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Cancer biomarker discovery via integrative medicine and bioinformatics analysis of sequencing, gene expression and clinical oncology data

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This work is addressed to the molecular diagnostics and prognostic data management system of cancers. This system is developing and implementing via integrative medicine, computational genomics and statistical bioinformatics methods. Adequate multivariate and multifactorial models of high-throughput data pre-processing, quality control, de-noising of diverse sources of complex data influence to correct interpretation of the results of molecular diagnostics, stratification and prognosis. We analysed TCGA/NCI and other massive genome-wide sequencing, gene expression and clinical oncology data and developed the appropriate statistical and computational methods of automatic identification and improvement of systematic errors including the batch effects, occurring due to technical and clinical series and distinct protocols. We proposed a novel feature selection methodology, which ranks-order and weights of the individual or/and composed molecular features associated with a given disease outcome and forms a sub-space of potential clinical biomarkers providing a high-confidence and robust stratification of cancer patients into two or more disease' recurrence risk groups. Our data analysis strategy allows us (i) to specify clinically relevant molecular processes, pathways, and biomarkers essential for progression of ovarian serous carcinoma, breast cancer, lung adenocarcinoma, (ii) to stratify the patients by the risks of disease recurrence, (iii) to identify a relatively small number of specific, sensitive and reliable biomarkers (ncRNAs, mRNA, CNV/ SNP and mutations) which after in-deep validation could be quantified to assays/kits useful in personalize diagnostics, prognosis and treatment prediction of the cancer patients.

Biography

Vladimir A. Kuznetsov has completed his Ph.D from Moscow State University in 1984. In 19981-2006 he has carried out his studies in Institute of Chemical Physics of Russian Acad of Sciences, Moscow. In 1994, he was elected as Corresponding Member of Russian Acad of Natural Sciences and awarded by P.L. Kapitsa's named medal. In 1996 he was awarded by International Society for Cancer Research/American Cancer Society and in 1996-2004 his was a research scholar and a senior scientist at US FDA, National Cancer Inst. and National Institute of Child Health and Human Development/NIH, USA. Since 2007 he is Senior Principal Investigator, Head of Division and Deputy Director Graduate Affairs at Bioinformatics Institute, Singapore. He has published more than 100 papers in reputed journals and serving as an editorial board member of several journals.

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