



EPICO platform: a reference cyber-infrastructure for comparative epigenomics. The BLUEPRINT Data Analysis Portal as a practical case

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Abstract

The development of the next generation sequencing techniques opened the door to explore epigenetic changes related with DNA and associated histones. Reference epigenomes are being generated by different large consortia including BLUEPRINT, CEMT, CREST, DEEP, ENCODE, CEEHRC and NIH ROADMAP. The impact of large and complex epigenomic datasets on biology insights or clinical applications is limited by the lack of accessibility by easy, intuitive and fast tools. The EPICO cyber-infrastructure is an open access reference set of libraries to develop comparative epigenomic data portals. EPICO offers a framework in which large epigenome projects can make available their rich datasets to the community without requiring specific technical skills.

As a first EPICO instance we have implemented the BLUEPRINT Data Analysis Portal (BDAP). BDAP provides a desktop for the comparative analysis of epigenomes of hematopoietic cell types based on the results of the basic epigenetic analysis pipelines, i.e., position of epigenetic features. The BDAP user-friendly interface enables the interactive exploration of genomic regions, genes and pathways in the context of differentiation of the hematopoietic lineages. The EPICO system source code can be accessed at <https://github.com/inab> and BDAP at <http://blueprint-data.bsc.es>