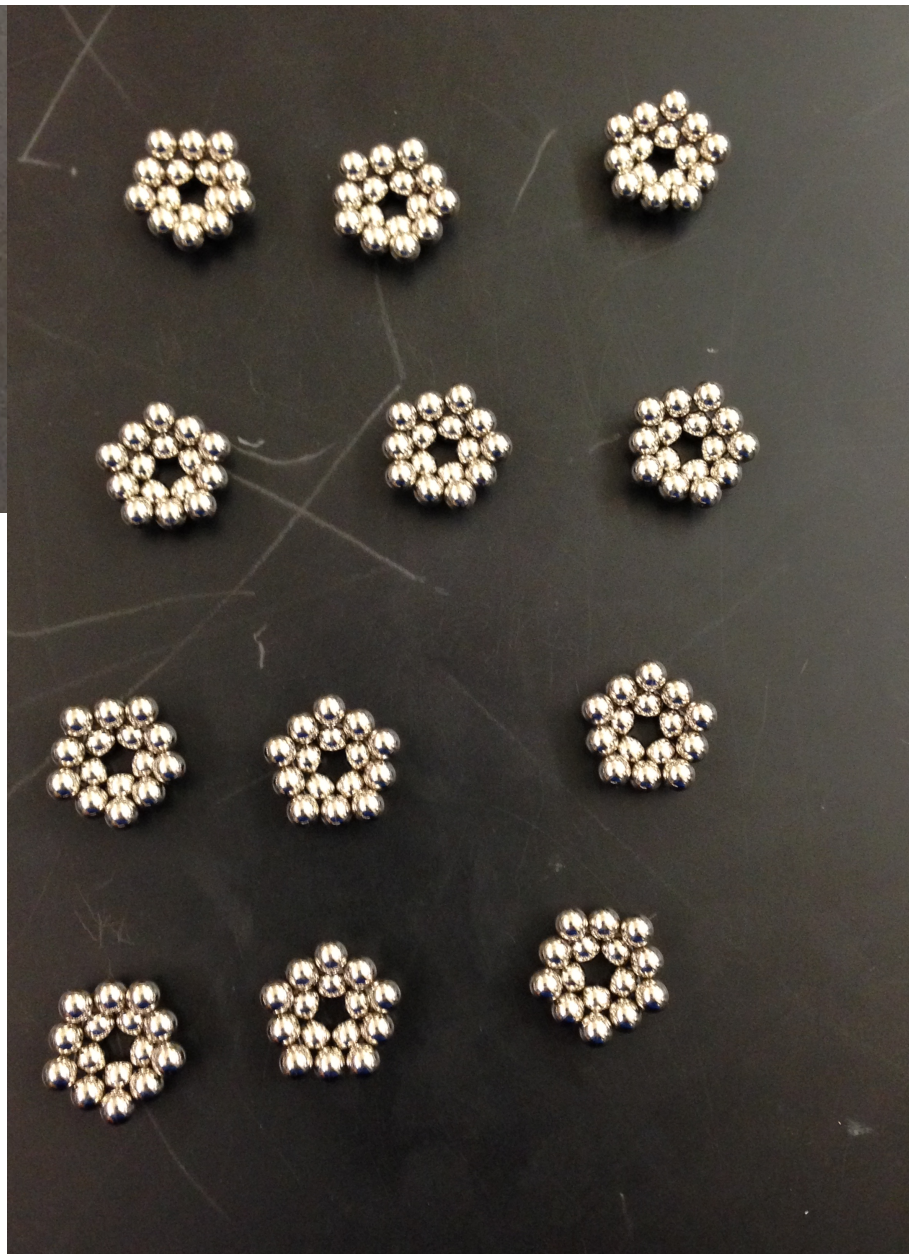


Figure 2: Pentagons

Icosahedron:

How'd that go? Ready to try another form? If you take the dodecahedron form and rotate it, you can see a triangles inscribed by line segments drawn between the centers of each pentagon. It would take 20 such triangle to make roughly the same structure.

Figure 3: dodecahedron with triangle revealed.

You will form triangles out of 9 spheres each. Watch this video. Getting them to form can be tricky. If the two beads adjacent to each corner keep coming apart, try rotating them slightly with your fingers as you push them together.
Again, the interaction along the edges of the triangle will need to be antiparallel. If you bring two triangles together and they want to link up incorrectly, flip one of them over.
Once you get 20 triangles made, you can make sure they are the right polarity by forming them into one long band (Figure 4).

Figure 4: 20 triangles

Then you cut them into groups of 4 and form an odd, "star" type structure. Watch this video to see how to start it and check out the finished structure in Figure 5.
Then watch this one last video. Too Cool, right!?

The finished product is shown in Figure 6. You can see the vertices of the triangle easily enough. But, Look at the structure where the vertices are. It has five beads. If I rotate it over, you see the view on the right, centered on the pentagon, this time.

Figure 5: unfolded icosahedron. Just like Origami!

Before you move on

Figure 6

1. Were you surprised by how easily these went together? Discuss what properties lead to this ease of assembly and what happens when the properties aren't quite right (say, the magnets have the wrong polarity in a particular interface). Discuss how this is (or is not) analogous to how real proteins fold.
2. Would truly random motion of these triangles or the pentagons efficiently give rise to the correct structure? If not…why not?

Want to play with a real Virus?

Well, sort of. Figure 7 is a model of rhinovirus, which causes colds. As you can see, it really is made of pentagons (which are themselves made of several smaller, roughly triangular proteins).

You may find it interesting to know that when Crick and Watson proposed the structure of viruses based on Platonic solids, the idea was met largely with derisive laughter. For the most part, the scientific community learned not to laugh at Francis…no matter how outlandish what he was saying seemed.

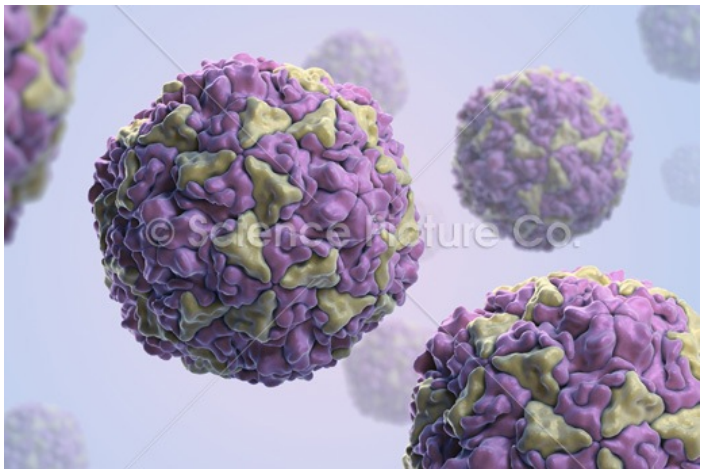


Figure 7

Proteins are better than magnets

One of the problems we had with the magnet-bead viruses is that there were too many "wrong ways" for them to interact. When we pushed the subunits together, they seemed to want to assemble…but sometimes got stuck in the wrong configuration. This is due to the relative non-selectivity of magnet fields in space. Importantly, **the wrong interactions were just as strong as the right ones**.

However, if the interactions are mediated by specific hydrogen bonds and hydrophobic regions that have a more limited number of ways to interact, and incorrect interactions were not as stable, could one get assembly of complex structures through truly random motion?

Obtain a virus shaker-bottle from me. Please do not unscrew the cap…I know it's tempting.

You can see the pentagon structure easily enough. We are again using magnets to stand in for intermolecular forces. However, we put the magnets in very specific places, analogous to how the intermolecular interactions would be constrained.

Shake well until done.

Experiment with different shaking speeds and observe what happens. In my experience, simple shaking and occasional rolling work best. It also helps not to look at the jar too much. Random generally works better than "intentional" shaking.

Pretty impressive, isn't it. You should note that what you just did is considered impossible if you are a creationist or an intelligent design advocate (really the same

thing). The fellow who made these virus shakers for me used to have a video on youtube showing this running in a jar just rotating slowly on a machine. I wish I could find the old page to show you all the comments from creationists explaining how he had to be running the video backwards because what he was showing is impossible. He set it up with a watch along side so you could see the second hand moving. They claimed that he obviously altered the watch to run backwards, so he could film the structure coming apart, reverse the video, and have the virus seem to self assemble…which it obviously cannot really do. Except…you just did it.

Questions for ELN.

1. What happens if you shake the jar too fast?
2. What happens if you shake it too slowly?
3. To what is the speed of shaking analogous? (Hint: think about energy)
4. If the analogy holds up, what effect might a fever have on virus assembly in your cells?
5. Why is that last shape so hard to get to assemble? Would that same problem occur if this were inside the cell and there were thousands of pentagons available?