

Single-cell Sequencing and Bioinformatic Modeling of Cancer Heterogeneity (ERC-funded postdoc position)

On a new project funded by the European Research Council (ERC) we are recruiting a postdoc interested in **single-cell sequencing technologies** and/or **bioinformatic algorithms** for dissecting **cancer heterogeneity**.

Our group is based at the **CeMM Research Center for Molecular Medicine of the Austrian Academy of Sciences in Vienna**. It combines a strong focus on biomedical technology (epigenomics, single-cell sequencing, drug screening, mass spectrometry, imaging, etc.) with a deep interest in computational modeling. We are also working closely with physicians at the Vienna General Hospital and the Medical University of Vienna, in order to advance precision medicine through the use of computation and high-throughput technology.

The Project

Cancer is the most heterogeneous of all diseases – a microcosm of tightly interlinked evolutionary and developmental processes. We want to understand this complexity at the level of single cells – including the cancer cells competing with each other for resources, but also the microenvironment that supports the cancer and the immune cells that try to fit the cancer. Using a combination of single-cell genome, epigenome, and transcriptome sequencing and computational modeling, we seek to establish a full evolutionary map of the dynamics underlying cancer development. Moreover, we pursue an engineering-inspired “build it to understand it” approach to cancer epigenetics, using CRISPR technology and computationally designed drug combinations to rationally reprogram normal cells into cancer cells and vice versa. This project seeks to establish a quantitative understanding of cancer heterogeneity and a predictive model for advancing precision therapies.

The Candidate

We are looking for highly motivated and academically outstanding candidates who want to pursue a scientific career in the field of computational and medical epigenomics. A strong candidate may have a background in the computational sciences (bioinformatics, statistics, physics, engineering, etc.) and some prior experience with collaborative research in high-throughput biology. In the same way, we are considering applicants with a background in medicine or in biology (e.g., functional genomics, chemical biology, human genetics, molecular medicine, etc.) who have strong quantitative skills and a keen interest in pursuing systems medicine projects. We are fully equipped and experienced with both computational and wet-lab work, such that it is an option – but by no means mandatory – to build a unique skill set by combining and fully integrating these two approaches through own work and collaborations.

The Lab (<http://www.medical-epigenomics.org/>)

The Medical Epigenomics Lab at CeMM pursues an interdisciplinary and highly collaborative research program aimed at understanding the cancer epigenome and establishing its utility for precision medicine. The lab is internationally well-connected and active in several fields:

- *Epigenomics*. We perform large-scale epigenome mapping in order to dissect the dynamics of cancer development and emerging drug resistance. This work is part of the European BLUEPRINT project and the International Human Epigenome Consortium.
- *Technology*. Exciting biomedical research is often driven by new technologies. Our lab is therefore heavily invested into technology development, including single-cell protocols, nanopore sequencing, CRISPR, and epigenome editing.
- *Bioinformatics*. New algorithms and advanced computational methods allow us to accurately infer epigenetic cell states from large-scale datasets, in order to reconstruct the epigenetic landscape that controls cellular differentiation and reprogramming.
- *Diagnostics*. Using large-scale DNA methylation mapping, bioinformatic prioritization, and functional characterization, we strive to develop clinically relevant biomarkers for informing personalized cancer therapy.

The Principal Investigator (<https://scholar.google.com/citations?user=9qSsTcIAAAAJ>)

Christoph Bock is a principal investigator at CeMM, guest professor at the Medical University of Vienna, scientific coordinator of Vienna's Biomedical Sequencing Facility, and adjunct group leader at the Max Planck Institute for Informatics. Previous appointments include the Max Planck Institute for Informatics (PhD studies) and the Broad Institute of MIT and Harvard (postdoctoral research). CB is a 2009 recipient of the Otto Hahn Medal by the Max Planck Society for pioneering work in computational epigenetics, and he recently received two major career development grants – a New Frontier Group award by the Austrian Academy of Sciences (EUR 1.4 million) and an ERC Starting Grant by the European Research Council (EUR 1.3 million). CB leads Genom Austria, which is the Austrian contribution to the International Network of Personal Genome Projects, and he is a member of several European and global initiatives on epigenetics & precision medicine.

The Institute (<http://www.cemm.at/>)

CeMM is an international research institute of the Austrian Academy of Sciences. Driven by medical needs, CeMM integrates basic research and medical expertise to pursue innovative approaches focused on cancer, inflammation, and immune disorders. CeMM is located at the center of one of the largest medical campuses in Europe, within walking distance of Vienna's historical city center. A study by “The Scientist” placed CeMM among the top-5 best places to work in academia world-wide (<http://the-scientist.com/2012/08/01/best-places-to-work-academia-2012>). Vienna is frequently ranked the world's best city to live. It is a United Nations city with a large English-speaking community. The official language at CeMM is English, and more than 30 different nationalities are represented at the institute.

Please apply online (<https://prescreen.io/j/0wzehoj>) with cover letter, CV, academic transcripts, and contact details of 3 referees. Applications will be reviewed on a rolling basis. Any application received by 15 August 2016 will be considered. Start dates are very flexible.

