Interested to do a Postdoc at the DKFZ? Get in touch with us!

Current opportunities for Bioinformaticians at the German Cancer Research Center

Name of DKFZ research division/group:
Clinical Cooperation Unit Molecular Hematology/Oncology (A360)

Contact person: **Prof. Alwin Krämer, Phone: +49-6221-42-1440, Email: a.kraemer@dkfz.de**

Group homepage: **https://www.dkfz.de/en/mol-haem_onk/index.php**

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

RESEARCH PROFILE AND PROJECT TOPICS:

If you're interested in this project please get in touch with the respective contact person.

The Clinical Cooperation Unit Molecular Hematology/Oncology of DKFZ and University Hospital Heidelberg has a basic science focus on causes and consequences of chromosomal instability, a nearly universal feature of human malignancies and a major contributor to genetic heterogeneity, clonal evolution and metastasis, themselves being at the center of cancer development, progression, relapse, and therapy resistance in solid tumors. Its clinical/translational research centers around carcinoma of unknown primary (CUP syndrome), a paradigm metastatic malignancy in which only metastases but no primary tumor can be identified. Within an interdisciplinary team between University Hospital Heidelberg, National Center for Tumor Diseases (NCT), German Cancer Research Center (DKFZ) and Roche Pharma we currently analyze the treatment response of patients with CUP syndrome by a variety of sequencing readouts. For the analysis of genome sequencing, DNA methylation sequencing and gene expression analysis data from patients treated within a large, international clinical study (CUPISCO), which compares 12 different targeted therapies with standard chemotherapy, we are seeking a postdoctoral fellow to conduct bioinformatic analyses in tight interaction with lab-based scientists and clinicians. The work will include standard sequencing data analysis methods as well as machine learning based approaches. The primary goal is to evaluate DNA sequencing, methylation and gene expression data in terms of their ability to identify the tissue of tumor origin, explain patient and disease heterogeneity, and to predict tumor recurrence and treatment response. You will have the opportunity to shape your own research profile by pursuing research in method

development and collaborative analysis of novel datasets. We are looking for someone with strong computational skills and capable to handle large scale data sets who wants to work in an interdisciplinary team. A PhD or equivalent qualification in quantitative sciences (mathematics, physics, systems/quantitative biology, computer sciences and related fields). Experience in the computational analysis of omics data, solid programming skills in a high-level programming language (e.g. C, C++, Java) and/or appropriate scripting languages such as R or Python, as well as familiarity with Linux compute clusters is highly beneficial.