

POSTER PRESENTATION

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# Graph algorithms for machine learning: a case-control study based on prostate cancer populations and high throughput transcriptomic data

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## Background

The continuing proliferation of high-throughput biological data promises to revolutionize personalized medicine. Confirming the presence or absence of disease is an important goal. In this study, we seek to identify genes, gene products and biological pathways that are crucial to human health, with prostate cancer chosen as the target disease.

## Materials and methods

Using case-control transcriptomic data, we devise a graph theoretical toolkit for this task. It employs both innovative algorithms and novel two-way correlations to pinpoint putative biomarkers that classify unknown samples as cancerous or normal.

## Results and conclusion

Observed accuracy on real data suggests that we are able to achieve sensitivity of 92% and specificity of 91%.

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