Investigating White Matter Tract invasion by single-cell sequencing data analysis

A post-doctoral position (12 months, extendable) is available in the **Bioinformatics team** at the IBGC, UMR 5095 CNRS in Bordeaux (**France**), to work with **Dr. Macha Nikolski and Dr. Thomas Daubon**. The research project consists in developing methods and analyzing human and culture samples by **single cell RNA sequencing** for understanding invasion processes in **glioblastoma**.

Glioblastoma (GBM) is the most deadly type of human cancer. Most patients diagnosed with this grade IV malignant glioma **survive for about 15 months**. Even with optimal treatment, the estimated recurrence rate is more than 90%. Recurrence is mostly caused by the **regrowth of highly invasive cells that spread from the tumor bulk and are therefore not removed by resection.** A large number of GBM cells are invading around the tumor core. Invasion on blood vessels is a well-described phenomenon, but a majority of cells **invade along white matter tracts**. This latter mode, also known as perineuronal satellitosis, is not well described in the literature (observed by Scherrer in 1950). Furthermore, the molecular relationship between glioma and white matter tracts remains **largely unknown**. Recent publications described **neurogliomal synapses** in glioblastoma (Venkataramani et al, Nature), in pediatric glioma (Venkatesh et al, Nature), or in cerebral metastasis (Zeng et al, Nature), which interconnects the neuronal network to the cancer network. Glutamate influx *via* NMDAR induces calcium flux into the glioma network, and by consequence, tumor cells are invading the surrounding tissues. **Single-cell transcriptomics** was performed in the publications related to glioma, and massive amount of data was generated in Venkataramani et al. By using these data, the candidate will develop a methodology for integrating these already acquired datasets for deciphering molecular and metabolic pathways, used for increasing invasion. Indeed, due to differences in experimental platforms and biological sample batches, the **integration of multiple scRNA-seq datasets remains challenging**. These bioinformatics analyses will be extended by **integrating newly acquired data**, generated by the team of Thomas Daubon (IBGC, UMR 5095 CNRS) for several glioblastoma models in co-culture with neurons or white matter tracts in acute brain slices. **Bulk and single-cell transcriptomics** will help to elucidate the invasive mechanisms in play.

Candidate Profile and main duties:

- PhD degree in bioinformatics, high level engineer or equivalent
- Dedicated, pro-active and with a personal fit into the team
- Good communication skills that allow productive interactions with biologists and clinicians (e.g. discussing models / analyses choices)
- Programming skills (R, Python) in Unix environment are essential
- Prior experience in NGS data analysis is essential, experience in sc-RNAseq data analysis would be a plus
- Ability to communicate in both spoken and written English
- Autonomous and rigorous with a critical mind

Job offer

There are several unique features of this job opportunity:

1. Working with enthusiastic teams and an already-setup laboratories.
2. CNRS and Bordeaux University offer access to state-of-the-art infrastructure and a competitive salary.
3. Basic science approaches to address clinically relevant issues in collaboration with clinicians.
4. Two international-friendly teams.

Cover letter, CV and references contacts may be directed to Macha Nikolski and Thomas Daubon, macha.nikolski@u-bordeaux.fr and thomas.daubon@u-bordeaux.fr.