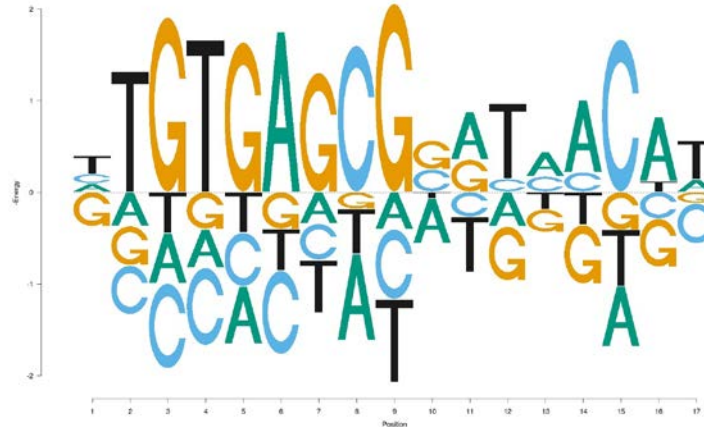




Forty Years of TF Motifs: Lessons and Challenges



The invention of DNA sequencing allowed for the rapid determination of binding sites for regulatory proteins, such as transcription factors (TFs). An early lesson was that they could be highly variable with different sequences determining different binding affinities. Motifs were invented to represent their specificity, how their activity varied as a function of the binding site sequence. But motifs can be made in various ways, using a variety of different types of data and of various degrees of complexity. Recent advances in experimental methods have greatly facilitated the determination of motifs for a large number of TFs. This talk will cover some of the history of motifs, up to the current approaches that take advantage of the newest methods. An important issue is how to assess the quality of a motif, the accuracy of its quantitative predictions, and how to make improved motifs if necessary. It will also describe some uses of motifs, such as in the design of TF with novel specificities. And it will describe some challenges in the utilization of motifs to better model regulatory networks *in vivo*.

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Hosts: Drs. Jack Greenblatt
and Timothy Hughes

Date: December 11, 2018
Time: 3:00 PM
Place: CCBR Red Room