Automated Cell Segmentation in Julia

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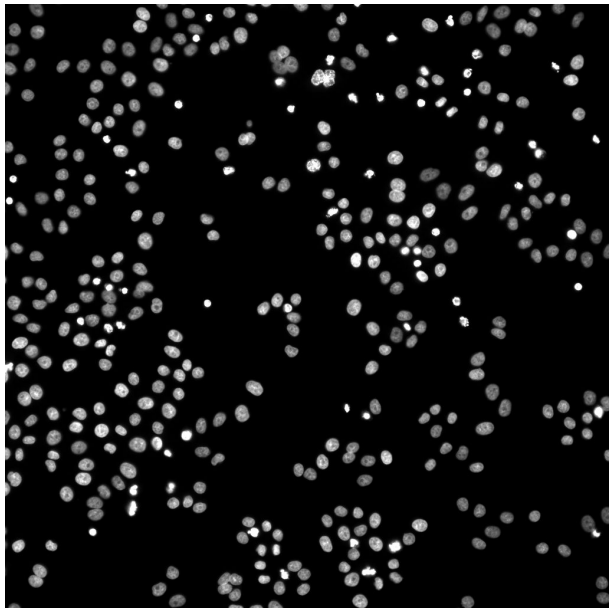
Cell Segmentation

- Traditionally, images of cultured cells for biological research were both acquired and reviewed manually
- However, it is becoming increasingly common to acquire large datasets with **tens of millions** of cells
    - Our dataset has 900 images of >220,000 cells
- Segmentation on this dataset takes ~30 minutes as currently implemented in Python
- A dataset with 10 million cells (which could be a single large plate) would require **~1 day**
- Many other tasks in image processing are similarly time-consuming but independent across images: easily parallelizable

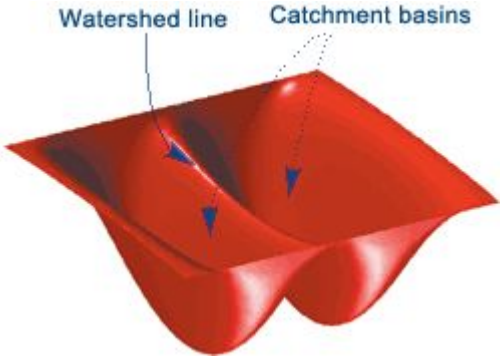
Our goal: **parallelize segmentation with Julia!**

Cultured cells with DNA stain



Marker-Based Watershed Algorithm

- Watershed algorithm: treats image as a topographic surface where bright pixels are peaks dark pixels are valleys
    - The algorithm floods from valleys: boundaries formed when water from different sources merge
- For cell segmentation, a marker-based version of the algorithm is commonly used
    - Cell nuclei act as markers from which topographic surface is flooded
- Add final thresholding step based on cell background to erode regions that meet (allow spaces between cells)



Parallelization

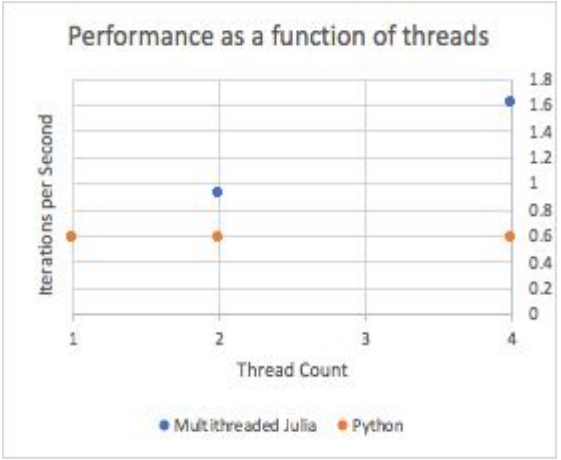
Three main approaches to parallelization in Julia:

- **Multi-threading**
  - Allows atomic operations to be conducted simultaneously
  - “Experimental” in Julia 1.0
- Multi-core or distributed processing
  - Divide operations across multiple CPUs
  - Limited by speed of the individual CPUs and speed of the memory access operations
- Coroutines (green threading)
  - Use “Tasks” to switch among multiple computations
  - Relies on a VM dynamic scheduler to allocate resources to particular tasks at different times

Performance Analysis

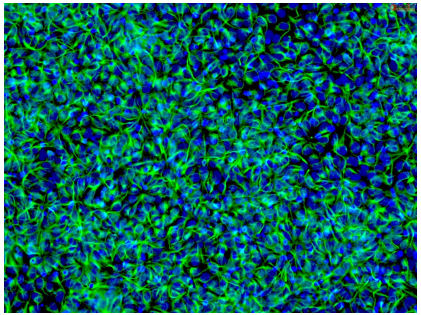
To process 900 1024x1024 .tif files:

Algorithm	Runtime
Native Python Code	25 min 47 sec, avg 0.58it/s
Julia Watershed - Unparallelized	25 min 36 sec, avg 0.59it/s
Julia Watershed - Parallelized (multi-threading, 4 threads)	9 min 19 sec, avg 1.61it/s
Julia Watershed - Parallelized (multi-threading, 2 threads)	16 min 3 sec, avg 0.93it/s
Julia Watershed - Parallelized (distributed)	Future directions

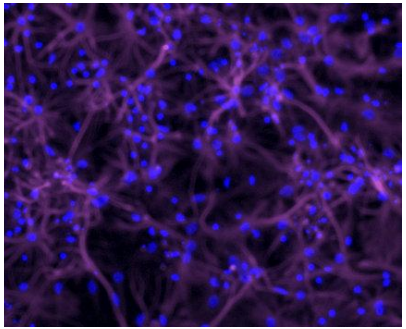


U-Net Based Segmentation: Motivation

- Marker-based watershed still has segmentation errors and requires a nuclear stain for the marker, which is not always available
- Works well enough for many cultured cells, but not well in tissues, where cells are three-dimensional
  - In addition, some cells have unusual shapes or imaging preparations

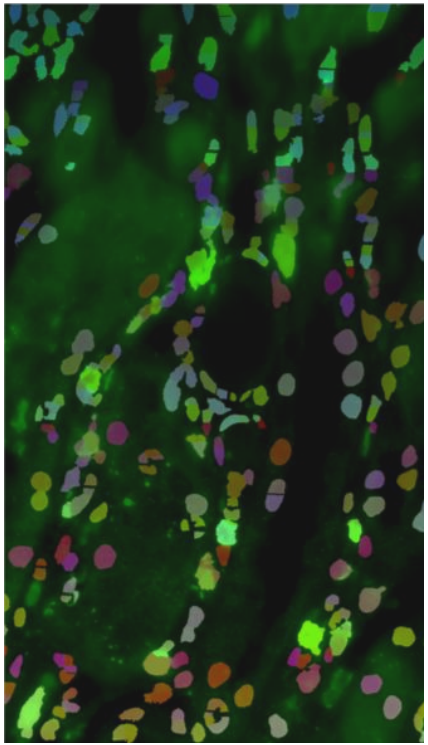


Dense cells

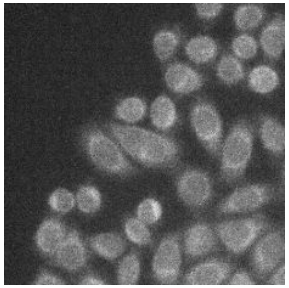


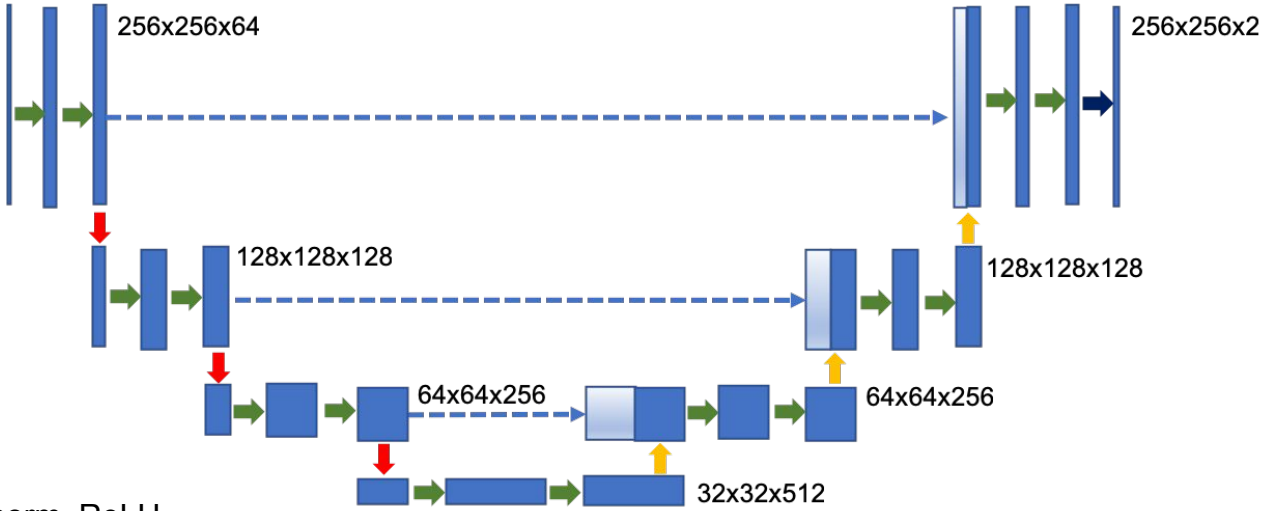
Neurons

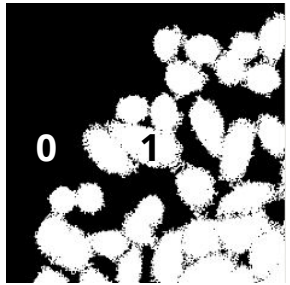
Tissue section



U-Net Implementation







conv 3x3, batchnorm, ReLU

Max pool 2x2

Bilinear upsamling

Conv 1x1, softmax

Limitations and Future Directions

- *Underway:*
  - Implementing distributed processing
  - Training the U-Net model
- Which of the three parallelization strategies offered by Julia is the most powerful and generalizable?
- How robust is DL-based segmentation compared to Watershed?
- Potential of transfer learning: Can we use the DL network to segment cells...
  - That are organized in dense structures?
  - That have unusual shapes (e.g. multinucleated, mitotic)?
  - In tissue sections?
- Can we parallelize other imaging operations in Julia?