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MR4Cancer: A web server prioritizing master regulators for cancer

Master Regulator (MRs) collectively orchestrates the regulatory program of almost all critical biological processes involved in development and homeostasis. Deregulation of MRs has been demonstrated to result in a wide variety of diseases, including cancer. Therefore, identification of MRs in context-specific condition may provide new insights into the underlying mechanism of oncogenesis. In this study, we develop a web server named MR4Cancer, which aims to identify potential MRs regulating the differentially regulated genes critical for the initiation and progression of cancers. Based on over-representation analysis (ORA) or gene set enrichment analysis (GSEA), it outputs five categories of ranked MRs: Transcriptional regulators, recurrently mutated genes, kinases, phosphatases, proteins from protein-protein interaction (PPI) network. Gene Ontology and pathway analyses are also conducted to assist function annotation of MR candidates. For transcriptional regulators, user can browse its expression level of tumor and normal samples, relation to cancer hallmarks, and effect of gene mutation on its activity and expression. More importantly, our tool provides network visualization for above results, especially interactions between MRs and their targets. Users can interactively customize the network and save high quality figures for their publications. We hope that this user-friendly and powerful web application could help biologists gain deep insights into the key regulators of oncogenesis with profound implication in cancer diagnosis, prognosis, and therapeutic intervention. MR4Cancer is freely accessible at: http://cis.hku.hk/MR4Cancer/.

Biography

Jiangwen Zhang graduated from Johns Hopkins University with PhD. He has worked at Harvard University Genome Center as Senior System Biologist for years before joining University of Hong Kong in 2013. His lab has broad interest in genetic and epigenetic regulation in development and diseases. Currently, his lab is focusing on epigenetic regulation of tumorigenesis. His lab employs high through-put 'omics' assays and large scale computation to dissect the gene regulatory network and signaling pathways involved in oncogenesis.

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