

Project Title:

Transcriptome assembly and differential expression analysis

Name: ○Juan Pascual Anaya

Laboratory at RIKEN: Laboratory for Evolutionary Morphology.

My research project is two fold: on one hand, I am analyzing the embryonic transcriptomes of lamprey and hagfish. For that, the analysis and processing of the huge amount of data produced by Next Generation Sequencing technologies require the use of powerful computational resources, not possible to do with normal desktop computers. On the other hand, I am involved in my lab in a ChIP-seq and RNA-seq project of the turtle CR. In this project, I plan to analyze the differential expression of mRNAs in the turtle CR when compare with the limbs and body wall, and also the chomosomal signatures that defines different states of the chromatin in the CR, in order to identify new enhancers.

However, we finally did not use RICC because of the time limitations in computation. Although we started some jobs within RICC with some assembler like Velvet, those jobs were stopped after 24h. Some of these jobs needed weeks to complete, so eventually I acquired my own high-memory server at CDB and use it to perform the transcriptome assembly, read mapping and other genomic analyses.