Computational software for cancer diagnosis and prognosis

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Technology description

Summary

Carcinomas are a subset of cancers that originate in epithelial tissues. They represent the majority of cancers worldwide including lung, ovarian, and esophageal cancers. These epithelial cancers are thought to become invasive and pass through an epithelial-to-mesenchymal cell transition, but the process is poorly understood creating significant hurdles for diagnosing, treating, and predicting the prognosis of a patient's cancer. This technology is computational software that can identify biomarkers characteristic of particular metastasis stages in an unbiased manner. It can be developed into a diagnostic tool to evaluate a patient's prognosis, monitor disease progression, predict drug responses, and suggest appropriate courses of treatment.

Software identifies a coordinated gene expression signature characteristic of particular metastatic stages

The computational technique utilized by this technology identifies clusters of genes that are overexpressed together during a cancer's transition to a particular metastasis stage. These coordinately overexpressed genes signal a cancer's stage with a high degree of specificity. This technology has successfully identified metastasis related biomarkers, and it has been used to confirm the hypothesis that a core signature of overexpressed genes is shared among multiple cancers. It can also be used as a research tool to identify drug targets for inhibiting the metastasis transition.

Publications

Ou Yang TH, Cheng WY, Zheng T, Maurer MA, and Anastassiou D. "Breast cancer prognostic biomarker using attractor metagenes and the FGD3-SUSD3 metagene." Cancer Epidemiol Biomarkers Prev. 2014 Dec;23(12):2850-6.

Cheng WY1, Kandel JJ, Yamashiro DJ, Canoll P, Anastassiou D. "A multi-cancer mesenchymal transition gene expression signature is associated with prolonged time to recurrence in glioblastoma." PLoS One. 2012 Apr 6;7(4):e34705.

Kim H1, Watkinson J, Anastassiou D. "Biomarker discovery using statistically significant gene sets." J Comput Biol. 2011 Oct;18(10):1329-38.

Application area

Computational tool for identifying biomarkers in a range of disease states

Computational tool for diagnosis and staging of cancer

Computational tool for predicting cancer drug response

Computational tool for suggesting cancer treatment

Research tool for the development of metastasis-inhibiting therapeutics

Advantages

More accurate diagnosis and staging of cancer

Institution

Columbia University

Inventors

Dimitris Anastassiou