





Der Fachbereich Informatik der Johannes Kepler Universität Linz¹ lädt in Zusammenarbeit mit der Österreichischen Gesellschaft für Informatik (ÖGI) zu folgendem Vortrag ein:

Victor Greiff ETH Zürich, Department of Biosystems, Science & Engineering

Deciphering the rules of antibody repertoire complexity using a systems biology approach

Monday, August 22, 2016, 15:30 Room JKU S3-318 in Science Park 3

Abstract:

Antibody repertoires ensure highly specific host protection. They thereby lay the foundation for many of the most prominent medical success stories such as vaccines, therapeutic monoclonal antibodies and immunodiagnostics. However, as of yet, the immense complexity of antibody repertoires (>1020 potential unique antibodies) prevented the quantitative investigation of the molecular rules, which govern their formation. Deciphering these rules is crucial for developing novel precision vaccine and therapeutic approaches.

The recent advent of high-throughput sequencing constituted a paradigm-changing event for the rapidly expanding field of systems immunology as it has enabled for the first time to interrogate antibody repertoire diversity in its entirety.

We have recently created one of the largest antibody repertoire high-throughput sequencing datasets to date. Combining this dataset with mathematical simulation, high-performance computing, machine learning and graph theory, I will present in my talk our progress in answering two of the longest-standing questions in the field of antibody immunology: (i) is the immense diversity of antibody repertoires predictable and (ii) what is the architecture of antibody repertoires?

Short Bio:

Dr. Victor Greiff received his PhD in Theoretical Immunology from the Humboldt University of Berlin (Germany, 2012) where he had studied the specificity of antibody repertoires using high-throughput antibody-binding proteomics data and mathematical modeling. In 2013, he joined the Laboratory for Systems and Synthetic Immunology (Prof. Sai T. Reddy) located at ETH Zürich where his main focus lies on gaining a systems view of antibody repertoire complexity by coupling large-scale immunogenomics data to computational immunology.

Einladender: Univ.-Prof. Dr. Sepp Hochreiter Assoz.Univ.-Prof. Dipl.-Ing. Dr. Ulrich Bodenhofer Institute of Bioinformatics

Der Fachbereich (http://informatik.jku.at) besteht aus folgenden Instituten:

Application Oriented Knowledge Processing (FAW), Bioinformatics, Computational Perception, Computer Architecture, Applied Systems Research and Statistics, Computer Graphics, Formal Models and Verification, Networks and Security, Integrated Circuits, Pervasive Computing, Software Systems Engineering, System Software, Telecooperation, Signal Processing

