

Pre-Trained models for Developmental Neuroscience

render nbviewer

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Pre-trained deep neural networks like ResNet are being used in various industries where they help make our lives easier. But these kinds of models are not yet being used for microscopic images on a large scale. With the right model architecture and training approaches, it is possible to get pre-trained models which would help in the research efforts of many. These models would help accelerate data driven research in developmental biology.

Hello devolearn

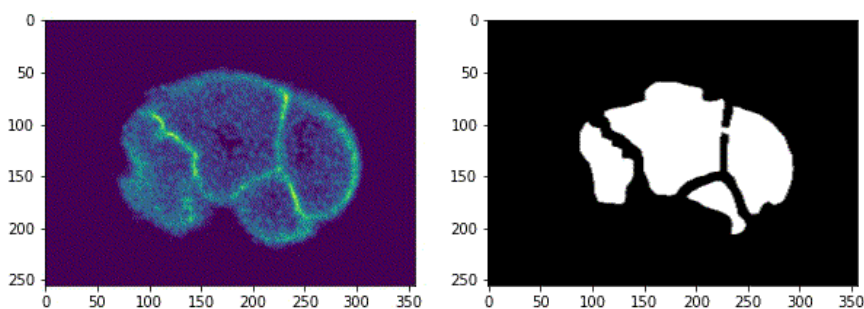


Accelerate data driven developmental biology research with computational learning models

Devolearn is a python library that helps accelerate data driven research on the C. elegans embryo by automating the process of collecting metadata from microscopic images/videos with the help of deep learning models. It's been already released on PyPI as `pip install devolearn`.

- [devolearn main repo](#)
- [devolearn quickstart notebook](#) on colab.

Deep segmentation model to segment the C. elegans embryo



Another segmentation model to extract features from a C.elegans embryo

- This model was trained on the [WormImage dataset](#) with manually labelled masks. You can download the segmentation dataset [from this link](#)
- The architecture is built on a [resNet18 backbone](#).
- Augmentations were made within a custom instance of the `torch.utils.data.Dataset()` with the help of [albumentations](#). We had to make sure that the input image and the mask went through the exact same augmentative transforms in the pre-processing stage.
- Interestingly enough, the model's output is less noisy than the augmented mask as seen below

□

Extracting metadata from embryo time-lapses using the ResNet18

The dashed lines are the predictions and the solid lines are the real annotations made by researchers. The model's performance is almost at par with that of the researchers. The orange line shows the predictions made by the deep learning model, while the blue line shows the real populations of the "A" lineage of cells.

- We trained a ResNet18 architecture to determine the population of cells of various lineages within the C. elegans embryo. All videos were sourced from the

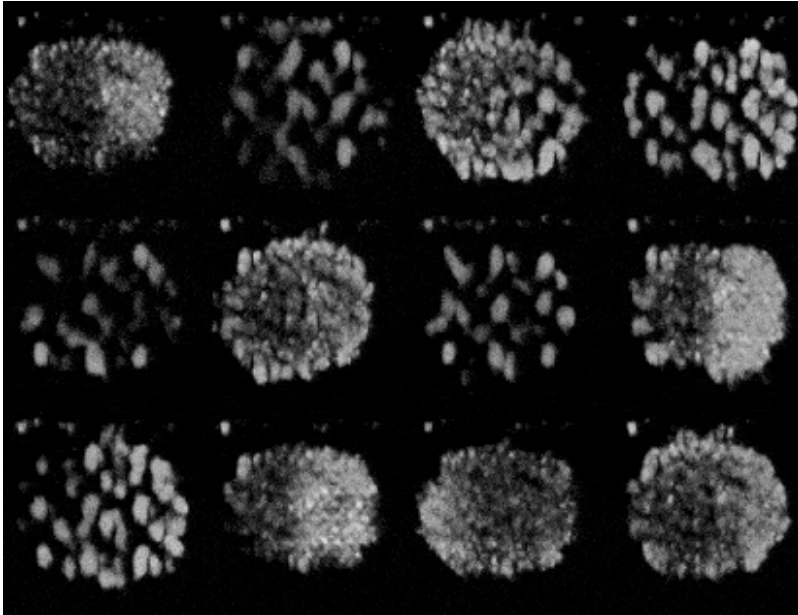
[EPIC dataset](#).

- The prediction for each frame of the model is a 1 dimensional tensor which contains the populations of the lineages ['A', 'E', 'M', 'P', 'C', 'D', 'Z'] in that order
- The model was trained on a reformatted version of the raw metadata, feel free to contact any of the members in this project for the reformatted data that was used for training.

Trained model making predictions on generated images from a GAN

□

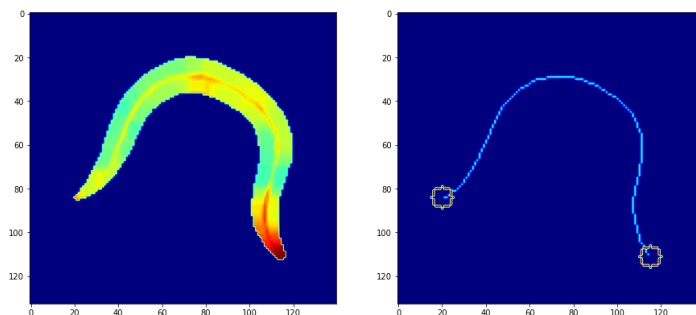
Generative Adversarial networks making "fake" embryo images



Worm movement tracking and metadata extraction

- This was built mostly using [openCV](#) with tools like thresholding and contour finding algorithms. It tracks and segments worms from video feeds specifically from the [Open Worm Movement Database](#)

- The cropped images of the worms were then used for time series analysis with the distance between the head and the tail as the parameter. The head and tail of the worm were also extracted using openCV.



Deep learning on cell position metadata of a *C. elegans* embryo * Training was done on the [EPIC dataset](#) * The model can predict the lineage name of a cell (or the cell name itself, depending on the time value) given it's position, size and time value. One can get a better understanding of the lineage tree of cells from the diagram given below:

- The model can be re-trained on any embryo instance available on the dataset.

Time series prediction on worm metadata

- Predicting the "curvature" of a worm's body from time series data containing the distance between the head and the tail of the worm's body.
- Note that the distance between the head and the tail is inversely proportional to the curvature. □

Principal component analysis on worm embryo metadata

PCA helped us visualise how cells descending from common ancestors are closer to each other in the lower dimensional space with the two principal components as the `x` and `y` axis.

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