Protocols and programs for standardized chromatin research

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Abstract
Here we present our efforts to further standardize chromatin research -- both experimentally and also computationally. First we explore the application of our **NEXSON** protocol (Arrigoni *et al. 2016*) to more challenging samples and very low cell numbers (less than 10,000 cells). In the process, we also investigate the treatment of clinical samples, that are often frozen before fixation for storage in biobanks. We compare genome-wide ChIP-seq results from standard fixation protocols with those obtained from clinical studies.
With ***deepTools2*** (Ramirez, Ryani *et al. 2016*) we present a software suite to perform complete bioinformatic workflows ranging from quality controls and normalizations of aligned reads to integrative analyses, including clustering and visualization approaches. Since we first described deepTools in 2014, we have implemented new solutions for many requests from the community and our users. Here, we introduce significant enhancements and new tools to further improve data visualization and interpretation. deepTools continue to be open to all users and freely available as a Galaxy web service at deeptools.ie-freiburg.mpg.de. The new deepTools2 suite can be easily deployed within any Galaxy framework via the toolshed repository, and we also provide source code for command line usage under Linux and Mac OS X. A public and documented API for access to deepTools functionality is also available.

Arrigoni L, Richter AS, Betancourt E, Bruder K, Diehl S, Manke T, Bönisch U. Standardizing chromatin research: a simple and universal method for ChIP-seq. Nucleic Acids Res. 2016 Apr 20;44(7):e67. doi: 10.1093/nar/gkv1495. Epub 2015 Dec 23. PubMed PMID: 26704968; PubMed Central PMCID: PMC4838356.

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