

Carl D
Homework 3

2.

a. SELEX-seq and PBM are both in vivo experiments. SELEX-seq stands for Systematic Evolution of Ligands by Exponential Enrichment. SELEX-Seq is the best high throughput experiment for determining DNA binding specificity of transcription factors. PBM stands for Protein Binding microarray. PBM allows for the discovery of specific DNA binding sites used by transcription factors. Materials needed consist of a microtitre plate and nitrocellulose membrane.

b. ChIP-seq uses Chromatin immunoprecipitation and DNA sequencing to locate the DNA-binding sites used by desired proteins.

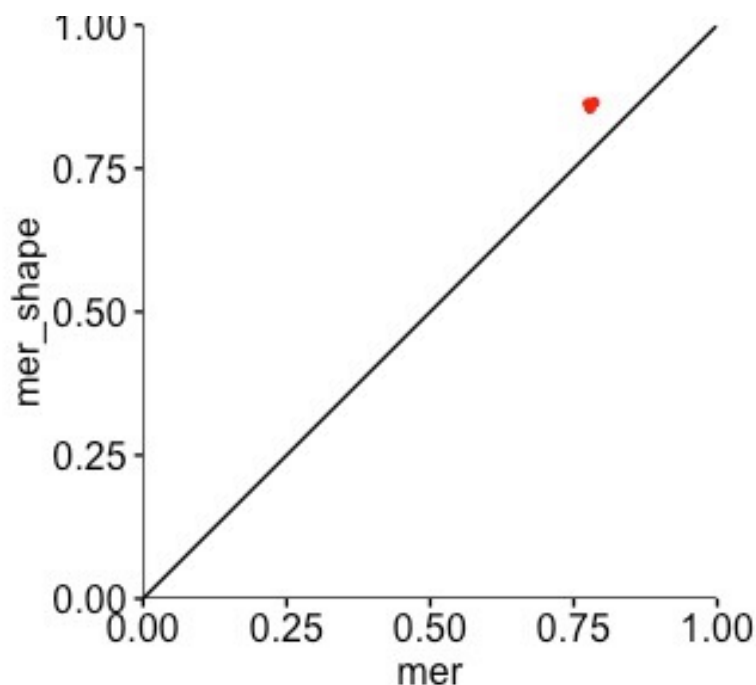
c. SELEX-seq can determine the affinity of any DNA sequence for desired transcription factors. SELEX-seq and PBM are quantitative and can be used with large quantities of proteins.

Disadvantages include the difficulty of using surfaces that will not allow the proteins to denature during the experiment or allow the proteins to interact with the surface itself and other, undesired molecules present in the experiment. An advantage of ChIP-seq is its ability to generate large amounts of data. Its disadvantage is its qualitative nature. This test does not give details of bond strength in the binding process.

4.

	1-mer	1-mer+shape
Mad	0.776	0.863
Max	0.786	0.864
Myc	0.778	0.855

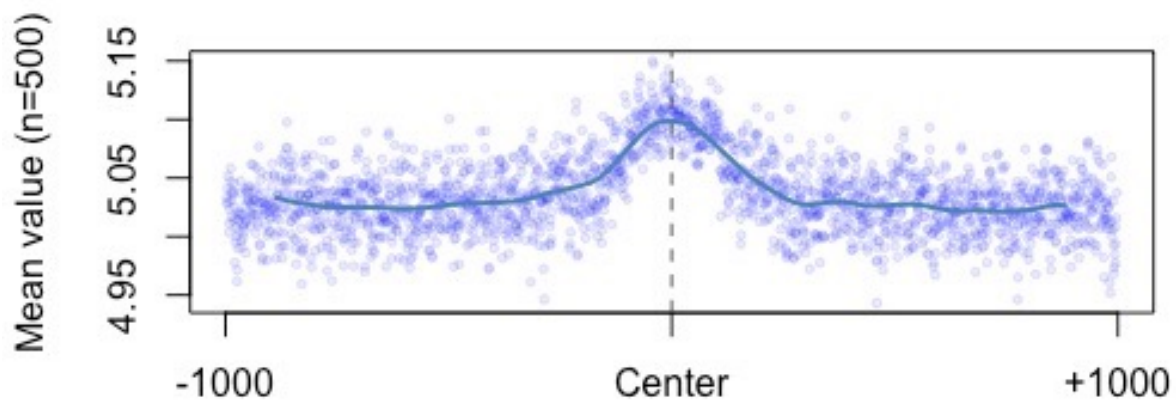
5.



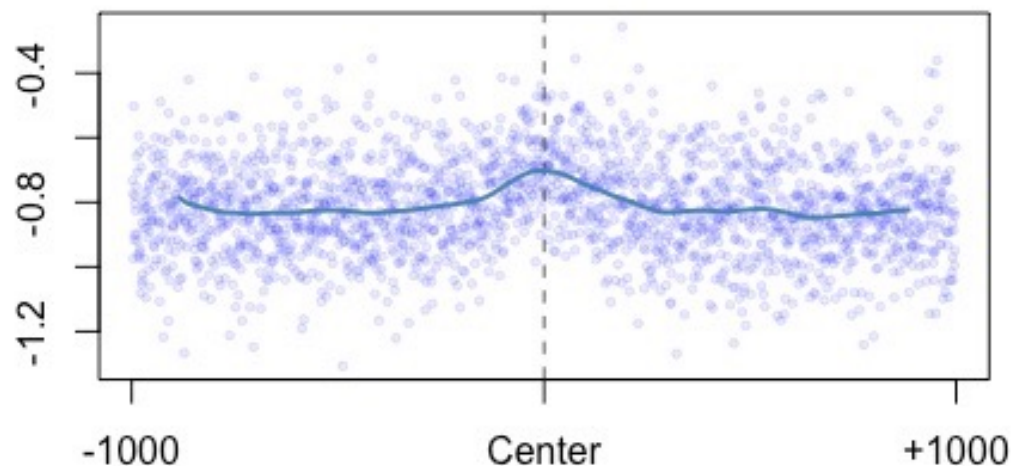
1-mer R squared values lie on the x-axis, while 1-mer+shape R squared values lie on the y-axis. The three, red data points lie above the line ($y = x$), which means which show the 1-mer+shape R squared values are higher than the 1-mer R squared values. Adding additional parameters to the model increased the validity of the R squared values obtained from the test. The diminished distance between the cluster of red points shows this is true for all of the values.

7. a.

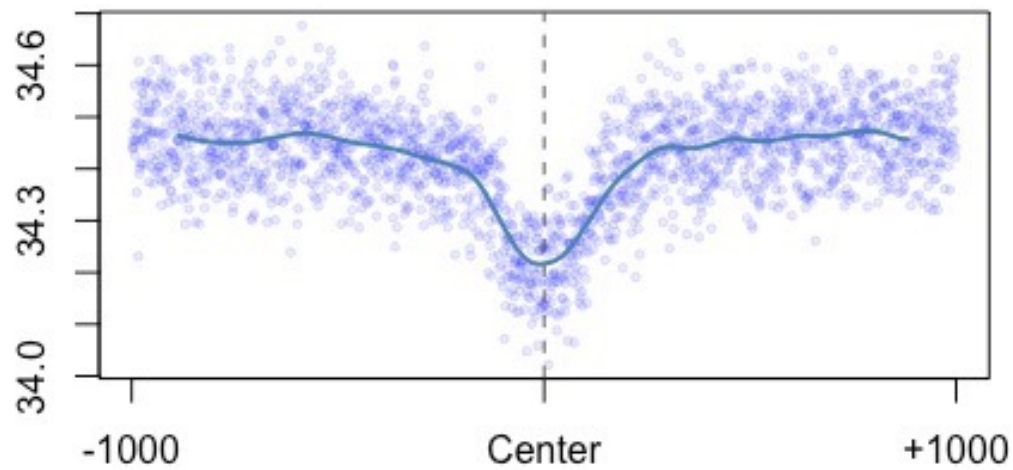
MGW: The Minor Groove width is greatest at the center.



Roll: The Roll, although does not increase as greatly as the Major Groove width, is greatest at the center.

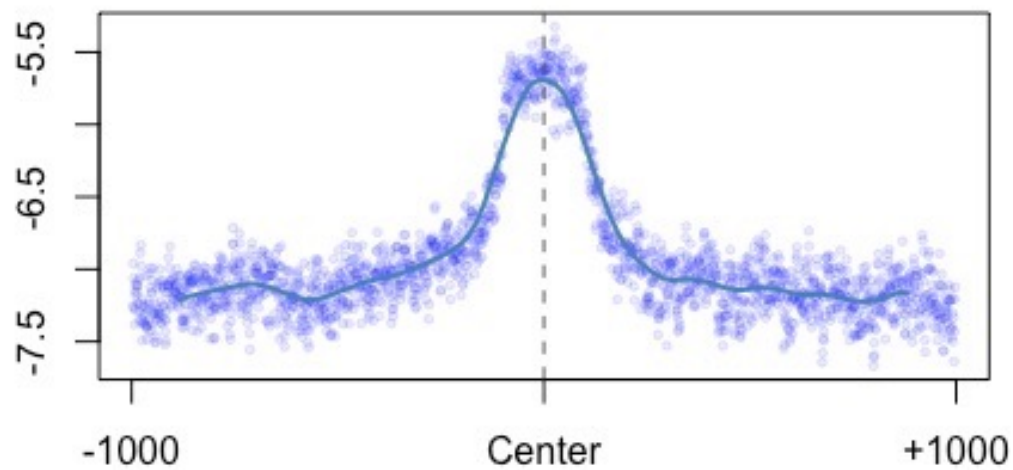


HelT: The Helix Tist, unlike the Major Groove width and Roll, is smallest at the center.

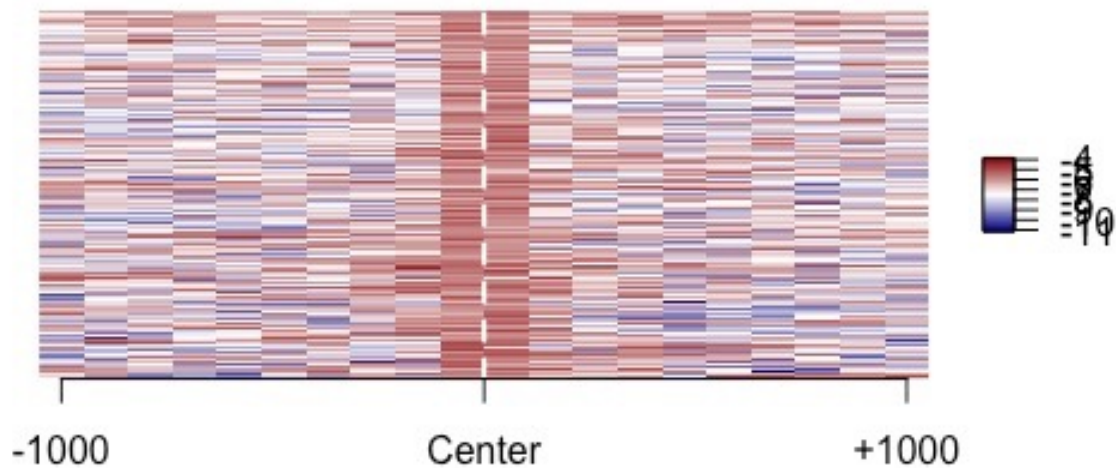


ProT

The Propeller Twist is greatest at the center. It also increases the more drastically than any of the other parameters.

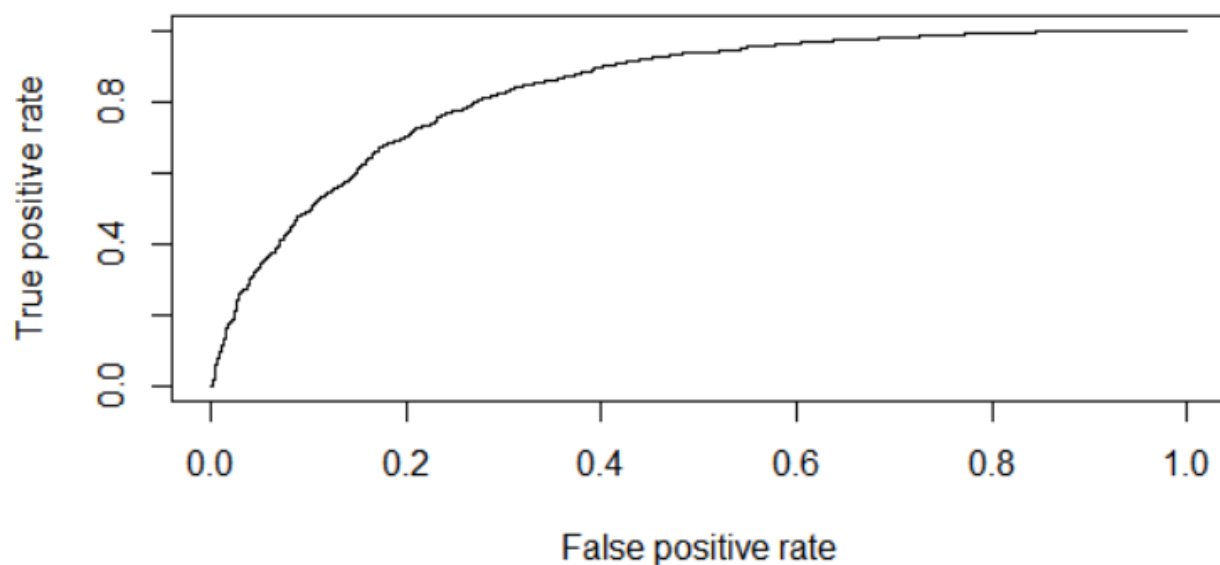


ProT: The deep red shows the extreme increase in the Propeller Twist at the center of the parameter.

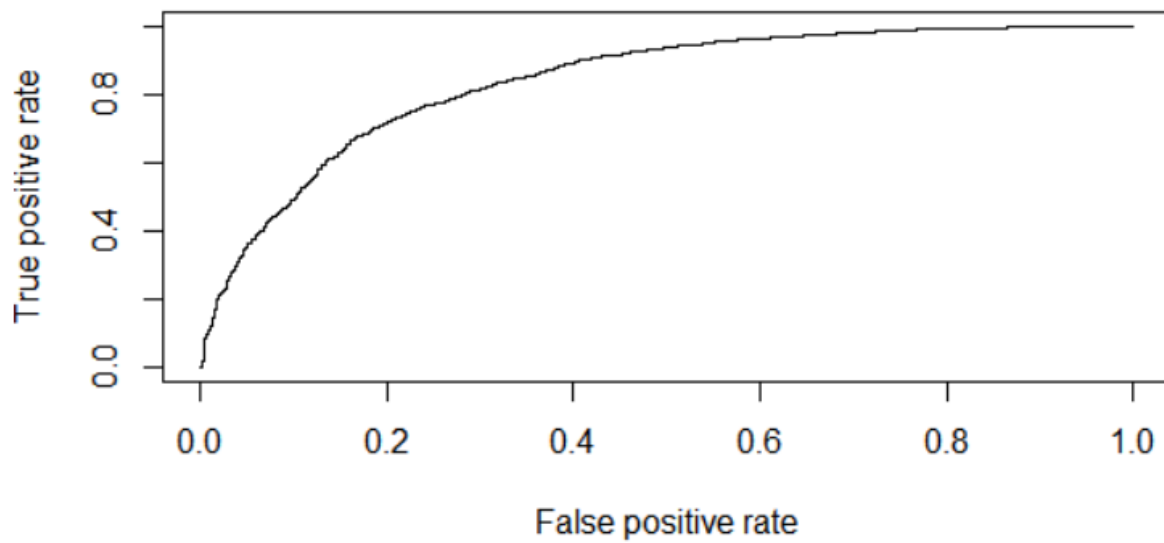


b: The minor groove width is expected to be deepest at the center. This is demonstrated in the plot above. The Roll plot shows, although there is a slight increase in the center, the roll value remains steady around -0.8. This means there is very small difference in rotation. The Helix Twist tells us about base pair orientation. This plot shows us that arc or the helix is smallest at the center. All other parts of the arc remain constant near 34.4 Å. Propellor twist describes the angles of bases along the axis, with respect to other bases. The plot shows the Propellor Twist has a negative value (on the negative axis).

8.
1-mer



1-mer+shape



The AUC for 1-mer+shape is 0.839, while the AUC for 1-mer is 0.838. The values differ very slightly, showing adding the shape parameter neither increases nor decreases the accuracy of the results.