

# Analyzing microbial ChIP-Seq data with Pique

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## ABSTRACT

### Motivation:

While numerous effective peak finders have been developed for eukaryotic systems, we have found that the approaches used can be surprisingly error prone when run on high-coverage bacterial and archaeal ChIP-Seq datasets.

### Results:

We have developed Pique, a conceptually simple, easy to use ChIP-Seq peak finding application for bacterial and archaeal ChIP-Seq data. The software is cross-platform and Open Source, and based on Open Source dependencies. Output is provided in standardized bioinformatic formats, and easily imported by the Gaggles Genome Browser for manual curation and data exploration, or into statistical computing and graphics software such as R for further analysis.

### Availability:

The software is available under the BSD-3 license at

<http://github.com/ryneches/pique>.

A tutorial and test data are included with the documentation.

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## 1 INTRODUCTION

Next generation sequencing coupled with chromatin immunoprecipitation (ChIP-Seq) is revolutionizing our ability to genomically map protein-DNA associations for a wide variety of proteins. The growing popularity of ChIP-Seq has spurred the development of over thirty peak picking algorithms (for a nearly completely list see [10]). The relative performance of representative peak detection algorithms on eukaryotic data and methods to assess performance have been recently reviewed by several authors [6, 3, 9, 2, 7]. Many of these peak picking methods have employed a number of sophisticated strategies to detect peaks in the typically sparsely covered eukaryotic datasets for which they are designed.

While ChIP-Seq has been predominantly used to interrogate protein-DNA interactions in eukaryotic systems, there are clear advantages to adopting this technology for studying microbial systems. Microbial genomes typically are much smaller than eukaryotic genomes (the genome of *E. coli* is  $\approx 2000$  times smaller than the human genome), and have simpler replicon and chromatin structure.

Only one other peak finding package, CSDeconv [5], has been explicitly developed for finding peaks in microbial ChIP-Seq data.

This MATLAB package successfully finds peaks in microbial ChIP-Seq data, but its application is limited by its dependency on costly proprietary software, slow performance, lack of support for manual curation. Herein we describe Pique, a conceptually simple, Python-based peak finding package that enables easy and rapid peak finding in bacterial and archaeal ChIP-Seq datasets.

## 2 APPROACH

ChIP-Seq in bacteria and archaea yields coverage several orders of magnitude larger than in eukaryotic systems. This generates data with continuous signal across the microbial chromosome rather than the sparse coverage typically present in eukaryotic ChIP-Seq data. This feature of microbial ChIP-Seq data permits simpler, faster algorithms to be used. We have based our algorithm on classic noise reduction techniques from signal processing.

Pique is designed for use in systems that have genomic complexities such as IS elements, gene dosage polymorphisms and accessory genomes that cause variations in sequence coverage unrelated to ChIP, or in cases where the organism under study is not identical to the reference genome. The resulting enrichment “pedestals” and “holes” can be very problematic for detecting peaks and calculating enrichment levels. Pique allows the user to optionally supply a map of these features as a GFF file, and the software will automatically perform a segmented analysis.

Pique has integrated curation support through the Gaggles Genome Browser. This permits interactive curation of the peak list and analysis of the ChIP-Seq data in the context of other Gaggles-enabled resources. Interactive curation of a microbial ChIP-Seq data set can typically be completed in a few minutes.

## 3 METHODS

Pique requires BAM files as input [4]. Therefore, prior to using Pique, Illumina (Solexa) reads should first be quality filtered, quality trimmed, and aligned to a reference genome, preferably using all contigs of the reference genome as the mapping target. We suggest using all contigs of the reference genome as the mapping target, but the user may prefer to proceed with one contig at a time if desired.

By default, Pique treats each contig as a single analysis region, but the user may optionally designate regions within a contig for separate analysis by supplying a feature map. This may be useful when coverage level are systematically altered over large regions. Pique supports three feature types: analysis regions, masking regions, and normalization regions. Masking

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regions are simply masked out of their respective analysis regions, and are useful for removing coverage variation due to repetitive DNA. Normalization regions selected within an analysis region, are used to compensate for total coverage discrepancies between the background and ChIP alignments.

The user launches the primary analysis stage by providing alignment an file for the ChIP data, an alignment file for the control data, and optional an coverage feature map. The primary analysis proceeds thusly :

- The alignment files are digested into coverage tracks, and the analysis regions are initialized in memory. Provided masking regions are applied.
- The coverage noise threshold is measured by comparing the relative total coverage within the normalization regions. (The user should choose normalization regions that contain neither peaks nor coverage level aberrations.)
- High- $k$  noise in coverage is removed using a Wiener-Kolmogorov filter. The filter delay  $\alpha$  is chosen to approximate to the expected footprint size of the targeted protein. The choice of filter implies the existence of two inputs; a “true” signal, and a noise source. Both are assumed to be stationary stochastic processes combined additively.
- A Blackman window of a diameter equal to the read length is convolved with the filtered coverage track to remove features smaller than one read.
- The noise threshold in the ChIP coverage track is measured by comparing the coverage distribution in the ChIP track to the control track within user-annotated non-peak regions. Features that exceed the noise threshold are identified.
- To determine if a feature corresponds to a binding event, we require that the stop coordinate of the forward strand enrichment envelope must fall between the coordinates of the reverse strand enrichment envelope, and that the start coordinate of the reverse strand enrichment envelope fall between the coordinates of the forward strand enrichment envelope. (We call this the overlap criterion.)

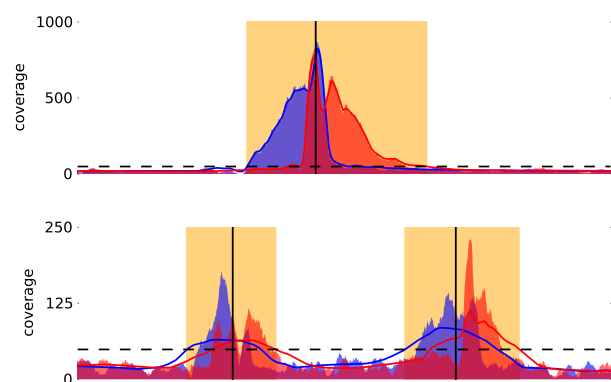
For each putative peak, Pique calculates the enrichment ratio of the ChIP alignment to the control alignment, the binding coordinate, and the enrichment normalization factor for that analysis region.

## 4 DISCUSSION

The coverage enrichment is distributed differently between the forward and reverse strands because the possible read orientations are constrained by the fragment size.

Pique does not attempt to filter peaks that are statistically insignificant. We have found that this part of the analysis is rather specific to the data and to the experiment. Pique is designed to achieve a low false-negative rate, which comes at the cost of a relatively high false-positive rate. Thus, some kind of post-filtering is necessary. Pique provides the user with output that can be used to support a variety of such statistical tests.

Some recommended filtering might include eliminating peaks that are significantly narrower than the size range of the sequencing library, peaks with a normalized enrichment ratio below unity, or peaks that have predicted binding sites that are very skewed from the center of the enriched region. Depending on how many peaks are recovered, the user may wish to try one or all of these, perhaps with clustering. However, if a “perfect” peak list is required, we do not recommend relying on statistical refinements alone. To facilitate manual curation, Pique outputs a track file of the coverage, a quantitative positional data of the estimated binding sites, and a bookmark file annotating the peaks. These files are simple to process



**Fig. 1.** Peaks found in the included sample dataset, derived from ChIP-seq of tfbD in *Halobacterium salinarum* sp. NRC1. Blue and red shading indicate coverage of reads aligned from the ChIP-derived data to the forward and reverse strands, respectively. Blue and red lines represent the filtered coverage levels for the forward and reverse strands, respectively. The dashed line is the detected noise threshold for the region. Orange indicates a detected peak.

by a variety of tools, and can be loaded directly into the Gaggie Genome Browser.<sup>1</sup>

## 5 CONCLUSION

We note that Pique should also work well with eukaryotic datasets provided they are gathered with greater coverage than has been previously reported.

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