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BISC481 Homework 3

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2. SELEX-seq is a method that is used for the characterization of the complete repertoire of the binding site preferences for transcription factor complexes. PBM or protein binding microarray is a method that is used for the characterization of DNA-protein interactions. It allows rapid high throughput characterization of the in vitro DNA binding site sequences specificities of transcription factors, other DNA binding proteins or synthetic compounds. These in vitro experiments allow measurement of the binding intensities of one transcription factor to numerous double stranded DNA sequences in a single experiment. ChIP-sequencing is a method used to analyze protein interactions with DNA. it combines chromatin precipitation (ChIP) with massively parallel DNA sequencing to identify the binding sites of DNA-associated proteins. In vitro experiments including the SELEX-seq and PBM tend not to be complicated by nuclear components. The in vitro experiments generate quantitative results pertaining to the binding data i.e the affinity. In vitro experiments on the other hand, including ChIP-seq give us the qualitative binding data i.e they give us information on binding vs non-binding interactions.

4.b) R2 values obtained have been tabulated

|  |  |  |
| --- | --- | --- |
| **Dataset** | **Sequence:** | **Sequence+ Shape** |
| Mad | 0.7752453 | 0.8627805 |
| Max | 0.7855357 | 0.8647366 |
| Myc | 0.7783882 | 0.8547946 |

5. After following the procedure, we generate a plot that compares the two models 1mer+1shape and 1mer. The plot obtained is as follows:

../Rplot.pdf

7. b) Certain functions were used in order to generate ensemble plots of various DNA shape parameters. The graphs obtained were as follows:

Minor groove width plot:

MGWplot.pdf

Propeller Twist (20) plot:

PROT20plot.pdf

Propeller twist plot:

PROTplot.pdf

Roll Plot:

ROLLplot.pdf

Helix twist plot:

HELTplot.pdf

The plot of the minor groove width tells us the orientation of the groove and its depth. As expected we would find it to be deepest at the center of the groove which can be verified by the plot. The degree propellor twist is known to correlate with the flexibility of the dinucleotide step that they constitute. The propellor twist angles the bases along the axis and with respect to one another. The plot of the propellor twist shows that the bases are angled along the negative axis with the least negative value being at the center. The roll plot shows us that there is little difference in the rotation along the side axis with values being mostly centered around -0.8 approximately. The helix twist gives us information about the orientation of a base pair with respect to the helix axis. This value tells us how big an arc the base pair traces as it is measured from one base pair to the next. From the plot we can see that the arc is seen to be smallest at the center, with the rest of the arc being approximately close to 34.5 angstrom.