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BioEnvAda

Easily investigating protein adaptation to environmental conditions

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The analysis of protein evolution requires many steps and tools, starting from collecting DNA data to predicting protein structure. We developed a NextFlow (BioEnvAda) pipeline to investigate protein adaptation to changing environmental conditions. It considers multiple aspects of protein evolution comparing changes in amino acid sequences while considering both phylogenetic information and measures of evolutionary pressure. It calculates tendencies for specific biophysical behaviours accounting for the local sequence environments and incorporates predicted 3D structures of a protein.

HSP20 is a regulatory element in the temperature response of many organisms. To demonstrate the functionality of the BioEnvAda pipeline, we applied it to the HSP20 of the ubiquitous marine cyanobacterium, *Synechococcus*. Using a set of 60 high quality protein sequences BioEnvAda rapidly identified regions that likely play a role in temperature adaptation.

The pipeline is available on the Bio2Byte GitHub (<https://github.com/Bio2Byte/nf-pipelines>).

