

# Identification of Key Player Genes in Gene Regulatory Networks

Maryam Nazarieh<sup>1,2</sup>, Andreas Wiese<sup>3</sup>, Thorsten Will<sup>1,2</sup>, Mohamed Hamed<sup>1,2</sup> and Volkhard Helms<sup>1</sup>

<sup>1</sup>Center for Bioinformatics, <sup>2</sup>Graduate School of Computer Science and <sup>3</sup>Max Planck Institute fuer Informatik, Saarbruecken, Germany

Identifying the gene regulatory networks governing the workings and identity of cells is one of the main challenges in understanding processes such as cellular differentiation, reprogramming or cancerogenesis. One particular challenge is to identify the main drivers and master regulatory genes that control such cell fate transitions. In this work, we reformulate this problem as the optimization problems of computing a Minimum Dominating Set (MDS) and a Minimum Connected Dominating Set (MCDS) for directed graphs. Both MDS and MCDS are applied to the well-studied gene regulatory networks of the model organisms *E. coli* and *S. cerevisiae* and to a pluripotency network for mouse embryonic stem cells. The results show that MCDS can capture most of the known key player genes identified so far in the model organisms. Moreover, this method suggests an additional small set of transcription factors as novel key players for governing the cell-specific gene regulatory network which can also be investigated with regard to diseases.

The work proposes a new method to identify key player genes in gene regulatory networks. The tools explained in the paper are available as a Cytoscape plugin and as supplementary material in [1].

[1] Maryam Nazarieh, Andreas Wiese, Thorsten Will, Mohamed Hamed, Volkhard Helms (submitted).