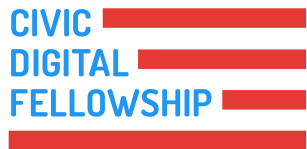


Using Machine Learning to Find Interesting Features of Cell Migration

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The Problem

- Researchers at NIDCR CBS spends hours at a time looking at videos of cells moving over two decades to find 'interesting features'
- What would machine learning mark as interesting?
- Applications to cancer research, difference in what's interesting between healthy and cancerous cells

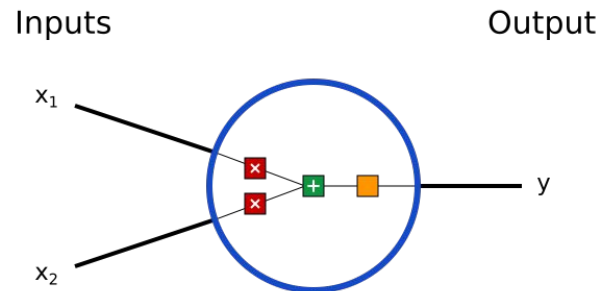


Why the Problem is Hard

- 'Interesting' is not a quantitative target
- 'Cellular migration' is also not a quantitative target, so interesting with respect to what?
- Machine learning benefits from lots of data, but biologists don't collect that volume
- So machine learning model must:
 - Be unsupervised
 - Have 'interesting' emerge organically from the model

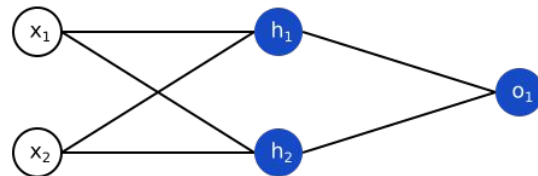
Background: What is a Neural Network

- Layers of 'neurons' that do a calculation and pass their information forward to the next layer
- Layers in between input and output are called 'hidden' layers, deep learning has multiple hidden layers



A single neuron multiplying inputs by weights and adding

Input Layer Hidden Layer Output Layer

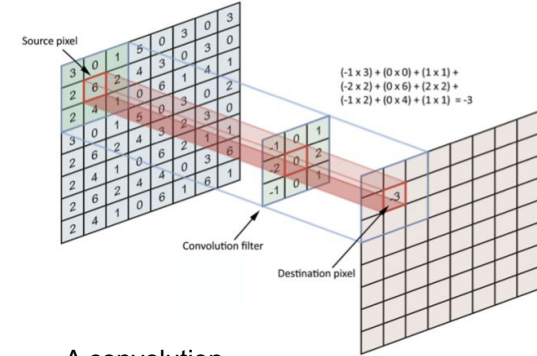


Input neurons passing data forward to hidden neurons, which then pass their data to an output neuron

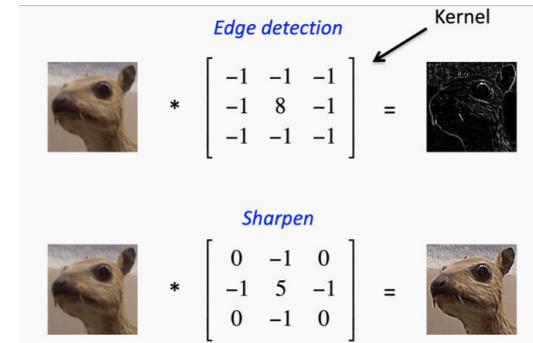
Source: Towards Data Science [1]

Background: Convolutional Neural Network

- Learn kernels to convolve against input image and extract features
- Many sequential convolutional layers create more and more complex features, extracting features from previous features
- These 'deep features' are hard to interpret from a human perspective



A convolution

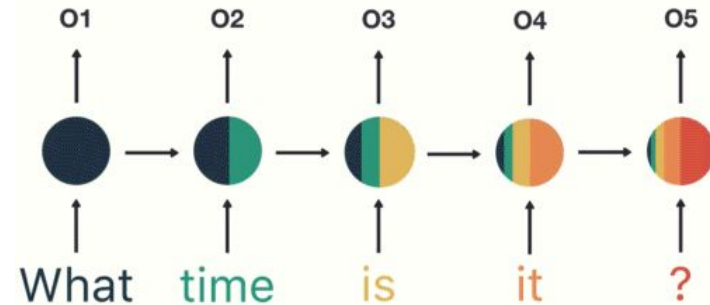
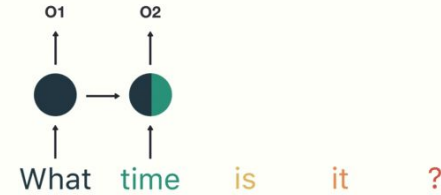
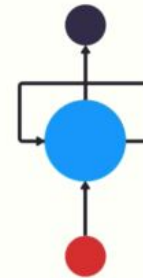


Effect of convolving filters against an image

Source: Towards Data Science [2]

Background: Recurrent Neural Network

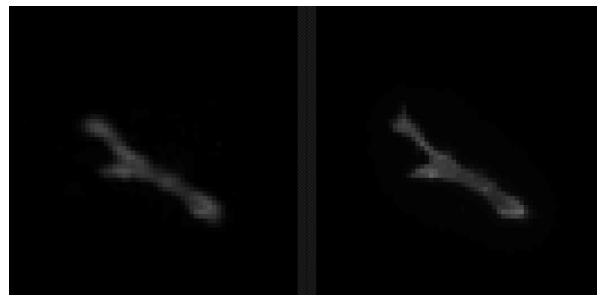
- Process input, produce output and hidden state
- Process next input along with hidden state from previous input via same network
- Keep passing hidden state forward to collect a numerical 'summary' of the inputs seen
- Very difficult to interpret final hidden state from a human perspective



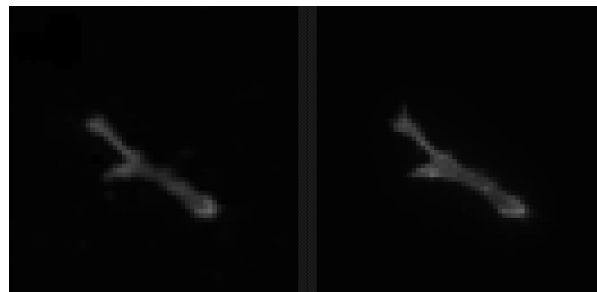
Source: Towards Data Science [3]

Convolutional-Recurrent Neural Network with Attention

- Get visual features from images via convolutional network, pass features to LSTM⁶ RNN³ and allow network to attend^{7,8} to images in the sequence differently
- Attention weights can be used as a measure of relative importance for each image in a sequence
- As target, generate last image via DCGAN^{4,5} image generator in order to capture all visible aspects of migration, including morphology and motion



Generated via dot product based attention^{8,9}
(prediction on left and real image on right)



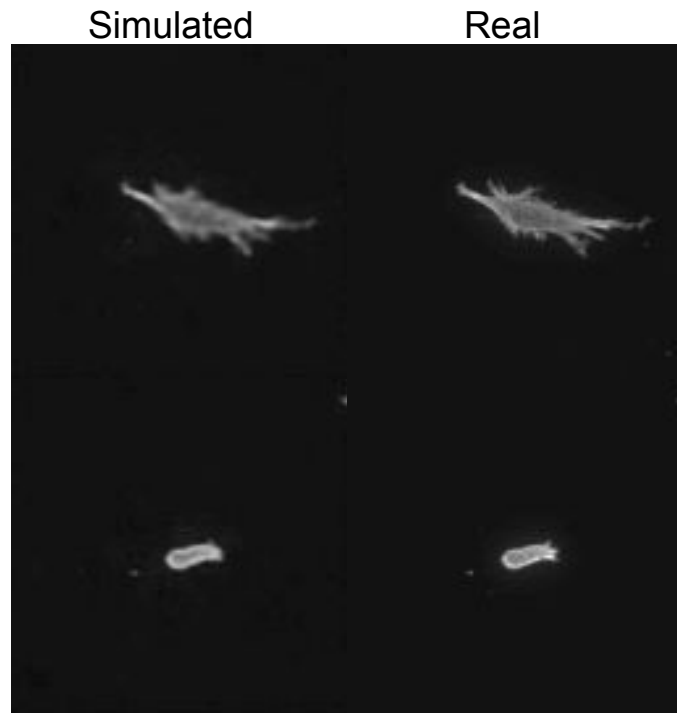
Generated via locality based attention using the concat method^{8,9}. Notice the improved shape of the bottom left point.

Kullback-Leibler Divergence

- What CRNN+Attention lacks:
 - Want average attention to be distributed evenly across input sequence
 - Want attention to only spike when very important
- Apply secondary loss to neural network based off Kullback-Leibler (KL) divergence of attention from uniform distribution
 - Used in variational autoencoders¹⁰, so there's precedence
- But found that due to location-based attention, found that sequences shifted by one had similar attention distribution shapes, not what we want

Convolutional Transformer

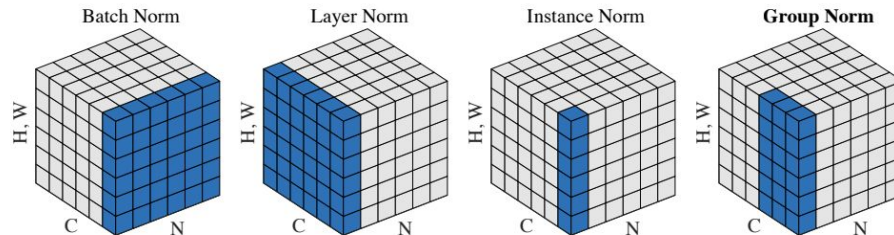
- Get more robust attention mechanism by using a Transformer¹¹
- Predict next sequence of images instead of single next image
 - Better captures cellular motion
- But much more complex so potentially will overfit more on small dataset



Example predictions of cell motion for a short subsequence. (left is simulation and right is real)

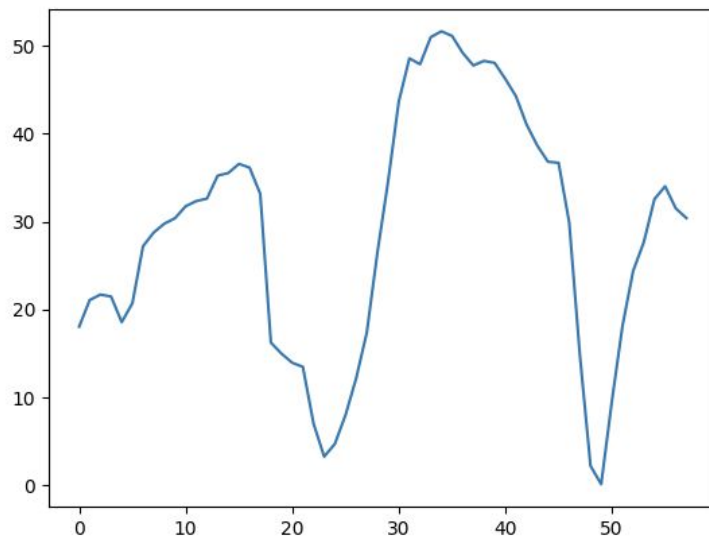
Batch Normalization in Convolutional Sequential Networks

- Batch normalization is essential for modern convolutional neural networks¹² (CNN)
- Since CNNs don't have a concept of time, hard to separate temporal and batch dimensions and still train effectively
- To predict sequence with Transformer, need to use teacher forcing¹³, which when generating messes up batch normalization exposed to temporal dimension
- Switch to group normalization¹⁴ in CNN feature extractor and DCGAN^{4,5}-based image generator solves problem since normalizes orthogonally to batch-temporal dimension



Normalizing Transformer Attention

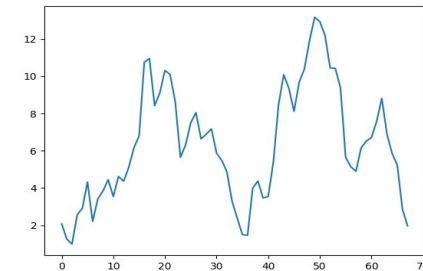
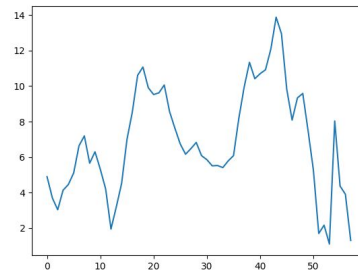
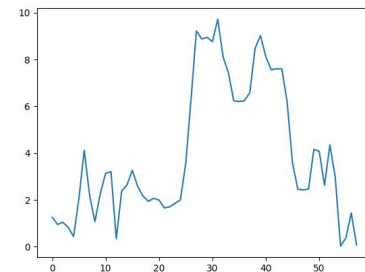
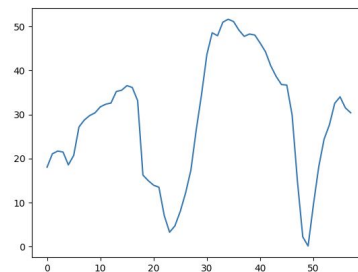
- Transformer attention still is on average unevenly distributed across input sequence
 - Instead of using KLD loss, normalize after training
- Normalize by smallest value in each sequence so relative importance within sequence captured
- Use log of attention probability as measure of information content in event¹⁵



Graph of attention-based importance, importance on y-axis and frame number (time) on x-axis

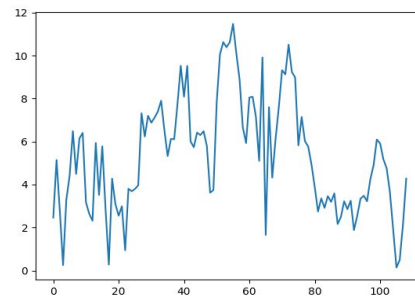
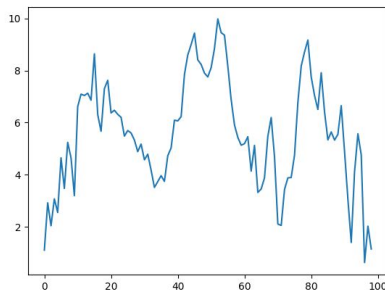
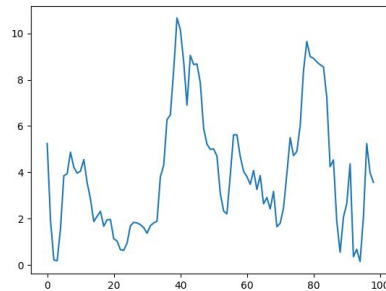
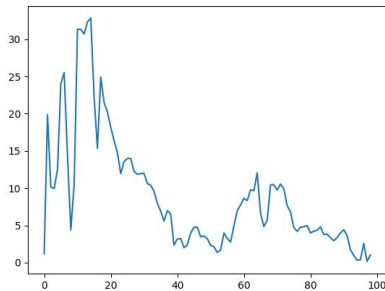
Attention from Different Networks

- Ideally, attention-based importance rating would be similar for different networks
- In practice, differences between networks are significant
- Suggests directly using attention weights as measures of importance may not be optimal



Graphs of importance for one video from different networks. Top left: large network trained for 1000 epochs, top right: small network trained for 500 epochs, bottom left: small network trained for 1000 epochs, bottom right: small network trained for 1000 epochs on shorter sequences

Worse Attention from Different Networks



Next Steps

- Better to get important subsequences
 - Classify importance based on degree of attention variation in short image sequence, likely more stable across different networks
- Use LIME¹⁶ and classification of important or not based off thresholding attention variance to see why a sequence is important
- Use Deep Continuous Clustering¹⁷ (or other unsupervised clustering technique) to group importance sequences for better understanding of what the network thinks is important

Limitations

- Only suitable for in-sample analysis, not a general model of cell migration
- Based entirely on videos so any features aren't necessarily meaningful from a proteomics or genomics perspective
 - And some of the model is memorizing changes that couldn't be predicted solely from observing previous motion
- Due to small dataset size, any features found aren't necessarily generalizable
- Still requires human interpretation of features either via direct analysis of important frames or via inspecting LIME¹⁶ output
- Work is pre-publication, pre-peer review, and not quite finished

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- Jess Mazerik - NIH OD
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Citations

(In order of appearance)

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and cell images courtesy of Andrew Doyle at NIDCR CBS