Geometry and Physics of Proteins

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Proteins can replicate, with errors. This is good for natural selection.

Proteins fall into an intermediate size region which makes them difficult to analyse physically. They are too large for simple mechanics, but not numerous enough to statistical mechanics. Any picture of protein structures must explain common physical and chemical characteristics as well as the specific characteristics of each protein. These include:

-rapid and reproducible folding
-expel water from the interior
-co-op transition to a folded state with few intermediates
-flexible and versatile
-~10^5 proteins, ~1000 folds
-buildings blocks are helices and sheets
-form determines function
-amyloid formation (long proteins form placque-like materials associated with Alzheimer's disease and Mad Cow disease
-helices and sheets are periodically repeatable structures for which H_2 bands provide scaffolding

Contributions have been made by Bernal (1939), Linus Pauling (1954) and Ramachandran (1994).

The quantum chemistry approach to protein structure is probably too complex to solve.

The physics approach uses symmetry and geometry. There is a gap between polymer physics and properties of proteins. Polymer physics uses chain of hard spheres as a model. This does not predict helices and sheet structures.

Sam Edwards introduced a string model with delta functions to discourage self-interaction and overlapping.

The author proposed a garden hose segment (tubular) model of non-zero thickness, or spaghetto model (singular of sphaghetti). If the size of the tube is ~ the range of interaction, tube segments tend to be parallel rather than perpendicular. This results in the right kind of helices, where the pitch is within 2% of the radius. Analysis of this model shows a prediction of helices and sheet structures similar to protein structures.

Papers on this have been published in Nature.