



Master project 2024-2025

Personal Information

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Project

Structural bioinformatics

Project Title:

Construction of a pipeline for enzyme design using generative network models and the empirical valence bond model

Keywords:

enzyme design, generative neural networks, molecular simulations, empirical valence bond, protein structure-function relationships

Summary:

Enzyme design is evolving fast thanks to the irruption of ML/DL in the field a few years back. In particular, generative neural models are one of the main tools of choice to produce new scaffolds for enzyme design. Most current methods base their approach in the exploitation of the structural features of existing enzyme active sites and they try to cope with catalytic activity enhancement while keeping control of protein stability. Few models include the use of the free energy profiles of the enzymes under scrutiny during the protein design phase. The empirical valence bond method has been extensively used to unravel the features that help an enzyme to be an active catalyzer in hysiological conditions. Lately, the interest on EVB has increased as it provides a fast and insightful tool to discriminate protein variants based on their activity. In this project we propose exploring the interface between generative neural networks and EVB calculations of free energy of activation, in order to describe a model to increase the toolbox for protein design pipelines. The project includes the development of ML/DL pipelines linked to the use of extensive molecular simulations in GROMACS.

References:

<https://pubs.acs.org/doi/10.1021/acs.jctc.3c00714>

Expected skills:

Python programming (desirable some expertise in ML/DL programming with keras and tensorflow); interest in free energy calculations and molecular simulations; good understanding of biochemistry

Possibility of funding:

No

Possible continuity with PhD:

Yes

Comments:

The candidate should be willing to work in a hybrid basis, but mostly presential at the IRIS-CC / UVic-UCC premises in Vic.

