

1-2020

Statistics of Tumor Micro-environment

Brenton Maisel

Thomas Jefferson University, brenton.maisel@jefferson.edu

Inna Chervoneva

Thomas Jefferson University, Inna.Chervoneva@jefferson.edu

Follow this and additional works at: https://jdc.jefferson.edu/si_ctr_2022_phase1



Part of the [Oncology Commons](#), and the [Translational Medical Research Commons](#)

[Let us know how access to this document benefits you](#)

Recommended Citation

Maisel, Brenton and Chervoneva, Inna, "Statistics of Tumor Micro-environment" (2020). *Phase 1*. Paper 40.

https://jdc.jefferson.edu/si_ctr_2022_phase1/40

This Article is brought to you for free and open access by the Jefferson Digital Commons. The Jefferson Digital Commons is a service of Thomas Jefferson University's [Center for Teaching and Learning \(CTL\)](#). The Commons is a showcase for Jefferson books and journals, peer-reviewed scholarly publications, unique historical collections from the University archives, and teaching tools. The Jefferson Digital Commons allows researchers and interested readers anywhere in the world to learn about and keep up to date with Jefferson scholarship. This article has been accepted for inclusion in Phase 1 by an authorized administrator of the Jefferson Digital Commons. For more information, please contact: JeffersonDigitalCommons@jefferson.edu.

SI/CTR Abstract

Word count: 250 words

Statistics of Tumor Micro-environment

Brenton Maisel, Inna Chervoneva*

(*) indicates primary project advisor

Introduction:

Immune cells play a prominent role in keeping tumors suppressed, but how the distribution of these immune cells within a tumor's microenvironment remains poorly understood. The long-term goal of this project is to study how statistical spatial distributions of different immune cells is associated with clinical outcome. The first objective is developing an algorithm for identifying different types of immune cells.

Methods:

The data motivating this project includes spatial localization information (x-y coordinates) and expression levels of immune cell CD markers quantified by immunofluorescence immunohistochemistry (IF-IHC) in ~1,500 cases of invasive breast cancer. Using expression levels of CD markers in cancer cells (viewed as background noise), we compute upper nonparametric tolerance limits for CD expression in cancer cells. The stroma cells with CD expression above this tolerance limit are considered to be immune cells of the corresponding CD marker type.

Results:

We have developed a Python program allowing us to quickly process a dataset of x-y coordinates of various cells that took up IHC stain, and creates a dataset of coordinates

that are true immune cells. We have additionally analyzed multiple parameters for the development of a tolerance interval and concluded that a combination of 95%-confidence 99%-content allows for a minuscule chance of including the stroma cells that are not immune while maintaining enough data for analysis. Exploratory analysis of spatial point patterns of identified immune cell populations and their association with progression-free survival is in progress.

Discussion:

We have developed an algorithm for the identification of different types of immune cells associated with type-specific CD markers quantified using IF-IHC. These tools enable further studies of spatial arrangement of immune cells in the tumor tissue and relating them to clinical outcome.