

SEMINAR

“HOW TO FIND EPISTASIS IN FITNESS LANDSCAPES?”

Dr. Dmitry Ivankov

October 18, 2018

12.30 - 14.00

Room 403,

TPOC-3



SEMINAR ABSTRACT:

Epistasis, a non-additive contribution of single amino acid substitution to the fitness, is one of the most important factors of molecular evolution. Epistasis can be described differently; among the other types, researchers use the concepts of higher-order and multidimensional epistasis. To study epistasis, one has to find hypercubes of dimensionality two and higher in experimental genotype-to-phenotype maps. The (quasi-)random mutagenesis experiments potentially contain a lot of epistatic data. The topic of the seminar is how to study epistasis in random mutagenesis experiments.

First, Dr Ivankov will present a method for finding all hypercube structures in huge protein genotype-phenotype map produced by random mutagenesis. Second, he will show that there is a limited relationship between higher-order and multidimensional types of epistasis. Third, Dmitry will tell how to extend the framework to find epistasis in sparse data. And the last, he will present a new type of multidimensional epistasis, which is finer than sign and reciprocal sign types of epistasis. All suggested methods were successfully applied to two experimental datasets and it turned out that epistasis is abundant in high-throughput experimental data.

SPEAKER INTRODUCTION:

Dr. Dmitry Ivankov graduated from Moscow Institute of Physics and Technology in 1999. Then he worked for 10 years in the field of protein folding at the Institute of Protein Research. He defended his PhD “Theory of protein folding rates” in 2006. In 2010-2013 he worked in Technical University of Munich analyzing new signal peptides produced by proteogenomics. Starting from 2014 he has been working on the analysis of epistasis in Evolutionary Genomics group headed by Fyodor Kondrashov.