

Finding regulatory motifs in front of genes can be approached in a variety of ways. If only sequences/genomes are observed, two complementary methods are: Observing independent genes with some commonality to their regulation and then search for common segments to these genes. An example of this approach is Lawrence et al. (1993). An alternative is footprinting that takes related genes and searches for slowly evolving segments or even more powerful, segments with a common mode of evolution (Satija et al. (2010), Moses et al., (2004)). We will mainly be concerned with footprinting, but the framework can be extended to incorporate independent sequences as well.

Alternatively or supplementary to the above pure sequence approach additional data can be available and this situation is increasingly predominant. Four major sources are expression levels, ChIPSEQ, nucleosome positioning, and DNA Hypersensitive Sites (DHS).