MACS (Model-based Analysis of ChIP-Seq) is a command line tool designed by X. Shirley Liu and colleagues to analyze data generated by ChIP-Seq experiments in eukaryote, especially in mammal. Given the ChIP-Seq data with or without control samples, MACS can be used to identify transcription factor binding sites and histone modification enriched regions.

- can be used on Unix-based operating systems (Mac OS X, Debian or Ubuntu Linux)
- peak identification for ChIP-Seq data
- can be used with or without control samples
- applied in affinity enrichment based DNA methylation studies, such as MeDIP-Seq data

- detect histone modification enriched regions
- speed of MACS analysis: For FoxA1 ChIP-Seq experiment on human with 4 million 36 nt tags for treatment and 5 million tags for control, it will take MACS(version 1.3) less than 3 min and no more than 65M memory to complete the analysis on a 2.0G Hz computer, using the default parameter. Actually, every tag will take 6 bytes in memory. So for instance, 500M tags will take 3G memory, considering other data like peak information and temporary data, then its memory usage will normally be around 4G mem

Reference

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