Special Track: Tumor evolvability and heterogeneity

1st International Symposium on Mathematical and Computational Oncology (ISMCO'19)

http://www.ismco.net

Lake Tahoe, Nevada, USA
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Scope

Growing from a single somatic cell, by the time of detection a human tumor typically comprises of billions of cells that belong to different subclonal populations, with genetic and non-genetic differences among them - a phenomenon known as intra-tumor heterogeneity (ITH). Moreover, tumor heterogeneity can be found among tumor within different patients, interpatient heterogeneity, or multiple tumors found in one patient, intertumor intrapatient heterogeneity. During tumor progression and treatment, natural selection operates on phenotypic variation among tumor cell populations driving somatic evolution in tumor - leading to adaptations such as increased proliferative, invasive phenotypes, emergence of resistance during treatment, and ultimately metastasis.

This special track is intended to cover the latest advances in development and application of computational methods and mathematical models for studying tumor evolution and heterogeneity.

Topics

The topics of interest include, but are not limited, to the following areas:

- Inference of clonal architecture from genomic data
- Estimation of the extent of intra-tumor genetic and non-genetic heterogeneity
- Inference about mode of tumor evolution
- Emergence of resistance

- Spatio-temporal dynamics of cancer progression
- Order of events in cancer
- Tumor dormancy and metastasis
- Visualization
- Interpatient drug response

Organizers

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Important Dates

See http://ismco.net/

Paper Submission Procedure

See http://ismco.net/index.php/paper-submission/