**Project 1.14. Towards understanding functions of microglia in brain homeostasis and tumor progression through analysis of single cell sequencing data**

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**Background:**

Complex organisms and tissues are characterized by molecular heterogeneity of their cells. Thanks to recent advances in sequencing technologies, it is now possible to study gene expression and chromatin accessibility at the level of individual cells. Single-cell genomics studies can reveal distinct cell subpopulations and dissect their function. Our recent study used immunosorted myeloid cells (CD11b+) from glioma and naïve mouse brains to study the subpopulations of these cells. The results demonstrated that microglia in healthy brain contribute to brain homoeostasis, while in tumor they adapt a tumor supporting role. Distinct gene expression profiles of microglia and monocytes/macrophages were demonstrated and marker proteins have been selected (*Ochocka et al., 2021*).

**Aim:**

The project aims to achieve a better understanding of functional roles of microglia through computational analyses of acquired single cell sequencing data. For this end, we will use data from single cell transcriptomics (scRNA-seq) and accessible chromatin (scATAC-seq) assays. scRNA-seq data on transcriptomes of CD11b+ cells from glioma and naïve brain at three time-points, would allow to study gene expression trajectories in tumor progression. Further experiments will involve drug-induced depletion of microglia followed by its spontaneous repopulation. We expect that the repopulated cells could have a permanently altered cell state, and that the precision of the repopulation may deteriorate with age. We will follow an integrative approach, in particular we will use available data on chromatin conformation from Hi-C experiments to interpret the observed cell differences in the context of genome organization into topologically associating domains. Finally, we expect that the computational methods developed in this project will be generalizable to other models.

**Requirements:**

- Master's degree in exact or natural sciences (biology, biotechnology, bioinformatics, computer science, mathematics, physics etc.),
- Experience in biological data analysis, preferably in analyzing next generation sequencing data.
- Interest in tackling biological problems using computational methods,
- Good programming skills, preferably in R or Python,
- Fluency in written and spoken English.