Survey of Nature Methods

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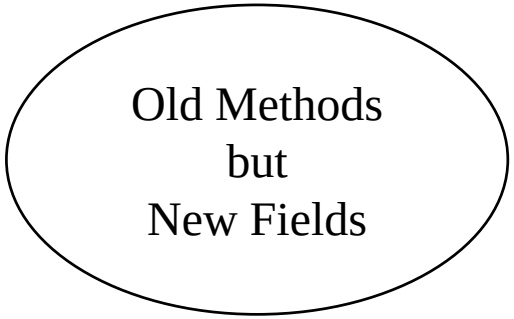
Outline

- Nucleus segmentation competition

- Bio-image Analysis Tools
  - Real-time cryo-electron microscopy data preprocessing
  - Interactive machine learning for (bio)image analysis

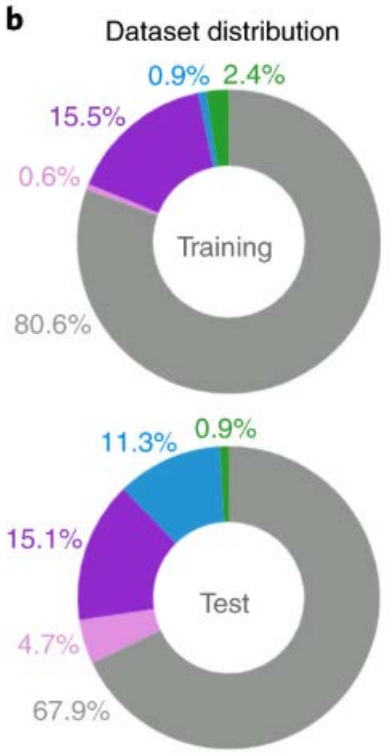
- Deep Learning Applications
  - Unified deep representation of amino-acid sequences
  - Data denoising with transfer learning
  - Particle picking in cryo-electron micrographs



Nucleus segmentation competition[1]

- 2018 Data Science Bowl[2]
- 37333 training data

Data Category



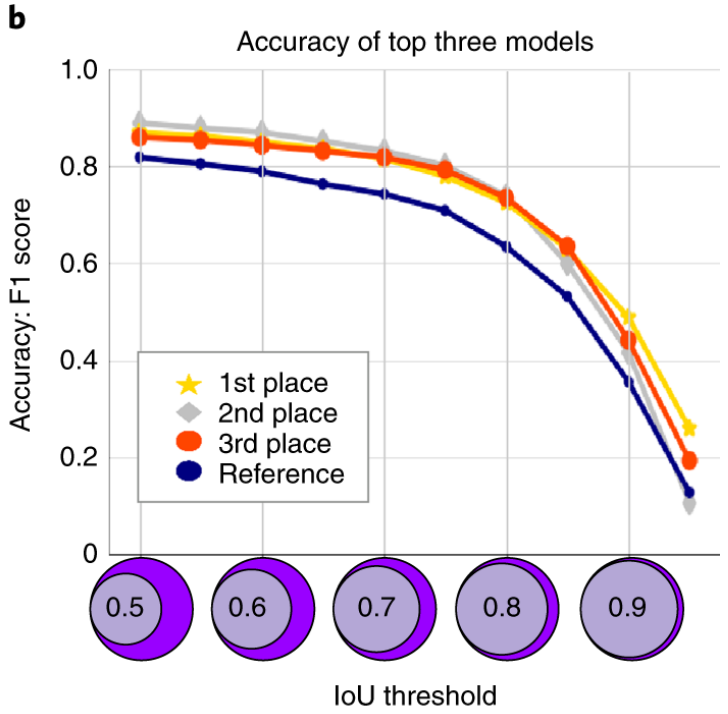
Data Distribution

1. https://www.nature.com/articles/s41592-019-0612-7#article-info
2. https://www.kaggle.com/c/data-science-bowl-2018

Nucleus segmentation competition

$$S = \frac{1}{|T|} \sum_{t \in T} \frac{\mathrm{TP}(t)}{\mathrm{TP}(t) + \mathrm{FP}(t) + \mathrm{FN}(t)}, \text{where } T = \{0.10, 0.15, \ldots, 0.95\}$$

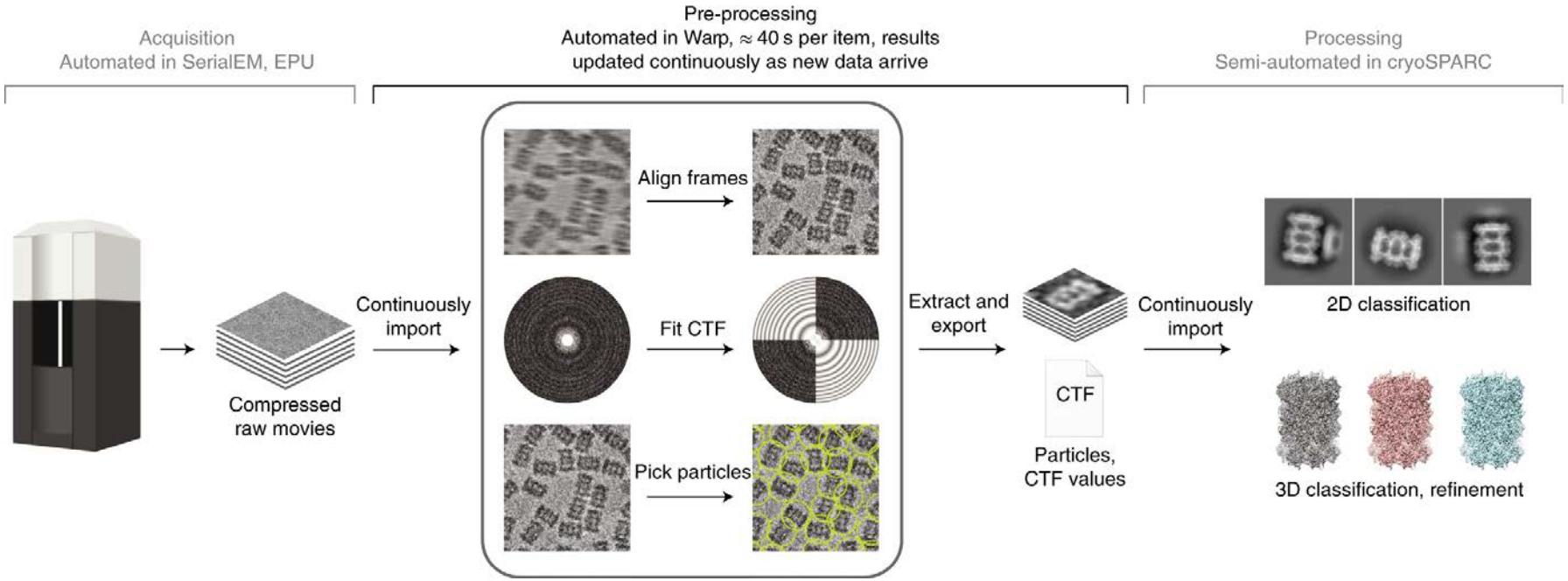
Team	Core model	Competition score
[ods.ai] topcoders[1]	32× U-Net/FPN	0.6316
Jacobkie[2]	1× FC-FPN	0.6147
Deep Retina[3]	1× Mask-RCNN	0.6141
CellProfiler	-	0.5281



1. https://github.com/selimsef/dsb2018_topcoders/
2. https://github.com/jacobkie/2018DSB
3. https://github.com/Lopezurrutia/DSB_2018

Warp

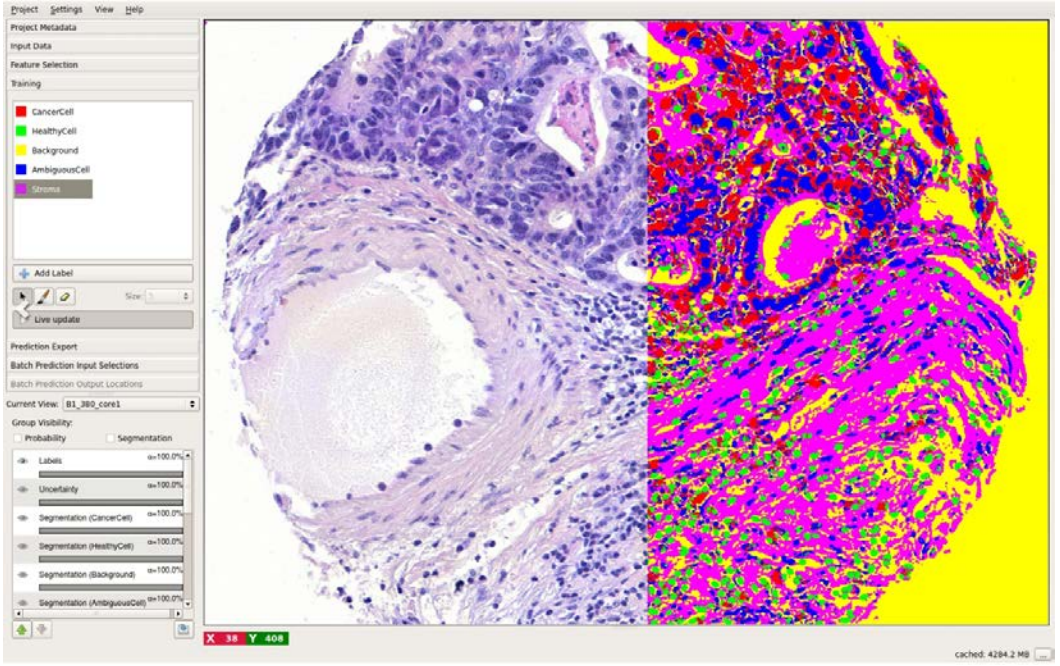
- Real-time cryo microscopy preprocessing[1]
- Automated Pipeline (~40s per item)
  - A nice GUI, an ongoing community, various functions, good compatibility



1. https://www.nature.com/articles/s41592-019-0580-y

Ilastik[1,2]

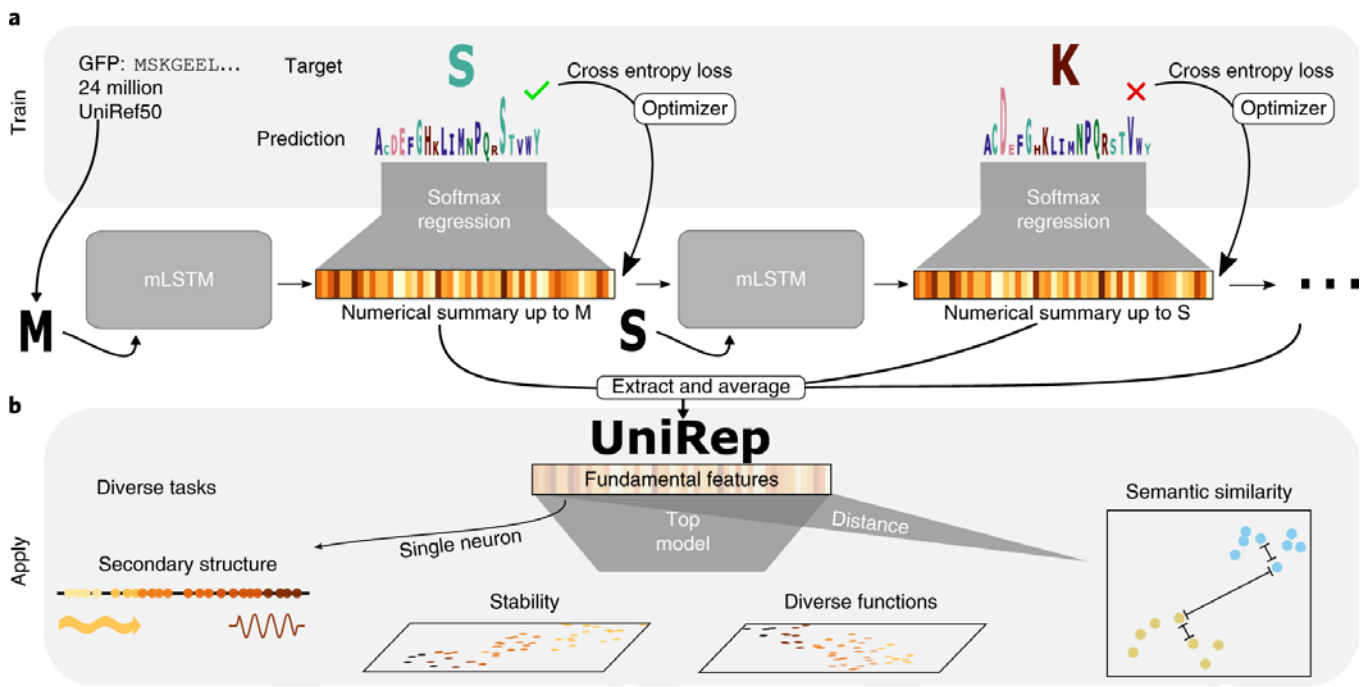
- An interactive learning and segmentation toolkit
  - No machine learning expertise required
- Support different analysis tasks with convenient annotation tools attached
  - Pixel classification, multicut, carving, object classification, counting, tracking…



1. https://www.nature.com/articles/s41592-019-0582-9#article-info
2. https://www.ilastik.org/index.html

UniRep[1]

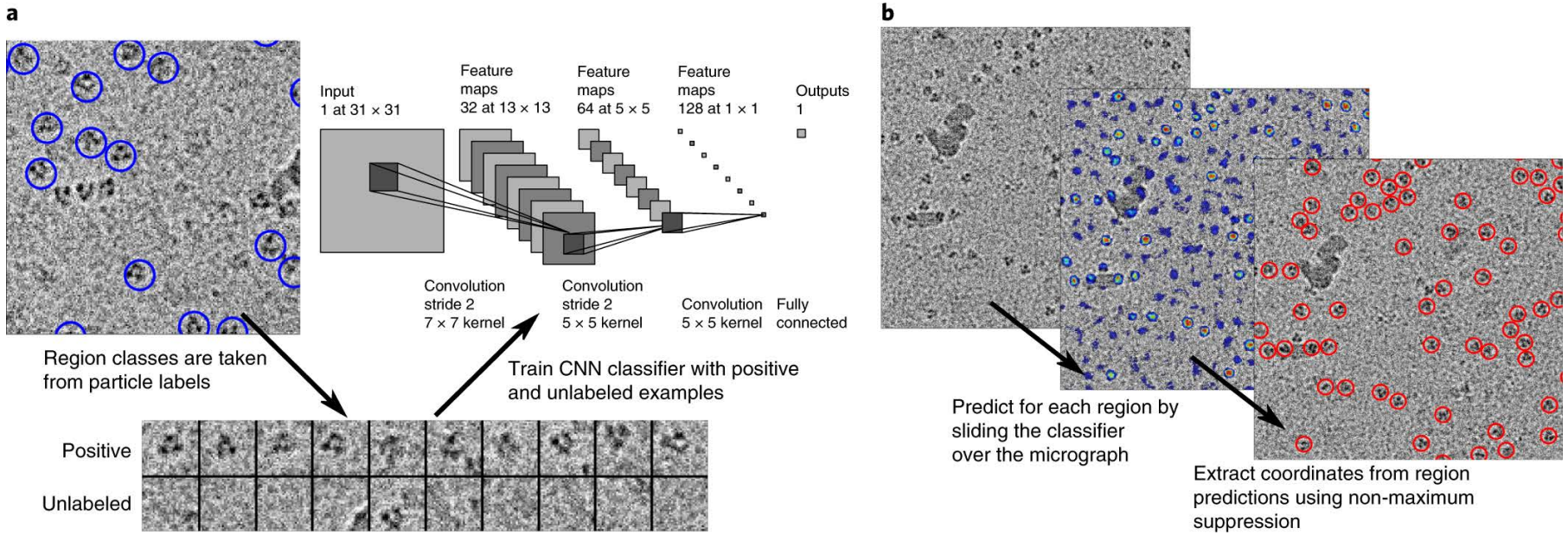
- A **unified** representation of amino-acid sequences
- Representations: features from mLSTMs
  - Support **various** down stream analysis
- Goal: sequence & function



1. https://www.nature.com/articles/s41592-019-0598-1#article-info

Topaz[1,2]

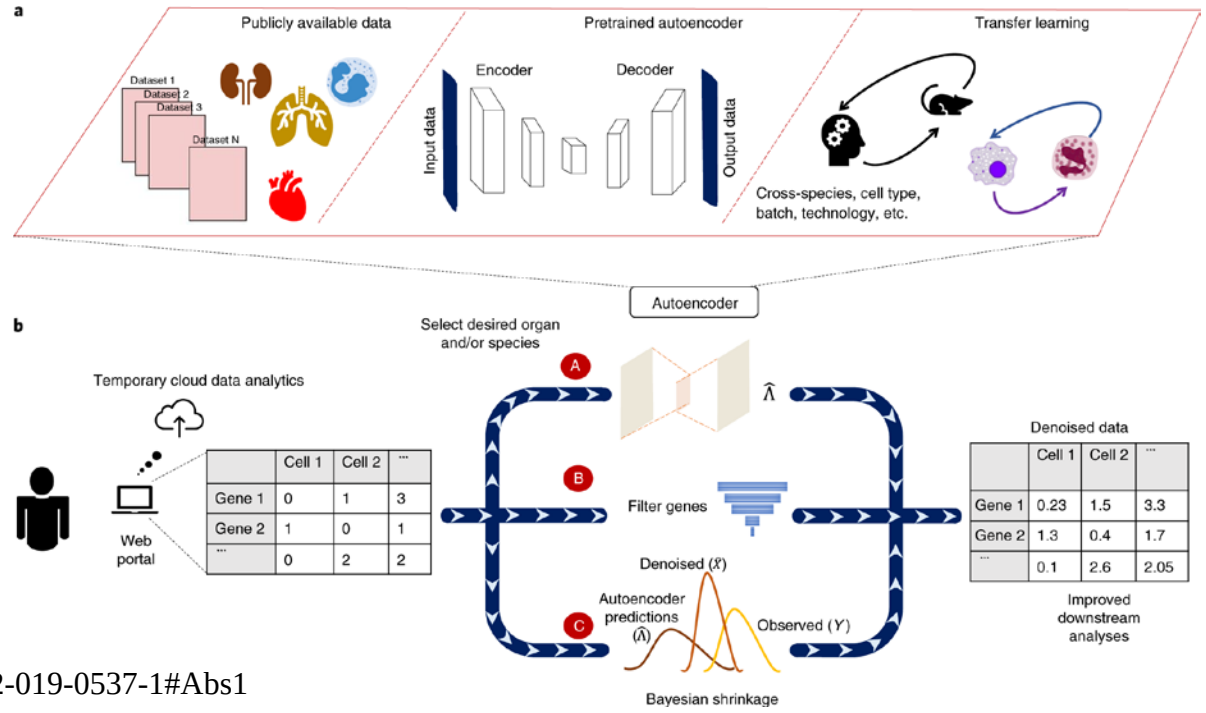
- A particle picking pipeline for cryo-electron micrographs
- CNN-based (quite like classical detection tools, such as Yolo)
  - Region-based classification(detection) + NMS



1. https://www.nature.com/articles/s41592-019-0575-8
2. http://cb.csail.mit.edu/cb/topaz/

SAVER-X[1]

- A denoising tool for single-cell transcriptomics
  - Autoencoder + Bayesian Shrinkage
  - Transfer learning (pre-trained)



1. https://www.nature.com/articles/s41592-019-0537-1#Abs1