

# STRUCTURAL MOTIF ENUMERATION IN TRANSCRIPTIONAL REGULATION NETWORKS

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**Abstract:** Network motifs are small connected subnetworks within a larger network that occur in statistically significant quantities and may indicate functional regions of the network. Network motif software tools employ algorithms that compare a network to randomly generated networks in order to identify subnetworks that occur in frequencies higher than would be expected by random chance. The transcriptional regulation network of *E. coli* has been represented as a network and evaluated using both full enumeration and an edge sampling algorithm. Several significant network motifs were identified, including feedforward loops and bipartite graphs. This paper applies both full enumeration and a different sampling algorithm, randomized enumeration, to the *E. coli* network using the newer software tool FANMOD. Evaluating the *E. coli* transcriptional regulation network with FANMOD also identified feedforward loops and bipartite graphs as significant network motifs. Sampling identified fewer and less significant motifs than full enumeration, however, sampling enables the evaluation of larger subgraph sizes.

## 1 INTRODUCTION

Graph theory provides a useful mathematical model to represent many systems as graphs composed of vertices, or nodes, and edges that connect the pairs of vertices. Network motifs are small connected subnetworks within a larger network that occur in higher frequencies than would be expected in random networks (Kashtan 2004, Schreiber and Schwobbermeyer 2005, Wernicke and Rasche 2006). Network motifs are the building blocks of networks, providing information about the behavior or design of the network; they may identify functional regions within biological systems. A range of network motif detection software tools have been developed to analyze network systems and to identify network motifs. Systems ranging from social networks to biological systems have been represented as graphs and analyzed for network motifs using these software tools. However, there is still room for improvement in network motif detection software tools. Since the most common network motifs in biological systems are different

than those found in other systems, it may be useful to optimize software tools specifically for network motif detection in biological systems. This could improve both outcome and performance.

### 1.1 Network Motifs and *E. Coli*

The transcription regulation networks of *E. coli* and *Saccharomyces cerevisiae* have been evaluated with network motif detection software tools by Alon and Lee respectively. There are three significant motif patterns in the transcriptional regulation network of *E. coli*. Each of these network motifs becomes apparent while comparing subnetworks of a particular size in the *E. coli* network with those of the same size in randomly generated networks. Significant motif patterns in *E. coli* depend on the number of nodes within the system. For a graph with only three nodes, the only significant network motif found by the Alon team is the feedforward loop. The feedforward loop is characterized by three nodes; X, Y and Z. A transcription factor X regulates a second transcription factor Y, which both

jointly regulate the operon Z. Alon terms the X the ‘general transcription factor’, Y the ‘specific transcription factor’ and Z the ‘effector operon’. Feedforward loops are also significant network motifs in networks with more than three nodes; in this case, transcription factors X and Y jointly regulate one or more operons  $Z(1) \dots Z(n)$ . The feedforward loop has other significant characteristics, of which the most important is coherence. Shen-Orr describes coherence, “A feedforward loop motif is ‘coherent’ if the direct effect of the general transcription factor on the effector operons has the same sign (negative or positive) as its net indirect effect through the specific transcription factor. For example, if X and Y both positively regulate Z, and X positively regulates Y, the feedforward loop is coherent. If, on the other hand, X represses Y, then the motif is incoherent” (Shen-Orr, Shai, Milo, Mangan and Alon, 2002). Most feedforward loops are coherent (85%). The feedforward loop occurs much more often within the *E. coli* transcriptional regulation network than would be expected by random chance. Shen-Orr suggests that the coherent feedforward loop has a significant functional structure; the ability to act as a circuit that rejects transient activation signals from the general transcription factor and responds only to persistent signals, while at the same time allowing a rapid system shut down through the control of the general transcription factor. This structure is useful way to coordinate a rapid response to an external signal. Also, the abundance of coherent feedforward loops over incoherent loops suggests a functional design. Lee’s research on the transcriptional regulatory networks of *Saccharomyces cerevisiae* suggest that the feedforward loop is also a significant network motif within that system (Lee *et al.*, *Science* 02). This suggests that the feedforward loop may also be significant within other biological system networks. Additional network motifs emerge as subgraphs of increasing numbers of nodes are evaluated. When subgraphs of four nodes are evaluated, the overlapping regulation motif becomes apparent. In the overlapping regulation motif, two operons are regulated by the same two transcription factors. This type of overlapping regulation motif is a smaller and specific form of dense overlapping regulons (DORs), which are discussed later.

Other significant motif patterns within the transcriptional regulation network of *E. coli* can be seen when graphs with higher numbers of nodes are evaluated. When subgraphs of larger than three nodes are evaluated, the single input module (SIM)

network motif becomes significant. The SIM is defined by a set of operons that are controlled by a single transcription factor, where all of the operons are under control of the same sign (positive or negative). There is no additional transcriptional regulation of the operons. The transcription factors involved in SIM systems are mostly autoregulatory (70%). Most of the autoregulatory transcription factors are autorepressive. There is a higher rate of autoregulatory transcription factors within SIM motifs than in the overall system. In the *E. coli* transcription regulation network, 70% of the transcription factors involved in SIM motifs are autoregulatory, compared to 50% in the overall dataset. SIMs are found in systems of genes that function stoichiometrically to form a protein assembly (*e.g.* flagella) or a metabolic pathway (*e.g.* amino acid biosynthesis). SIM systems may involve temporal ordering, where the first gene activated is the last to be deactivated.

Dense Overlapping Regulons (DORs) are a type of network motif found within *E. coli* when evaluating larger subnetworks. DORs are composed of layers of overlapping interactions between operons and a group of input transcription factors organized in a bipartite graph that is much more dense than corresponding structures in randomized networks. DORs are not a homogenous mesh of interconnections; rather, they contain several loosely connected, internally dense regions of combinatorial interactions. The regions are somewhat overlapping, and different criteria can yield slightly different groupings. One way to quantify DORs is by the frequency of pairs of genes regulated by the same two transcription factors. Shen-Orr uses a clustering approach to define DORs. An algorithm detects locally dense regions in the network with a high ratio of connections to transcription factors. Within the *E. coli* network, there are six DORs, where operons in each DOR share common biological functions. Usually, every output operon is controlled by a different combination of input transcription factors, but there are multi-input modules in rare cases where several operons in a DOR are regulated by precisely the same combination of transcription factors with identical regulation signs (termed ‘multi-input modules’). DORs are significant in the larger structure of biological networks; they seem to partition the operons into biologically meaningful combinatorial regulation clusters. DORs also govern how several different network motifs connect together within the larger network. Shen-Orr describes patterns in the overall structure of the *E. coli* network, “A single

layer of DORs connects most of the transcription factors to their effector operons. Feedforward loops and SIMs often occur at the outputs of these DORs. The DORs are interconnected by the global transcription factors, which typically control many genes in one DOR and a few genes in several DORs” (Shen-Orr *et al.*, Nature 02). Over 70% of the operons are connected to DORs; the rest of the operons are in small disjoint systems, with most disjoint systems having only one to three operons.

## 1.2 Motif Detection Tools

There are a number of software tools dedicated to network motif detection. Most of them employ different algorithms to achieve this task. In order to find network motifs, the software tool must find which subgraphs occur in the input network and in what number, determine which subgraphs are isomorphic (equivalent), and determine which subgraph classes of isomorphic graphs are displayed at higher rates than in random graphs. This means random graphs must also be generated. FANMOD is a newer motif detection tool that uses a random enumeration sampling algorithm. FANMOD uses the NAUTY algorithm (McKay, 1981) in order to group isomorphic graphs together into subgraph classes. It also supports colored graphs, a useful feature that other software tools do not support. Support of colored graphs is a highly useful feature for motif detection in biological networks because elements that should not be connected to one another, such as in a bipartite system, can be assigned the same color. This is a computationally effective way to avoid the generation of unnecessary random graphs for comparison. FANMOD employs a randomized enumeration algorithm called RAND-ESU. It works by first taking an algorithm for full enumeration and then modifying it to skip over some subgraphs randomly as the algorithm is executed. FANMOD also has the advantage of running much faster than similar programs. Other software tools include MAVISTO, which visualizes occurrences of a motif in a network by a force-directed graph algorithm, and MFINDER, which uses a different algorithm called edge sampling (Wernicke and Rasche, 2006). Edge sampling works by first selecting a random edge in the input graph, and then the edge is randomly extended until a connected subgraph with the desired number of vertices is obtained. However, edge sampling has distinct disadvantages. Wernicke has shown that the edge sampling algorithm results in a sampling bias, and

that the bias cannot be estimated from the number of edges neighboring the oversampled subgraph alone.

## 1.3 This Study

Enumeration of the subgraphs of a particular size within a larger graph is a computationally expensive and time consuming task. As the size of the subgraphs increases, the process becomes unwieldy and current algorithms take far too long to execute. Two of the major aspects involved in improving network motif detection tools are improving full enumeration algorithms for faster runtimes, and improving the sampling of motifs so that the algorithm is able to identify those motifs most likely to be functionally relevant. The transcriptional regulation network of *E. coli* has been analyzed by Shen-Orr using a Markov-chain algorithm to generate random networks for comparison. FANMOD uses the previously discussed RAND-ESU randomized enumeration algorithm to generate random networks. We chose to evaluate Shen-Orr’s *E. coli* transcriptional regulation network data with FANMOD in order to see if other algorithms would also identify the network motifs the Shen-Orr team found significant.

The study consisted of analyzing Shen-Orr’s *E. coli* transcription regulation network using the FANMOD motif detection software tool. We downloaded the *E. coli* transcription regulation network data from the Uri Alon lab website to use as the input file for FANMOD. Next, we ran both the full enumeration and sampling algorithms with FANMOD for subgraphs of increasing size, from three nodes to five nodes. The sampling algorithm takes less time to execute, but provides less information and identifies fewer network motifs than full enumeration. Sampling improves runtime, but at the loss of the identification of functional network motifs. The fact that the FANMOD sampling algorithm returns far fewer significant network motifs than full enumeration shows that there is room to improve the sampling algorithm. However, the more important quality in a sampling algorithm is not so how many motifs it identifies compared to full enumeration, but whether it is able to identify those motifs that are most functionally relevant. There are a few features that could improve the user experience of FANMOD. FANMOD generates diagrams of the most significant network motifs. It would be useful to be able to highlight substructures within these diagrams; for example, to highlight all feedforward loops within subgraphs of a particular size larger than three. Also, network motif detection

tools could allow the user to specify the types of network motifs that person is most interested in seeing. For example, the ability to show graphs that are bipartite or nearly so (80-90% of edges connecting different colors) would be useful for those studying such systems.

## 2 RESULTS

FANMOD provides several statistical values alongside significant network motifs. The Z-score is one way of determining how significant a network motif is. The Z-Score is the original frequency minus the random frequency divided by the standard deviation. Motifs with the highest Z-scores are the most significant, so the following tables of motifs are organized in order of decreasing Z-score. P-Values range from zero to one; smaller p-Values indicate more significant motifs because a smaller p-value indicates that the motif occurs more often in the network than would occur by random chance. The p-Value is calculated in the following way, "The p-Value of a motif is the number of random networks in which it occurred more often than in the original network, divided by the total number of random networks."

The following tables show the results for full enumeration and sampling of the *E. coli* network, enumerating subgraphs of size three. All graphs are ordered by descending Z-Score, so that the most significant network motifs are listed first. Full enumeration of the network at subgraph size three identified two significant network motifs, whereas the sampling algorithm just identified one significant network motif. The full enumeration data shows the average values from three trials. Two of the five trials for the sampling algorithm of subgraph size three resulted in no identification of significant network motifs. The sampling data shows the average values from the remaining three trials.

The table below shows the three most significant network motifs of subgraph size four identified using full enumeration. All of the seven significant network motifs for subgraph size four using full enumeration are bipartite graphs or contain at least one feedforward loop. The two motifs with the highest Z-scores contain two feedforward loops, and the third most significant is a bipartite graph. The remaining four motifs contain one feedforward loop. For sampling of subgraph size four, only one trial out of three trials identified any significant network motifs at all. The one network motif identified was

the sixth most significant according to the full enumeration data.

Table 1: Significant network motifs identified using FANMOD, full enumeration and subgraph size 3 (n=3).

(Three trials)	Feedforward Loop 	Bipartite Graph 
Average Frequency [Original]	0.80676%	91.76%
Average Mean-Frequency [Random]	0.14468%	91.216%
Average Standard-Deviation [Random]	0.00058784	0.00048442
Average Z-Score	11.264	11.221
Average p-Value	0	0

Table 2: Significant network motifs identified using FANMOD, sampling and subgraph size 3 (n=3).

(Three Trials)	Feedforward Loop 
Average Frequency [Original]	0.99259%
Average Mean-Frequency [Random]	0.10969%
Average Standard-Deviation [Random]	0.0015703
Average Z-Score	5.6127
Average p-Value	0.003667

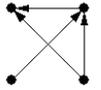
The full enumeration algorithm identified the 20 most significant network motifs for subgraphs of size five. Each of the three trials identified 20 network motifs; 22 distinct motifs total. All of the 22 motifs are either bipartite graphs or contain at least one feedforward loop. Two of the 22 network motifs contain three feedforward loops and three of the motifs are bipartite graphs. Ten of the motifs contain two feedforward loops, and the remaining seven graphs contain only one feedforward loop each. The table below shows the two network motifs found with full enumeration of subgraph size five that contain three feedforward loops. The first

network motif listed was found to have the highest Z-score for all three trials, and the second was in the top ten motifs in every trial. The next table shows the three bipartite graphs.

Table 3: Significant network motifs identified using FANMOD, full enumeration and subgraph size 4 (n=4).

Network Motif	Average Z-score	Motif Rank		
		Trial 1	Trial 2	Trial 3
	24.927	1	1	1
	15.641	2	2	2
	10.533	3	3	3

Table 4: Significant network motifs identified using FANMOD, sampling and subgraph size 4 (n=4).

Network Motif	
Frequency [Original]	0.62167%
Mean-Frequency [Random]	0.050375%
Standard-Deviation [Random]	0.00074301
Z-Score	7.6889
p-Value	0.001

The sampling algorithm identified five significant motifs in one trial and ten in another. The third trial identified no significant motifs. The two trials together identified 12 distinct motifs. 9 of these 12 motifs are included in the 22 motifs identified using full enumeration. Of the 12 motifs identified using sampling, one motif contains three feedforward loops, one motif contains two feedforward loops, and seven contain one feedforward loop. The remaining three motifs contain no feedforward loops. The second motif containing three feedforward loops in the table below was also identified in one of the sampling trials, ranked first with a Z-score of 10.528. As can be seen in the table below, the average Z-score for the same motif identified using full enumeration is 16.047.

Table 5: Significant network motifs containing three feedforward loops, identified full enumeration and subgraph size 5 (n=5).

Network Motif	Average Z-score	Motif Rank		
		Trial 1	Trial 2	Trial 3
	206.22	1	1	1
	16.047	6	8	9

Table 6: Significant network motifs that are bipartite graphs, identified full enumeration and subgraph size 5 (n=5).

Network Motif	Average Z-score	Motif Rank		
		Trial 1	Trial 2	Trial 3
	17.474	7	7	6
	11.31933	10	11	10
	5.6591	18	19	17

### 3 CONCLUSIONS

Every single significant network motif identified using full enumeration for subgraph sizes of three, four and five is either a bipartite graph or contains one or more feedforward loops. Most of the network motifs identified using sampling also contain one or more feedforward loops. The data supports the notion that the feedforward loop and bipartite graphs are statistically significant structures in the transcriptional regulation network of *E. coli*. The data supports Shen-Orr's research that shows the feedforward loop as the most significant network motif at subgraph size three. Additionally, the second network motif that was detected using full enumeration is a bipartite graph, suggesting that bipartite graphs are significant in the *E. coli* transcription regulation network. Many of the network motifs found to be significant from the enumeration and sampling of larger subnetwork sizes contain feedforward loops or are bipartite graphs. When the subgraph size is increased to four, the full enumeration data shows that the two most

significant network motifs each contain two feedforward loops. The third most significant motif is the previously-described overlapping regulon motif, a bipartite graph. All of the remaining identified motifs for full enumeration of size four graphs contain one feedforward loop with one additional edge. Overall, six out of the seven significant motifs contain at least one feedforward motif, with the two most significant motifs containing two feedforward loops. The remaining motif is a bipartite graph. This further supports that feedforward loops and bipartite systems are significant within the *E. coli* transcription regulation network. The sampling data for subgraphs of size four only identified one of the significant motifs, the sixth most significant according to the full enumeration data. It consists of a feedforward loop with one additional edge. The most significant motifs at subgraph size five also contain feedforward loops, with those ranked highest containing two or three feedforward loops. The sampling data showed fewer network motifs than full enumeration in all cases. For subgraphs of sizes four and five, the most significant motif identified by sampling was not represented in the top five most significant motifs identified using full enumeration. Sampling has major shortcomings when compared to full enumerations; it identifies both fewer and less significant network motifs. Overall, the FANMOD data shows that feedforward loops and bipartite graphs are significant network motifs in the transcriptional regulation network of *E. coli*.

#### 4 FUTURE WORK

There are several ways to improve network motif detection tools. One way to improve sampling results in FANMOD could be to alter the default probability settings in order to better favor sampling the network more evenly. This is discussed in detail in Section 5 of the FANMOD manual. The default settings are 0.5 for all probability fields, but organizing the probability fields with high probabilities in the left fields and lower probabilities in the right fields increases the chance that the network will be sampled more evenly. However, preliminary results for sampling using the probabilities 0.8, 0.5 and 0.3 for subgraph size three resulted in identification of the feedforward loop with a lower average Z-score from three trials (4.8304) than sampling subgraphs of size three with the probabilities 0.5, 0.5, 0.5 (Z-score 5.6127). This indicates that the feedforward loop was actually

found to be *less* significant using the alternative descending probabilities. More trials could be conducted using subgraphs of different sizes to determine whether an altered probability pattern improves the results from sampling compared to those from full enumeration.

FANMOD also supports several models for randomized network generation. Our study used the local constant model, where directed edges are exchanged with one another and the number of edges connected to each vertex remains constant. FANMOD also supports a global constant model that preserves the total number of edges, but the number of edges connected to a specific vertex may or may not remain the same. The transcriptional regulation network of *E. coli* could also be evaluated using the global constant model with full enumeration and sampling in order to see whether the motifs identified as significant change. Additionally, it would be useful to test other transcriptional regulation networks to see if structures such as the feedforward loop are significant in other biological networks.

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