Speckle Pattern Clustering Strategies for Detecting Glaucoma

Seth Chatterton · Ian Kleinemolen · Josh Marchant Sandip Mondal

Background and Motivation

• Glaucoma leads **reduced vascular branching** in patients [ref].

Alterations in vascular → reduced tissue function

Reduced tissue function → alterations in vasculature

- **Potentially important biomarker** for diagnosis.
- High resolution vasculature imaging using optical coherence tomography (OCT) is technically challenging and expensive, **limiting widespread clinical** viability.

Background

• Instead of directly imaging vasculature, lasers could be used to scatter light off

of vasculature and produce unique network-specific speckle patterns.



(simulated) vascular network



(simulated) diffraction pattern



Hypothesis: clustering speckle data or relevant latent variables may enable characterization of higher ("healthy") vs. lower ("pathological") branching patterns.

Tools:

- K-Means
- t-SNE
- Frequency space clustering
- Variational autoencoder (VAE)

Data generation:

3 sets of "toy model" networks:



- Set 1: 1%:10%, Set 2: 3%:7%, Set 3: 5%:6% branching probability

Data split (for each set):

- Train: 75+75, Test: 25+25 pathological+healthy

Diffractio Python toolbox used for generating light diffraction patterns.

- Raleigh Summerfield approximation of diffracted light propagation

We want to see if there is sufficient signal within our generated diffraction data to distinguish the "healthy" from the "pathological" cases.

- Clustering (K-Means)
- t-SNE
- PCA

All of the above are from the scikit learn library

For each of the methods, we flatten the 400x400 far-field diffraction image into a vector of 160,000 elements.

Frequency Space

We want to explore whether transformation to the frequency space improves the ability to distinguish the "healthy" from the "pathological" cases, especially when diffraction values are normalized to simulate a more representative measurement.

- 1. FFT run on diffraction images, frequencies shifted, and magnitude extracted
- 2. PCA used for feature extraction
- 3. K Means clustering







VAE:

- Created custom torch-compatible datasets (see link here)
- VAE and vector quantized (VQ)-VAE: github.com/Jackson-Kang/Pytorch-VAE-tutorial
- Trained anew for each dataset



VAE:

- Aside: vector quantized (VQ)-VAE: github.com/Jackson-Kang/Pytorch-VAE-tutorial



Figure 1: Left: A figure describing the VQ-VAE. Right: Visualisation of the embedding space. The output of the encoder z(x) is mapped to the nearest point e_2 . The gradient $\nabla_z L$ (in red) will push the encoder to change its output, which could alter the configuration in the next forward pass.

VAE: How should we use the **16x16** latent space?

Ideas for clustering:

Global metric (average, max)

Most critical pixels in the latent space

```
for ii in range(xdim):
for jj in range(ydim):
    z[:,ii,jj] = 0
    xhat_test = model.decoder(z)
    recon_loss = mse_loss(xhat_test, x)
```

"LIME"-esque interpretability strategy...

"Loss effect landscape"





Results: a baseline intensity approach

Total diffraction intensity increases as branching probability increases, because there is more transmission.



Results: a baseline intensity approach

Total diffraction intensity increases as branching probability increases, because there is more transmission.



Results: t-SNE

Visual inspection: does it look like we will be able to separate the two classes?



Dataset 1: high separation

Dataset 2: some separation

Dataset 3: little separation

Results: k-Means



Dataset 1: high separation Test Accuracy: 100.00% Train Accuracy: 100.00% Dataset 2: some separation Test Accuracy: 100.00% Train Accuracy: 98.00% Dataset 3: little separation Test Accuracy: 52.08% Train Accuracy: 52.00%

Results: PCA



Dataset 1: high separation

Dataset 2: some separation

Dataset 3: little separation

Results: PCA Visualization

Principal components for Dataset 1 (high separation)



Principal components for Dataset 3 (low separation)



Results: Clustering in Frequency Space

Data1

× Cluster 0

× Cluster 1

0

PCA Feature 1

healthy

pathologica

50

-40

×

-100

-50

-150

*X

150

100

1500 -× Cluster 0 × Cluster 0 × × Cluster 1 Cluster 1 1000 ** healthy 1000 healthy × pathological pathological 1000 750 500 500 500 **** ** * **** 250 -250 -500 -500 ×* -500 -1000 -750 -1000 -1500 -1000 -500 500 1000 1500 2000 -1000 -500 500 1000 -1000 -750 -500 -250 250 500 ò ò PCA Feature 1 PCA Feature 1 PCA Feature 1 × Cluster 0 60 -60 × Cluster 1 healthy 40 pathological × Fourier 20 CAF Q -20 -20 -20 -40 × Cluster 0

**

PCA Feature 1

× Cluster 1

-60 -

healthy

-60 -40-20 0 20 40 60 80

pathological

Data2

×

×

×

-60

-40 -20

Data3

× Cluster 0

Cluster 1

healthy

XX

750 1000

*1

20

0

PCA Feature 1

××

40

60

pathological

Spatial

Results: Clustering in Frequency Space with Normalization



Autocorrelation of a signal can represent the structure or "memory" of a signal which could provide additional information on magnitude and phase of fourier transform.



Data1 PSD using Normalized and mean-subtracted Diffraction



Autocorrelation of a signal can represent the structure or "memory" of a signal which could provide additional information on magnitude and phase of fourier transform.



Data1 PSD TEST data using Normalized and mean-subtracted Diffraction



Data2 PSD using Normalized and mean-subtracted Diffraction

Data3 PSD using Normalized and mean-subtracted Diffraction



Autocorrelation of a signal can represent the structure or "memory" of a signal which could provide additional information on magnitude and phase of fourier transform.



Data1 Autoencoder of Fourier Space With Normalized Diffraction (1st Attempt, needs refinement)



Set 1 - **not** normalized:

Input



Reconstructed



16x16 latent space

15 epochs

Set 1 - **not** normalized:





Set 1 - normalized:





Set 2, not normalized







Set 3, not normalized





Set 1, normalized, larger latent space (6x16x16):

Input



Reconstructed

6x16x16 latent space

15 epochs

Set 1, normalized, larger latent space (6x16x16):



Conclusions + Next Steps

- We used several unsupervised methods to see if differences in the far-field speckle pattern of vasculature with different branching probabilities could be identified
- Some techniques, like t-SNE and k-Means can be used to identify different clusters of vein branching if the difference between "healthy" and "pathological" branching is large enough (and depending on normalization)
- Variational Autoencoders may underperform in our experiments due to the limited amount of data we had access to. Further work is needed to optimal parameters (number of encoding layers, latent variables) and latent variable characterization.

Possible next exploration: Conditional Diffusion Model

Can we generate the true vasculature using the far field speckle pattern?



- Current step of vasculature image
- Error of noisy vasculature speckle pattern and true vasculature speckle pattern

We think this might work because although we do not have any information about the phase of the light, we do have a good amount of prior knowledge in that we know what vasculature is supposed to look like.