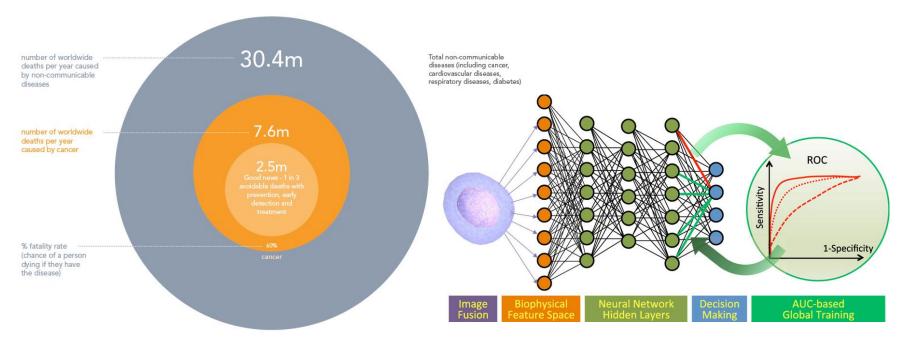
Scalable Informatics Tools for Investigating Intra-Tumor Heterogeneity in Breast Cancer

Alex Andonian

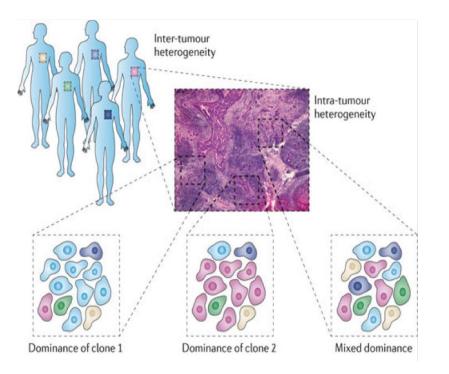
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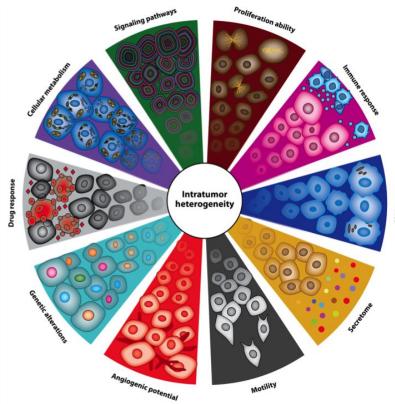


Cancer mortality compared to other diseases



Tumor Heterogeneity

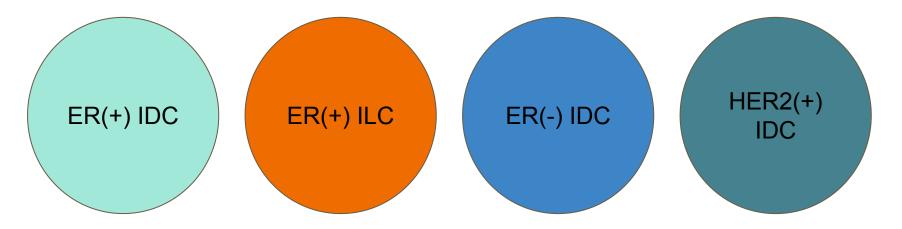






Tissue microarray of 99 samples consisting of triplicate, 1mm diameter cores from 24 invasive breast tumor tissues.

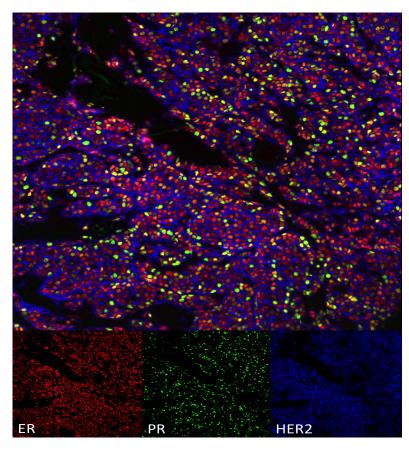
Immunohistochemical staining revealed 4 cohorts:

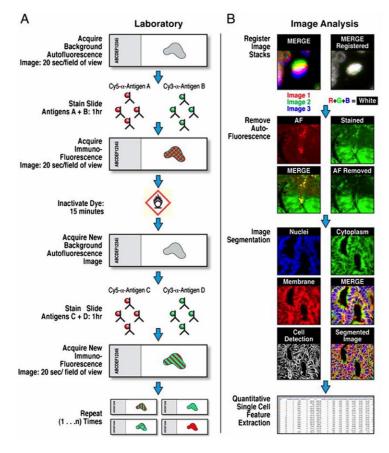


IDC - invasive ductal carcinoma

ILC - invasive lobular carcinoma

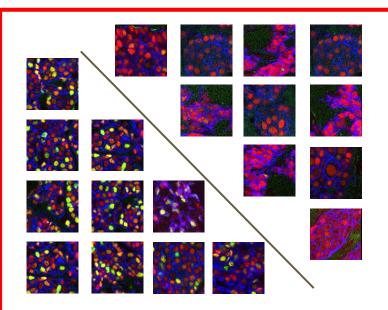
Multiplexed Immunofluorescence Imaging



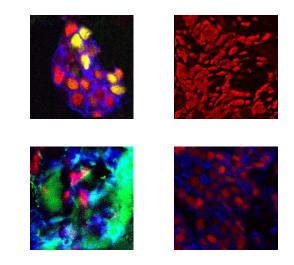


Research Goals

Develop high throughput informatics tools for integrating and analyzing cancer data obtained from a variety of imaging modalities

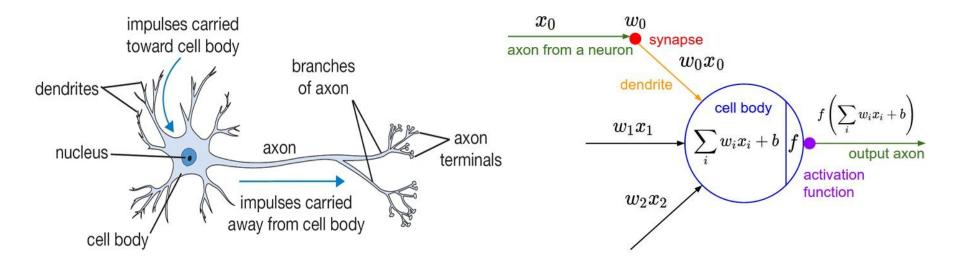


1. Cancer Classification



2. IF Signatures

Neural Networks - Biological Motivation

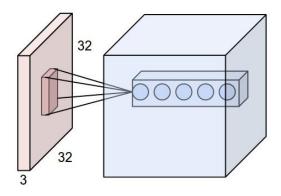


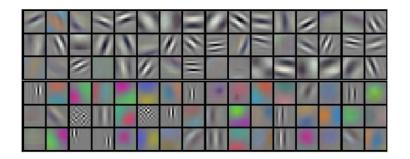
Convolutional Neural Networks

CNNs are very similar to ordinary neural networks, but...

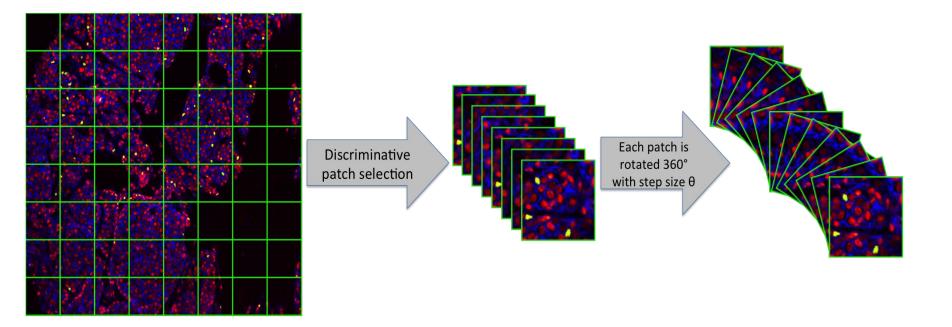
• Now, we make the explicit assumption that input are **images**

• Since fully connected layers don't scale well - take advantage of the fact that portions of images are correlated





Patch Selection and Augmentation





Classification accuracy by configuration:

	256 imes 256				512×512	
heta step size	3	6	6	18	36	9
patch overlap	-	-	64	-	-	-
CNN Acc	0.79	0.77	0.81	0.76	0.75	0.78

Classification accuracy:

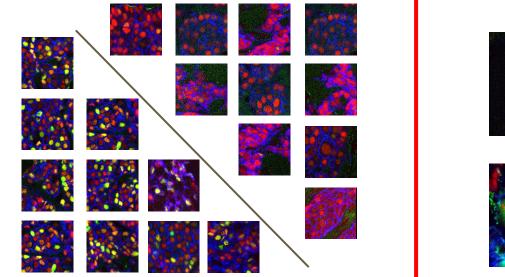
increases with patch overlap decreases with rotation step size

Ground Truth	ER(+) IDC	0.75	0.03	0.16	0.05	
	ER(+) ILC	0.33	0.59	0.00	0.07	
	ER(-) IDC	0.08	0.02	0.87	0.03	
ŀ	IER2(+) IDC	0.04	0.00	0.09	0.86	
		ER(+) IDC ER(+) ILC ER(-) IDC HER2(+ Predictions				

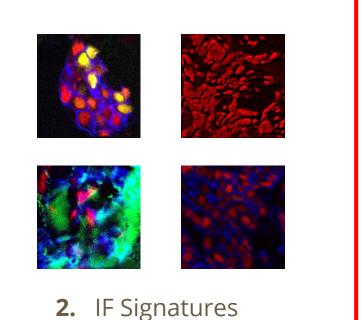
Confusion matrix for best performing configuration

Research Goals

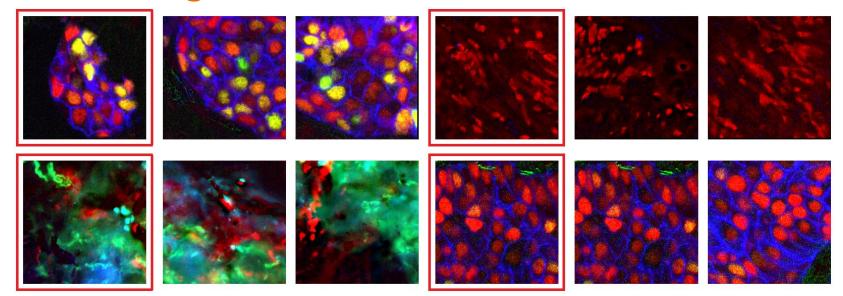
Develop high throughput informatics tools for integrating and analyzing cancer data obtained from a variety of imaging modalities



1. Cancer Classification



Nearest Neighbor Visualization

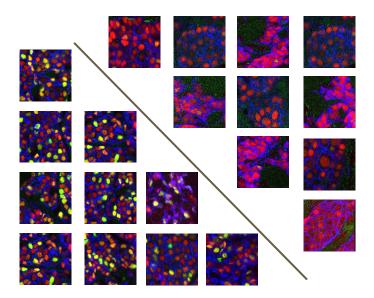


Could form the basis for a powerful and interactive visualization tool for clinicians

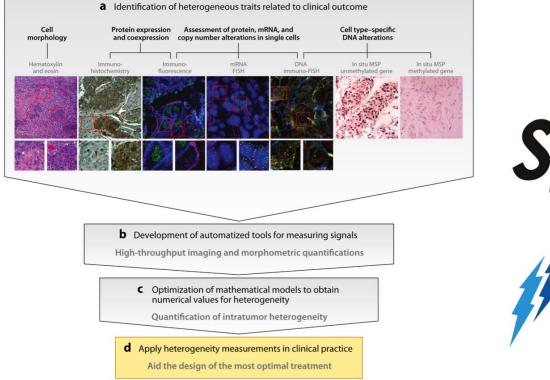
Conclusions

The main contributions of this work:

- classify cancer subtypes with respectable accuracy
- Identify immunofluorescent signatures associated with a cancer subtype



Future Work

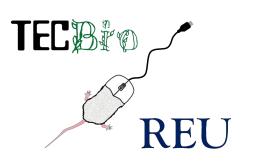


Spark



Acknowledgements

TECBio REU @ Pitt is supported by the National Science Foundation under Grant DBI-1263020 and is co-funded by the Department of Defense in partnership with the NSF REU program. Many thanks to Dr. Chennubhotla and his lab group.







References

- 1. Siegel, R. L., Miller, K. D. and Jemal, A. (2015), Cancer statistics, 2015. CA: A Cancer Journal for Clinicians, 65: 5–29. doi: 10.3322/caac.21254
- 2. Marusyk, A., et al. "Intra-tumor heterogeneity: a looking glass for cancer?." Nature Reviews Cancer 12.5 (2012): 323-334.
- 3. Almendro, V., et al. "Cellular heterogeneity and molecular evolution in cancer." Annual Review of Pathology: Mechanisms of Disease 8 (2013): 277-302.
- 4. Gerdes, Michael J., et al. "Highly multiplexed single-cell analysis of formalin-fixed, paraffin-embedded cancer tissue." PNAS 119.29 (2013): 11982-11987.
- 5. Jia, Y., et al. "Caffe: Convolutional architecture for fast feature embedding." arXiv preprint:1408.5093 (2014).

