Supporting material to article “Modeling DNA-binding of sigma70 exhibits a characteristic energy landscape around strong promoters”

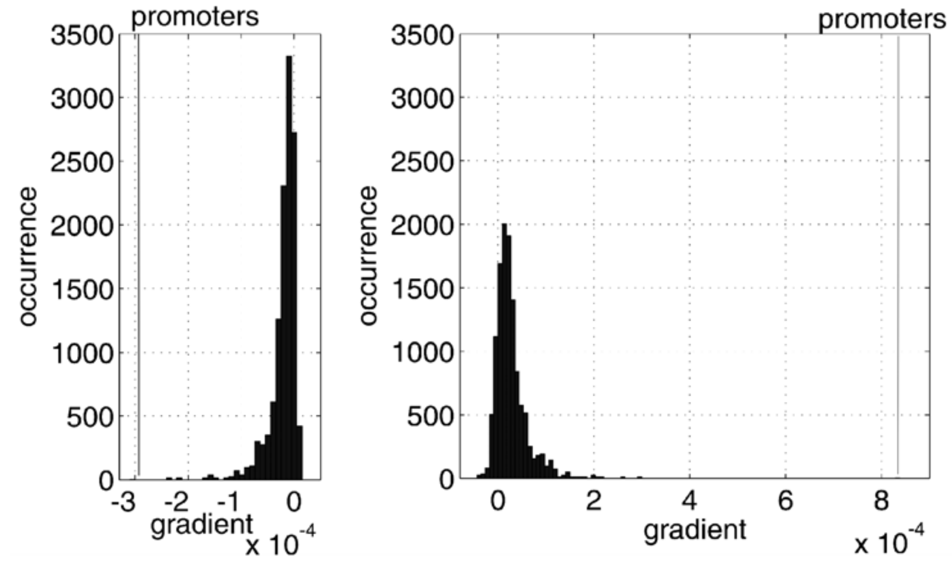

Figure 1. Analysis of gradients before and after the target sites obtained for the 12000 performed random permutations of W and $\varepsilon(s)$. **Left:** Histogram of gradients in the first 250 bps of the analyzed region (500 bps around the random target sites). **Right:** Histogram of gradients in the last 150 bps of the analyzed region.

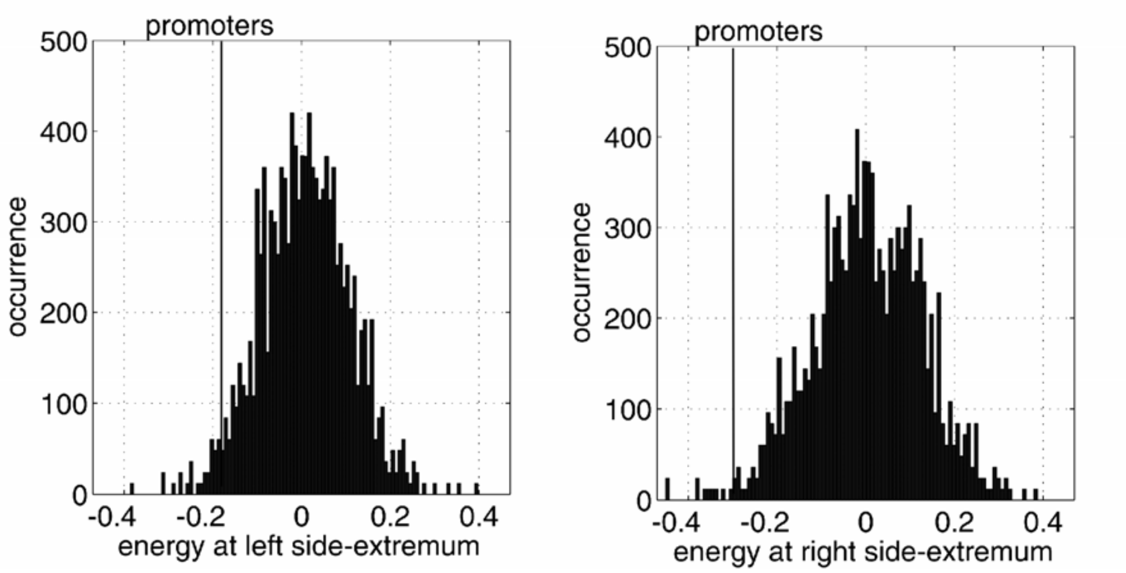

Figure 2. Analysis of binding energies at the side-extremals obtained for the 12000 performed random permutations of W and $\varepsilon(s)$. **Left:** Histogram of binding energies at the extremum 23 bp before the target site. **Right:** Histogram of binding energies at the extremum 23 bp after the target site.

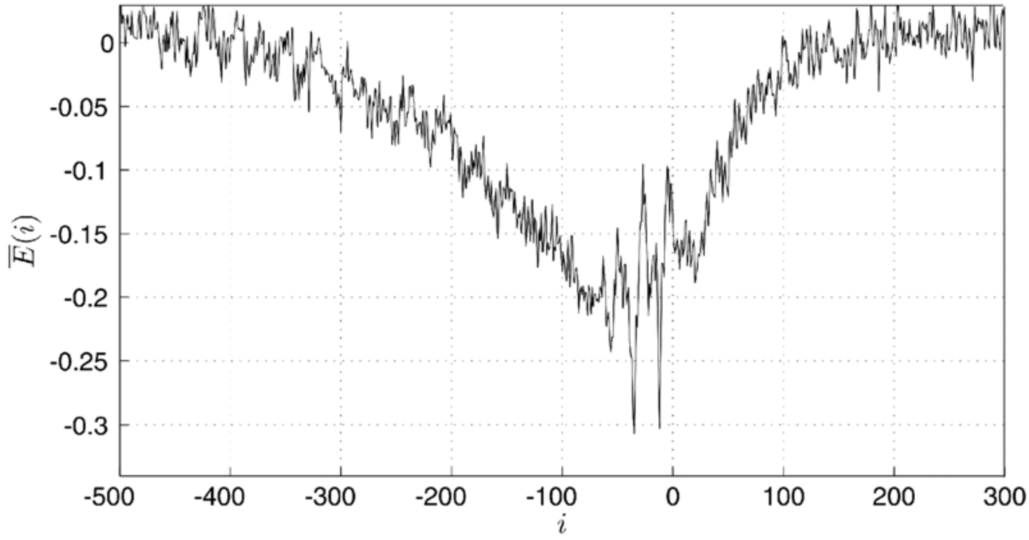

Figure 3. Application of the weight matrix derived from promoter strength data to a set of 651 experimentally verified sigma70-promoters downloaded from RegulonDB (version 5.7).

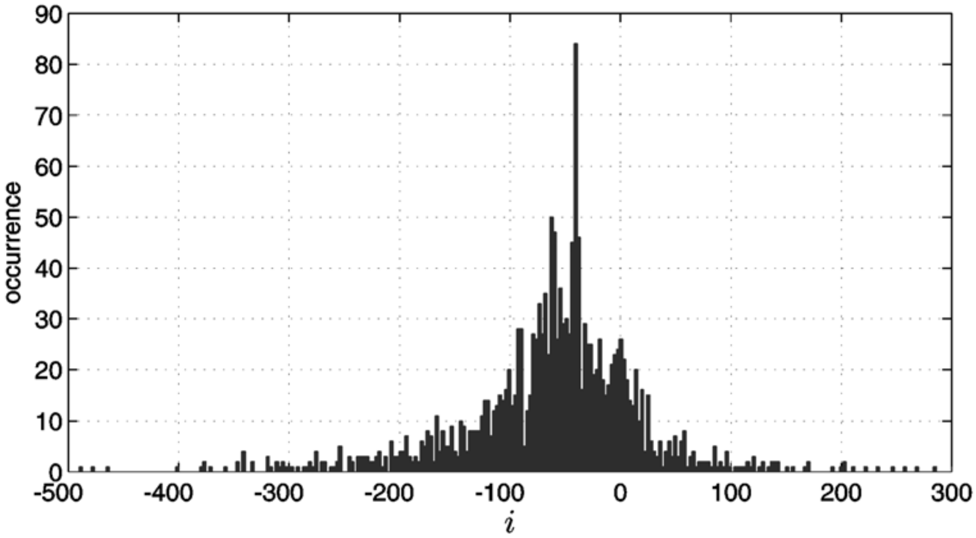

Figure 4. Positional distribution of the 2015 *E.coli* transcription factor binding sites downloaded from RegulonDB. Position 0 references the transcription start site.