

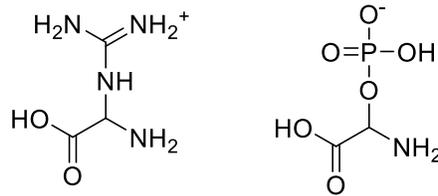
The following submission came from William Sikkema November 23 2015:

Perry,

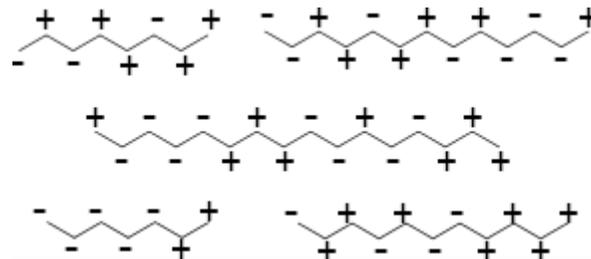
I came up with a solution that I think addresses the shortcomings of my last solution. This one encodes high level information in a very abstract format. I've attached the idea to this email - let me know what you think.

William Sikkema

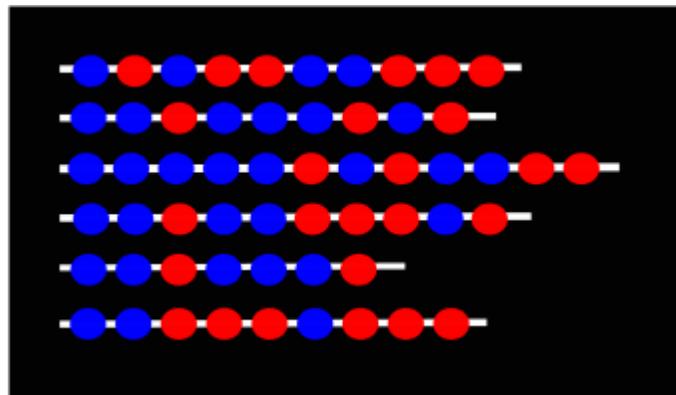
Take two amino acids: one with a positive charge and the other with a negative charge. (Amino acids can be formed in nature.)



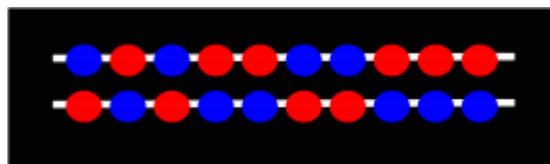
Assemble them randomly into short polymers. (This can happen in nature.) You'll get a mixture of polymers with positive and negative charges along the backbone. Something like this:



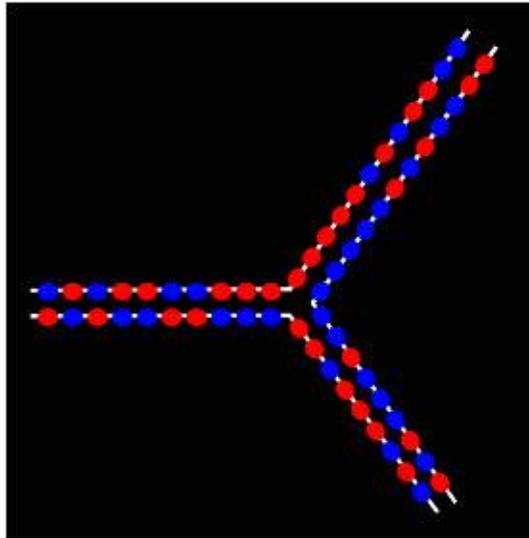
Here, each point along the chain represents one amino acid from above. Every polymer has a unique code. The negative can be assigned 0, and the positive 1. Thus, the polymer can be represented by or considered to be an abstract string of 1s and 0s. We can also represent them as a string of spheres, where blue indicates negative, and red indicates positive like so:



The structure of these is such that two complimentary strands tend to self-align:



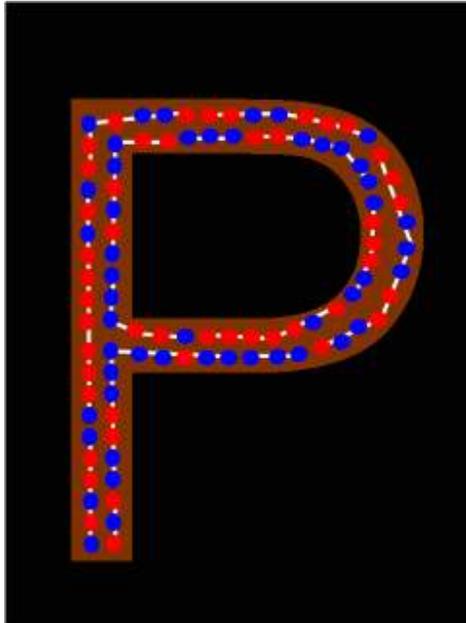
Or, multiple strands can make defined shapes, similarly to DNA origami:



Now we take a 2 dimensional surface with some depression in it. Here we have a flat mica surface (which exist in the real world), with a brown depression in it (which exist in the real world). The depression shown below is in the shape of a P, but it could be an arbitrary shape.



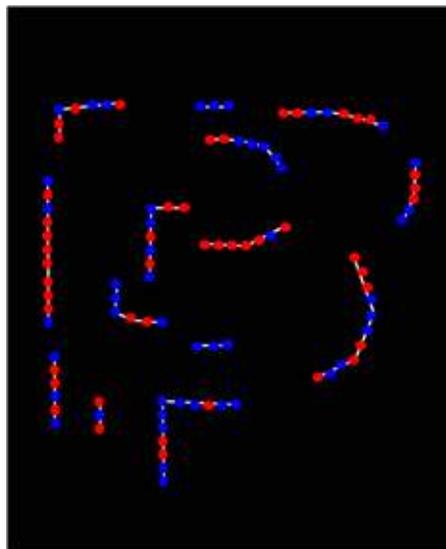
Now, you take the mixture of polymers you've made and flow them over this depression. Some will stick and fill the depression. Polymers that do not stick well or do not find a pair that sticks well will leave the depression. This will continue until the depression is full and every positive charge is matched with an adjacent negative charge – this is the lowest energy configuration. This can be aided with low salt concentration, as salt will stabilize mismatched charges. This is the encoding part of the process.



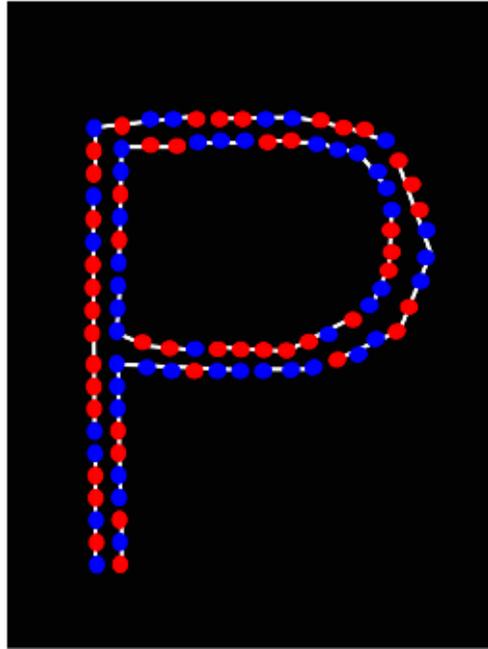
This image only has two side by side polymers, but for larger shapes, many side by side polymers could be imagined to fill the space

Now, rinse away the other polymers that haven't fit into the depression. Then, add salt or heat to remove the stuck polymer from the depression.

The information stored in the shape of the object has now been digitized into a string of digital polymers.



To decode the information in this digital system, cool it down or remove salt, and it will reform the original structure – its lowest energy configuration:



1. Humans can design the experiment, with all manner of state-of-the-art laboratory equipment, ideal conditions etc. They just can't cheat: the submitted system cannot be pre-programmed with any form of code whatsoever.
 - a. No code to begin with – only the amino acids that get randomly assembled
2. Since the origin of DNA is unknown, the submitted system cannot be a direct derivative of DNA or produced by a living organism. Bee waggles, dogs barking, RNA strands and mating calls of birds don't count. Such codes are products of animal intelligence, genetically hard-coded and/or instinctual.
 - a. Amino acids can be produced naturally and assemble naturally
3. The origin of the submitted system must be documented such that its process of origin can be observed in nature and/or duplicated in a real-world laboratory according to the scientific method.
 - a. This could be done in the lab, but doing it would not be cheap, as systems for imaging on the single molecule scale are necessary.
4. The submitted system must be digital, not analog.
 - a. It's digital, as it can be represented as a series of 1s and 0s.
5. The submitted system must have the three integral components of communication functioning together: encoder, code, decoder.
 - a. See above
6. The message passed between encoder and decoder must be a sequence of symbols from a finite alphabet.
 - a. The alphabet has two letters
7. A symbol is a group of k bits considered as a unit. We refer to this unit as a message symbol m_i ($i=1, 2, \dots, M$) from a finite symbol set or alphabet. The size of the alphabet M is $M = 2^k$ where k is the number of bits in the symbol. For a binary symbol, $k = 1$, $M = 2$. For a quaternary symbol in DNA, $k = 2$, $M = 4$.
 - a. For my system, $k=1$, $M=2$.
8. A character is a group of n symbols considered as a unit. We refer to this unit as a message character c_i ($i=1, 2, \dots, C$) from a finite word set or vocabulary. The maximum size of the character set C is $C = M^n$. For a standard computer byte, $M = 2$, $n = 8$, $C=256$. For a triplet group of quaternary symbols in DNA, $M = 4$, $n = 3$, $C=64$.
 - a. Calling the triplet in DNA as a unit of information is to oversimplify the issue. Certain information in DNA looks like it has a n of 3, but there's lots of information in there that doesn't have $n=3$. Likewise, my code doesn't have a set unit length – it can and does vary.

9. The submitted system must be labeled with values of both encoding table and decoding table filled out.
 - a. One such encoding and decoding example is given. Others are trivial to imagine.
10. For the submitted system, it must be possible to objectively determine whether encoding and decoding have been carried out correctly. For example when you press the “A” key on the keyboard, a letter “A” is supposed to appear on the screen and there is an observable correspondence between the two. In defining biological gender, a combination of X and Y chromosomes should correspond to male, while XX should correspond to female. For any given system, a procedure should exist for determining whether input correctly corresponds to output.
 - a. It's possible to do this in the lab, but it's not cheap.