Journal of Oncology

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Special Issue on
Bioinformatics in Cancer and Immune Microenvironment

CALL FOR PAPERS

Tumor cells do not exist in isolation in the microenvironment of malignancy but rather in a diverse ecosystem that includes not only heterogeneous tumor cell clones, but also normal cell types like fibroblasts, vasculature, and a large pool of immune cells at various stages of activation and differentiation. As a consequence, there is now a complicated interaction of different cellular signaling pathways with the immune cell component influencing cancer development and therapeutic response. To capitalize on potential therapeutic and biomarker findings, it is challenging and time-consuming to thoroughly and systematically characterize these different cell types from diverse tumor samples using immunohistochemistry. We have now entered an era of digital cancer treatment, fueled by the increasing availability of omics technologies, in which varied and global molecular profiling may drive therapeutic discovery and predict immunotherapy responses. Computationally extracting cell-type specific information directly from bulk tumors is one promising answer to this problem. The benefit of using bioinformatics to predict accurate immune signatures from bulk native tumor tissue is that the functional intracellular and intercellular transcriptome profiles are preserved, whereas when purified immune cells are isolated from native tissue, the molecular profiles will have inherently different patterns. Such in silico methods are beneficial because they may capture cell-type specific characteristics as well as cell-cell interactions at the tissue system level.

Predicting tumor patterns accurately and completely is a significant problem to solve, especially considering the effectiveness of immunotherapeutic medication therapy for many human malignancies. This is particularly difficult for subgroups of closely similar immune cell phenotypes with modest gene expression variations but significant functional differences. It will be very beneficial to use bioinformatics strategies to profile the tumor immune landscape because it will allow us to systematically profile one immune cell population's patterns and immune cell networks in tumors with higher resolution, which will aid in the discovery of immune-modulatory drugs.

The goal of this Special Issue is to bring together original research and review articles that will help researchers better understand the complex interactions that exist between tumors, immune cells, and the microenvironment, as well as the discovery of new biomarkers and molecular targets in various cancers.

Potential topics include but are not limited to the following:

- Bioinformatics research into new cancer diagnosis and treatment methods based on the immune microenvironment
- Immunological, gene regulatory, and pathophysiological mechanisms involved in carcinogenesis
- The crosstalk between immune and nonimmune cells in the tumor microenvironment
- Drug target discovery and targeted drug design
- Therapeutic strategies that modulate the immune response
- Meta-analysis to identify the function of tumor microenvironment in cancer

Authors can submit their manuscripts through the Manuscript Tracking System at https://review.hindawi.com/submit?specialIssue=827345.

Papers are published upon acceptance, regardless of the Special Issue publication date.

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