

Hosting group information for applicants

Name of DKFZ research division/group:

Molecular Genetics/B060

Contact person: **Team Leader Dr. Marc Zapatka, Tel. 06221 42-4584, m.zapatka@dkfz.de**

Group homepage: <https://www.dkfz.de/en/genetics/index.php>

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

RESEARCH PROFILE AND PROJECT TOPICS:

The bioinformatics team develops and applies methods and algorithms for the analysis of molecular genetics data in the clinical context. Currently the main focus is the understanding of biological processes in the context of clinical applications through the analysis of high throughput sequencing data. We are mainly analyzing the genome using small RNA, RNA, DNA sequencing and the epigenome using ChIP-Sequencing and whole genome bisulfite sequencing. In addition, we use single cell technologies to disentangle tumor compositions and understand the tumor microenvironment. Furthermore, we are interested in bacterial and viral contributions to cancer analyzing the microbiome components of tumor samples to make use of the identified microbiota for tumor characterization and patient stratification.

Research Interests

The main focus of the bioinformatics team is to improve and apply methods to interpret high throughput data especially to understand tumor diseases, their causes and clinical consequences. In the context of several projects we work on the following aspects:

- Improve and apply bioinformatics in the context of molecular tumor boards leading to improved treatment of breast cancer cases

In two clinical projects (CATCH and COGNITION) we perform the bioinformatic analyses and clinical interpretation of the genomic aberrations in breast cancer patients to guide treatment decisions [3]. In collaboration with Prof. Dr. med. Andreas Schneeweiss we work on clinical trials in gynecological oncology (Clinical Trials at NCT) and support the decision process in the personalized patient treatment by performing the variant calling and interpretation as well as preparation of the molecular tumor boards.

- Understanding of tumor development, microenvironment and clonal evolution based on transcriptomic, epigenetic and genomic changes applying bulk and single cell approaches We recently analyzed the clonal evolution in chronic lymphocytic leukemia [2] and now together with Martina Seiffert use single cell methods to understand the tumor microenvironment in CLL. In addition, we analyze the tumor and microenvironment



CONNECTING THE DOTS.
TO ADVANCE RESEARCH CAREERS

International Postdoc Program
www.dkfz.de/postdoc

composition applying single cell technologies in brain metastases of breast cancer to understand the establishment of these metastases and their interactions with immune and brain cells.

- Identifying and characterizing the microbiome component in tumors and tumor patients.

Recently we analyzed the viral contribution to cancer in a large cohort of cancer samples collected in PCAWG [1] and could identify relevant genomic lesions linked to viral infections. We now are analyzing the viral contribution to cancer in additional cohorts and extend our analysis to the bacterial microbiome especially in the context of chemo- and immune therapy of cancer.



**CONNECTING THE DOTS.
TO ADVANCE RESEARCH CAREERS**

[International Postdoc Program](https://www.dkfz.de/postdoc)
www.dkfz.de/postdoc