

## Master project 2020-2021

### Personal Information

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<b>Group</b>	Cancer Resistance & Bioinformatics

### Project

## Computational genomics

#### Project Title:

Discovery of "Dr Jekyll & Mr Hyde" genes

#### Keywords:

Cancer, genetics, outcome, tumor suppressor, oncogene

#### Summary:

Integration of genomic and clinical information using the Cox proportional hazard model is commonly used to identify biological factors that influence cancer outcome. Typically, this is applied to analyze the connection between gene expression and cancer progression, therapeutic response or patient survival. This approach has generated hundreds of biomarkers, of which several are nowadays applied in the clinic. However, some genes might not show a single facet during the course of the disease: they can act as tumor suppressors or as oncogenes depending on other variables (so called "Dr Jekyll and Mr Hyde" genes). These genes, their features and impact on cancer outcome remain completely unknown. Objectives In this project, we aim to identify this type of genes by pan-cancer interrogation of gene expression and clinical outcomes. This proposal will be integrated into experimental assays performed at the recipient group.

#### References:

An Integrated TCGA Pan-Cancer Clinical Data Resource to drive high quality survival outcome analytics. Cell. 173, 2: p400-416.e11, 10.1016/j.cell.2018.02.052 (2018). Kourou et al., Machine learning applications in cancer prognosis and prediction. Comput Struct Biotechnol J 13, 8-17 (2015).

#### Expected skills::

Candidate(s) are expected to be proficient in programming in R and to have strong background on statistics.

#### Possibility of funding::

To be discussed

**Possible continuity with PhD: :**

To be discussed

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