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With the coming of personal genomics era, the biomedical data will be accumulated fast and then it will become reality for the personalized and accurate diagnosis, prognosis and treatment of complex diseases.

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Immune and stromal cells are two major components of tumor microenvironment (TME) which play an important role in judging the prognosis of tumor and influencing the progression of malignant, inflammatory, and metabolic disorders.

~~Bioinformatics Analysis to Screen the Key Prognostic Genes ...~~

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Conclusion: Bioinformatics analysis revealed that COL10A1 might be considered as a predictive biomarker for prognosis of breast cancer. Further experiments and clinical trials are essential to elucidate the value of COL10A1 in breast cancer treatment.

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~~Bioinformatics analysis of prognostic significance of ...~~

Bioinformatics for Medical Diagnostics: Assessment of Microarray Data in the Context of Clinical Databases Dugas M , 1 Merk S , 1 Breit S , 2 Schoch C , 3 Haferlach T , 3 and Kääh S 4 1 Department of Medical Informatics

~~Bioinformatics for Medical Diagnostics: Assessment of ...~~

Background: Reliable noninvasive biomarkers for hepatocellular carcinoma (HCC) diagnosis and prognosis are urgently needed. We explored the potential of not only microRNAs (miRNAs) but other types of noncoding RNAs (ncRNAs) as HCC biomarkers. Methods: Peripheral blood samples were collected from 77 individuals; among them, 57 plasma cell-free RNA transcriptomes and 20 exosomal RNA ...

~~Noncoding RNAs Serve as Diagnosis and Prognosis Biomarkers ...~~

Conclusion: Bioinformatics analysis revealed that RRM2 might be used as a predictive biomarker for prognosis of breast cancer. Further studies are needed to more precisely elucidate the value of RRM2 in evaluating breast cancer prognosis. Keywords: Biomarker; Breast cancer; Prognosis; RRM2. © 2019 The Author (s).

~~Bioinformatics analysis revealing prognostic significance ...~~

With the coming of personal genomics era, the biomedical data will be accumulated fast and then it will become reality for the personalized and accurate diagnosis, prognosis and treatment of complex diseases. The book covers both state of the art of bioinformatics methodologies and the examples for the identification of simple or network biomarkers.

~~Bioinformatics for Diagnosis, Prognosis and Treatment of ...~~

Andrew J Sedgewick, Kristina Buschur, Ivy Shi, Joseph D Ramsey, Vineet K Raghu, Dimitris V Manatakis, Yingze Zhang, Jessica Bon, Divay Chandra, Chad Karoleski, Frank C Sciurba, Peter Spirtes, Clark Glymour, Panayiotis V Benos, Mixed graphical models for integrative causal analysis with application to chronic lung disease diagnosis and prognosis, Bioinformatics, Volume 35, Issue 7, 01 April ...

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Of these nine validated pro-oncogenes, we found by bioinformatics analysis, TTK was chosen to verifying its role as a biomarker for

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prognosis in NSCLC by using a tissue microarray. According to the expression of TTK, 90 cases of NSCLC were divided into the low TTK group and high TTK group with 45 cases in each group.

~~Bioinformatics analysis and experimental validation of TTK ...~~

The detection of DEGs using bioinformatics analysis might be crucial to understanding the pathogenesis of ovarian cancer, especially the molecular mechanisms of its development. The association between PSAT1 expression and the occurrence, development, and prognosis of ovarian cancer was further verified by immunohistochemistry.

~~Identification of molecular marker associated with ovarian ...~~

Prognosis-related genes and factors such as HCAR3, PPY, RFWD2, WSPAR and Amcinonide were screened and investigated. The multi-regulatory networks constructed in this study are not only beneficial to improve treatment and evaluate patient prognosis with pancreatic cancer, but also favorable for implementing early diagnosis and personalized ...

~~Identification of prognosis related genes and construction ...~~

The aim of the present study was to identify molecular biomarkers related to the initiation and development of HCC via bioinformatics analysis, so as to provide a certain molecular mechanism for individualized treatment of hepatocellular carcinoma. Three datasets (GSE101685, GSE112790, and GSE121248) from the GEO database were used for the bioinformatics analysis.

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