

## Master project 2020-2021

### Personal Information

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<b>Group</b>	Epitranscriptomics and RNA Dynamics

### Project

## Computational systems biology

### Project Title:

Understanding the role of RNA folding in neurodegenerative diseases using third-generation sequencing technologies (oxford nanopore)

### Keywords:

Oxford Nanopore sequencing; RNA modifications; RNA structure; machine learning;

### Summary:

RNAs are not simple intermediary molecules between DNA and protein, but are in fact functional molecules capable of regulating central cellular processes. Because RNA is a single-stranded molecule, it tends to fold back on itself, forming stable secondary and tertiary structures by internal base pairing and other interactions. The function of RNAs can vary depending on the specific folding that the molecule, and therefore accurate RNA structural maps are needed to understand the complexity, function, and regulation of these molecules. Unfortunately, current methods generating RNA structure maps employ second-generation sequencing technologies (e.g. Illumina), which are unable to produce information on highly repetitive regions of the genome. Here we will use Oxford Nanopore Technologies (ONT), capable of producing full-length RNA molecule reads, to produce RNA structure maps for highly repetitive regions, such as those involved in neurodegenerative diseases such as Amyotrophic Lateral Sclerosis (ALS) or Fronto-temporal dementia (FTD).

### References:

1. Liu H\*, Begik O, Lucas MC, Ramirez JM, Mason CE, Wiener D, Schwartz S, Mattick JS, Smith MA and Novoa EM#. Accurate detection of m6A RNA modifications in native RNA sequences. Nature Comm 2019, 10:4079. doi:10.1038/s41467-019-11713-9
2. Beaudoin JD\*, Novoa EM\*, Vejnar CE, Yartseva V, Takacs CM, Kellis M and Giraldez AJ. Analyses of mRNA structure dynamics identify the embryonic RNA regulome. Nat Struct Mol Biol 2018, 25, 677-686
3. Smith MA\*, Ersavas T\*, Ferguson JM\*, Liu J, Lucas MC, Begik O, Bojarski L, Barton K and Novoa EM#. Barcoding and demultiplexing Oxford Nanopore native RNA sequencing reads with deep residual learning. bioRxiv 2019, 864322 (under review in Genome Research)
4. Cozzuto L, Liu H, Prysycz LP, Hermoso Pulido T, Ponomarenko J and Novoa EM#. MasterOfPores: a workflow for the analysis of Oxford Nanopore direct RNA sequencing datasets bioRxiv 2019, 828336 (accepted in Front in Genet)

### Expected skills::

Mandatory: Python, R. Desirable: machine learning, handling of third-generation sequencing data

**Possibility of funding::**

Yes

**Possible continuity with PhD: :**

To be discussed

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