

ChIP-Seq Analysis

Chromatin Immunoprecipitation Sequencing (ChIP-Seq) uses high-throughput DNA sequencing to map protein-DNA interactions across the entire genome. Partek Genomics Suite offers convenient visualization and analysis of ChIP-Seq data.

In this tutorial, we will use the Partek Genomics Suite ChIP-Seq workflow to analyze aligned data from a ChIP sample versus a control sample in .bam format.

This tutorial illustrates:

- [Importing ChIP-Seq data](#)
- [Quality control for ChIP-Seq samples](#)
- [Detecting peaks and enriched regions in ChIP-Seq data](#)
- [Creating a list of enriched regions](#)
- [Identifying novel and known motifs](#)
- [Finding nearest genomic features](#)
- [Visualizing reads and enriched regions](#)

*Note: the workflow described below is enabled in Partek Genomics Suite version 7.0 software. Please fill out the form on [Our support page](#) to request this version or use the **Help > Check for Updates** command to check whether you have the latest released version. The screenshots shown within this tutorial may vary across platforms and across different versions of Partek Genomics Suite.*

Description of the Data Set

The data for this tutorial comes from Johnson et al. 2007, which first described the ChIP-Seq technique.

This study mapped genomic binding sites for neuron-restrictive silencer factor (NRSF) transcription factor across the genome. There are two samples: an NRSF-enriched ChIP sample (chip.bam) and a control sample of input DNA without antibody immunoenrichment (mock.bam). The chip.bam file contains ~1.7 million mapped reads and the mock.bam file contains ~2.3 million mapped reads. These .bam files contain the aligned genomic locations and sequences of mapped reads. This data set contains reads from a single-end (SE) library; the differences in processing paired-end (PE) reads will be discussed when applicable.

Data for this tutorial can be downloaded from the Partek website using this link - [ChIP-Seq tutorial data](#). To follow this tutorial, download the 2 .bam files and unzip them on your local computer using 7-zip, WinRAR, or a similar program. Because of the large size of the .bam files, we recommend saving them to a local drive instead of trying to access them on a network drive. The first time a .bam file is read by Partek Genomics Suite, the file will be sorted to allow for faster access. Therefore, you must have write permissions for the .bam files after download and on the file folder where they are stored.

References

Johnson, D. S., Mortazavi, A., Myers, R. M., & Wold, B. (2007). Genome-Wide Mapping of in Vivo Protein-DNA Interactions (Vol. 316). New York, NY: Science.

Additional Assistance

If you need additional assistance, please visit [our support page](#) to submit a help ticket or find phone numbers for regional support.



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