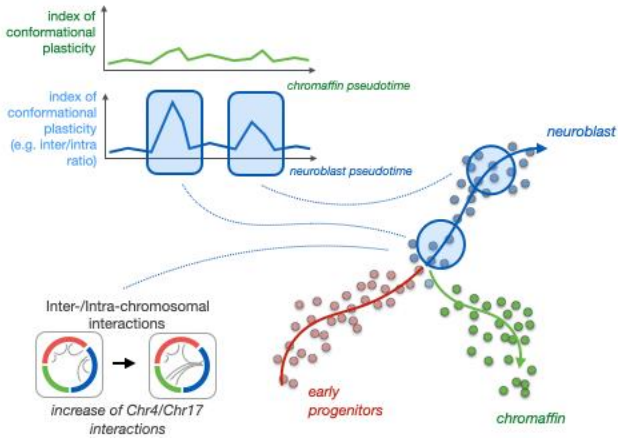
Postdoc (3 years) position in computational single-cell multiomics analysis in neuroblastoma

***Health Data Science Unit** – Medical Faculty Heidelberg and BioQuant (Dr. Carl Herrmann)*



Neuroblastoma, an embryonal tumor accounting for 15% of cancer-related death in children, is a devastating disease, which arises during development of the sympathetic lineage involving neural crest cells. The vast clinical diversity corresponds to a **molecular heterogeneity, which is partly shaped by the chromatin conformation and the epigenetic landscape**. In prior work, the **Health Data Science Unit** (www.hdsu.org) in collaboration with our partners at the German Cancer Research Center (DKFZ) has contributed to the description of this diversity at bulk and single-cell level, highlighted the role super-enhancers, and connected the oncogenic process in different subtypes to distinct phases and lineages in normal embryonal development (adrenal medulla) (Gartlgruber *et al.*, 2021; Jansky *et al.*, 2021).

Within the DFG special priority program (SPP) "3D Genome Architecture in Disease and Development", our 3-year funded project "**Modeling embryonal neuroblastoma tumorigenesis by activation of chromosomal 3D super enhancer interactions and genomic instability"** aims at going further in the understanting of the role of 3D genome architecture in driving the malignant transformation during neuroblastoma. **We want to test the hypothesis that certain timepoints during normal embryonal development show higher susceptibility to oncogenic transformation**, and that these are defined by certain conformational and chromatin properties. In collaboration with the group of Frank Westermann, DKFZ, we are thus planning to:

1. Complement our high-resolution scRNA-seq atlas of neuroblastoma tumors and normal adrenal glands with **scATAC-seq** and use this multiome data to reconstruct **single-cell gene regulatory networks**.
2. Perform **scHi-C** on normal adrenal medulla and establish a **temporal map of chromatin conformation** changes along normal developmental trajectory
3. Identify **perturbations in the regulatory networks** driven by conformation changes through integration of the different data modalities.

The computational predictions will be validated by functional assays based on hiPSC using CRISPR-induced looping and enhancer surgery in the group of Frank Westermann.

For the computational part of this project, we are looking for a highly motivated postdoctoral researcher in computational genomics.
What we expect:

- Prior experience and expertise in computational single-cell analysis.
- Expertise in cancer (epi)genomics.
- High-interest in a collaborative project involving computational and experimental groups.

We are offering:

- A 3-year funded postdoc position according to german salary scale TV-L E13
- An excellent scientific environment in the middle of the Heidelberg Campus, with many opportunities for exchanging with groups involved in single-cell analysis within the Heidelberg-Mannheim Alliance
- Being involved in a network of many research project within the special priority program with many opportunities for scientific exchange and scientific meetings with groups involved in this SPP

Please send your application (CV + letter + publications) together with 2 references to Dr. Carl Herrmann before October 30th (carl.herrmann@bioquant.uni-heidelberg.de)