Computational Methods in Inferring Cancer Tissue-of-Origin and Cancer Molecular Classification

Inferring cancer tissue-of-origin and molecular classification are two critical problems in personalized cancer therapy. It is known that there are about 5% cancers of unknown primary (CUP) site. These kinds of patients are under empirical chemotherapy, which leads to a very low survival rate. Thus, it is important to infer cancer tissue-of-origin. However, experimental methods usually fail to identify the exact tissue-of-origin even after the death of a patient, which provides a need for computational methods, especially in the era of big biomedical data. Based on the finding that gene expressions of metastasis cancer cells are more similar to those of original tissue than metastasis tissue, there have been a few computational methods developed in this area. However, the accuracy of the methods is yet to be improved to assure a clinical usage. In addition to CUP, inferring cancer tissue-of-origin is also important in avoiding misdiagnosis even if the cancer origin is known.  
  
Cancer molecular classification has also been proven to be useful in optimizing treatment methods. With the accumulation of genetic and prognosis data, it is possible to improve molecular classification for most cancer types based on historical data, especially when more and more single-cell data are available. A better cancer molecular classification and better set of markers are critical for developing more efficient cancer treatment and new drugs.  
  
This Research Topic will comprehensively discuss cancer tissue-of-origin and molecular classification, including not only methods/algorithms to infer the origins and molecular classification, but also translational studies for cancer treatment in hospitals. We welcome investigators to contribute Original Research as well as Review articles on methods and clinical applications of these two topics. Potential topics include but are not limited to the following:  
  
-Inferring tissue-of-origin for pan-cancers based on tissue data including gene expression, methylation, somatic mutation, etc.

-Inferring tissue-of-origin for pan-cancers based on liquid biopsy including cfDNA, cfRNA, methylation, circulating tumor cells, etc.

-Tissue and liquid biopsy-based methods in inferring tissue-of-origin for cancer subtypes

-Inferring cancer site-of-origin for multiple nodules at a specific tissue

-Machine learning methods in molecular classification of a specific cancer

-Clinical applications of cancer tissue-of-origin identification

-Clinical applications of cancer molecular classification

-The association between cancer molecular classification and immunotherapies

-The association between cancer molecular classification and other important cancer features like MSI, TMB, PD1-PDL1, etc.

-Single-cell analyses for tissue-of-origin and cancer molecular classification

-Medical image-based methods in cancer tissue-of-origin and molecular classification  
  
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**Keywords**: cancer, NGS, tissue-of-origin, molecular classification, cancer treatment, medical image, machine learning, liquid biopsy