Project Check-in #2

Project title: Cell Segmentation using a CNN-based classification algorithm.
Team name: Artificial in-cell-igence.
Members: Lexi Henrion (Ehenrion), Serena Agarwal (sagarw56), and Valeria Quero (vquero).

Paper we are replicating: U-Net: Convolutional Networks for Biomedical Image Segmentation by Ronneberger et al.

Goal: Cell segmentation, a technique for defining and distinguishing individual cells' boundaries in biomedical images, has benefited increasingly from DL approaches as opposed to traditional methods. The paper we chose introduced a CNN-based, state-of-the-art architecture for the cell segmentation problem, which led them to win the ISBI tracking challenge in 2015. Their architecture outperformed the prior best method (a sliding-window convolutional network) on the ISBI challenge dataset using just **30 annotated training images**. For reference, segmentation of a 512x512 image takes less than one second on a GPU.

Related Work

For a related article, we chose Understanding Cell Segmentation: A Key Tool in Spatial Imaging. This article provides a foundational understanding of cell segmentation and its importance in spatial imaging. Cell segmentation both distinguishes and defines individual cell boundaries within biomedical images, which in turn is helpful for researchers whose goal is to understand cell architecture. It helps with cell counting (relevant for biological assessments), morphological analysis (for understanding cell function), and cell tracking (monitoring of cell movement), useful for dynamic biological studies. The article elaborates on the two main approaches for cell segmentation: thresholding and watershed transformation (traditional) and DL-based approaches based on CNN architectures. For choosing the right method, they proposed the metrics of accuracy and adaptability to different imaging modalities and efficiency with various cell types. The article also provided some examples of different pipelines for cell segmentation performance compared to manual segmentation marking, which functioned as the ground truth for the sake of visual comparative analysis.

Current Implementations:

- PyTorch U-Net Implementation
- ArcGIS U-Net Guide

Data

Dataset: CTC Datasets: Pancreatic stem cells and Human hepatocarcinoma-derived cells.

- **Structure:** Folders include raw TIFF images (300 per folder), ground truth masks (`*_GT/`), segmentation masks (`*_ST/`), and error-corrected masks (`*_ERR_SEG/`).
- **Preprocessing:**
  - Convert "black" masks to visible formats by scaling pixel values (e.g., 0/1 to 0/255).
  - Align raw images (e.g., `01/000.tif`) with corresponding masks (e.g., `01_GT/man_track000.tif`).
  - Parse tracking text files (e.g., `"214 150 228 946"`)
- **Training Split:** 80% training, 20% validation.

Methodology

- **Architecture:**
  - **Contracting Path:** Repeated application of two 3x3 unpadded convolutions (ReLU) + 2x2 max pooling (stride 2). Doubles feature channels at each step.
  - **Expansive Path:** Upsampling with 2x2 transposed convolutions, concatenation with cropped skip connections, followed by two 3x3 convolutions (ReLU). Halves feature channels at each step.
  - **Final Layer:** 1x1 convolution to map 64-component features to class labels (cell vs. background).
- **Training:**
  - **Loss Function:** Weighted cross-entropy prioritizes cell edges to separate touching cells (common in microscopy).
  - **Batch Size = 1:** this maximizes GPU memory for the large input tiles.
  - **Optimizer:** SGD with high momentum (0.99) to stabilize the small batches.
  - **Data Augmentation:**
    - *Elastic deformations*: used to simulate the variations in tissue shapes
    - *Rotations/flips*:
    - *Intensity shifts*: for lighting variations.
- **Challenge:** overlap-tile strategy for large images mentioned in paper.

Metrics: To evaluate accuracy, we plan on using:

- **Warping Error**: Measures topological consistency (target: <0.0004, as in the original paper).
- **Rand Error**: Quantifies cell instance separation (target: <0.05).
- **Pixel Error**: Baseline pixel-wise accuracy (target: <0.07).
- **Intersection-over-Union (IoU)**: Overlap accuracy for segmentation masks (target: >75% for DIC-HeLa, >90% for PhC-U373).

Ethics

- **Broader Impact:** Accurate cell segmentation is essential for biomedical research but errors could lead to incorrect conclusions, which is a bigger concern in settings were a rapid solution must be delivered (e.g., in pandemic times, we strive to deliver a solution as quickly as possible and may sacrifice the appropriate testing / experiments).
- **Dataset Concerns:** Annotations in `*_GT/` may reflect lab-specific biases. Limited cell types (pancreatic/hepatocarcinoma) might reduce generalizability to other cell types.

Division of Labor

- **Data Preprocessing & Augmentation:** Serena Agarwal
- **U-Net Implementation:** Lexi Henrion
- **Training Pipeline & Evaluation:** Valeria Quero
- **Ethics & Documentation:** All members