

Locating Transcription Factor Binding Sites: Methods in search of *moralistic* motifs

Saket Choudhary

March 13, 2016

Introduction

With the completion of human genome sequence[1], an imposing challenge has been to decipher its underlying its functional pattern and their biological implications. Application of emerging technology over the years has enhanced our knowledge about the regulatory genome responsible for controlling various cellular processes. Transcription factors(TFs) are DNA-binding proteins responsible for regulating expression of the gene by activating or inhibiting the transcription machinery. The TF machinery plays a central role in ma

Mutations in TFs have been known to be associated with developmental disorders [2], cancer[3] and other human diseases [4, 5]

References

- [1] Eric S. Lander, Lauren M. Linton, Bruce Birren, Chad Nusbaum, Michael C. Zody, Jennifer Baldwin, Keri Devon, Ken Dewar, Michael Doyle, William FitzHugh, and others. Initial sequencing and analysis of the human genome. *Nature*, 409(6822):860–921, 2001.
- [2] Franklin H. Epstein and David S. Latchman. Transcription-factor mutations and disease. *New England Journal of Medicine*, 334(1):28–33, 1996.
- [3] Simon J. Furney, Desmond G. Higgins, Christos A. Ouzounis, and Nria Lpez-Bigas. Structural and functional properties of genes involved in human cancer. *BMC genomics*, 7(1):3, 2006.
- [4] Ruslan Medzhitov and Tiffany Horng. Transcriptional control of the inflammatory response. *Nature Reviews Immunology*, 9(10):692–703, October 2009.
- [5] Andrew P. Sage, Yin Tintut, and Linda L. Demer. Regulatory mechanisms in vascular calcification. *Nature Reviews Cardiology*, 7(9):528–536, September 2010.