JAMM: A Peak Finder for Joint Analysis of NGS Replicates

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DEMO DESCRIPTION:

We introduce JAMM: a peak finder that can integrate biological replicates and determine enrichment site widths accurately. JAMM is a universal peak finder that is applicable to different types of datasets. It is available for free and can run on Linux machines through the command line: http://code.google.com/p/jammpeak-finder

We will describe JAMM via three main sections:

– Peak Finding Approach and Benchmarking
– Tutorial: How to Call Peaks with JAMM
– An Open Q&A Session

1- Peak Finding Approach and Benchmarking (10 minutes)

We will briefly describe the approach JAMM employs for peak finding, and the main advantages of using these methods. This includes the method for fragment length calculation, the method for defining enriched windows as well as replicate integration via mixture model clustering.

We will also describe various benchmarks we used to validate JAMM and we will demonstrate how it performs compared to some of the more commonly used peak finders (example: MACS) and some of the recently published ones (example: DFilter).

2- Tutorial: How to Call Peaks with JAMM (10 minutes)

- Formatting input for JAMM: How to prepare read alignments for JAMM. How to specify sample replicates and biological control for JAMM.

- JAMM's three peak calling modes: How to set them and how they affect output

- User-defined parameters: Parameters affecting read pile-ups and enriched window determination.

- JAMM's Output: How to interpret the narrowPeak files JAMM outputs and a brief description of JAMM's peak scores and p-values. Some quick suggestions for downstream analysis.

During the tutorial, we will also run JAMM live on a test dataset.

3- A Q&A Session (5 minutes)

This is an open Q&A session for the audience.