Proteins, from the smallest amoeba to the largest living organisms, are the building blocks of all life on our planet.  With the advent of modern sequencing techniques, we possess a copy of these organism's (and our own) genetic code.  Deep within the ribosome, cells within continually build new proteins from DNA.  Given the same blueprint, though, we cannot accurately model what Mother Nature does so easily.  
  
Molecular structures obey the laws of nature.  In theory, we are masters of the atom: we have enough knowledge of physics, chemistry and math to be able to predict any interaction correctly.  But, in practice, biology remains frustratingly difficult to quantify.  With modern machines we can perform a billion simulations in the blink of an eye but still cannot accurately replicate what a single protein knows how to do with nothing more than its very own DNA sequence.  
  
Some of this is because our tools, be they computers or algorithms, are still relatively limited.  Some of this is because we, the proteins commanding the machine, have not improved very much ourselves over the past million years.  Computational modeling of molecular structures is a very, very new field.  In the decades hence they will surely laugh at both our machines and methods.  We are, for the most part, fools stumbling about the dark.  
  
But, we must try.  If we can command the rules of life, we can command the cosmos.  If we cannot, then we are nothing better than a virus, replicating endlessly without understanding its existence.  It is, therefore, our duty to try and understand what is happening.  Only then can we claim to be more then mere collections of molecules.  Therefore, consider this document a tiny attempt at self-awareness.