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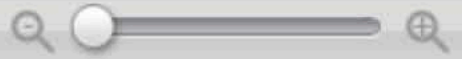
Powerful quantifiers for cancer transcriptomics

Iacobas DA. Cancer Transcriptomics Quantifiers

Dumitru Andrei Iacobas

Abstract

Every day, investigators find a new link between a form of cancer and a particular alteration in the sequence or/and expression level of a key gene, awarding this gene the title of “biomarker”. The clinician may choose from numerous available panels to assess the type of cancer based on the mutation or expression regulation (“transcriptomic signature”) of “driver” genes. However, cancer is not a “one-gene show” and, together with the alleged biomarker, hundreds other genes are found as mutated or/and regulated in cancer samples. Regardless of the platform, a well-designed transcriptomic study produces three independent features for each gene: average expression level, expression variability and coordination with expression of each other gene. While the average expression level is used in all studies to identify what genes were up-/down-regulated or turn on/off, the other two features are unfairly ignored. We use all three features to quantify the transcriptomic change during the progression of the disease and







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## Spatially Resolved Transcriptomics ... - Cancer Research

Cited by: 10

Author: Kim Thrane, Hanna Eriksson, Hanna Eriks...

Publish Year: 2018

Spatially Resolved Transcriptomics Enables Dissection of Genetic Heterogeneity in Stage III ... scRNA-seq is a powerful tool for addressing transcriptional het- ... Studying Melanoma with Spatial Transcriptomics [www.aacrjournals.org](http://www.aacrjournals.org) Cancer Res; 78(20) October 15, 2018 5971 ...

<https://cancerres.aacrjournals.org/content/canres/78/20/5970.full.pdf>

## Identification and transfer of spatial transcriptomics ... [翻译此页](#)

作者: Niyaz Yoosuf

Spatial transcriptomics (ST) is an in situ capturing method, which allows quantification and visualization of transcriptomes in individual tissue sections. In the past, studies have shown that breast cancer samples can be used to study their transcriptomes with spatial resolution in individual tissue sections.

<https://breast-cancer-research.biomedcentral.com/...>

## INsPeCT: INtegrative Platform for Cancer ... [翻译此页](#)

Cited by: 6

Author: Piyush B. Madhamshettiwar, Piyush B. Ma...

Publish Year: 2014

位置: 8600 Rockville Pike, Bethesda, MD

Here we present INsPeCT (INtegrative Platform for Cancer Transcriptomics), which allows users with basic computer skills to perform comprehensive in-silico analyses of microarray, ChIP-seq, and RNA-seq data. INsPeCT supports the selection of interesting genes for advanced functional analysis.

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3956744>

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**Publish Year:** 2014

## [Single-Cell Transcriptomics in Cancer Immunobiology: The ...](https://www.ncbi.nlm.nih.gov/pubmed/30483257)

<https://www.ncbi.nlm.nih.gov/pubmed/30483257>

Nov 12, 2018 · in these **transcriptomic** analyses of bulk **tumor cell populations**. Massively-parallel single-cell RNAseq analysis has emerged as a **powerful** method to unravel heterogeneity and to study rare cell populations in **cancer**, through unsupervised sampling and modeling of **transcriptional** states in single cells. In

**Cited by:** 15

**Author:** Fatima Valdes-Mora, Fatima Valdes-M...

**Publish Year:** 2018

## [Spatially Resolved Transcriptomics ... - Cancer Research](https://cancerres.aacrjournals.org/content/78/20/5970)

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Oct 15, 2018 · Although scRNA-seq is a **powerful** tool for addressing **transcriptional** heterogeneity, knowledge about the spatial origins of single cells is vital when studying the TME. We aimed to optimize and apply spatial **transcriptomics** (ST) technology for the in situ and **quantitative** detection of gene expression in stage III melanoma lymph node metastases. For this purpose, we analyzed the **transcriptomes** ...

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**Author:** Kim Thrane, Hanna Eriksson, Hanna Er...

**Publish Year:** 2018





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Cited by: 1

Author: Greta Ali, Rossella Bruno, Anello Marcell...

Publish Year: 2019

## Cancer transcriptome profiling at the juncture of clinical ...

<https://www.nature.com/articles/nrg.2017.96>

Dec 27, 2017 · RNA sequencing (RNA-seq) has the potential to **bridge tumour genotypes** (for example, mutations) and their phenotypic consequences (for example, **cancer molecular subtypes**). The field of...

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Author: Marcin Cieřlik, Arul M. Chinnaiyan

Publish Year: 2018

## Cancer Transcriptomics | myGenomics - Quality NGS, FAST ...

[www.mygenomics.com/cancer-transcriptomics](http://www.mygenomics.com/cancer-transcriptomics)

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**Cancer RNA-Seq** enables detection of strand-specific information, an ...

## Spatially Resolved Transcriptomics ... - Cancer Research