Differential analysis of combinatorial protein complexes with CompleXChange

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Many proteins operate in multiprotein complexes and not on their own. Unlocking this complexome in a condition-specific manner thus promises a deeper understanding into the cellular wriring and what happens upon cell fate transitions. Although there exist large amounts of transcriptomic data and an increasing amount of data on proteome abundance, quantitative knowledge on the dynamics of complexomes is lacking.
We present CompleXChange, a tool for differential analysis of protein complexes based on predicted complexes and inferred complex abundances. For simulated data the results obtained by our complex abundance estimation algorithm are in better agreement with the ground truth and biologically more plausible than previous efforts that used linear programming. Also, execution time is much shorter. The practical usability of the method was assessed in the context of transcription factor complexes predicted for human monocyte and lymphoblastoid samples. We demonstrate that our new method is robust against false-positive detection and reports deregulated complexomes that can only be partially explained by differential analysis of individual protein-coding genes. Furthermore we show that deregulated complexes identified by the tool potentially harbor significant yet unused information content compared to gene- and protein-centric analyses.