**Comparison of NGS DNA methylation profiles of different types of pluripotent cells**

In the field of cellular reprograming, a lot of research has been performed in the last years in the search for the so called “Epigenetic somatic memory” and several controversies have arisen in relation to its existence and biological impact. Several researchers have tackled the problem searching for Differentially Methylated Regions (DMRs) between ESCs and iPSCs.

In this project several DNA methylation profiles form Next Generation Sequencing (NGS) from fibroblasts, Embryonic Stems Cells (ESCs) and Induced Reprogrammed Stems Cells (iPSCs) will be download from public databases and it will be analyzed the DNA methylation differences between them.

For such task it will be used the program P3BSseq (Parallel processing pipeline for analysis of bisulfite sequencing data) that can be download from https://sourceforge.net/projects/p3bsseq/