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.

Lead Inventor:

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Applications:

- 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

**Patent Information:**


Tech Ventures Reference: IR 2734

**Related Publications:**


**Inventors**

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