



THE UNIVERSITY OF
CHICAGO

Department of Statistics

MASTER'S THESIS PRESENTATION

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**Assessing the Additive Model of Protein-DNA
Sequence Interactions: Drosophila Hunchback as a
Test Case**

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110 Eckhart Hall, 5734 S. University Avenue

ABSTRACT

Identification of protein-DNA sequence binding sites is important for understanding gene regulatory networks, and modeling the specificity of DNA motifs is crucial to this question. Several methods provide insights about specificity of protein-DNA binding sequences, but most of them are limited in scope by assuming additive interactions. This article first describes a new approach G.D. Stormo (2011) proposed, which uses simplex encoding of DNA motifs in the modeling and is efficient in extending into higher-order models; then put forward merits and limitations about this method. In addition, assessment and quantitative analysis are applied on the Drosophila hunchback gene experimental dataset, leading to the conclusion that the additive model of hunchback binding site is not sufficient, and enough information is contained in the adjacent-dinucleotides.

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