Research profile for applicants

Name of DKFZ research division/group:	*Division of Computational Genomics and Systems Genetics (B260)*
Contact person:	*Oliver Stegle* *o.stegle@dkfz-heidelberg.de*
Group homepage: *Visit this website for further information on current research and recent publications.*	*https://www.dkfz.de/en/bioinformatik-genomik-systemgenetik/*
Eligibility:	• **DKFZ Postdoctoral Fellowships**

RESEARCH PROFILE AND PROJECT TOPICS

Our laboratory develops and applies computational approaches to study molecular variations and their phenotypic consequence. How does our genetic background shape phenotypic traits or cause disease? How are genetic and environmental factors integrated at different molecular layers, and how variable are molecular states between individual cells? We use statistical inference and machine learning as our main tools to address these scientific questions.

Our interdisciplinary and international team is jointly located at German Cancer Research Center (DKFZ) and European Molecular Biology Laboratory (EMBL) Heidelberg.

Project 1:
Possible projects in our lab at the DKFZ center around one of the following topics and will be tailored to the particular interests, opportunities and the background of the postdoctoral candidate.

1. *Computational Genetics*: We develop statistical and machine-learning methods to dissect often overlooked dimensions of the genotype-phenotype relationship, including genetic effects of rare genetic risk factors, and gene-environment interactions.
2. *Spatial Multi-Omics*: We develop foundational methods to integrate high-dimensional molecular profiles assayed in bulk or at the single-cell level. This includes innovations to allow for integrating multi-omics readouts across time and space, as well as methods for spatial omics technologies.
3. *Causal Models and Transcriptomics:* We develop methods to model genetic perturbation effects and infer causality. We leverage opportunities provided by engineered perturbations using CRISPR screens combined with a single-cell readout.

Project 2:
We are also looking for another candidate for one specific, well-defined project. This collaborative project investigates the epigenetic changes during the progression of human metastatic colorectal cancer. Your tasks will include i) data analysis to identify cis-regulatory elements, ii) analysis of 3D genome organization for the identification of transcription factors (TFs) and gene programs and iii) spatial profiling in primary tumors to identify spatial gene signatures.

We are looking for a candidate who is ambitious, kind and possesses the ability to work both independently and in a team. Many of our project are designed in close collaboration with experimental partners at DKFZ, where we apply these approaches to gain new insights on tumor evolution and principles of metastases formation, among other questions.