Computational prediction and experimental validation of modular transcriptional enhancer elements regulating gene expression during eye development in *Drosophila melanogaster*

We tested the algorithm STUBB for its ability to predict binding sites of known transcription factors. We selected the paradigm of eye imaginal disc development because it provides an ideal experimental setting for testing intersection of signal transduction pathways and modular transcriptional regulation. Various signal transduction cascades funnel into transcriptional regulatory apparatus of genes controlling eye development and each signalling pathway is used reiteratively for neuronal differentiation, induction and cell fate specification. It must be emphasized that developmental decisions are taken by a cell in context dependent: action of various transcription factors in specific combinatorial pattern result in spatio-temporal regulation of gene expression. Accurate prediction of such input points of signal transduction into the transcriptional regulatory machinery enables precise correlation with developmental outcome with specific inputs. This allows us to have a better understanding of cellular developmental decisions.

From the above results we see that our prediction algorithm is efficient in predicting binding site information for known transcription factors. We could interpret previously known data and correlate precious experimental evidence with our predictions. Once these predictions are verified *in vivo*, where artificially incorporated enhancer modules can recapitulate predicted or known expression pattern, we can have a better understanding of the complexity of the gene network in action during development.