

[P9] Impact of enzymatic gene coexpression of cellular networks on disease comorbidity

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The diverse interactions of numerous cellular ingredients in cellular networks have proved to be essential for understanding disease prevalence patterns. For instance, we have previously shown that the metabolites controlled by genetically-correlated enzymes are robust; the prevalence of their associated diseases is low. Yet, it remains elusive how the intricate connectivity pattern of cellular networks affects the relationship - a positive or negative correlation - between distinct diseases. Here we consider the distance between two metabolites at different layers of cellular networks - gene coexpression, protein interaction, and metabolism - and how much they can explain the correlation of distinct disease modules quantified by their comorbidity.