Supplementary Material

# Supplementary Tables

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Cascades** | | **Downlinks** | | **Uplinks** | | **Cycles** | | **FFLs** | |
| **Organism** | Z-score | P-value | Z-score | P-value | Z-score | P-value | Z-score | P-value | Z-score | P-value |
| ***E.coli*** | -7.92 | <0.01 | -7.27 | <0.01 | -14.52 | <0.01 | -1.37 | 0.13 | **7.4** | 0 |
| ***S. cerevisiae*** | -1.88 | 0.04 | -1.94 | 0.03 | -13.49 | <0.01 | -0.68 | 0.32 | **9.11** | 0 |
| ***M. musculus*** | -5.66 | <0.01 | -5.20 | <0.01 | -9.42 | <0.01 | -1.83 | 0.03 | **4.92** | 0 |
| ***H. sapiens*** | -4.90 | <0.01 | -4.68 | <0.01 | -6.33 | <0.01 | -2.33 | <0.01 | **1.45** | 0.72 |

**Table S1. Motif enrichment in Transcriptional interaction graphs**

## Supplementary Figures

**Figure S1. Topological properties of simulated networks (*S. cerevisiae)*.** FFL-motif node participation, average sparsity, in- and out-degree distribution in simulated networks. For FLL-motif node participation counts, up to three participations for each node were allowed  (in different roles).

**Figure S2. Topological properties of simulated networks (*M. musculus)*.** FFL-motif node participation, average sparsity, in- and out-degree distribution in simulated networks. For FLL-motif node participation counts, up to three participations for each node were allowed  (in different roles).

**Figure S3. Topological properties of simulated networks (*H. sapiens)*.** FFL-motif node participation, average sparsity, in- and out-degree distribution in simulated networks. For FLL-motif node participation counts, up to three participations for each node were allowed  (in different roles).

**Figure S4. Mean runtime for FFLatt algorithm.** Ten datasets at each size were used for determining mean run time when generating networks with various numbers of FFL-motifs present.