



## Master project 2021-2022

### Personal Information

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<b>Group</b>	High Content Genomics and Bioinformatics (HCGB)

### Project

## Web development & bioinformatic tools

#### Project Title:

Development of new modules in NGS analysis pipelines

#### Keywords:

transcriptomics, RNAseq, WGS, visualization, integration

#### Summary:

Our unit serves as a core bioinformatics services facility within a research institute associated to a large hospital. We work at the interface between basic and translational research and analyze datasets of many sorts of omics data, generated in house as well as externally. Students interested in exposure to such environments are encouraged to apply. We have developed two NGS analysis pipelines that are in production stages and that could benefit from addition of new functionalities and implementation of advanced versions of these tools. The first pipeline is XICRA, dedicated to small RNA sequencing analysis which currently processes paired end data for precise miRNA analysis at the isomiR level. Future plans are to include other small non coding RNAs such as piRNAs and tRFs. The second tool is Bacterial Typer which is a whole microbial genome analysis tool with modules adapted to different needs specific to different species. In addition, we would like to expand usability by developing GUI for non expert bioinformaticians in the clinic using R shiny or python Dash and to package the pipeline in a docker container for easy deployment.

#### References:

Sanchez-Herrero JF, Pluvinet R, Haro de Luna A, Sumoy L (2021) Paired-end small RNA sequencing reveals a possible overestimation in the isomiR sequence repertoire previously reported from conventional single read data analysis. BMC Bioinformatics (Suppl.) (in press) Lacoma A, Laabei M, Sánchez-Herrero JF, Young B, Godoy-Tena G, Gomes-Fernandes M, Sumoy L, Plans O, Arméstar F, Prat C. (2021) Genotypic and Phenotypic Characterization of Staphylococcus aureus Isolates from the Respiratory Tract in Mechanically-Ventilated Patients. Toxins (Basel). 13(2):122. doi: 10.3390/toxins13020122. PMID: 33562023.

#### Expected skills::

R, Python, NGS, shiny, dash, docker

#### Possibility of funding::

To be discussed

#### Possible continuity with PhD: :

