

Network diffusion-based discovery of genes and modules associated to antibiotic resistance in *E. coli* K12

Spreading of antibiotic resistance *Escherichia Coli* represents a real concern worldwide. Furthermore, *Escherichia coli* remains one of the most frequent causes of several common bacterial infections in humans and animals. Studies assessing the role in the resistance of genes to particular drugs classify antibiotic resistance due to mutated/alterd genes or presence of particular genes. Some genes participate to a common general resistance role in the bacteria, such as multidrug efflux pumps and their expression modulators, and other can be directly targeted by antibiotic to produce a negative effect on the bacteria. In this context, we use molecular interaction networks to analyze at a genome scale resistance associated genes in the model organism *Escherichia coli* K12. We employ a recent network diffusion-based algorithm to gather information from the topology of the interactions. This allow us to unveil a set of connected genes neighbouring the described genes in the literature and functionally related to them. Most of the predicted genes are involved in key genome related pathways such as protein synthesis, DNA replication, mismatch repair, or involved in membrane efflux pump activities.

Summary

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Session Classification : Posters