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Jacqueline M Dresch* (jdresch@clarku.edu), Clark University, Worcester, MA. *Using bioinformatic and mathematical analyses to predict protein-DNA binding preferences.*

When mathematically modeling gene regulation from DNA sequence information, a critical first step is to predict where on the DNA sequence transcription factor (TF) proteins might bind, and the biophysical affinity of such binding. Since the 1980s, one of the most popular bioinformatic approaches for predicting TF binding sites involves constructing a Position Weight Matrix (PWM) and scanning a DNA sequence for subsequences with a high probability of binding the TF of interest. The question remains whether the bioinformatic scores obtained using PWM-based approaches relate directly to the binding affinities of the TF binding sites. Focusing our efforts on a set of TFs known to drive gene expression during early fruit fly development, we have used known binding sites within the genome, bioinformatic tools, clustering and statistical analyses to investigate and predict the relative TF-DNA binding preferences. (Received September 15, 2020)