

Constructing, analyzing and predicting disease-specific or developmental stage-specific transcription factor and miRNA co-regulatory networks

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TFmiR is a freely available web server developed in our group for deep and integrative analysis of combinatorial regulatory interactions between transcription factors, miRNAs and target genes that are involved in disease processes in human [1]. We are currently extending this work by integrating a number of new features such as the MCDS algorithm to identify key player genes in the selected network, construction of tissue-specific networks, and support of mouse networks (beside human). Besides disease processes, the successor of TFmiR can now also be applied to identify regulatory motifs associated with the transitions between different developmental stages from the set of dysregulated genes and miRNAs provided by the user.

[1] Mohamed Hamed, Christian Spaniol, Maryam Nazarieh and Volkhard Helms, *Nucleic Acids Res.* 43: W283-W288 (2015).