Galaxy HiCExplorer: HiCExplorer, deepTools3 and pyGenomeTracks

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Hi-C and ChIP-seq comprise a powerful combination of techniques that can be used to reveal genomic structure and its influence on gene expression. Chromosome conformation capture techniques are widely used to analyse the 3D conformation of chromatin inside the nucleus across a rising number of species, tissues and experimental conditions. In particular, the Hi-C protocol has helped to uncover folding principles of chromatin, demonstrating that the genome is partitioned into active (“A”) and inactive (“B”) compartments and that these compartments are further subdivided into topologically associating domains (TADs). Tracks derived from ChIP-seq showing histone modifications or protein interaction correlate with these structures and can be used to gain even deeper insight into the organisation, structure and function of the 3D chromatin conformation.

The Galaxy HiCExplorer web server combines HiCExplorer and deepTools to allow users with little bioinformatic background to perform every step of the analysis in one workflow. This inclusion facilitates the integration of ChIP-seq, RNA-seq, MNase-Seq, ATAC-Seq as well as other kind of datasets with Hi-C data. In combination with the newly created pyGenomeTracks, publication ready plots can be created with an endless combination of tracks. In this talk we will introduce new features and present real-world use-cases of HiCExplorer, deepTools3 and pyGenomeTracks.