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 Vázquez *et al.* 10.1073/pnas.0406024101.

Supporting Information

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Fig. 4. The distribution $P(T)$ of the number of triangles passing by a node. The solid lines correspond to the best fit to a power law. In the case of the *Saccharomyces cerevisiae* protein interaction network, the data are better fitted to two power laws, one for small T and one for large T . Since the subgraph abundance is mainly determined by the large k and T properties, we have estimated the exponent δ from the power law fit to the large T region.

[Supporting Figure 5](#)

Fig. 5.

Some examples illustrating the overcounting of subgraphs. In our approach, we count subgraphs with a central node connected to all other nodes in the subgraphs. In some cases a subgraph may have more than one

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node satisfying this condition. The number of potential central nodes of an (n,t) subgraph is counted by the combinatorial factor $1/g_{nt}$.

Supporting Figure 6

Fig. 6. (a) An example of a node with in-degree $k_{in} = 3$, out-degree $k_{out} = 2$, and one FFL passing by it (red arrows). The nodes with a link pointing to the central node (open circle) are called in-neighbors, whereas nodes that are pointed at by the central node are called out-neighbors. (b) Examples of directed n -node subgraphs, with a central node (open circle) and $n - 1$ in-neighbors, forming t FFLs.

Supporting Figure 7

Fig. 7.

FFL clustering coefficient for the two transcription regulatory networks studied here. The continuous line corresponds to the power law $C_{FFL}(k_{out}) \sim k_{out}^{-1}$.

Supporting Figure 8

Fig. 8. Subgraph over- and underrepresentation relative to the randomized network for type I subgraphs ($t \leq (n - \gamma)/\alpha$). Positive and negative values of z_{nt}^I correspond to over- and underrepresented subgraphs, respectively. The symbols correspond to $n = 3$ (circles), $n = 4$ (squares), $n = 5$ (diamonds), $n = 6$ (triangles), and $n = 7$ (crosses). Note that the value of t is given by the x axis.

Table 3. Network statistics after the removal of double links, self-loops, and isolated nodes

Network	N	E	$\langle k \rangle$	$\langle C \rangle$	$\langle k \rangle/N$
<i>E. coli</i> transcriptional	418	519	2.5	0.086	0.0059

<i>S. cerevisiae</i> transcriptional	688	1,078	3.13	0.047	0.0046
<i>E. coli</i> metabolic	884	2,739	6.2	0.169	0.0070
<i>S. cerevisiae</i> metabolic	551	1,698	6.2	0.227	0.0112
<i>S. cerevisiae</i> protein	5,068	15,117	5.97	0.085	0.0012

N is the number of nodes, E is the number of edges, $\langle k \rangle$ is the average degree, and $\langle C \rangle$ is the average clustering coefficient of the studied networks. The ratio $\langle k \rangle / N$ gives the average clustering coefficient for a random network with the same pair of parameters (N ; E).

Table 4. Clustering coefficient of the node of maximum degree, $C_{k_{\max}}$, and average clustering coefficient for the randomized graphs, C_{rd} , for the different biological networks studied in the paper

Network	C_{rd}	$C_{k_{\max}}$	$C_{k_{\max}}/C_{\text{rd}}$
<i>E. coli</i> transcription	0.10	0.0063	0.063
<i>S. cerevisiae</i> transcription	0.071	0.0044	0.062
<i>E. coli</i> metabolic	0.21	0.013	0.062
<i>S. cerevisiae</i> metabolic	0.19	0.024	0.12
<i>S. cerevisiae</i> protein	0.021	0.0030	0.14

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