Propuesta de Trabajo Fin de Máster
Año académico 2023-2024
MÁSTER EN MÉTODOS COMPUTACIONALES EN CIENCIAS

Proyecto Nº 10
Título: A new biochemical/bioinformatic tool to detect small circular RNAs
Departamento/ Laboratorio: RNA-based stress responses in neurodegenerative diseases
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Resumen: Circular RNAs (circRNAs) have been recently described as abundant, stable and very diverse RNA molecules that display unanticipated key roles in cell homeostasis. The advent of massive RNA sequencing methodologies provides an excellent substrate for the identification of circRNAs, based on the end-to-end contact of back splice junctions by using specific bioinformatic tools. As a limitation of current circRNA detection methods, the current RNAseq libraries and the bioinformatic methods fail to sensitively detect circRNA of small size. In our group, aiming to identify a small circular RNA (scRNA) of 26 nucleotides derived from the RNA encoding the XBP1 transcription factor, we have developed a biochemical method to isolate/enrich in small circular RNAs, and to copy them by rolling circle retrotranscription. The aim of this project is to complete the development of a bioinformatic tool that detect 1) the presence of reads corresponding to scRNA, 2) align the sequence of these reads with the genome and 3) finally provide the number and genomic location of scRNA molecules genome wide.

OPTATIVAS RECOMENDADAS 1. 2. 3. 4.