Hosting group information for applicants

Name of DKFZ research division/group:
Computational Genomics and System Genetics, B260

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Group homepage: **https://www.dkfz.de/en/bioinformatik-genomik-systemgenetik/**

Please visit our website for further information on our research and recent publications.

RESEARCH PROFILE AND PROJECT TOPICS:

Our interest lies in computational methods to unravel the genotype–phenotype map on a genome-wide scale. How do genetic background and environment jointly shape phenotypic traits or cause diseases? How are genetic and external factors integrated at different molecular layers, and how variable are molecular states between individual cells?
We use statistics and machine learning as our main tool to address these questions. To make accurate inferences from high-dimensional omics datasets, it is essential to account for biological and technical noise and to propagate evidence strength between different steps in the analysis. We develop methods that enable connecting genetic factors to phenotypes and to integrate multiomics data in health and disease.
Our methodological work ties in with biomedical collaborations, and we are developing methods to fully exploit high-throughput datasets from the most recent profiling technologies. In doing so, we derive computational methods to dissect phenotypic variability at the level of the transcriptome and the proteome and we derive new tools for single-cell biology.

Project topics:
We have open postdoc positions available at the interface of statistical genomics, single-cell biology and multi-comics technology. We are particularly interested in extension and applications of Multi Omics Factor Analysis [1] as a tool to identify disease-linked molecular variation. A second direction are novel methods for tying together genetic perturbations and single-cell dynamics, which will be conducted in the context of our ERC funded DECODE project [2]. Finally, we look for postdocs who are interested in developing novel strategies for integrating genetic factors with spatial omics readouts [3] .

Relevant publications and references:
[1] Argelaguet, Ricard, et al. "Multi-Omics Factor Analysis—a framework for unsupervised integration of multi-omics data sets." Molecular systems biology 14.6 (2018): e8124.

[2] https://cordis.europa.eu/project/id/810296
[3] Svensson, Valentine, Sarah A. Teichmann, and Oliver Stegle. "SpatialDE: identification of spatially variable genes." Nature methods 15.5 (2018): 343-346.
[4] McCarthy, Davis J., et al. "Cardelino: computational integration of somatic clonal substructure and single-cell transcriptomes." Nature methods 17.4 (2020): 414-421.