**NeighborhoodCoordination**

**Overview**

This repo consists of two parts: 1) Code used to generate the results for our publication “Coordinated cellular neighborhoods orchestrate antitumoral immunity at the colorectal cancer invasive front” and 2) Useful functions from our paper that we have generalized to make more user-friendly for the broader scientific community. These functions can be found in the “Neighborhoods” directory.

The following describes how to navigate the code we provide in the “Neighborhoods” directory. The code is implemented in python3 using jupyter notebooks. Some experience with installing python packages will be required to get up and running. Only a familiarity with python is required to follow and adapt these functions for your own use.

**Installation**

We recommend using the free package manager Anaconda (<https://www.anaconda.com)> to help install the packages required to use these scripts.

* Jupyter is most easily installed through Anaconda. Otherwise, one can follow the instructions here <https://jupyter.org/>
* The used scripts require very few dependencies. Packages required:
  + statsmodels
  + numpy
  + pandas
  + jupyter
  + seaborn
  + scikitlearn
  + tensorly
  + shapely

**Functions**

1. main\_fcs/main\_fcs\_csv: This is the data that we use in our publication and helps a user walk through these functions. This pipeline begins after Cell Types have been identified. The link to this file can be found via Mendeley Data, as indicated in our publication’s Supplementary Material.
2. Neighborhood Identification: This notebook walks a user through identifying Cellular Neighborhoods in high parameter imaging data as described in our publication.
3. Voronoi Generation: This notebook helps visualize the Cellular Neighborhoods on the tissue and allows the user to overlay a collection of cells over these neighborhoods to explore their spatial distribution.
4. Tensor Decomposition: This notebook describes how to perform tensor decomposition after each single cell has been allocated to a Cellular Neighborhood and Cell Type.
5. Neighborhood Mixing: This notebook allows the user to describe the spatial contacts between two Cellular Neighborhoods of interest.
6. Cell Type Differential Enrichment: This notebook allows a user to identify cell types that are differentially enriched within specific cellular neighborhoods across a set of conditions or clinical groups.