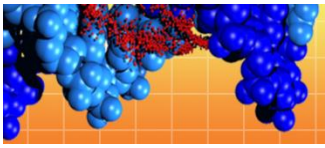

CENTER FOR BIOINFORMATICS & COMPUTATIONAL BIOLOGY

BIOINFORMATICS 2016 FALL SEMINAR SERIES

Hosted by: Department of Computer and Information Sciences,
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http://bioinformatics.udel.edu/Seminars/Current

MONDAY, November 14, 2016
3:30pm
DBI Room 102

Identification and functional study of nucleosome-depleting factors

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ABSTRACT: Nucleosomes present a barrier for the binding of most transcription factors (TFs). However, a special group of TFs can invade compact chromosome and deplete nucleosomes near their binding sites. These TFs, known as nucleosome-depleting factors (NDFs), direct the binding of other TFs and enable them to activate transcription. Despite NDFs' essential functions, we lack an experimental scheme to systematically categorize them and measure their nucleosome-depleting activities on a genome-wide scale. Here, by generating a complex library of synthetic regulatory elements and measuring the nucleosome occupancy on these sequences in vivo, we developed a high-throughput assay to identify NDFs from genome-wide TFs and to systematically evaluate the impact of the location, orientation, copy number, and combination of factor binding sites on the nucleosome-depleting activities. We applied this method to budding yeast and identified both new and established NDFs with variable nucleosome-depleting activities. We found that the activity of strong NDFs show topological relationships with nucleosome structure, and multiple closely-spaced weak NDFs can lead to significant nucleosome depletion, presumably through nucleosome-mediated cooperativity. By comparing the properties of TFs with different nucleosome-depleting activities, we propose that strong NDFs may function by directly competing with histones for the same DNA, while weak NDFs may have developed special structural features in recognizing nucleosomal DNA. Overall, our method presents a new framework to functionally characterize NDFs and further our understanding of the molecular mechanism of nucleosome invasion.