



# Workshop on Modeling of Genetic Regulatory and Metabolic Networks

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Abstract

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## Assessing the exceptionality of network motifs

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 exchangeable 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 compound Poisson approximation outperforms the Gaussian approximation. 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. Our methodology is applied on protein-protein interaction networks (PPI), and statistical issues related to exceptional motif detection are discussed.

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