Far frontiers of protein structure prediction

Tsinghua University: course syllabus

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Dr. Marcin J. Skwark is a coordinating postdoctoral researcher at Aalto University in Finland, and conducting independent research on the frontier of computational biochemistry, bioinformatics, statistical physics and machine learning.

This intensive course introduces protein structure prediction problem and classical approaches to solving it. The core of the course presents recently developed, novel methods that allow for computational prediction of proteins structures ab initio (i.e. without relying on already known protein structures). The novelty of the presented methods lies in vast reduction of computational time needed and significant improvement of prediction accuracy.

The course will run on every Tuesday and Wednesday in the afternoons between 3:20 and 5:00 pm. The course schedule:

March 25rd, 26rd: Introduction to proteins, protein evolution and folding
April 1th: Protein structure prediction
April 2th: Contact prediction: making ab initio structure prediction feasible
April 8th: Combining biology and physics for more accurate predictions
April 9th: Folding proteins with contacts and future of the field

The sessions will take place in **the Auditorium on the third floor of the Physics Building** of Tsinghua University.