The FANTOM5 web resource: from genome annotation to function

Knowing what are the genomic functional elements such as genes and regulatory regions responsible for all processes in life is crucial to understand how organisms survive. Genome sequencing techniques have allowed us to define genomes in terms of gene number, structure and abundance, and to learn about the regulatory interactions that fine-tune all cellular processes from differentiation to development and to evolution.

The FANTOM5 project, within the FANTOM consortium, has generated an invaluable collection of data comprising almost all distinct cell types and tissues sampled from several organisms; those datasets can be used to study gene expression and its regulation at several stages of differentiation or development, and in various system, in order to understand life. Here I summarize the FANTOM5 resource and give some examples how to use its data and web interfaces.