Abstract Submitted
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Mechanical function of proteins constrains sequence space to a low dimension: a simple physical model. TSVI TLUSTY, Inst for Basic Science, UNIST, and Institute for Advanced Study, ALBERT LIBCHABER, Rockefeller University, JEAN-PIERRE ECKMANN, University of Geneva — DNA genes are mapped to 3D arrangements of amino acids that make functional proteins. We will discuss this back-and-forth mapping, between the many-body physics within the protein and evolutionary forces acting on the gene. To look into the geometry of the map, we introduce a simple physical model in which proteins are treated as amino acid networks that adapt their connectivity to evolve a specific mechanical mode. Such large-scale conformational changes – where big chunks of the protein move with respect to each other – are known to be central to the function of many proteins. We will discuss how the collective physical interaction within the proteins projects the high-dimensional sequence space onto a low-dimensional space of mechanical modes: most of the gene records random evolution, while only a small non-random fraction is constrained by the biophysical function. Spectral analysis reveals a strong signature of the protein's structure and function within correlation 'ripples' that appear in the space of DNA sequences. These findings propose a testable basic principle of the protein as amorphous matter whose dynamics encode the evolutionary learning process. [1] Tlusty, Libchaber & Eckmann, *Physical model of the sequence-to-function map of proteins* (arXiv:1608.03145).

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