

## Visioning Tumor Immune Cell Composition Through Neural Networks

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### Keywords

Multispectral imaging, solid tumors, T cell immunity, neural networks, clustering algorithms

### Background

Generation of high-dimensional data in biological context has led to a wide range of applications of machine learning algorithms. This is most evident from differential pathway analysis performed on sequencing data and clustering algorithms applied to single cell cytometer data. Our and other laboratories have successfully applied such analysis techniques. However, current application to imaging data is still a challenge. Advances in multichannel image acquisition make it possible to acquire images visualizing up to 50 markers at the same time. Spatial as well as spectral overlap in these images pose enormous difficulty and time consumption to analyse such images. Furthermore, heterogeneity of patient materials limits application of such analysis to multiple images.

### Aim

To set up and train a neural network for analysis of immune contexts of tumor microenvironments in patient samples.

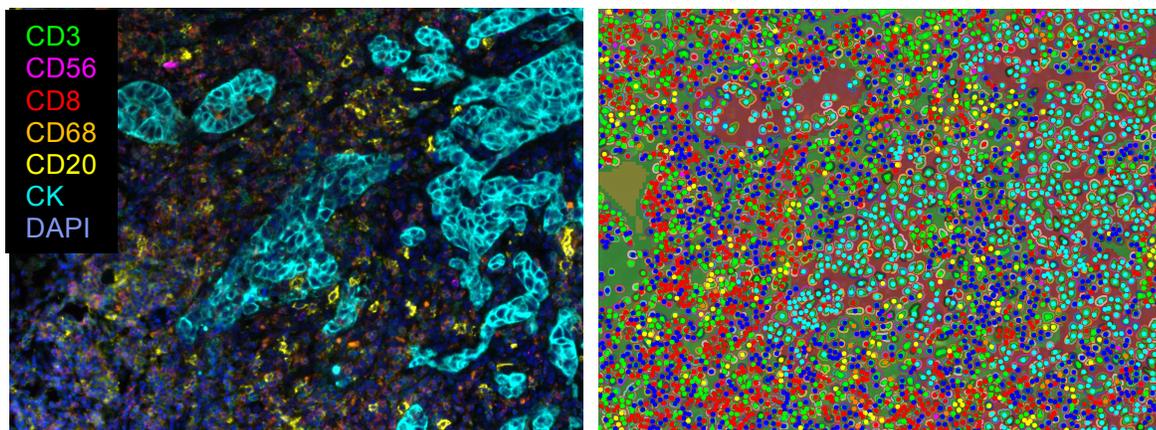
### Methodology

In the TME facility (coordinated by Balcioglu), embedded in our laboratory, we utilize a multispectral imaging approach for visualization of the immune micro-environment of tumors. To analyse such images, we have developed our in-house software implemented in python, providing the user with a 'what you see is what you get (WYSIWYG)' interface. This allows the analysis parameters to be easily changed on a patient and tissue basis and to address heterogeneity of biomaterials.

The image analysis workflow consists of tissue segmentation, cell segmentation and cell phenotyping, which are all suitable for machine learning algorithms. Making use of our wide database of quantified images (>1000 images analysed), there is a sufficiently large sample data set to further improve our workflow by addition of a neural network. In this project, separate tissue segmentation and cell segmentation neural networks will be trained and tested. Upon successful implementation of this discovery part, the outcome of single cell data will be subjected to unbiased clustering/mapping to validate our approach and at the same time identify different cell subsets and relating their abundance to survival data.

### Tasks and Opportunities

- Literature review on machine learning algorithms applied to biological images.
- Implementation of complex codes with simple interface for usage by biologists.
- Relating computational outcomes to clinical data.
- Gain insight in tumor-immunology, and acquisition and interpretation of biological data.
- Learn to give scientific presentations and prepare your work for peer-reviewed journals.



Left: Multispectral image of a triple negative breast cancer, right: corresponding segmentation and phenotyping