CDB SEMINAR

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Wednesday, July 23, 2014
16:00~17:00   A7F Seminar Room

How to visualize published ChIP-seq raw data

Summary

Background: ChIP-seq is a powerful method for comprehensively knowing the genomic regions occupied by proteins such as transcription factors and modified histones. Raw sequence data of published ChIP-seq experiments are all deposited in public databases and are publically available to every researcher. However, in order to visualize the ChIP-seq data of interest on genome browser, the corresponding raw sequence data must be downloaded and converted into a BigWig-formatted file through complicated command-line processing. Such hurdles hamper a wide range of biologists from exploiting the publically available ChIP-seq data.

Project 1: I developed a Mac GUI software package, SraTailor, which automatically converts ChIP-seq raw data into a BigWig-formatted file. Simplicity of use is one of the most notable features: entering an accession number of published ChIP-seq raw data and clicking the mouse are the only steps to graphically visualize the data on genome browser. Optionally, SraTailor is able to make peak calls, and also to process "your" ChIP-seq raw data as input. SraTailor is freely available at:
http://www.devbio.med.kyushu-u.ac.jp/sra_tailor

Project 2 (Ongoing): I am constructing a database to visualize all published ChIP-seq results on genome browser. You will be able to graphically know how much and which proteins are verified to bind to a genomic region of your interest.

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