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DRaCOoN: Differential Regulation and CO-expression Networks

To address challenges in identifying crucial regulatory elements, we introduce DRaCOoN, a data-driven method for differential co-expression and regulatory networks between unique conditions. DRaCOoN uses established metrics to better handle large datasets and offers algorithmic and benchmarking strategies for accuracy and relevance. The method employs permutation tests and a background model for significance estimation. Numba optimization enhances runtimes and scalability.

We tested DRaCOoN using simulated datasets and node-based perturbations. DRaCOoN's entropy-based metrics outperform others in multiple scenarios, particularly with datasets containing many perturbed genes. A GSEA-inspired approach revealed optimal performance when combining entropy-based association metrics with the shift differential metric.

In summary, DRaCOoN effectively identifies key factors in complex biological processes and shows promise for studying intricate conditions or diseases.

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Keywords

Differential Regulation Analysis, Co-expression Networks, disease mechanism elucidation, Differential networking,

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