Bioinformatician for single-cell developments in the context of viral infection

The Health Data Science Unit (HDSU, www.hdsu.org) is a newly created unit of the BioQuant and medical Faculty of the University Heidelberg, which focuses on research topics related to digital health and the integration of clinical and genomic datasets. HDSU is one of the major partners of the HighMed medical informatics consortium (www.highmed.org), and leads the effort to set up systems for clinical data integration. A further topic of the unit lies in the analysis of (epi)genomic datasets and single-cell datasets, as part of several consortia. We seek to develop novel approaches for the integration of multi-omics datasets, especially in a single-cell context.

Within the DFG-funded transregio project "Determinants and dynamics of elimination versus persistence of hepatitis virus infection" (www.trr179.de), the group of Dr. Carl Herrmann is planning to set up a central single-cell analysis facility, in collaboration with the single-cell Open Lab at BioQuant Heidelberg (https://malone.bioquant.uni-heidelberg.de/scopenlab/). We want to investigate the sources of variability in the cellular response to viral infection, in particular HCV virus, by combining several layers of single-cell omics in various cellular populations.

In this context, we are looking for a **bioinformatician** to support and coordinate this effort, with a focus on the following points:

- Development and implementation of standard single-cell analysis workflows for scRNA-seq and scATAC-seq datasets in an HPC environment;
- Implementation of such workflows in a cloud infrastructure (de.NBI cloud, ELIXIR,…);
- Development of data integration methods and strategies for multi-omics single-cell datasets;
- Analysis of single-cell datasets (scRNA-seq/scATAC-seq/CITE-seq) generated within the DFG consortium;
- Contribution to training efforts and documentation for external users of these workflows.

We are looking for a candidate with experience in large-scale high-throughput sequencing data such as RNA-seq, ChIP-seq and ATAC-seq, and the ability to set up analysis workflows (preferentially using snakemake). First experience with single-cell datasets as well as a solid statistical background would be a strong plus.
The position is funded for two years, with a possibility for further extension.

Application letters and CVs (as pdfs), together with contact information of two referees should be sent by mail to carl.herrmann@bioquant.uni-heidelberg.de