

DRAFT

# High Resolution Identification of Protein-DNA Binding Events and Quality Control for ChIP-exo data

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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  $\sigma^{70}$  factor in *Escherichia coli* (E. Coli) under aerobic (+O<sub>2</sub>) 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, additionally to our knowledge there are not established quality control pipelines for 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 [7], Carroll et. al. studied the use of the Strand-Cross Correlation (SCC) [8], 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 [9], CexoR [10] and peakzilla [11], 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 [12] and [13]), such as MACS [14], CisGenome [15] and MOSAiCS [16], 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 [17], GEM [18] (an improved version of [19]) and PICS [20] 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 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 Deeply sequenced E.Coli $\sigma^{70}$ ChIP-exo and ChIP-Seq data

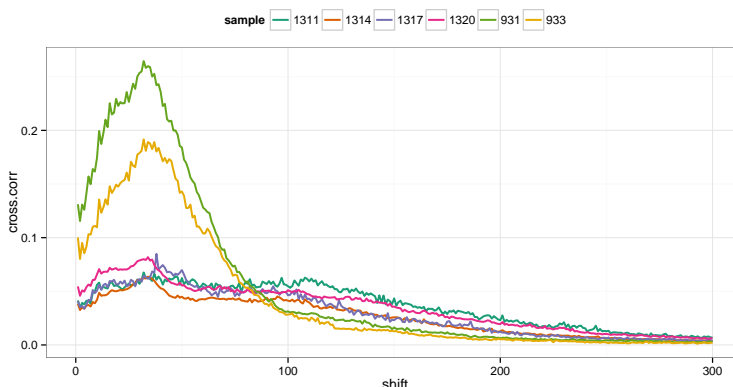
$\sigma^{70}$  factor is a transcription initiation factor of housekeeping genes in E. coli. In E. coli genomes, many promoters contain multiple transcription start sites (TSS) and these TSS are often closely spaced (10–150 bp). These closely spaced binding sites are considered to be multiple “switches” that differentially regulate gene expression under diverse growth conditions [21], [22]. Therefore, investigation of ChIP-exo’s potential for identification and differentiation of closely spaced binding sites are invaluable for elucidating the transcriptional networks of prokaryotic genomes.

### 2.2 Current guidelines and quality metrics

To have a first view on the data, we calculated a series of the most commonly used quality indicators for ChIP-Seq data, which are listed in table 1. The PBC, NSC and RSC were calculated as defined in [5] and the SSD was calculated as defined in [23]. Additionally, we calculated the FSR to compare the number of fragments in each strand. A few conclusions that we may get by observing the PBC in table 1 are all the samples have a quite low library complexity, hence it would be suggested to repeat the experiment.

| Condition | Rep. | Nr. reads | PBC    | SSD    | FSR    | NSC    |
|-----------|------|-----------|--------|--------|--------|--------|
| Aerobic   | 1    | 1,454,566 | 0.2156 | 0.0830 | 0.5012 | 114.14 |
| Aerobic   | 2    | 864,714   | 0.2471 | 0.0488 | 0.4923 | 160.93 |
| Rif-0min  | 1    | 960,256   | 0.2823 | 0.0361 | 0.4998 | 10.29  |
| Rif-0min  | 2    | 2,247,295 | 0.2656 | 0.1091 | 0.5047 | 25.08  |
| Rif-20min | 1    | 1,940,387 | 0.2698 | 0.0820 | 0.5054 | 17.69  |
| Rif-20min | 2    | 4,229,574 | 0.2153 | 0.1647 | 0.5071 | 14.11  |

**Table 1** Usual quality control indicators applied to our  $\sigma^{70}$  samples. PBC stands PCR-bottleneck coefficient, SSD for standardized standard deviation, FSR for forward strand ratio, NSC for normalized strand cross-correlation coefficient. We omitted the RSC (relative strand cross-correlation since ChIP-exo experiments don’t usually have an accompanying input file)



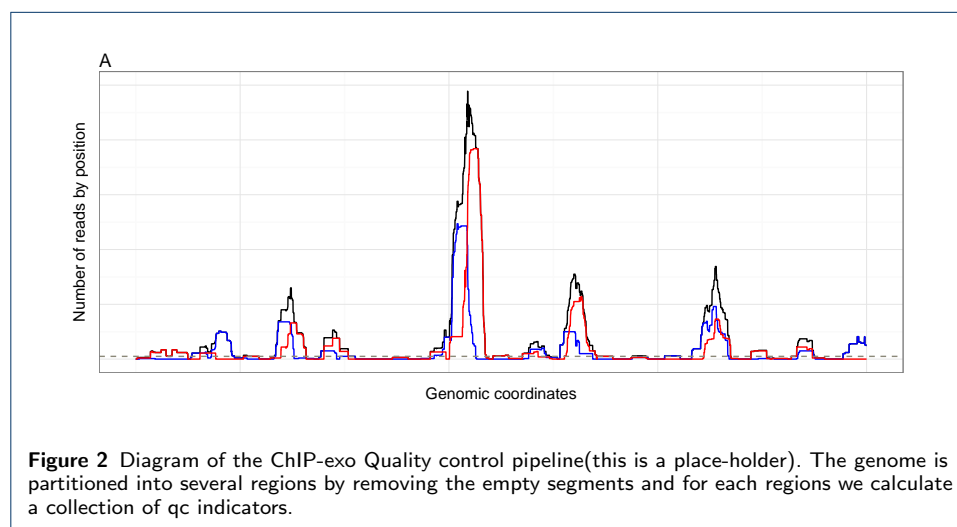
**Figure 1** Strand cross-correlation curves for  $\sigma^{70}$  samples.

In a good ChIP-Seq experiment the strand cross-correlation is maximized at the fragment length and there is also a “phantom peak” at the sample’s read length ([5] and [8]). However, in ChIP-exo’s case this two peaks are confounded. Hence

an enrichment measure based in the strand cross-correlation such as NSC or RSC is harder to interpret. In figure 1 we plotted the SCC curves for  $\sigma^{70}$  ChIP-exo experiments used to calculate the NSC and RSC values in table 1. According to ENCODE's quality metrics, NSC values close to one corresponds to low enrichment samples or bad quality datasets, hence in our case the last four samples would be considered to have higher quality than they actually have. On the other hand, all PBC values are considerably low and correspond to samples with severe bottlenecking issues, in particular we are going to show that for the first two samples we are obtaining a smaller resolution and identifying a comparable number of targets as in ChIP-Seq PET experiments.

### 2.3 ChIP-exo Quality Control pipeline

Figure 2 shows a flowchart for the ChIPexoQC pipeline. Which basically partitions genome by keeping the non-digested ChIP-exo regions. Then, for each region it calculates a series of independent statistics. Finally, it creates several visualizations designed to asses the overall quality levels of A ChIP-exo sample.



#### 2.3.1 Strand imbalance in ChIP-exo data

The strand imbalance assesment is based in the observation that the enriched regions usually have a higher concentration of fragments, therefore we examine the FSR (defined as the ratio of the number of forward stranded reads divided by the total number of reads in a given region) as the region with lower depth are being filtered out. This indicator is of particular importance, since several methods rely on the “peak-pair” assumption. In table 1, we calculated the FSR and noticed that for all the samples, it's value is close to 0.5, which means that there are roughly the same amount of reads in both strands. To asses

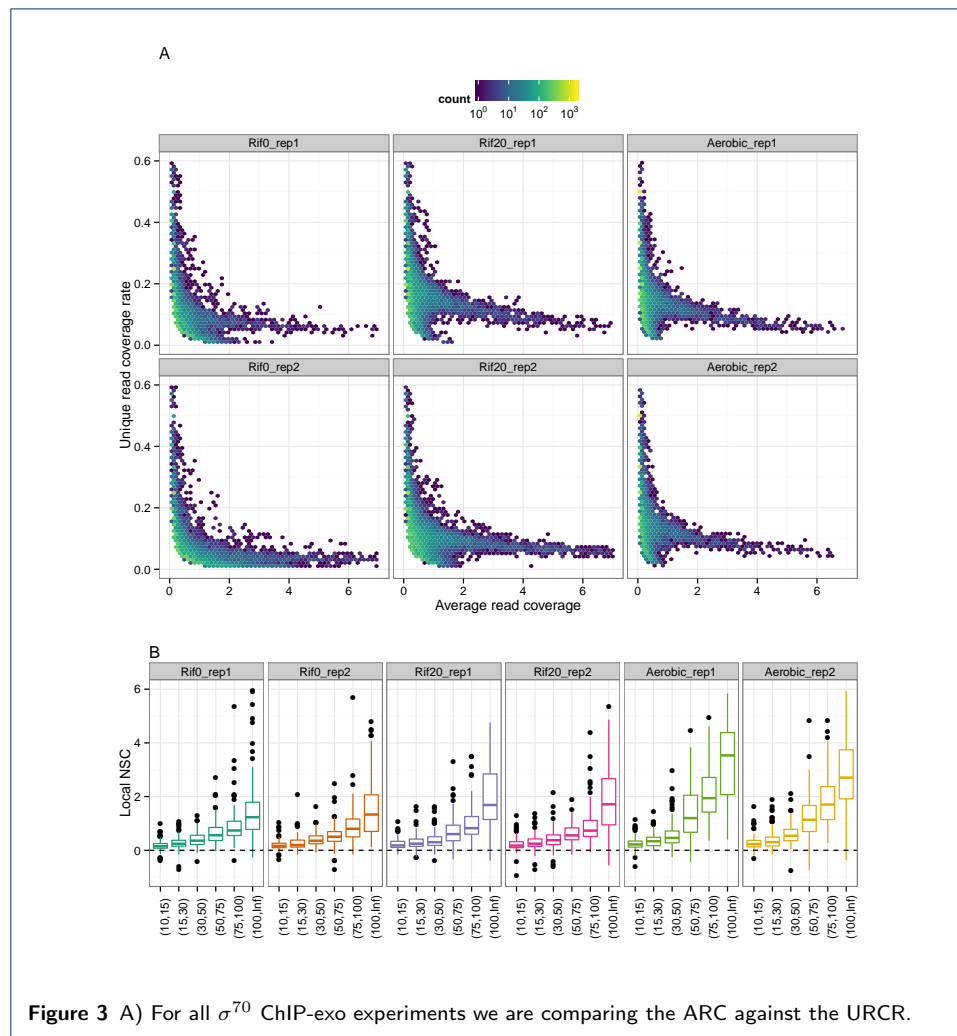
#### 2.3.2 Enrichment and library complexity in ChIP-exo data

In ChIP-exo experiments and input samples is often unavailable, therefore to determine the quality of a ChIP-exo experiment is necessary to address the balance between the enrichment and the library complexity of the experiment. To diagnose

this balance we considered the Average Read Coverage (ARC) and the Unique Read Coverage Rate (URCR) which are defined as:

$$\text{ARC} = \frac{\text{Nr. of reads in the region}}{\text{Width of the region}}$$

$$\text{URCR} = \frac{\text{Nr. of reads mapped to only one position in the region}}{\text{Nr. of reads in the region}}$$

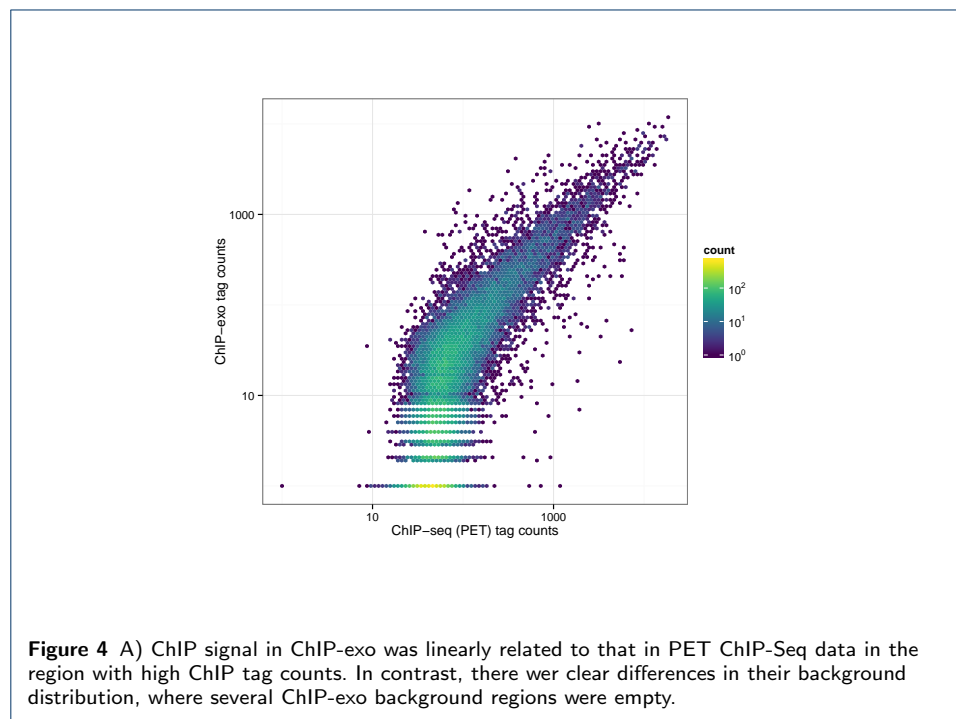


## 2.4 Comparison with ChIP-Seq data

We first compared various factors that could affect binding site identification between ChIP-exo and ChIP-Seq data. in order to compare distribution of signal and background between ChIP-exo and ChIP-Seq data, we calculated ChIP tag counts across the genome by counting the number of reads mapping to each of 150 non-overlapping window after extending reads by 150 to their 3' end directions. ChIP tag counts in ChIP-exo data were linearly related to ChIP tag counts in ChIP-Seq data for the regions with high ChIP tag counts (Figure 4A). This implies that signals

for potential binding sites are well reproducible between ChIP-exo and ChIP-Seq data. On the other hand, there was clear difference in the background distribution between them. In ChIP-Seq data reads were almost uniformly distributed over background (non-binding) regions and the ChIP tag counts in there regions were significantly larger than zero. In contrast, in ChIP-exo data, there was larger variation in ChIP tag counts among background regions and ChIP tag counts were much lower in these regions compared to ChIP-Seq data. There were also large proportion of regions without any read in ChIP-exo data. These results indicate that background distribution of ChIP-exo data is less homogeneous than that of ChIP-Seq data.

We next evaluated the “peak pair” assumption of Rhee and Pugh [2], MACE [?], CexoR, [10] and peakzilla [11], i.e. a peak of reads in the forward strand is usually paired with a peak of reads in the reverse strand that is located in the other site of the binding site.

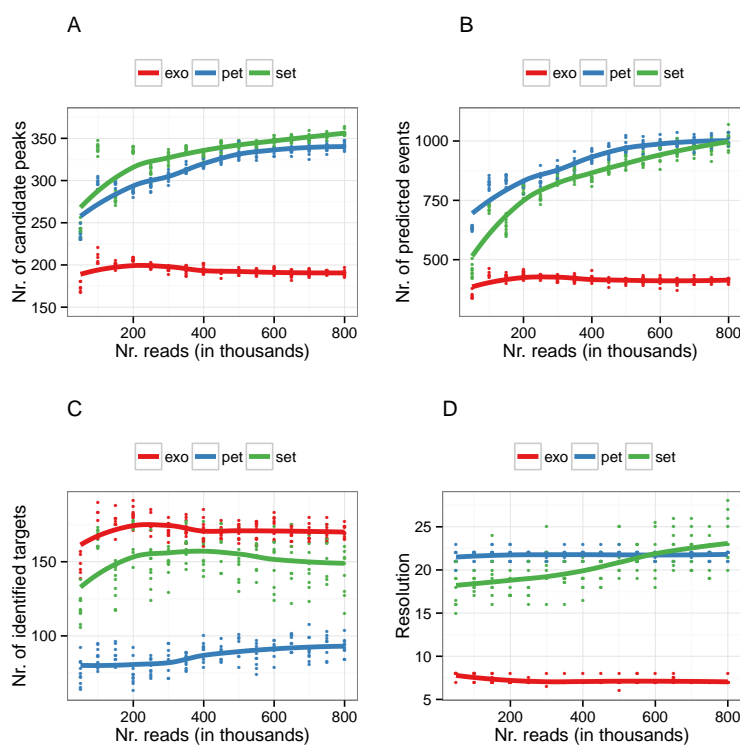


## 2.5 Recommendations for the design of ChIP-exo experiments

We sampled a fixed amount of fragments for each of the ChIP-exo, PET ChIP-Seq and SET ChIP-Seq datasets of the  $\sigma^{70}$  sample in aerobic conditions. For each sampled dataset we applied our lower-to-higher resolution pipeline by calling peaks with MOSAiCS [16] and then deconvolving the binding events by using dPeak [1]. For the ChIP-exo datasets we called peaks by using GC-content and mappability with MOSAiCS, and for the ChIP-Seq datasets we used their respective Input samples.

In figure 5 we compared the behaviour of each data type when their depth is fixed. It is remarkable that even when the number of candidate peaks or the number of predicted events is quite lower than for both ChIP-Seq cases, it outperforms them





**Figure 5** Comparison of the number of candidate regions (A), predicted events (B), identified targets (C) and resolution (D) among ChIP-exo, PET ChIP-Seq and SET ChIP-Seq. RegulonDB annotations are considered as a gold standard. A gold standard was considered identified if a BS was estimated inside a 15 bp window around it

in the number of identified targets and in resolution. This may suggest that with ChIP-exo less false positive peaks are being called and that when the targets are being identified, dpeak is able to estimate binding locations closer to the actual true cases. Additionally, we can see that as the read depth increases all four indicators do so as well, which may indicate that with ChIP-exo a smaller amount of reads is necessary to identify a higher number of targets, but it may also be possible that this is an artifact occurring due to ChIP-exo's lower library complexity.

### **3 Methods**

3.1 Growth conditions

3.2 ChIP-exo experiments

3.3 Library preparation, sequencing and mapping of sequencing reads

3.4 Method comparison for ChIP-exo

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