Assessing the exceptionality of network motifs

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Getting and analyzing biological interaction networks is at the core of systems biology. To help understanding these complex networks, many recent works have suggested to focus on motifs which occur more frequently than expected in random.

To identify such exceptional motifs in a given network, we propose a statistical and analytical method which does not require any simulation. For this, we first provide an analytical expression of the mean and variance of the count under any stationary random graph model. Then we approximate the motif count distribution by a compound Poisson distribution whose parameters are derived from the mean and variance of the count. Thanks to simulations, we show that the quality of our compound Poisson approximation is very good and highly better than a Gaussian or a Poisson one. The compound Poisson distribution can then be used to get an approximate p-value and to decide if an observed count is significantly high or not.

We compare our method to the Mfinder software on PPI data and discuss the choice of a relevant random graph model to detect over-represented motifs.

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