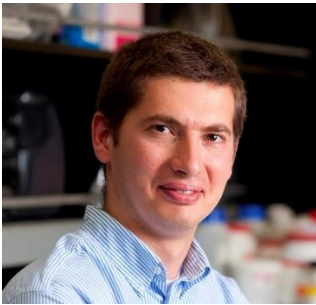# Lecturers:

Maxim Artyomov (PhD) / Washington University in St. Louis

Maxim Artyomov is an Assistant Professor at Immunology & Pathology Department of Washington University in St.Louis. Dr. Artyomov's lab applies next generation sequencing and novel computational techniques to address fundamental questions in immunology. His recent work is devoted to development of high-throughput RNA-seq approaches and applications of this technology to uncover relation between genes implicated in autoimmunity through genome-wide association studies. Dr. Artyomov obtained his PhD from MIT in 2009 working at Arup Chakraborty's lab where he studied stochastic behavior in the signal transduction networks at early stages of T-cell activation. For his postdoctoral studies Dr. Artyomov joined Broad Institute of MIT and Harvard, working with Aviv Regev to explore (both experimentally and computationally) the transcriptional networks that govern activation of dendritic cells in response to immune stimuli. Dr. Artyomov also serves as Co-Chair of Scientific Advisory Board (along with Doug Lauffenburger) for Cambridge based Immuneering Inc.

**Alexander Predeus (PhD) / Washington University in St. Louis**

Alexander has graduated from Moscow State University (Department of Chemistry) in 2003. In the fall of 2003 he joined the graduate school of Michigan State University to continue his studies in chemistry with Prof. William D. Wulff. His research focused on organometallic and supramolecular chemistry. He graduated with a Ph.D. in chemistry in 2009. Following this, Alexander has shifted his interests towards biological chemistry. During the two-year postdoctoral appointment with Prof. Michael Feig, Alexander have studied molecular dynamics methodology, and used it to get insights into mechanisms of action of RNA Polymerase II, MSH2-MSH6 DNA repair enzyme, and molecular crowding. After this Alexander have joined the lab of Prof. Maxim Artyomov to pursue his interest in fast-growing field of next-generation sequencing (NGS). He is currently working on integrative analysis of genetic and epigenetic information obtained by next-generation sequencing (RNA-Seq, ChIP-Seq of transcription factors and histone modifications, Dnase I hypersensitivity) applied to immune cells. Another current project involves analysis of co-expression patterns in publicly available datasets and creation of databases that would allow the discovery of biological similarities between unrelated samples based on gene co-expression.

Nikita Artomov / Harvard University, Massachusetts General Hospital, Broad Institute

Nikita is 4th year graduate student at Harvard University. He is working in the lab of Mark Daly at Analytic and Translational Genetics Unit (Massachusetts General Hospital) and Broad Institute. He is working on development of computational pipelines for full genome/exome sequencing data processing starting from raw data to the analysis ready dataset and following data analysis (GATK, Picard, etc.). Mostly working with germline cancer sequencing data of the patients with early onset and rare cancer type. He is interested in the development of tools for functional analysis incorporating protein-protein interaction maps for extracting affected protein pathways from sequencing studies.

Practice session:
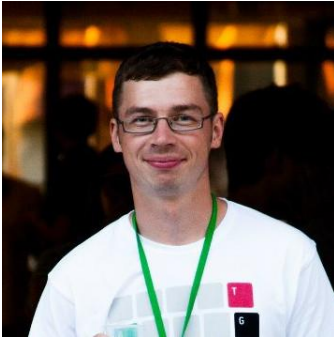
Pavel Fedotov / ITMO University

Pavel Fedotov works at Computer Technologies Laboratory, ITMO University since 2007. He graduated with Master's degree in applied math and informatics in 2011. After that Pavel has shifted to bioinformatics with focus on computational pipelines for next-generation sequencing data analysis, especially for genomics variants and genome assembly. Pavel was a visiting scientist at Washington University in St.Louis, the lab of Prof. Maxim Artyomov in 2013-2014. He has worked there on computational method for defining cell types from gene expressions data of mixed samples.

Alexey Sergushichev / ITMO University

Alexey graduated from ITMO University in 2013 and received his Master degree with honors in Computer Science. He was working on algorithms for genome assembly in Fedor Tsarev's lab (ITMO University). In the end of 2013 he was interning at Dr. Artyomov's lab working on a pipeline for integrated network analysis of transcriptional and metabolic profiling data. Now he continues this project in his PhD studies at Computer Technologies Laboratory at ITMO University.

Anton Alexandrov / ITMO University

Anton works as a researcher at Computer Technologies Laboratory of ITMO University. He received his Master's degree in Computer Science in 2013 from ITMO University. He has worked on a number of bioinformatic projects including developing genome assembly algorithms. In 2014, he was a visiting scientist at the lab of Maxim Artyomov, Washington University in St Louis where he worked on a pipeline for computational prediction of tumor-specific antigens.