

For students with a background on Bioinformatics, Computational Biology, Bioengineering, Biomedical engineering or related areas

Title: Investigating the function of antisense transcription in mammalian cells

Synopsis:

Antisense transcripts do not code for proteins but initiate inside or downstream of a protein coding gene and are transcribed in the opposite direction of that gene. Although antisense transcripts are increasingly recognized as important regulators of protein coding gene expression, very little is known about how they function. Moreover, identifying which of the many antisense RNAs made in cells are functionally important is a challenging task that requires development of improved research tools. We hypothesize that antisense transcription plays a general and physiologically important role in regulation of transcription and splicing of protein coding genes. We also reason that interventions targeted at antisense RNAs can be used to manipulate expression of the sense protein coding gene.

Main objective:

To identify at genome-wide level antisense transcripts that overlap either the promoter or splice sites of protein coding genes and experimentally test their role in transcription and splicing.

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Webpage of the group: <https://imm.medicina.ulisboa.pt/en/investigacao/labs/carmo-fonseca-maria-lab/>

Bibliography:

Nojima T, Gomes T, Grosso AR, Kimura H, Dye MJ, Dhir S, Carmo-Fonseca M, and Proudfoot NJ. (2015) Mammalian NET-seq reveals genome-wide nascent transcription coupled to RNA processing. *Cell* 161: 526-540.

Schlackow M, Nojima T, Gomes T, Dhir A, Carmo-Fonseca M, Proudfoot NJ. (2016) Distinctive patterns of transcription and RNA processing for human lincRNAs. *Mol Cell* 65: 25-38.

Remunerated or volunteer training: volunteer