Master project 2020-2021

Personal Information	
Supervisor	Toni Giorgino
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Project

Computational genomics

Project Title:

Machine learning-based assessment of SARS-CoV-2 genome variability

Keywords:

Coronavirus, machine learning, deep neural networks, genome

Summary:

We shall exploit the genetic-epidemiological evidence collected during the present SARS-CoV-2 outbreak to characterise the genomic regions with high mutation potential that could play a role in future outbreaks and in acquisition of drug resistance. Statistical learning and artificial-intelligence methods will be used to produce mutation models; the selected hot-spots will be cross-referenced in order to build early lead strategies of use in future outbreaks. The work is essentially computational. The student may work, either locally or remotely, with the computational group at the Institute of Biophysics of the Italian National Research Council, located at the University of Milan (Italy). Further collaborations are possible.

References:

* Smith M, Smith JC. Repurposing Therapeutics for the Wuhan Coronavirus nCov-2019: Supercomputer-Based Docking to the Viral S Protein and Human ACE2 Interface. 2020 Feb 20 (Chemrxiv) * https://viralzone.expasy.org/8996 * www.giorginolab.it * https://users.unimi.it/biolstru/molbd3-lab.html

Expected skills::

The project is heavily computationally focused. A good grasp of Python and an interest in machine learning are essential.

Possibility of funding::

To be discussed

Possible continuity with PhD: :

To be discussed

Comments:

Also: structural bioinformatics. Contact: toni.giorgino@cnr.it