Propuesta de Trabajo Fin de Máster
Año académico 2020-2021

Máster en Métodos computacionales en ciencias

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| **Project Nº 42** |
| **Título:** Metanalysis of RNA binding proteins implicated in cancer development |
| **Departamento/ Laboratorio** Gene Therapy and Regulation of Gene Expression, LncRNAs and Gene Regulation in Cancer, CIMA |
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| **Resumen**

 Human transcription covers 70% of the genome while only 25% entitle to protein-coding genes, leaving most of the remaining transcription to long noncoding genes (lncRNA). In the last years, we discovered that lncRNAs drive many biological processes and that their deregulation could lead to cancer disease and that lncRNAs differential expression helps to monitor and classify cancer prognosis. lncRNA are coated by RNA binding proteins (RPBs) that shuttle, modify, and finally control their faith and molecular mechanism of action. Therefore research over RBP lncRNA interoperability, classification, mode of action and co-evolution is gaining broad scientific interest.

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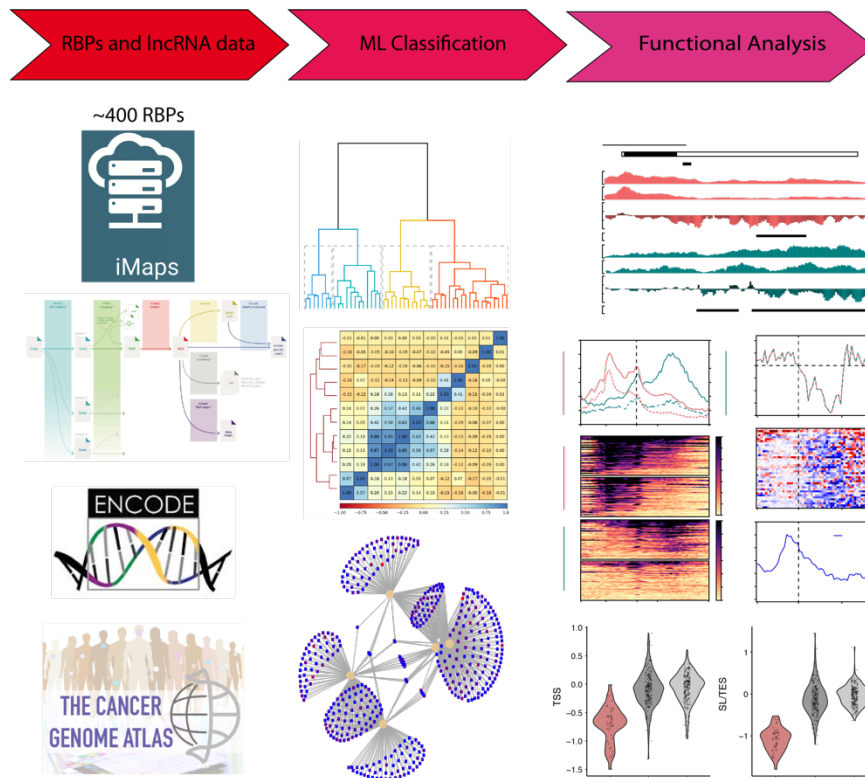
In this project, we will approach an RBP functional metanalysis over lncRNAs and their relation with cancer disease. To obtain sufficient comprehension, we will analyze hundreds of next-generation sequencing datasets unveiling RBP contact sites to lncRNA. We will also depict relevant lncRNA for cancer progression by assessing their expression in different cancer types. With all this knowledge and using machine learning clustering, multivariate approaches and multi-dimensional scaling methods, we will select RBPs binding lncRNAs, potentially implicated in cancer. Over these candidates, we will perform functional analyses with the aim to classify and better understand this inseparable coupling.

Necessary python or R programming knowledge.