Title: Bioinformatics methods to identify cellular types in GBM and develop prognostic models for cell fate using Artificial Intelligence

Starting date: October 2021
Location: Bordeaux, France
Laboratory: IBGC, CNRS

GLIONEUROMET - Metabolic crosstalk between glioblastoma cells and neurons - is funded by the National Cancer Institute, INCA and offers a fully funded PhD position at the intersection of two dynamic teams within the IBGC CNRS Institute, those led by Macha Nikolski and Thomas Daubon.

Glioblastomas (GBMs) are grade IV malignant gliomas mainly deriving from neural stem cells, which are progenitors of astrocytic or neuronal lineages. This cancer is one of the deadliest types in humans, with an **average survival time of less than 15 months upon diagnosis**, and an incidence increasing worldwide. Many clinical studies have been conducted on patients with GBMs, however **little progress has been made on patient survival** in the last decade. Cancer recurrence is mostly caused by the **regrowth of highly invasive cells that spread out from the tumor bulk,** in the close vicinity to the resection site**.** A large number of GBM cells are invading from the tumor core, partially due to hypoxic conditions, as demonstrated by recent publications (Daubon et al., 2019 Nature Communications).

Our recent results demonstrated that metabolic coupling between glycolytic and oxidative tumor cells, based on expression of LDHA and LDHB, is essential for GBM development (Guyon et al., submitted – available on Research Square). GBM cells invade the peritumoral space *via* different routes, one of those is **along white matter tracts**, which is not well described in the literature. The interactions of tumor cells with the peritumoral nervous parenchyma are also not well characterized, only recent findings described the formation of neuro-glioma-synapses to sustain GBM invasion. It is plausible that a metabolite exchange such as the lactate shuttle between astrocytes and neurons might operate between GBM and non-malignant cells. In this project, we propose to evaluate the importance and the regulatory mechanisms of metabolic coupling between glioma cells and neurons in GBM development, especially during cell invasion.

The bioinformatics Work Package of the project will be centered on the multi-omics single-cell data acquired by the experimental teams. More precisely, the candidate will:

- Define and apply bioinformatics pipelines to define GBM biomarkers from transcriptomics, metabolomics (targeted isotope-labeled data) and imaging datasets in a computationally efficient manner.
- Develop a bioinformatics methodology for integrative analysis of bulk and single cell transcriptomics and metabolomics.
- Using temporal series of omics data, build a predictive model of metabolic coupling.

The position is offered for 3 years. The hired researcher must enroll in Doctoral Programme at the University of Bordeaux, as well as to participate in complementary training activities.

HOW TO APPLY

Applicants should send full application by e-mail to Macha Nikolski and Thomas Daubon consisting of:

- Curriculum Vitae
- University transcripts (grades)
- A motivation letter addressing his/her research interests in relationship to the research project.
- Recommendation letters

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