**Natural selection does not affect the structural evolution of proteins**

Proteins diverge during biological evolution. At the level of sequences, different aminoacids evolve at different rates, which is a clear evidence of natural selection and its selective pressure. We recently proposed the “Stress Model” to explain such variation. According to this model, the rate of evolution of a site depends on the mutational stress of the active conformation, which is proportional to the local packing density of the site. However, at the level of structure, even though there are preliminary studies of structural divergence profiles, the role of natural selection has not been elucidated yet. Here, we deeply study the effect of natural selection on the structural divergence of a wide set of families of proteins. We compared experimental data with simulated data generated with the mutational model “Linearly Forced - Elastic Network Model”. We generated 2 sets of mutants; one without accounting for natural selection, and the other one selecting single mutations according to the fixation probabilities predicted by the “Stress Model”. The profiles we analyzed were both in Cartesian coordinates and projected on the normal modes of proteins. We found that the agreement between experimental and simulated profiles is high either considering or not natural selection in the simulation. Moreover, there are no clear differences between simulated profiles. These results suggest there is no evidence of natural selection on the evolution of the structure and go against the common belief that natural selection governs molecular evolution.