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| Computational Genomics  HMMicro: predicting miRNA targets from epigenetic data  Wu, Felix\*,1 and Nick Giangreco\*,1  1Department of Systems Biology, Columbia University, New York, NY, USA  \*To whom correspondence should be addressed.  Abstract  **Motivation:** Multiple gene regulatory layers give rise to complex phenotypes, which include redundant patterns to maintain homeostasis and other functions. Micro RNAs (miRNA) play an important regulatory role at the post-transcriptional level by binding longer messenger RNA (mRNA) transcripts, targeting them for degradation. These binding sites are difficult to obtain on a global scale for any given condition or treatment. Computational methods provide an effective alternative for identifying miRNA binding sites across the genome.  **Results:** We developed a Hidden Markov Model (HMM) for predicting miRNA binding sites in HEK293 cells using epigenetic information provided by ENCODE. Our model shows a low error rate and a high true positive rate. Our results indicate that leveraging known epigenetic information of a cell can potentially aid in predicting novel connections within post-transcriptional regulatory layers.  **Availability:** https://github.com/ngiangre/HMMicro  **Contact:** flw2113@cumc.columbia.edu, npg2108@cumc.columbia.edu  **Supplementary information:** Supplementary data are available at *Bioinformatics* online. |

# Introduction

Knowledge of the processes that give rise to cellular phenotype is a common and critical step in understanding specific biological phenomena such as developmental states, homeostasis, and disease. The phenotype of a cell is a product of the reactions and relationships between many molecular regulatory layers, ranging from transcription factor binding to chromatin confirmation. Each layer provides a regulatory logic, allowing the cell to integrate intracellular cues, environmental signals, and DNA-encoded information to achieve a specific state or activity.

Micro RNAs (miRNAs) – short approximately 22 nt- single-stranded RNA molecules – comprise one such layer and are involved specifically in post-transcriptional regulation. Canonically, miRNAs target messenger RNA (mRNA) transcripts for degradation by primarily binding to their 3'-untranslated regions (3'-UTRs), though evidence exists of binding across the transcript body. These binding sites can be difficult to experimentally identify, although methods do exist (CLIP ref).

With the advent of next generation sequencing and the popularity of high throughput experimentation, genome-wide assays of many regulatory layers such as histone modifications and transcriptome binding motifs have been made in a wide variety of cellular types and contexts (ENCODE ref). We hypothesized that a latent redundancy between the regulatory layers of the eukaryotic cell would allow us to predict miRNA binding sites using this corpus of existing regulatory data. ..

We present a hidden Markov Model (HMM) for prediction of miRNA binding sites. Focusing on the HEK293 cell line, we trained our model using various epigenetic experiments assayed through the ENCODE consortium, and tested our model using experimentally validated miRNA binding sites for this model system. We obtain a low prediction error and high prediction of known miRNA binding sites. This method can be expanded upon by leveraging the full complement of regulatory annotations associated with a particular cellular phenotype.

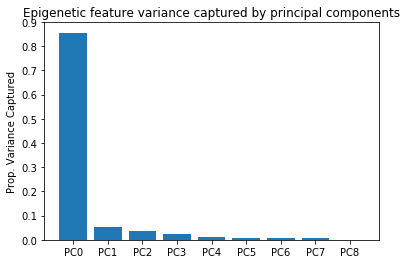
# Methods

We obtained HEK293 epigenetic signals at nucleotide resolution on chromosome 22 from ENCODE [ref]. We retrieved and processed the raw data via remote server using the R package *DeepBlueR* [ref].. We obtained normalized read signal (wiggle file signal) for 8 experiments (7 ChIP-Seq assays against KAP1, POL2RA, TCFL2, ZNF263, CTFC, ELK4, and H3K4me3; 1 DNase experiment) at nucleotide resolution across chromosome 22. We also developed in-house R scripts for querying and performing additional processing.

We generated a set of experimentally identified miRNA binding sites from argonaute (AGO) protein PAR-CLIP data by Hafner et al. Since miRNAs direct AGO binding, assaying its binding distribution across transcripts using PAR-CLIP is a standard way of assaying for novel miRNA binding sites. Since ENCODE epigenetic signal data uses hg19 reference genome coordinates while the PAR-CLIP data was aligned to the hg18 reference genome, we lifted over the set of miRNA binding sites to the hg19 reference using the UCSC online liftOver tool (https://genome.ucsc.edu/cgi-bin/hgLiftOver). All hg19 and refseq annotations were downloaded from the UCSC Genome Browser and the UCSC Table Browser.

The HMM was developed using the *Pomegranate* python package [ref]. We developed the HMM in three steps: pre-processing, training and testing. In the processing step, we computed the principal components of the epigenetic matrix. Also, using experimentally validated miRNA binding sites [ref], we modeled the distribution of start sites across chromosome 22 to identify an appropriate prior distribution of the binding state. In the training step, we used the Baum-Welch algorithm to learn emission parameters (epigenetic characteristics) and refine the prior transition (binding and non-binding miRNA states) probabilities from the training dimension-reduced epigenetic matrix. In the testing step, we applied a 5-fold cross validation to test the HMM. The code for these analyses are available at GitHub (https://github.com/ngiangre/  
HMMicro).

# Results



## Multiple epigenetic layers contain redundant information

We investigated the amount of variation present in normalized epigenetic signal from 8 different ChIP-Seq and DNase across chromosome 22 in HEK293 cells. This gave an indication of the amount of redundancy across the epigenetic layers. In agreement with our hypothesis of redundant patterns, we observed the first principal component captured about 85% of the variation across the epigenetic layers (Fig. 1).

### 3.2 *De novo* miRNA binding site discovery using a Hidden Markov Model

To model miRNA binding sites, we first identified an approximate prior distribution model by sampling all common distributions (Fig. 2). This best-fit model informed approximation of the binding state distribution in the HMM.

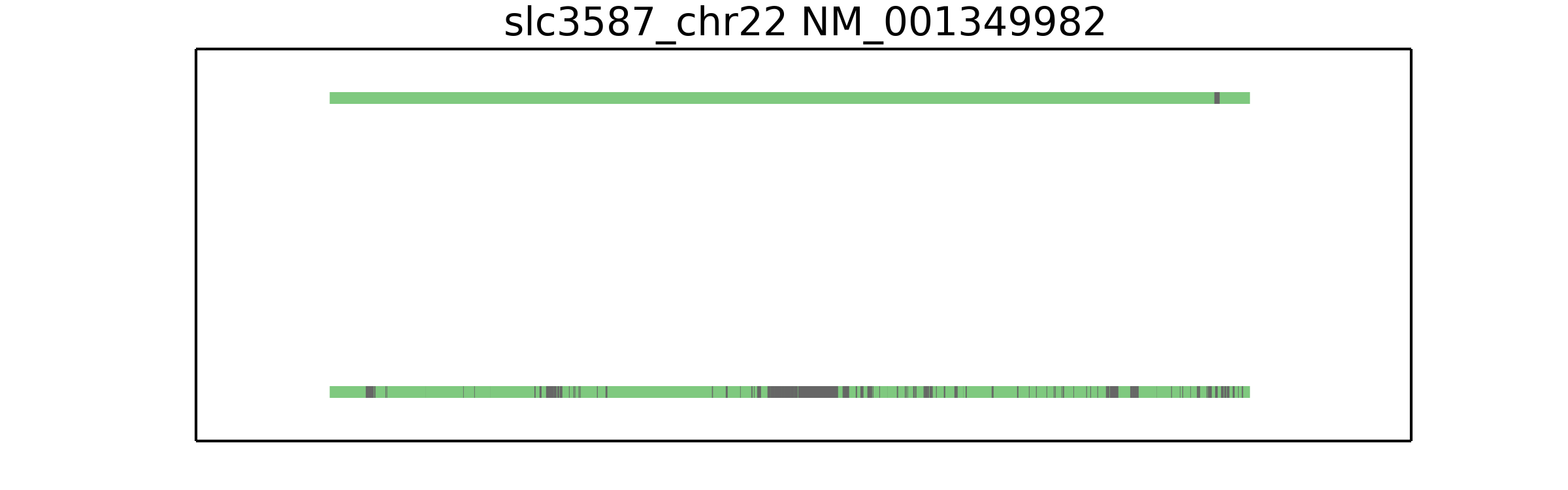
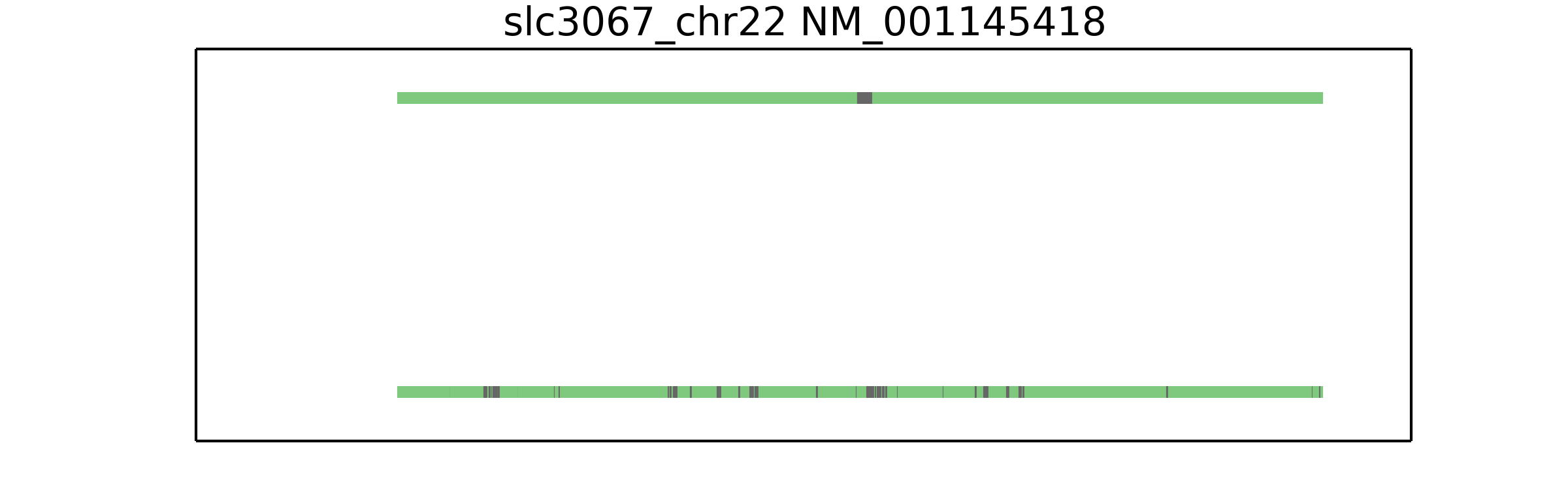
We developed a HMM that would take into account multiple epigenetic features of our HEK293 cell model system to guide predicting of miRNA binding patterns.

To test our HMM, we conducted 5-fold cross-validation. We found a low median error (calculated as the number of incorrectly predicted states normalized by the total number of states) in our validation strategy (Table 1).

Clearly, improvements can be made to the HMM model as it currently stands. Future efforts would include feature data from RNA-binding protein experiments as well as expand the analysis to chromosome 22. Moreover, other supervised learning models might be more suited for this problem and would be worth exploring.

**Table 1.**5-fold cross validation results

**True vs. predicted along transcript body**miRNA binding (purple) and non-binding sites (green). miRNA binding site names from Hafner et al. are given as well as transcript RefSeq id. True binding site location along the body (x axis) is given in the upper display of each plot and predicted on the bottom



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| *k* | Median error |
| 1 | 11.649 |
| 2 | 0.642 |
| 3 | 0.646 |
| 4 | 10.784 |
| 5 | 0.643 |

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*Conflict of Interest*: none declared.

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