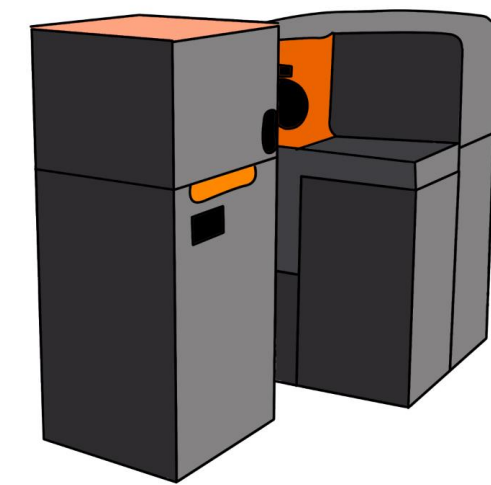


PURPOSE / OBJECTIVES



- Imaging mass cytometry technology producing high-throughput imaging of cells and proteins
- Multi-channel sub-cellular images, where each channel highlights expression level of a given protein
- Large amount of data produced, ideal for machine learning approaches

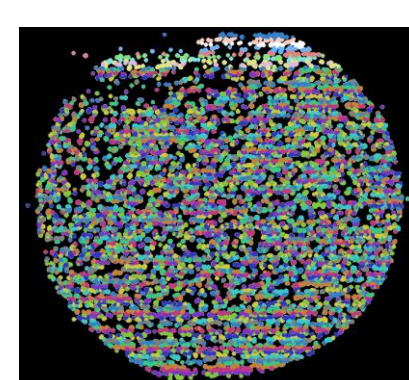
Identifying cell types in tissue sample (**cell phenotyping**) is crucial step in most analyses of cell-level data – typically a manual process which can result in user bias and difficulty scaling

OBJECTIVE: Automate the cell annotation process using deep learning

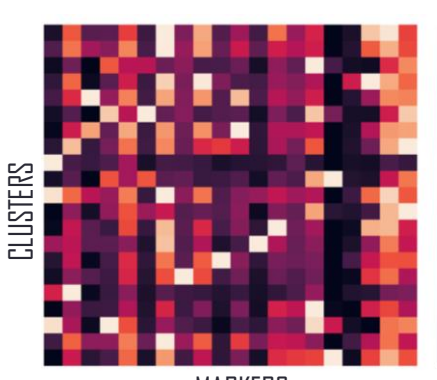
MATERIAL & METHODS



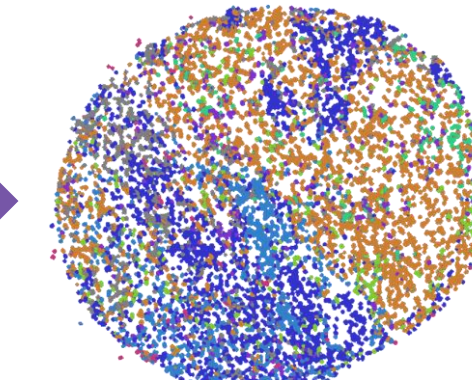
PRE-PROCESSING



Cell Segmentation



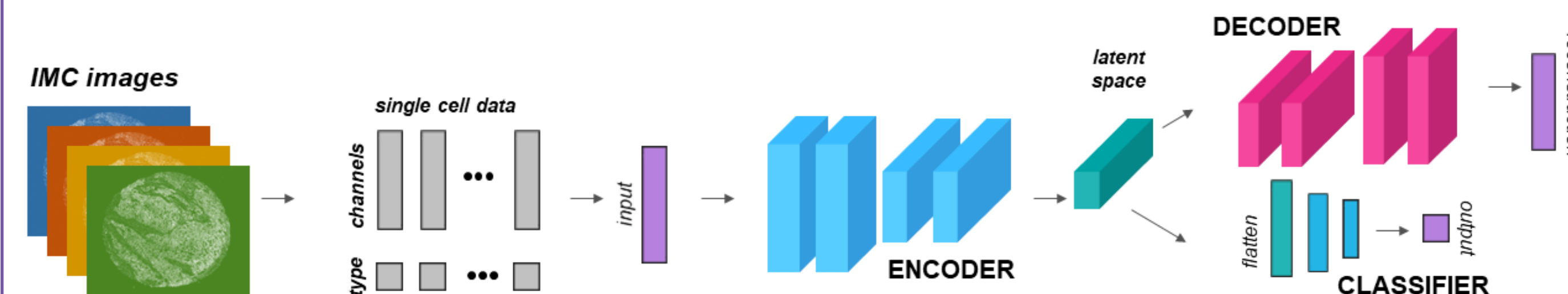
PhenoGraph Clustering



Cell Type Annotation

1. Segment data to create a cell mask using TITAN
2. PhenoGraph to cluster cells that have similar expression levels
3. Annotate cell types based on protein expression of each cluster

NETWORK ARCHITECTURE



Deep Joint Convolutional Autoencoder-Classifer

- Classifier identifies and phenotypes cells into four basic types: **immune**, **stomal**, **tumour**, and **other**
- Optimum values of structural parameters were determined based on classification accuracy
- Convolutional autoencoder was pre-trained alone to initialize network weights, then trained jointly for reconstruction loss and classification accuracy
- Model was evaluated using independent testing set; process repeated for 20 randomly generated sets, using average of performance metrics as measure of performance
- Conventional CNN was also implemented as a baseline to compare to

Imaging Mass Cytometry
A new advancement in tissue imaging that allows for a record number of proteins to be imaged at once

*Cell phenotyping
A necessary step for the analyses of this type of data*

Research Focus
To automate the process of cell phenotyping for imaging mass cytometry data for the first time

Results
Developed a deep convolutional autoencoder-classifier to automate cell phenotyping process into 4 basic cell types

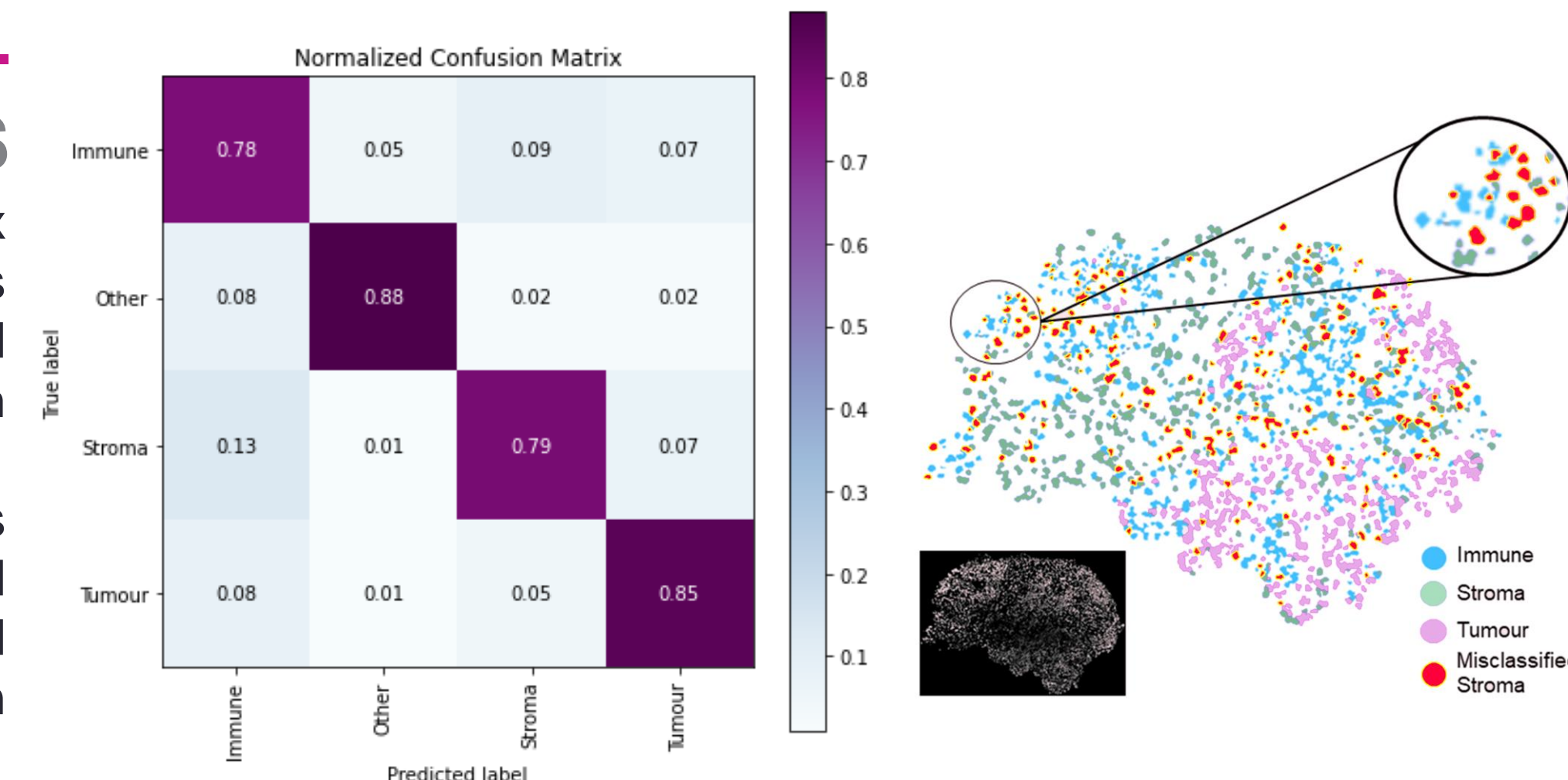
RESULTS

NETWORK PERFORMANCE

	Autoencoder Accuracy (%)	CNN (baseline) Accuracy (%)
Testing	81.9% +/- 0.3	79.9 +/- 0.7
Training	83.4 +/- 0.4	81.5 +/- 0.7

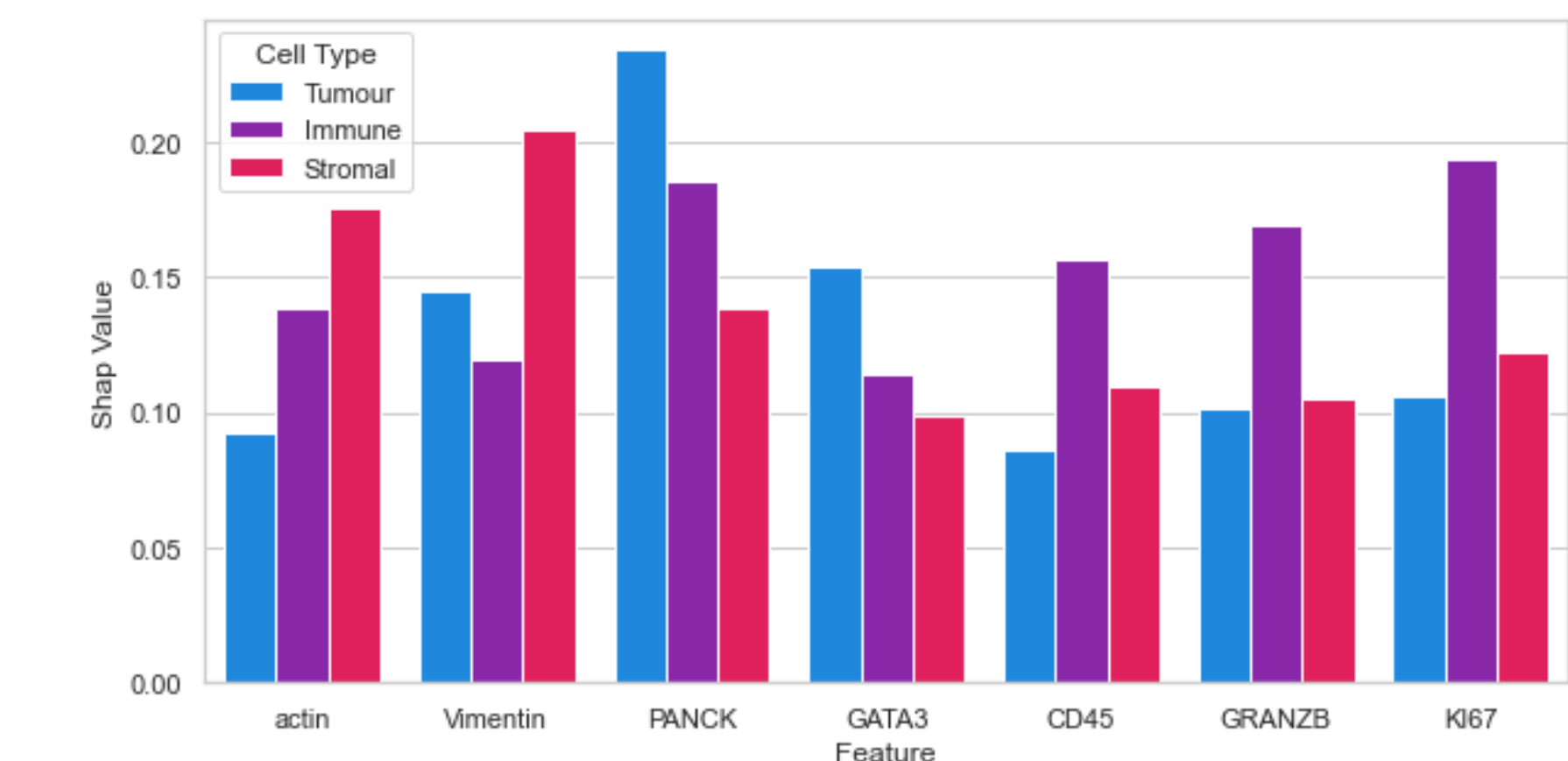
MISCLASSIFICATIONS

- Confusion matrix explores inter-class performance and indicates high performance
- Misclassified cells can be explained biologically and spatially, shown on right



FEATURE IMPORTANCE

- SHAP algorithm used to calculate each feature importance
- Top relevant features conform with what would be expected biologically



SUMMARY / CONCLUSION

- Developed convolutional autoencoder with joint classifier to identify cell types – first method to do this for imaging mass cytometry data
- Network shows the potential of using deep learning on imaging mass cytometry data for cell type annotation tasks
- Performance of network was biologically relevant
- Model was developed using bladder cancer tissue data but approach can be extended to imaging mass cytometry data of different tissue types

