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ChIP-exo: High Resolution Identification of Protein-DNA Binding Events and Quality Control

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Abstract

Recently, ChIP-exo has been developed to investigate protein-DNA interaction in higher resolution compared to popularly used ChIP-Seq. Although ChIP-exo has drawn much attention and is considered as powerful assay, currently, no systematic studies have yet been conducted to determine optimal strategies for experimental design and analysis of ChIP-exo. In order to address these questions, we evaluated diverse aspects of ChIP-exo and found the following characteristics of ChIP-exo data. First, Background of ChIP-exo data is quite different from that of ChIP-Seq data. However, sequence biases inherently present in ChIP-Seq data still exist in ChIP-exo data. Second, in ChIP-exo data, reads are located around binding sites much more tightly and hence, it has potential for high resolution identification of protein-DNA interaction sites, hence the space to allocate the reads is greatly reduced. Third, although often assumed in the ChIP-exo data analysis methods, the peak pair assumption does not hold well in real ChIP-exo data. Fourth, spatial resolution of ChIP-exo is comparable to that of PET ChIP-Seq and both of them are significantly better than resolution of SET ChIP-Seq. Finally, for given fixed sequencing depth, ChIP-exo provides higher sensitivity, specificity, and spatial resolution than PET ChIP-Seq.

In this article, we provide a quality control pipeline which visually assesses ChIP-exo biases and calculates a signal-to-noise measure. Also, we updated dPeak [1], which makes a striking balance in sensitivity, specificity, and spatial resolution for ChIP-exo data analysis.

Keywords: ChIP-exo; QC; TFBS; BS identification on High-Res

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1 Background

ChIP-exo (Chromatin Immunoprecipitation followed by exonuclease digestion and next generation sequencing) Rhee and Pugh ([2]) is the state-of-the-art experiment developed to attain single base-pair resolution of protein binding site identification and it is considered as a powerful alternative to popularly used ChIP-Seq (Chromatin Immunoprecipitation coupled with next generation sequencing) assay. ChIP-exo experiments first capture millions of DNA fragments (150 - 250 bp in length) that the protein under study interacts with using random fragmentation of DNA and a protein-specific antibody. Then, exonuclease is introduced to trim 5' end of each DNA fragment to a fixed distance from the bound protein. As a result, boundaries around the protein of interest constructed with 5' ends of fragments are located much closer to bound protein compared to ChIP-Seq. This is the step unique to ChIP-exo that could potentially provide significantly higher spatial resolution compared to ChIP-Seq. Finally, high throughput sequencing of a small region (25 to 100 bp) at 5' end of each fragment generates millions of reads or tags.

While the number of produced ChIP-exo data keeps increasing, characteristics of ChIP-exo data and optimal strategies for experimental design and analysis of ChIP-exo data are not fully investigated yet, including issues of sequence biases inherent to ChIP-exo data, choice of optimal statistical methods, and determination of optimal sequencing depth. However, currently, the number of available ChIP-exo data is still limited and their sequencing depths are still insufficient for such investigation. To address this limitation we gathered ChIP exo data from diverse organisms: CTCF factor in human [2]; ER factor in human and FoxA1 factor in mouse from [3]; and generated σ^{70} factor in *Escherichia coli* (E. Coli) under aerobic (+ O_2) condition, and treated by rifampicin by 0 and 20 minutes.

DNA libraries generated by the ChIP-exo protocol seem to be less complex than the libraries generated by ChIP-Seq [4]. Hence, most of current guidelines [5] may not be applicable on ChIP-exo. To address this challenge, we suggest a series of quality control visualizations to understand which biases are present in ChIP-exo data. Related to quality control, Previous ChIP-exo analysis used ChIP-Seq samples to compare the resolution between experiments ([2], [6], [3]). In [?], Carroll et. al. studied the use of the Strand-Cross Correlation (SCC) [7]. and showed that by filtering blacklisted regions the estimation of the SCC is improved. However, this method requires to know blacklisted regions in advance which may not be available. In our pipeline we propose two out-the-shelf metrics equivalent to RSC and NSC for the estimation of the signal-to-noise ratio for a ChIP-exo sample.

In order to achieve the potential benefits of ChIP-exo on protein binding site identification, it is critical to understand which are the important characteristics of ChIP exo data and to use algorithms that could fully utilize information available in ChIP exo data. Rhee and Pugh [2] discussed that reads in the forward and reverse strand might construct peak pairs around bound protein, of which heights were implicitly assumed to be symmetric. Hence, they used the “peak pair method” that predicts the midpoint of two modes of peak pairs as potential binding site. Mace [8], CexoR [9] and peakzilla [10], recently developed ChIP-exo data analysis methods, are also based on this peak pair assumption. However, appropriateness of such assumption was not fully evaluated in the literature yet. Furthermore, it is still

unknown which factors could affect protein binding site identification using ChIP exo data. In order to address this problem, we investigated various aspects of ChIP exo data by contrasting them with their respective ChIP Seq experiments.

Currently, research on statistical methods for ChIP-exo data is still in its very early stage. Although many methods have been proposed to identify protein binding sites from ChIP Seq data (reviewed in [11] and [12]), such as MACS [13], CisGenome [14] and MOSAiCS [15], these approaches reveal protein binding sites in lower resolution, i.e., at an interval of hundreds to thousands of base pairs. Furthermore, they report only one “mode” or “predicted binding location” per peak. Hence, these methods are not appropriate to evaluate the potential of ChIP-exo data for high resolution identification of protein binding sites. More recently, deconvolution algorithms such as CSDeconv [16], GEM [17] (an improved version of [18]) and PICS [19] have been proposed to identify binding sites in higher resolution using ChIP-Seq data. However, most of them are still not tailored for ChIP-exo and PET and SET ChIP-Seq data in a unified framework and as a result, currently available methods are not appropriate for fair comparison between ChIP-exo and ChIP-Seq. To address these limitations, we developed an improved of dPeak [1], a high resolution binding site identification (deconvolution) algorithm that we previously developed for PET and SET ChIP-Seq data, so that it can also handle ChIP-exo data. The dPeak algorithm implements a probabilistic model that accurately describes the ChIP-exo and ChIP-Seq data generation process.

In this paper, we demonstrate that the peak pair assumption of Rhee and Pugh [2] does not hold well in real ChIP-exo data. Furthermore, we found that when we analyze ChIP-exo data from eukaryotic genomes, it is important to consider sequence biases inherent to ChIP-exo data, such as mappability and GC content in order to improve sensitivity and specificity of binding site identification. dPeak outperforms or performs competitively with ChIP-exo data analysis such as GEM and MACE. More importantly, when comparable number of reads is used for both ChIP-exo and ChIP-Seq, dPeak couple with ChIP-exo data provides resolution comparable to PET ChIP-Seq and both significantly improve the resolution of protein binding site identification compared to SET-based analysis with any of the available methods.

2 Results and discussion

2.1 Data considered

2.1.1 Deeply sequenced *E.Coli* σ^{70} ChIP-exo and ChIP-Seq data

2.2 Characteristics of ChIP exo data

2.3 ChIP exo Quality Control pipeline

Methods

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