

## Machine Learning Guided Discovery of Protein Interactions and Functions

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### Abstract:

How can we find proteins that inhibit CRISPR? How can we train a computer to identify patterns in proteins sequences and structures to predict their anti-microbial properties? How can we identify interactions of different proteins and their binding sites?

Proteins - the workhorse of the biological cell - perform a variety of functions in the cell. These range from structural support to the regulation of different biological processes and often involve interactions of multiple proteins. Identification of biological functions and interactions of proteins in the wet lab requires specialized assays which can be limited in their throughput as well as being time consuming and labour intensive. Machine learning - training a computer to identify predictive patterns - is a useful tool to guide wet lab experiments for discovering protein functions and interactions. In this webinar, we shall discuss how machine learning can be applied for the discovery of a variety of protein functions and their interactions. We will discuss our recent work on the discovery of anti-CRISPR proteins in collaboration with the Doudna lab (winner of the 2020 Chemistry Nobel) as well as development of tools for anti-microbial peptide prediction and identification of viral binding proteins and their binding sites.

**Wednesday 10 February 2021**

**1.00pm-2.00pm**

Via MS Teams

[Link can be found here](#)

[MEETING LINK](#)

For queries, please email [bmsatgh@warwick.ac.uk](mailto:bmsatgh@warwick.ac.uk)