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Network based approach for analyzing complexities associated with diseases and its impact on personalized medicine

Priyanka Narad
Amity University, India

A standout amongst the most critical assignments of integrated Bioinformatics is to connect the gaps among different information areas, from the fundamental investigations of genomics, proteomics, and metabolomics to a level based system where all connections are represented in a coherent picture. A holistic understanding of the basic molecular mechanisms underlying any biological process is important for the application of biological science to personalized medicine. Issues of unavailable information, dissimilar information sources, wasteful work process, and incapable corresponding call for a better informatics approach needs to be addressed by providing an integrated approach. Increasing the elemental information of integrative Bioinformatics approaches useful for studying cellular complexities using new holistic data on gene expression and epigenetic marks. Two basic approaches, namely the representation in the form of networks and semantic web technology have been described for the management of the ever increasing high throughput data. An integrated approach to disentangle the biological intricacies would be highly beneficial in the field of medical and health sciences. With the cost of genome sequencing has fallen tremendously in the past decade, understanding of these complexities by developing a model framework is essential for personalized medicine. This model can serve as the base model and perturbations can be made and analyzed based on individual data.

pnarad@amity.edu

Long noncoding RNA Or3a4 promotes metastasis and tumorigenicity in gastric cancer

Xiaobo Guo
University of Shandonity, China

The contribution of long noncoding RNAs (lncRNAs) to metastasis of gastric cancer remains largely unknown. We used microarray analysis to identify lncRNAs differentially expressed between normal gastric tissues and gastric cancer tissues and validated these differences in quantitative real-time (qRT)-PCR experiments. The expression levels of lncRNA olfactory receptor, family 3, subfamily A, member 4 (OR3A4) were significantly associated with lymphatic metastasis, the depth of cancer invasion, and distal metastasis in 130 paired gastric cancer tissues. The effects of OR3A4 were assessed by overexpressing and silencing OR3A4 in gastric cancer cells. OR3A4 promoted cancer cell growth, angiogenesis, metastasis, and tumorigenesis in vitro and in vivo. Global microarray analysis combined with RT-PCR, RNA immunoprecipitation, and RNA pull-down analyses after OR3A4 transaction demonstrated that OR3A4 influenced biologic functions in gastric cancer cells via regulating the activation of PDLIM2, MACC1, NTN4, and GNB2L1 . Our results reveal OR3A4 as an inorganic lncRNA that promotes tumor progression; therefore, lncRNAs might function as key regulatory hubs in gastric cancer progression.

guo992352@hotmail.com