

ID: MSCA-2020-WVranken01

Title: Structural Bioinformatics

There are now 200 million protein sequences in UniProt, but for the majority of these nothing is known about their overall behaviour in terms of conformation and dynamics. A large proportion this 'dark proteome' likely exhibits ambiguous conformational behaviour that defies the traditional 'one-protein-one-fold' paradigm. In our lab (<http://bio2byte.be/>), we are creating a framework of protein sequence-based predictions, and the interpretation thereof, to obtain a more generally applicable, probabilistic view of protein behaviour. From core predictions of conformation and dynamics^{1,2}, we assess early folding³⁻⁵ and other characteristics such as disorder⁶ and aggregation⁷. The resulting biophysical view of a sequence can help in pairwise sequence alignment⁸ or global homology assessment⁹, without using evolutionary information, which is biased towards folded proteins¹⁰. We apply our computational methods in collaboration, both with computational groups, for example in relation to post-translational modifications (PTMs) (<https://iomics.ugent.be/scop3p/>), and with experimental groups, for example, in protein design to create RNA recognition motif domains (RRMs) for specific RNA binding (<http://rnact.eu/>).

We are looking for **postdoctoral researchers with excellent programming and computer science skills**, preferably in **Python** and with a **structural bioinformatics** background. It is important that you can show evidence of your research from **peer-reviewed publications in international scientific journals**, and that you have **strong communication skills in English**, as the group is very international. In this position, you would help further the framework, for example by i) predicting the effect of PTMs on protein biophysics, ii) connecting biophysical characteristics of proteins to their subcellular location, or iii) creating tools to use the biophysical space of proteins to improve protein (re-)design. This work will then be collaboratively applied in broader computational and/or experimental settings.

Supervisor: Wim.Vranken@vub.be

Research Group: <http://bio2byte.be/>

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