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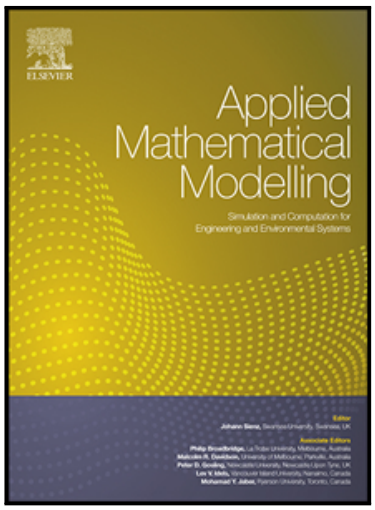

An Integrative Model for the Identification of Key Players of Cancer Networks

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Highlights

- A computational method for identification of cancer driver genes is proposed.
- Non-differentiable convex optimization identifies relationships between genes.
- Contributions of genomic data to cancer are formulated by convex maximization.
- Gene expression, copy number, and gene interaction are used to analyze breast cancer.

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