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Noise Filtering in Biological Networks

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In biology, networks serve as powerful representations of systems across various scales, from genetic interactions (GI) in organisms to food webs in ecological communities. However, biological networks are often plagued by multiple sources of error, including measurement inaccuracies, sampling biases, and incomplete data. While sophisticated algorithms have been developed to address these challenges, yielding notable successes, existing methods fail to fully exploit the rich second-moment statistical information (variances and covariances) present in biological data. Filling this gap requires methodological advancements.

We develop a network version of the generalized Wiener filter \cite{pratt1972generalized}, specifically tailored for filtering edge noise in biological networks. The core technical obstacle arises from the absence of a natural distance metric in network settings, distinguishing this task from traditional signal and image processing applications. Depending on the scenario, we resolve this issue by either uncovering the complete covariance structure of the network data or employing a network theoretic ansatz.

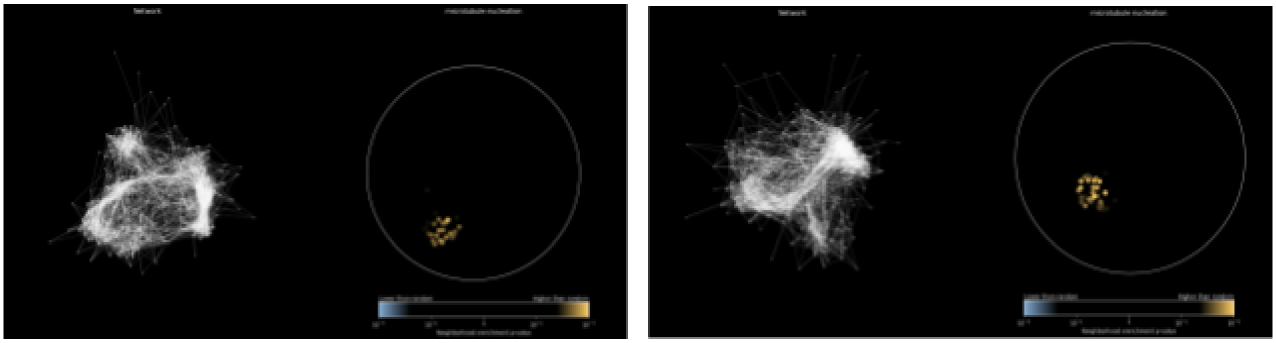

Figure 1: Original (left) and filtered (right) GI profile similarity networks for the essential genes of the yeast *Saccharomyces cerevisiae*, highlighting regions associated with microtubule nucleation using SAFE.

As an application of broad implications, we apply our approach to a state-of-the-art genetic interaction (GI) network mapped for the yeast *Saccharomyces cerevisiae*, which includes approximately 120,000 interactions between pairs of around 900 essential genes. The resulting filtered GI network exhibits greater symmetry and offers potential advantages in gene function prediction and other downstream analyses, suggesting the effectiveness of our method for biological discovery. This work paves the way for further exploration into advanced noise-filtering techniques in biological networks.

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