
A Study of Transcription and Its Affects

John Letey

David Knox

Abstract

Research project investigating hits calculated from yeast chromosomes and PSSMs and their correlations to each other. Transcription clusters and PSSMs have information about the transcription process, so modeling it can help us understand more about transcription. We hypothesized that the histogram of hits contains a pattern of having a peak around 30, or if not there, somewhere else close to 30, just as long as the number is roughly consistent). We were able to prove this [INSERT ACCURACY HERE]% of the time.

1 Introduction

2 Methods

PSSMs (Position Specific Scoring Matrices), have been used to calculate the affinity of an individual transcription factor for different sequences of DNA for a long time. DNA binding factors interact differently given different sequences of DNA. If an individual factor could only recognize a single unique sequence, then we could represent the interaction with two parameters: the on-rate and off-rate. This works well for free floating, well mixed environments where the molecules have a limited number of interactions depending on the molecule counts and volume of the environment. However, the positively charged transcription factors have a natural attraction to the negatively charged DNA, which leads to non-specific binding along the DNA. The non-specific binding may only be transient, but sequences that partially match the intended sequence will have stronger affinity for the factor than for random DNA sequences. High affinity binding sites will more likely be bound at low molecule counts, while low affinity sites will require high molecule counts before the site will be highly bound. The high affinity sites also have longer residency times than the transient binding of the low affinity sites.

A PSSM captures the affinity of a DNA binding factor for a sequence, position by position. The simplest method for determining a PSSM is to collect a set of sequence fragments that have been bound by a factor. These sequences are usually large fragments (20 - 100 nucleotides) and the factor generally only recognizes a few nucleotides (4 - 20), therefore a common sub-sequence within the collection would be expected. The most common or likely sequence would be the consensus motif that most biologists report as the binding sequence. However, the factor usually only has a few mandatory positions within the sequence and allows multiple different nucleotides to occupy the intervening positions. Aligning the pattern across multiple sequences, the number of times each nucleotide is found at each position can be calculated. Using the counts, we can calculate the log-odds of seeing a particular nucleotide at a particular position within a bound sequence of DNA. Storing the values for each nucleotide for each position results in a matrix. We can set the values of the matrix to be probabilities of each nucleotide at each position, or we can assign a score for each nucleotide at each position. The scores could be positive for a matching nucleotide or negative for an unlikely nucleotide, resulting in a PSSM. The PSSM contains the consensus motif as the highest scoring sequence, but also allows any sequence to be scored. Some alternative sequences to the consensus motif will still be able to score highly, indicating that even at low concentrations of the binding factor, sites with the alternate DNA sequence would also be bound. PSSMs provide a powerful tool for predicting the likely binding sites for any DNA sequence. We can iteratively pass sub-sequences

to the PSSM and use the high scores to predict not only the binding sites, but also the sites of high transcription factor residency times. Consider the REB1 transcription factor as an example (Figure 1). The transcription factor has particular sequences to which it preferentially binds, described by its PSSM. This matrix specifies the number of positions, as well as the nucleotides that are preferentially bound at each position. For any given sequence, we can calculate a score by adding up all the values for the sequence's nucleotide at each position. The resulting score indicates how well the given sequence matches the best sequence for the factor.

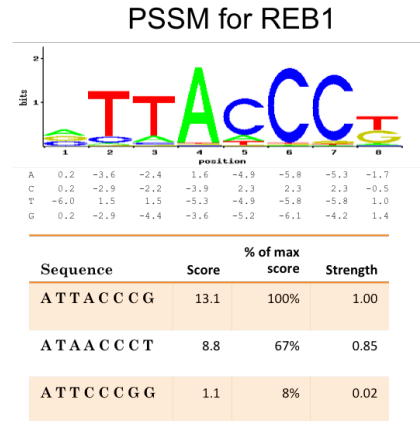


Figure 1: **TF affinity can be scored for any sequence by using the TFs PSSM.**

An example PSSM, here for REB1, describes the probability of binding at each nucleotide for any possible sequence. Positions are assumed to be independent and therefore the probability of a TF binding to any arbitrary sequence can be easily calculated. (Knox, Page 24, Figure 1.5)

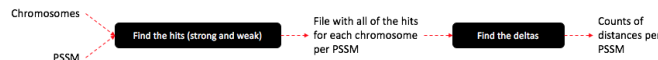


Figure 2: **The pipeline our code follows**

For visual purposes, Figure 2 clearly illustrates the process our program follows in our project. Assuming the above, we can then calculate each one of the scores for the entire DNA sequence given each transcription factor. When we do this, we can classify each score as being a strong hit, if it's greater than our set strong threshold (0.7), a weak hit, if it's greater than our set weak threshold (0.35) but less than our set strong threshold, and else, we don't classify it at all. After we calculated all of the hits, we can then analyze them.

3 Results

Unfortunately, since we are dealing with such a big data set, we only ran my code on 30 different transcription factors, over all 16 chromosomes (there were 18 in the data, but we discarded two of them). Here are some of the histograms we get from our analysis program:

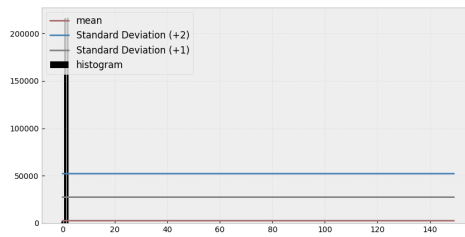


Figure 3: **Histogram for Transcription Factor HSF1**

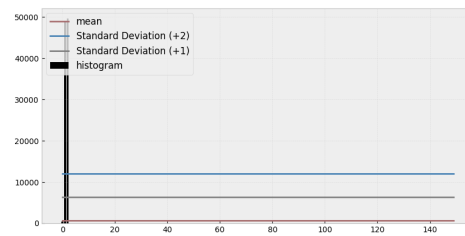


Figure 4: **Histogram for Transcription Factor RPN4**

Please note that this is only a small selection of output histograms that we get.

4 Code

All the code for this project is hosted on GitHub, located [here](#).

5 References

- [1] A special thanks to David A. Knox for the terrific guidance he gave on the project!
- [2] Thanks to Matt Shirley for making [pyfaidx](#)! It really helped in reading the FASTA data files quickly and efficiently.