

Using code to improve
people's health



OHSU is at the forefront of a digital revolution in medicine



Researchers, physicians, and teams like the Biomedical Engineering department at OHSU and across the world are working to improve patient outcomes through technological advancement.

- Advanced imaging and genetic/molecular sequencing are uncovering the molecular basis of healthy and unhealthy (disease) conditions
- These new technologies produce huge amounts of information which require computer-based advanced algorithms to understand
- Pharmaceutical: Computer algorithms are used to accelerate the development of new drugs

Digital Precision Medicine: Can computers and coding be used to make predictions about how to best treat a patient?

My research: using physics and python codes to predict cell behavior by making cell-state maps

predicting cell behavior → controlling cell behavior

Normal cell

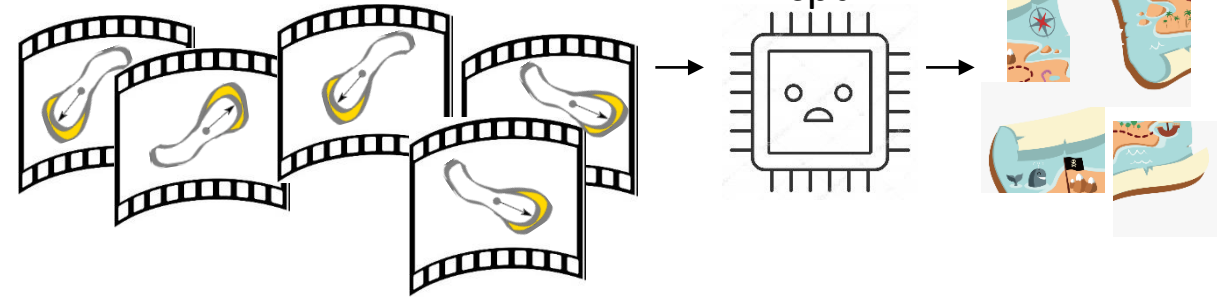


Example of one type of abnormal or cancerous cell



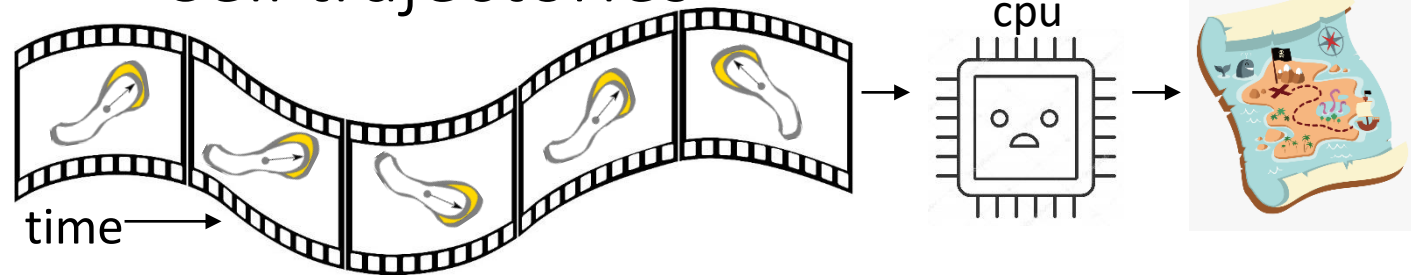
Goal: Create maps which can describe and predict cell-state outcomes, like a cell going from a normal cell-state to cancerous cell-state

Cell snapshots



Single-timepoint information is incomplete for cell behavior prediction

Cell trajectories



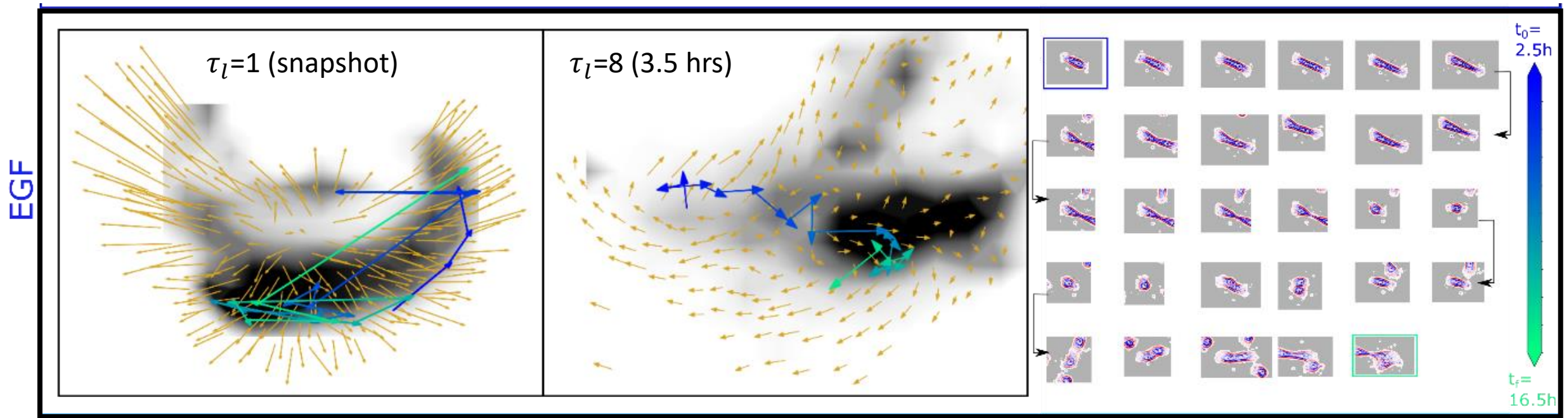
Trajectory information is complete for cell behavior prediction

Cell-state maps are built from microscope images of cells which are analyzed using python code

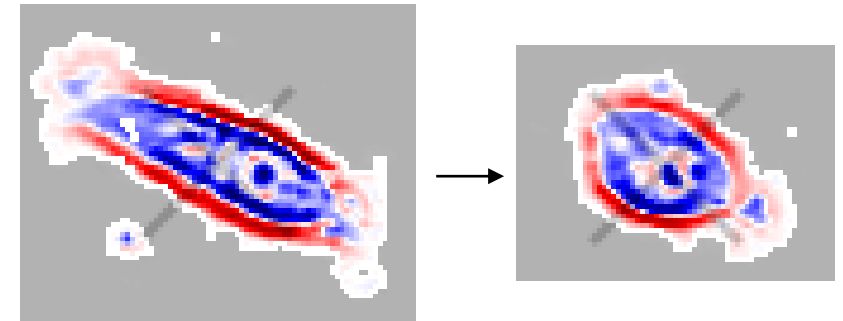


```
30 class cellTraj:
31     """Some cell trajectory analysis and embedding tools."""
32
33     def initialize(self, fileSpecifier, modelName):
34         self.modelName = modelName
35         pCommand = "ls " + fileSpecifier
36         p = subprocess.Popen(pCommand, stdout=subprocess.PIPE, shell=True)
37         (output, err) = p.communicate()
38         output = output.decode()
39         fileList = output.split("\n")
40         fileList = fileList[0:-1]
41         self.fileList = fileList
42         nF = len(fileList)
43         self.nF = nF
44         self.visual = True
45         self.imgdim = 2
46         try:
47             self.get_image_data(1)
48             self.imagesExist = True
49         except:
50             sys.stdout.write("problem getting images \n")
51             self.imagesExist = False
```

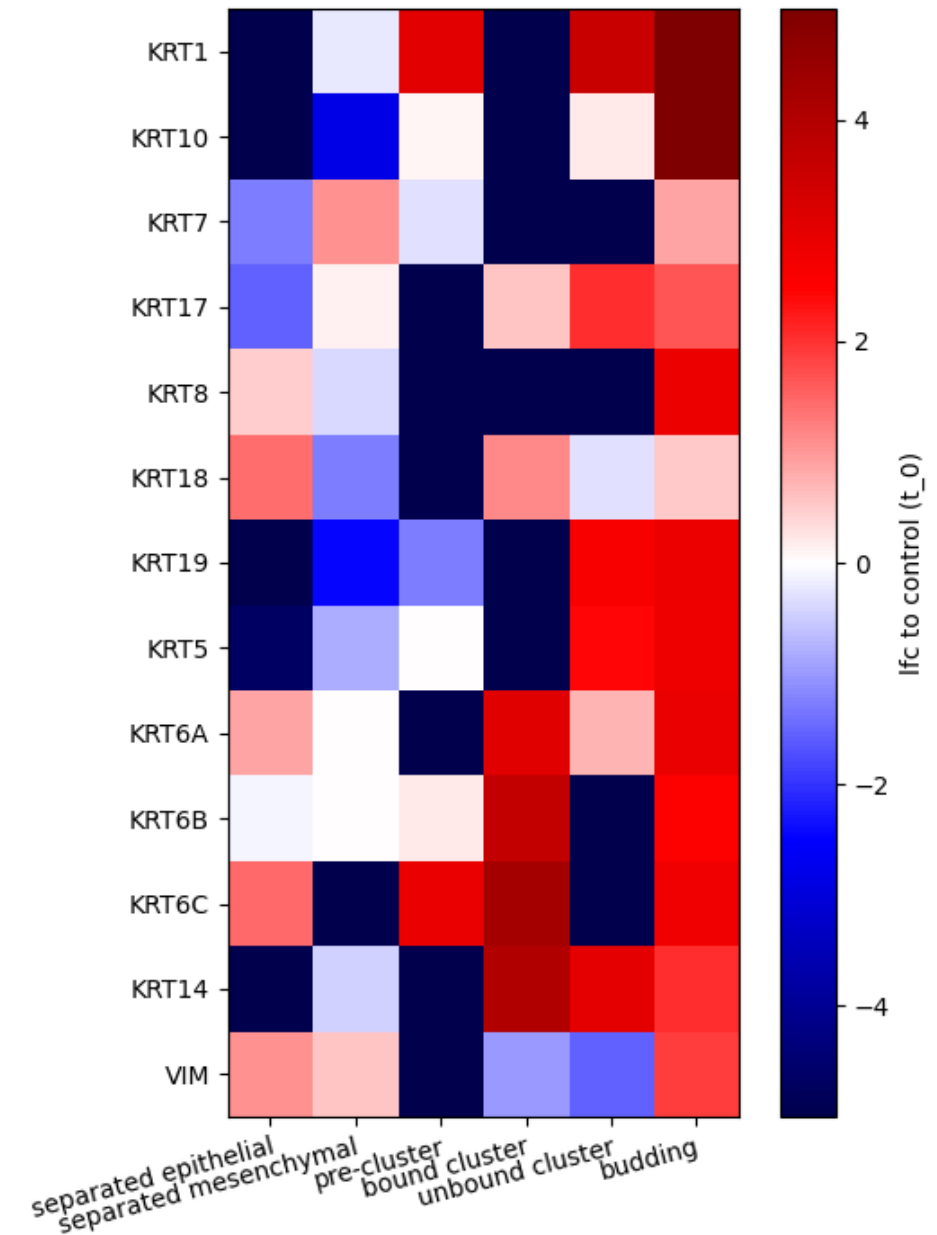
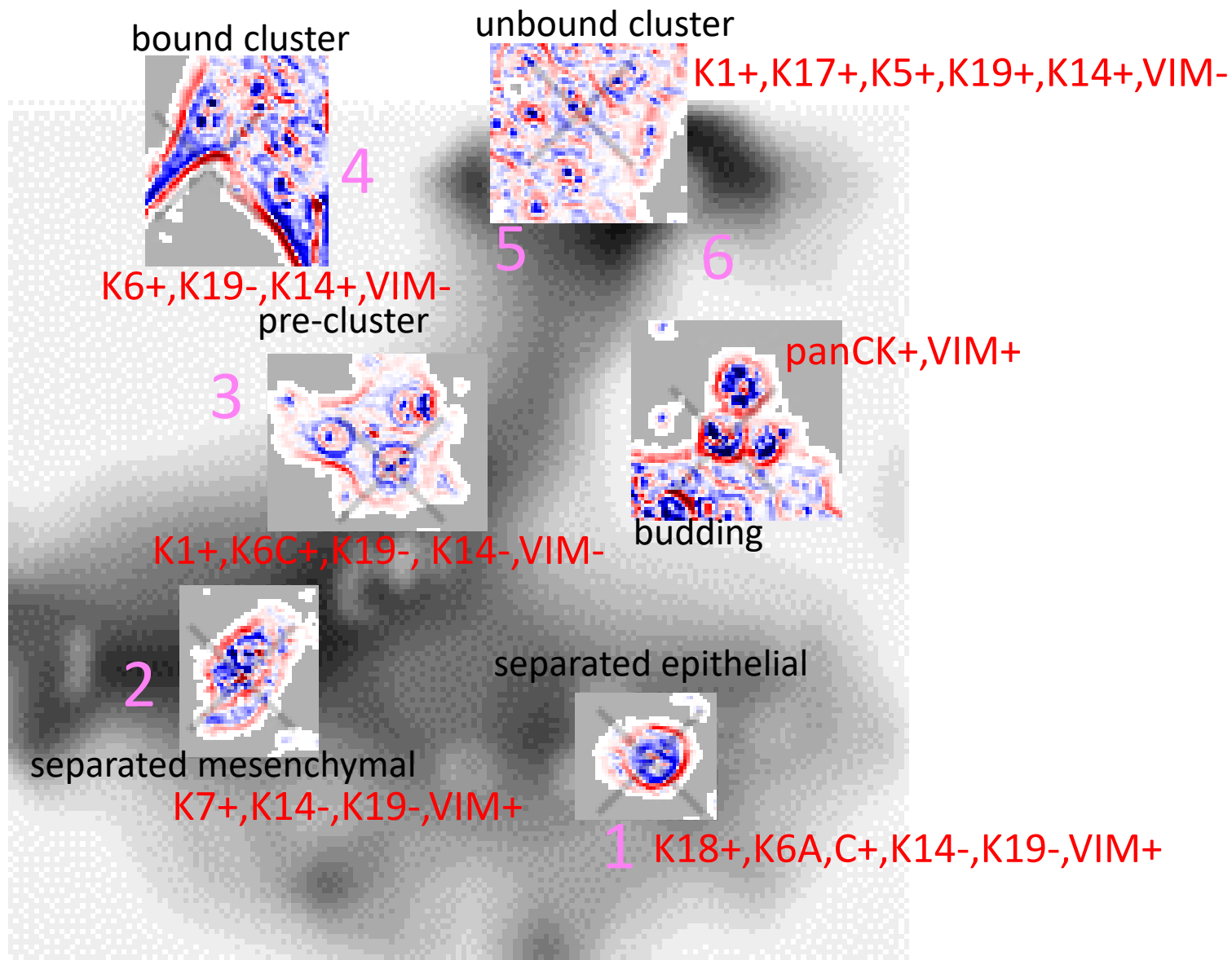
Cell-state maps from trajectories allow cell behavior to be predicted



- Maps based on cell snapshots (single-timepoint) seem random
- Maps based on trajectories show consistent, predictable cell-state trajectories



Current work: Combine cell-state maps with molecular information



Future work: Combine cell-state maps with computer-based models of cancer cells

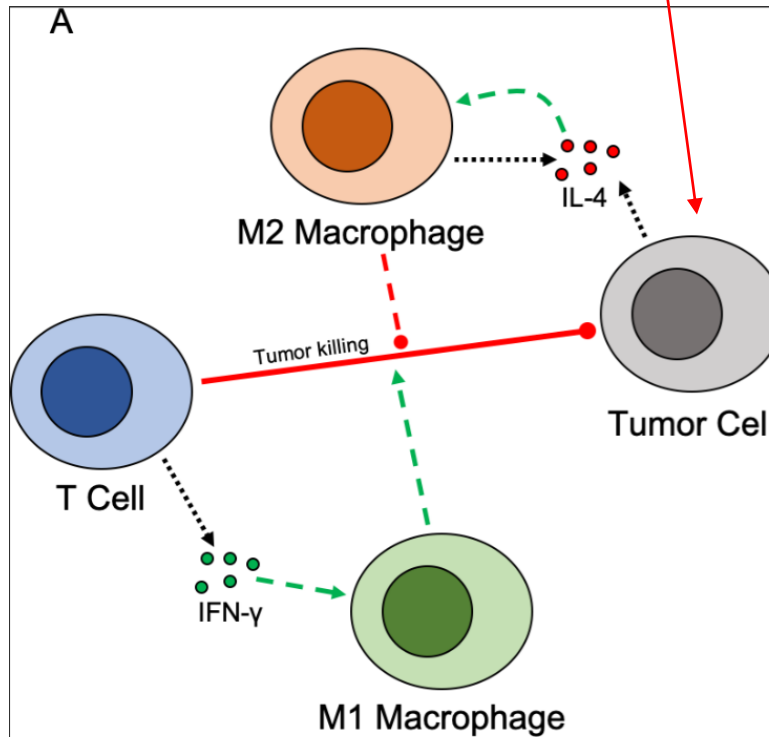
Groundbreaking computational cancer scientist

Stacey D. Finley, Ph.D.

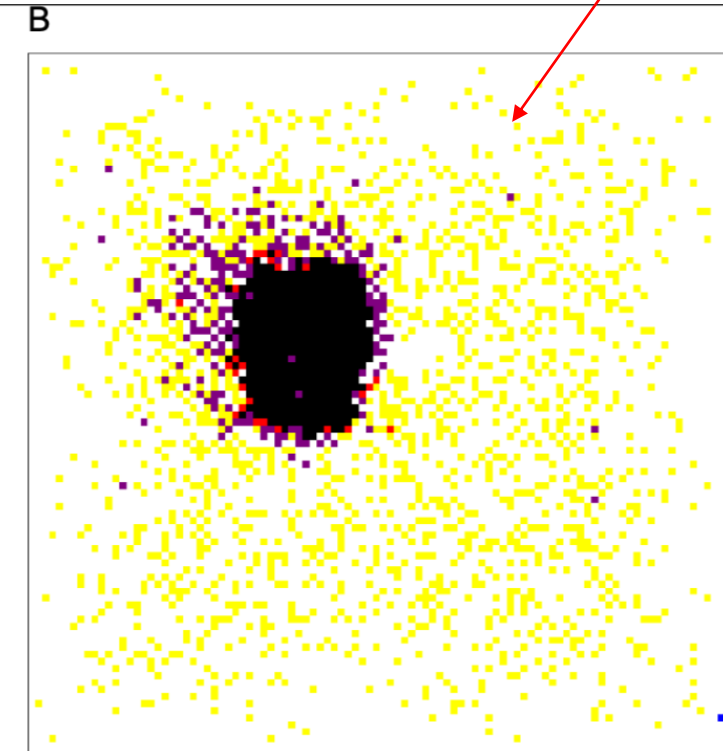


Associate Professor and Gordon S. Marshall Early Career Chair
Director, Center for Computational Modeling of Cancer

I plan to build off of her model of cancer cell / immune cells to include cell-state maps



This is Dr. Finley's computer-based model of cancer cells (black) being killed by immune cells (yellow, purple, red)



Cess, Colin G., and Stacey D. Finley. "Multi-scale modeling of macrophage—T cell interactions within the tumor microenvironment." *PLoS Computational Biology* 16.12 (2020): e1008519.

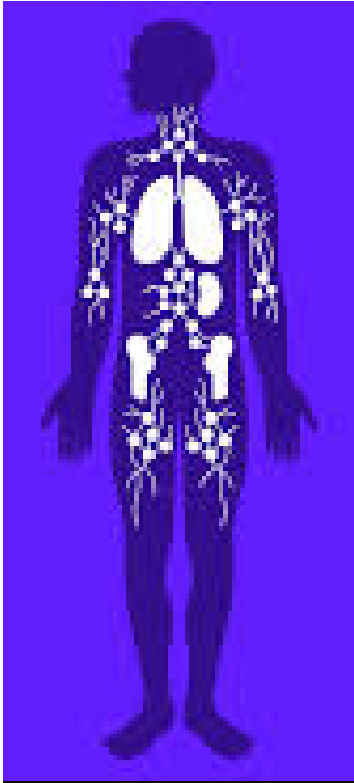
[FinleyLabUSC / Early-TME-ABM-PLOS-Comp-Bio](#)

Dr. Finley and many scientists share their codes on github so that other researchers (like me) can build off of their work

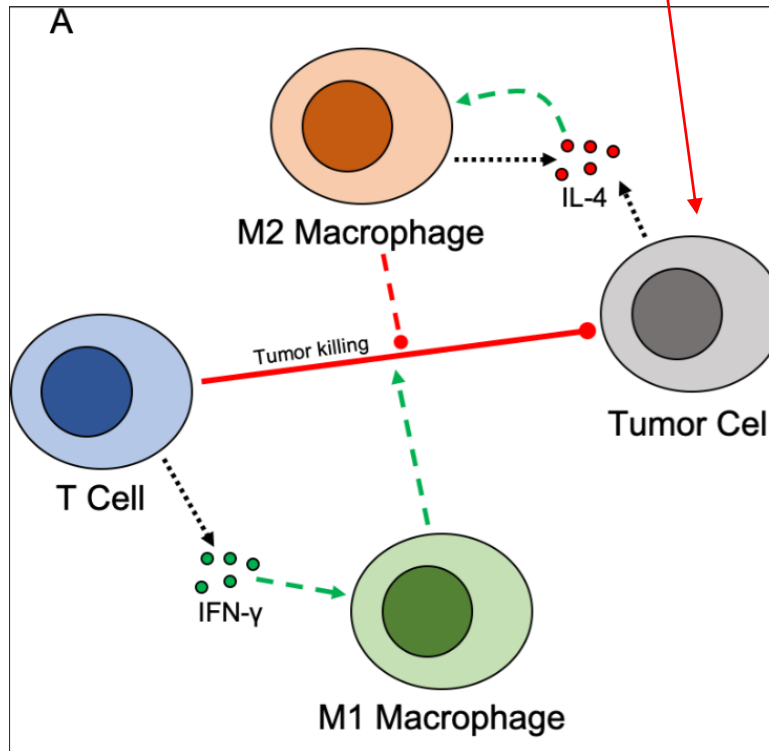
[Code](#) [Issues 1](#) [Pull requests](#) [Actions](#) [Projects](#) [Wiki](#) [Security](#) [Insights](#)

Long-term future work: Can computer-based models predict the best way to treat an patient's cancer?

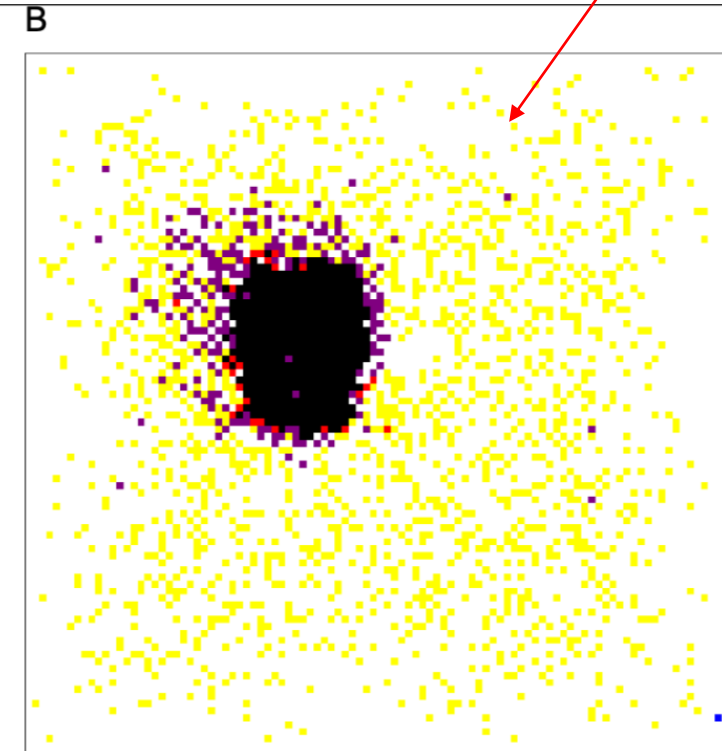
Obtain lots of information about an individual patient's cancer and immune system



Build an individualized model of cancer cell – immune cell interactions



Run simulations with different drugs and drug combinations to find the best treatment to control the cancer



Cess, Colin G., and Stacey D. Finley. "Multi-scale modeling of macrophage—T cell interactions within the tumor microenvironment." *PLoS Computational Biology* 16.12 (2020): e1008519.

Ambitious goals in digital precision medicine require a huge collaborative effort between researchers, coders, and physicians

Acknowledgements



- Laura Heiser
- Daniel Zuckerman
- Young Hwan Chang
- Joe Gray



- Heiser Lab
 - Sean Gross
 - Ian Mclean
 - Mark Dane
 - Nicholas Calitri
- Zuckerman Lab
 - John Russo
 - August George
 - Bassam Haddad (co w/ Reichow Lab PSU)
- Chang Lab
 - Luke Ternes

DAMON RUNYON
CANCER RESEARCH
FOUNDATION



