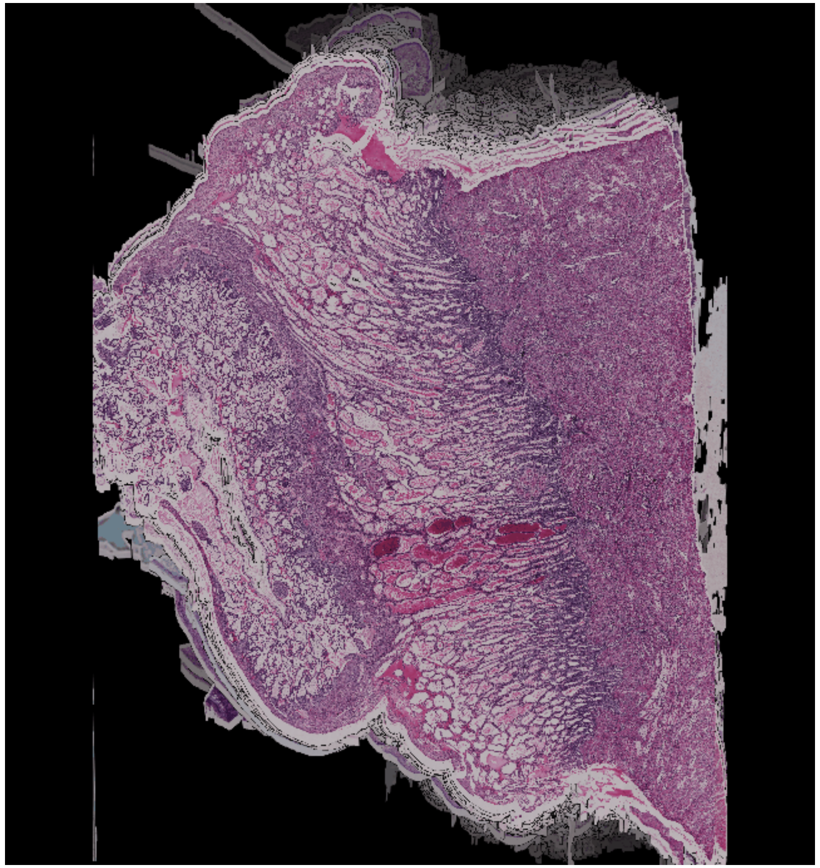
Creating a 3D Virtual Atlas of the Uterus



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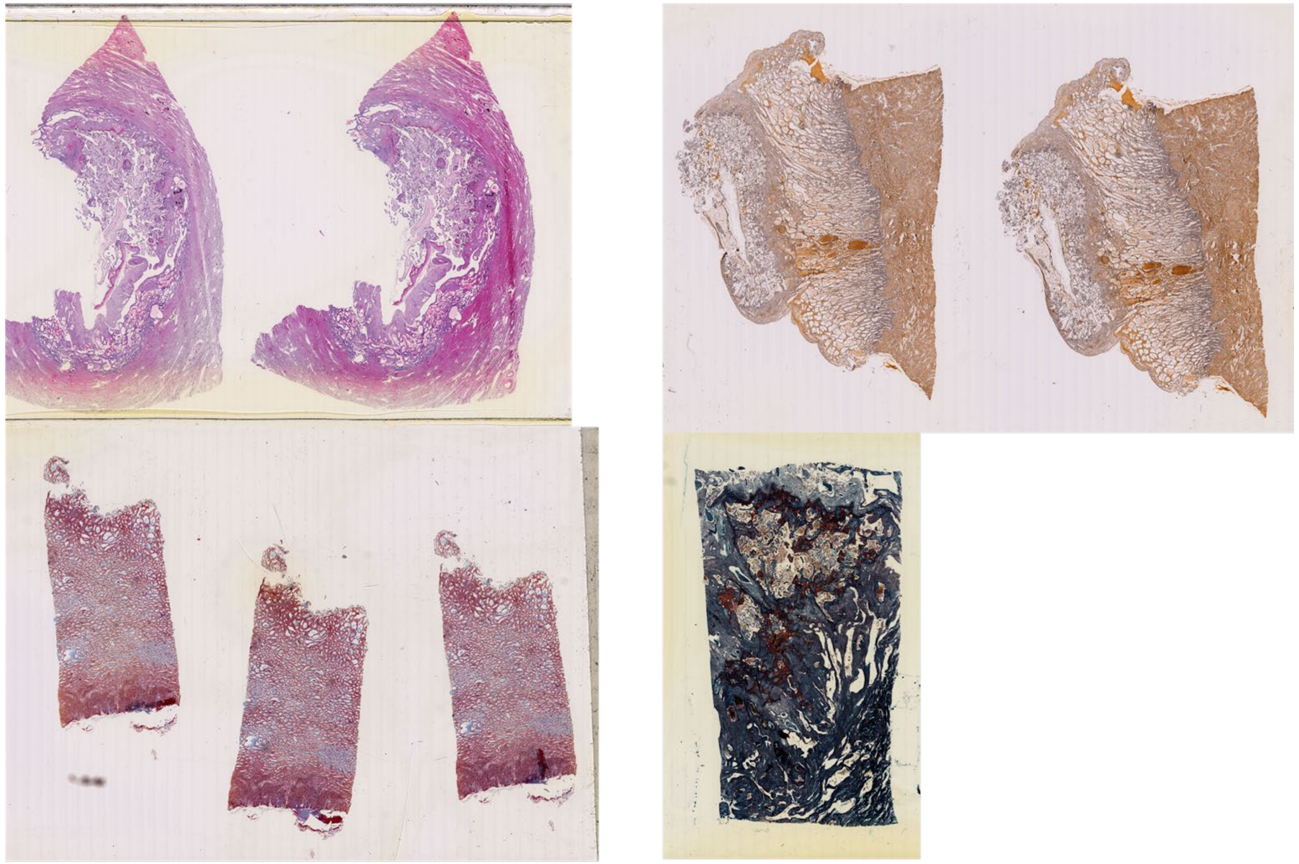
Associate Professor Alys Clark, ABI
Associate Professor Jo James, FMHS

Overview of project

- Masters project with the Placenta Modelling Group at the Auckland Bioengineering Institute
- Historical data set of uterine samples at varying gestations have been digitised
- Project outcomes:
  - Samples have been recreated into 3D reconstruction
  - Segmentation of key tissue types



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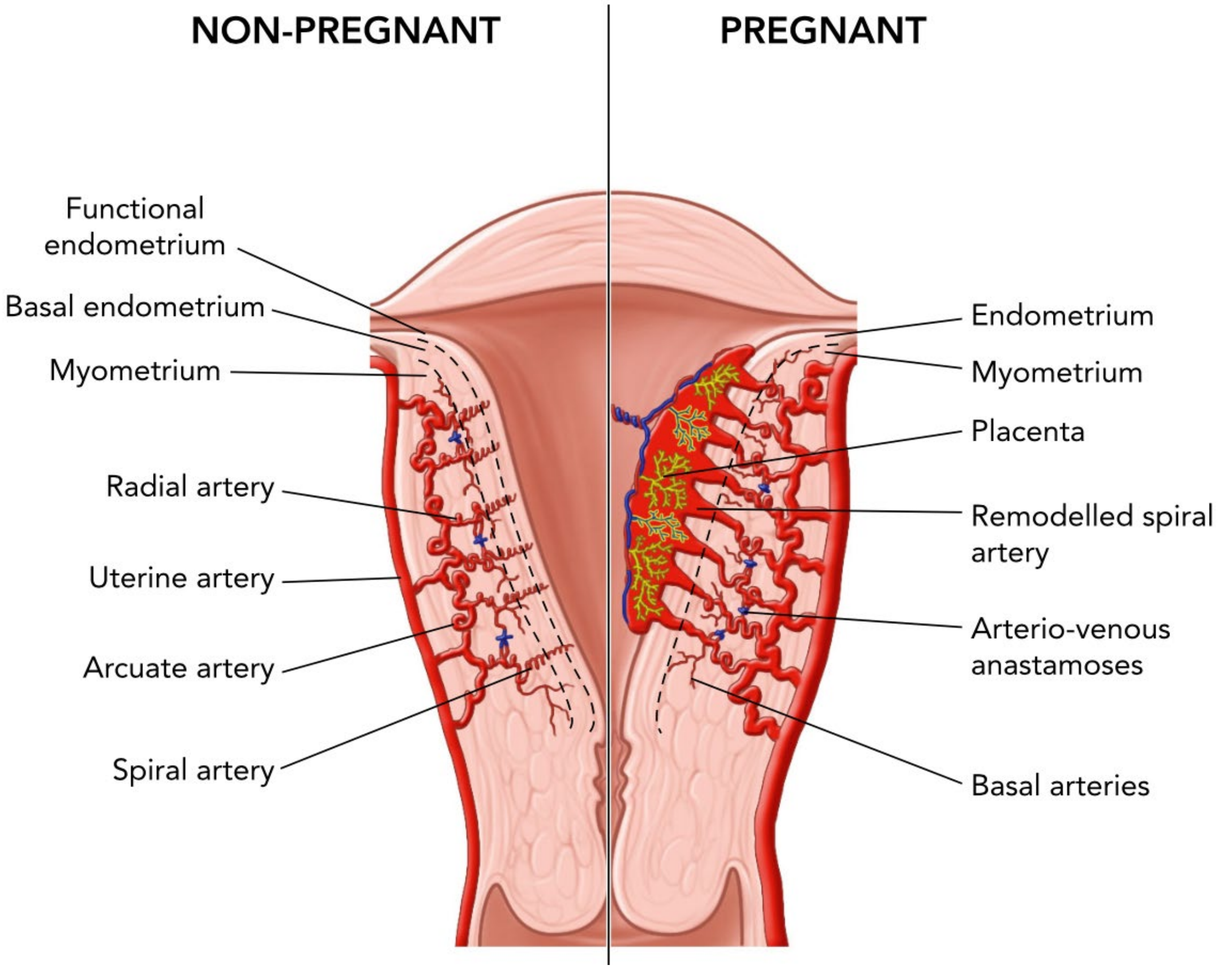
Why is this work important?

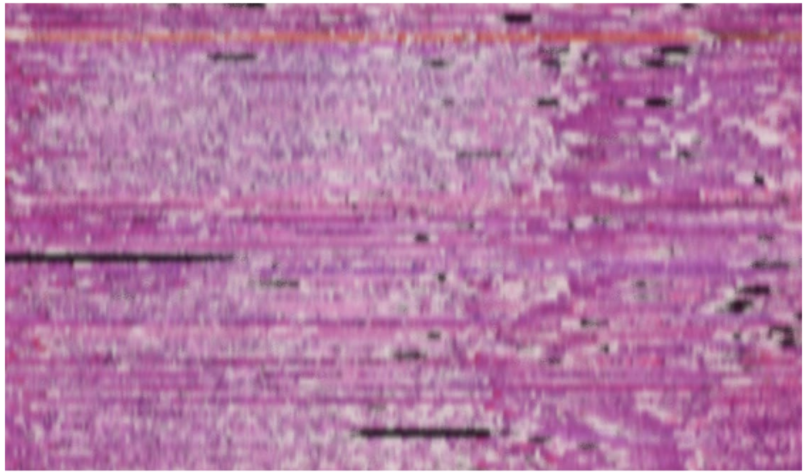
- One of the least understood organs in the human body
    - Mostly qualitative
    - Animal models or low resolution non-invasive imagery insufficient
- Fetal conditions are not well understood
    - e.g. Fetal Growth Restriction (FGR) is poorly diagnosed during pregnancy
- Visualisation is key to quantitatively describing the uterine vasculature



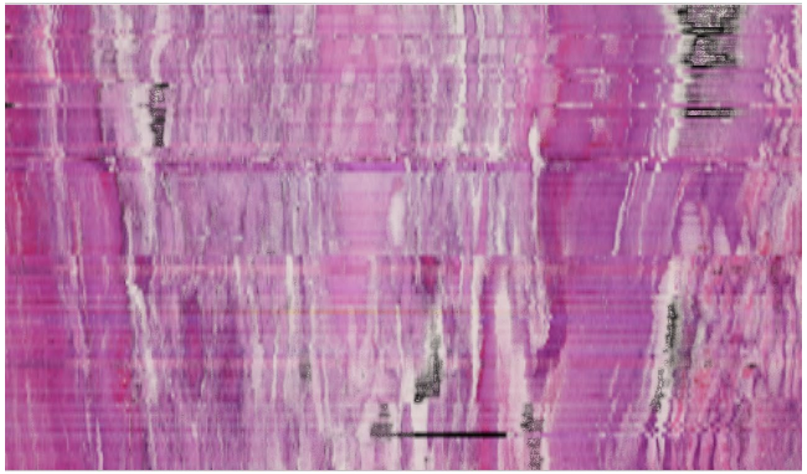
J. L. Joana, L. W. Chamley and R. A. Clark, "Feeding Your Baby In Utero: How the Uteroplacental Circulation Impacts Pregnancy," *Physiology*, vol. 32, pp. 234-245, 2017.

Registration

- Features exhibit large linear and nonlinear deformations
  - Linear registration minimises translation and rotation errors
  - Non-linear registration is the abstract correction of visual continuity
- Key to alignment is how you measure sample deformations



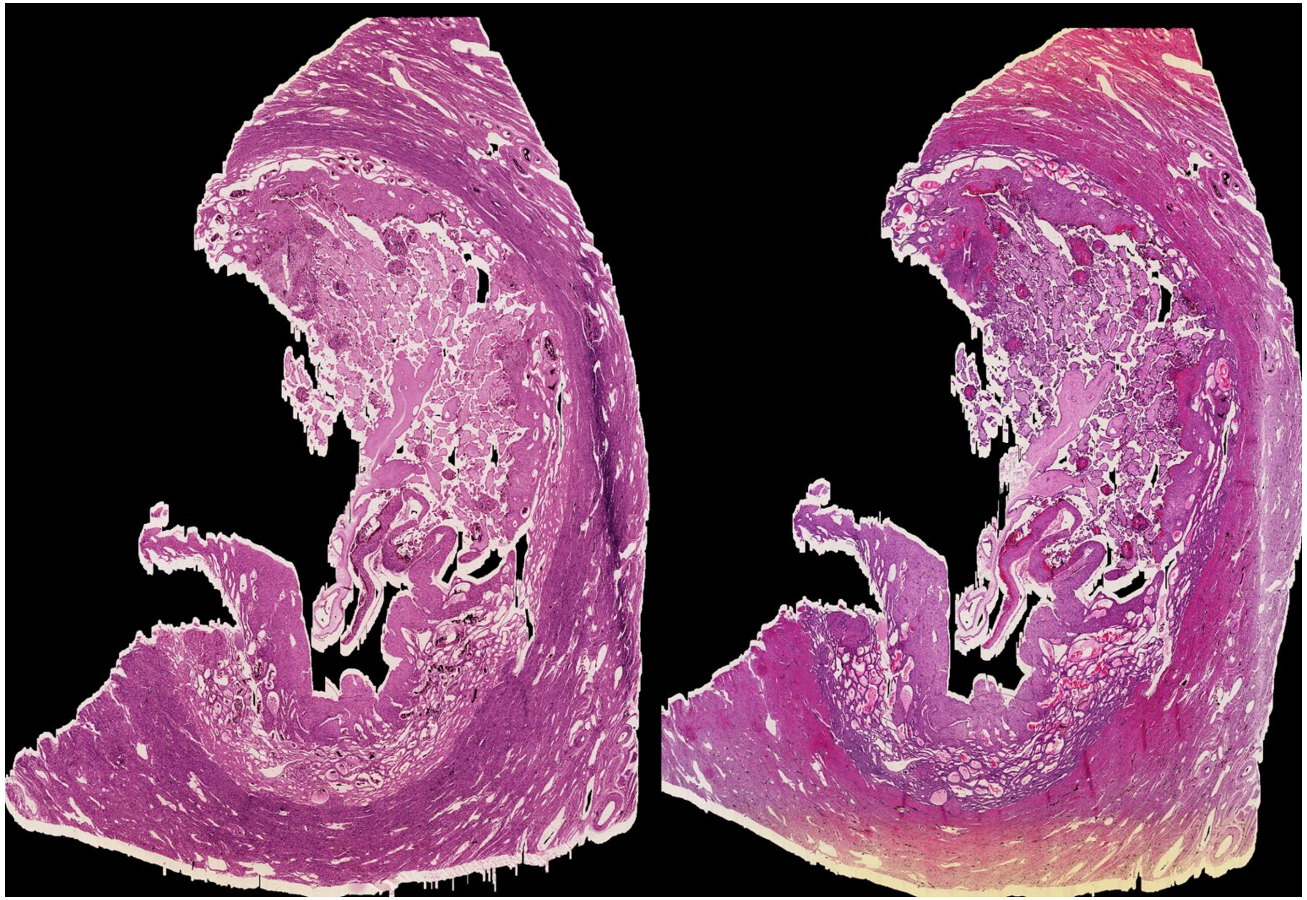
Unregistered specimen



Registered specimen

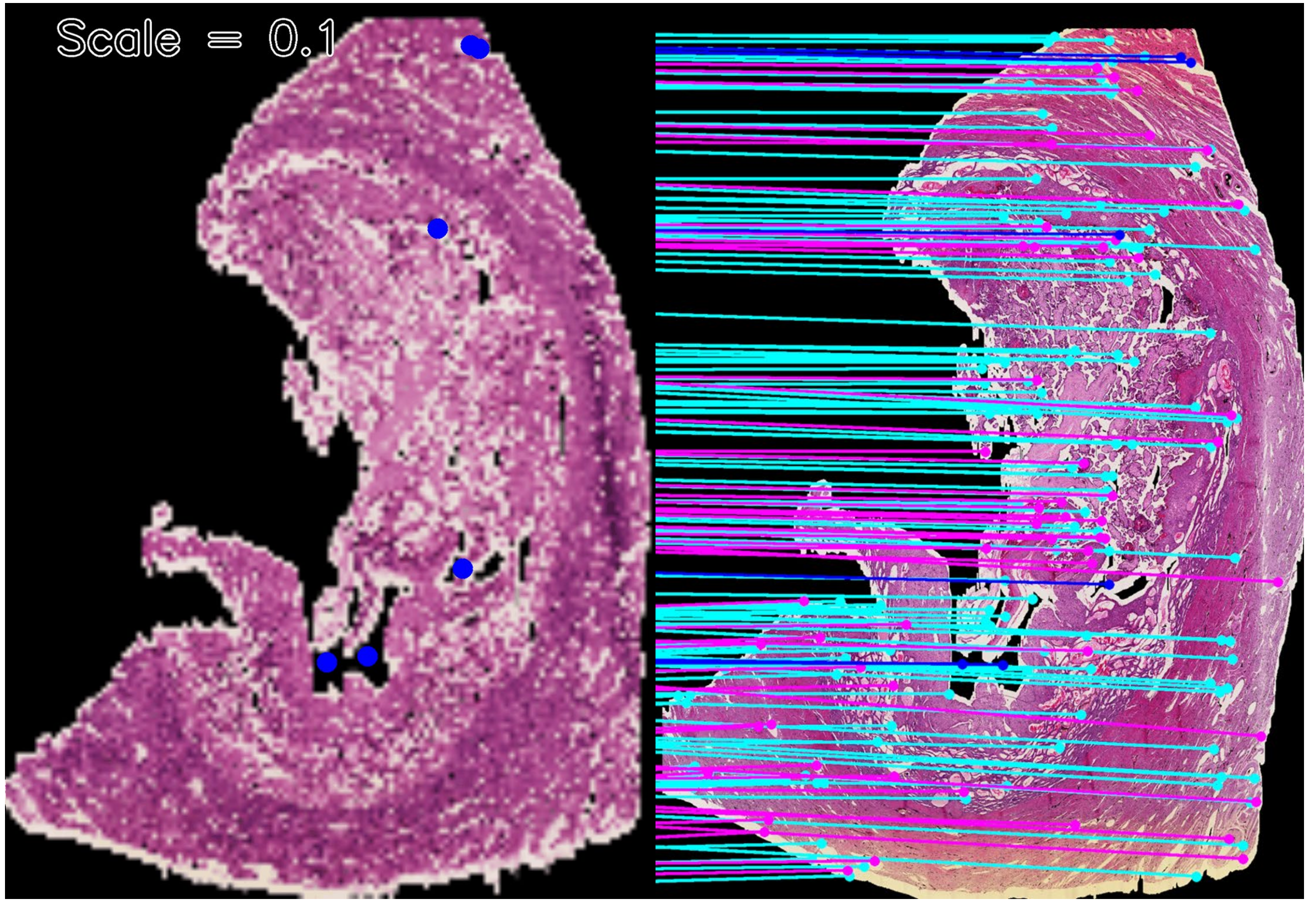
Linear Registration, Feature finding

- Features represent the most robust method for identifying the relative positions of the samples
- Feature finding performed by SIFT in particular to rotation invariance []
- Naive SIFT is not useful or intuitive
- “Spatial cohesiveness” is finding features which are biologically relevant



Linear Registration, Feature finding

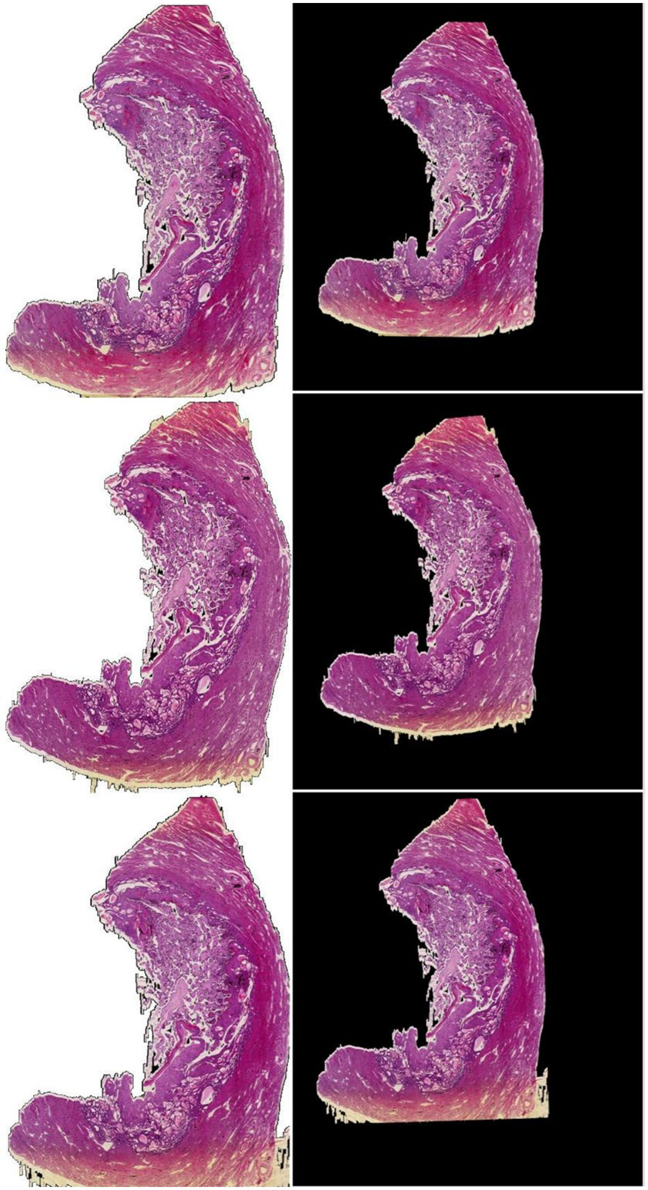
- Manual feature identification is considered “gold standard”, however very slow and high variability
- Codified the process of manually finding features: find prominent feature first and use those to find other features
- Multi-resolution feature search using low res/high strength features to initiate feature searching



Linear Registration

- Linear registration minimises rotation and translation of the **features**
- Performed using scipy.optimise.minimize
- If not below threshold, features of highest error removed and repeated

```
while True:
        featureTran = translate(features)
        featureMod = rotate(featureTran)
        err = errorPerFeature(FeatureMod)
        if err < threshold:
                break
        else:
                features =
```



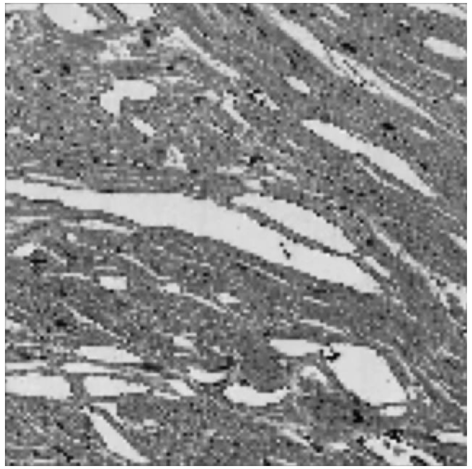
0th image, Reference image
Translation (pixels moved from top left) = (0, 0)
Rotation (angle anti-clockwise, centre of rotation) = 0°, (0, 0)

1st image, aligned to 0th image
Translation = (127, 1)
Rotation = 5.4°, (672, 1022)

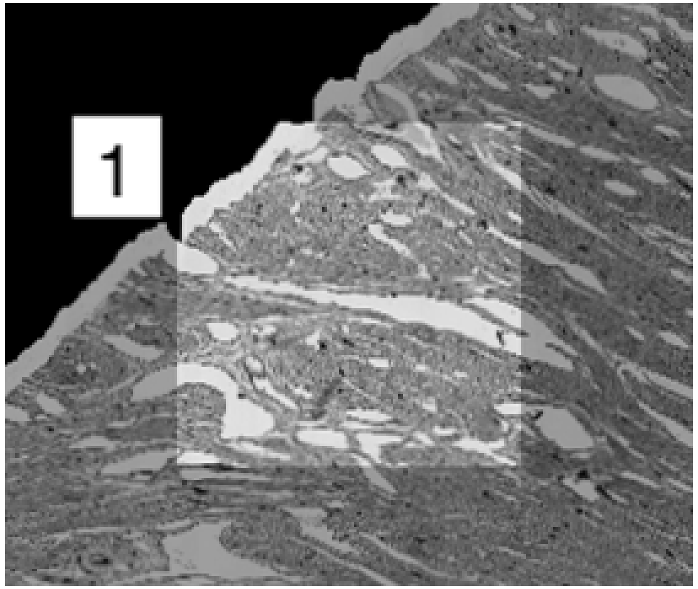
2nd image, aligned to 1st image AFTER translation
Translation = (135, 87)
Rotation = 1.7°, (703, 825)

NL Registration, Feature tracking

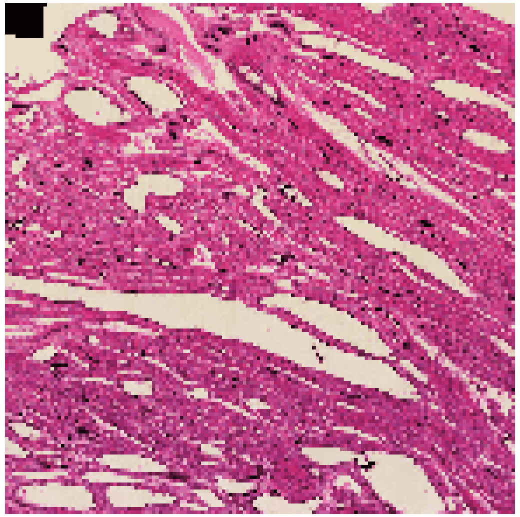
- Finding spatially cohesive features as well as visually similar features
- Uses Phase Cross-Correlation to minimise the visual differences



Reference section



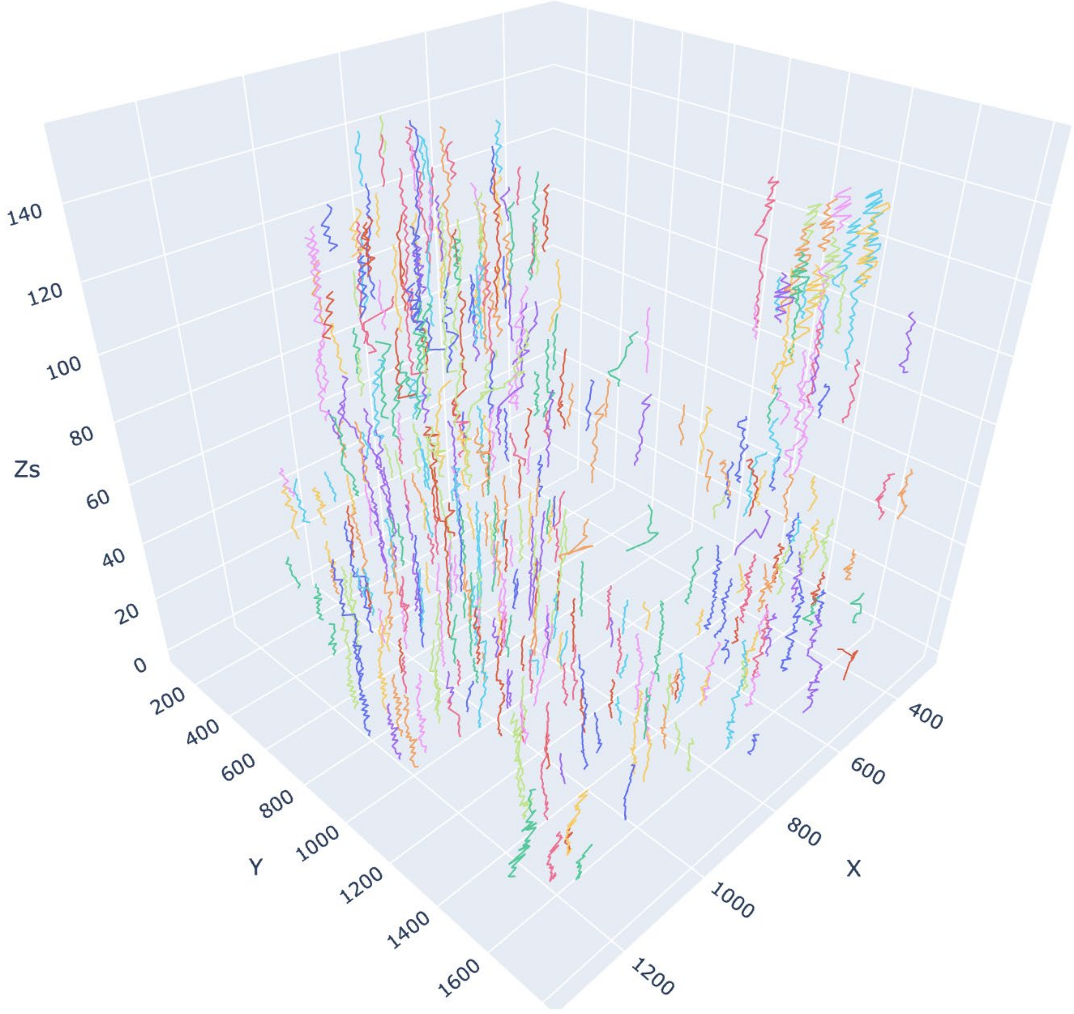
Target section search



Final feature through specimen

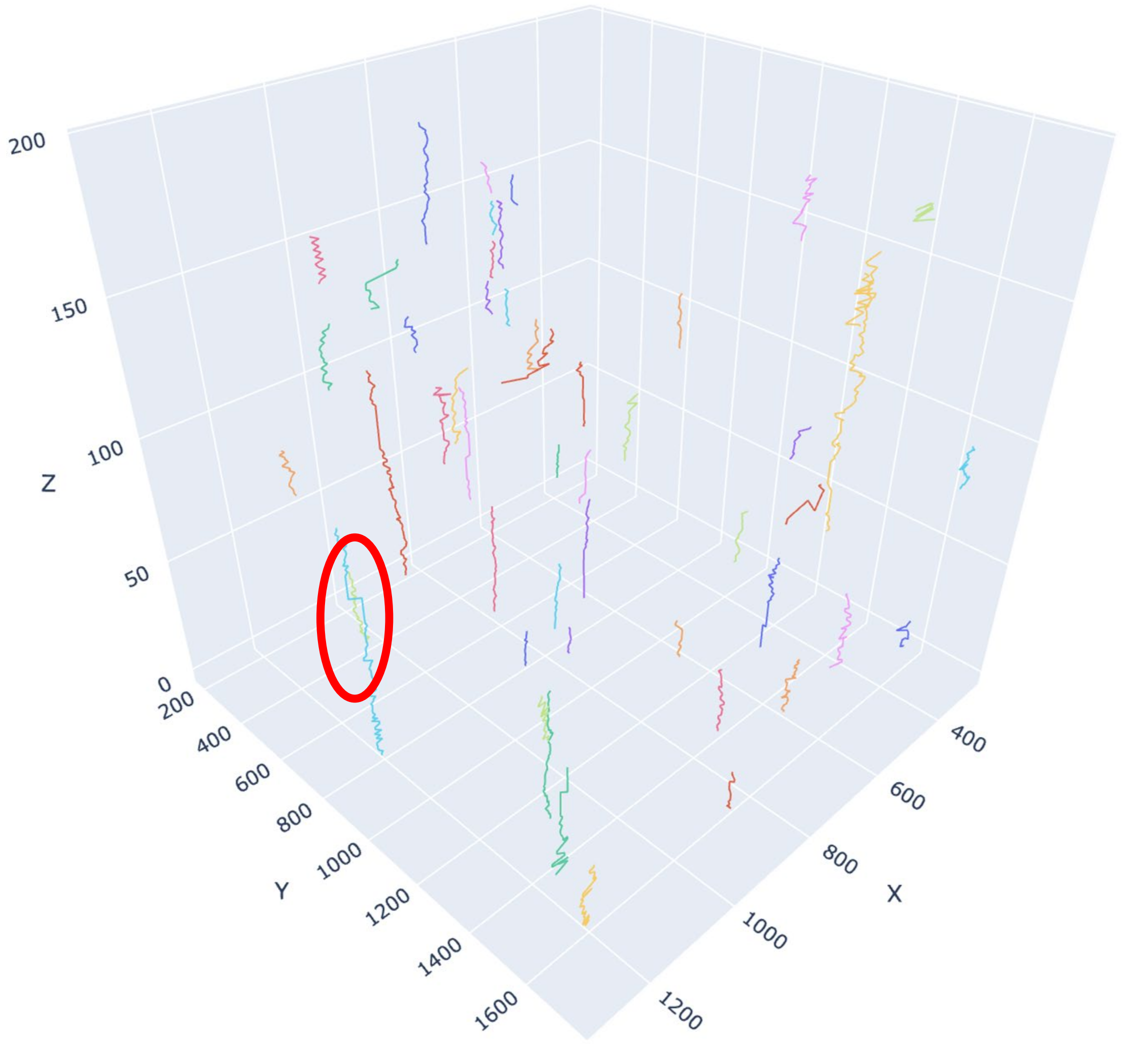
NL Registration, Feature tracking

- The features are tracked through the entire specimen
- Spatial cohesion is checked at each sample
- Feature stops when no longer spatially cohesive



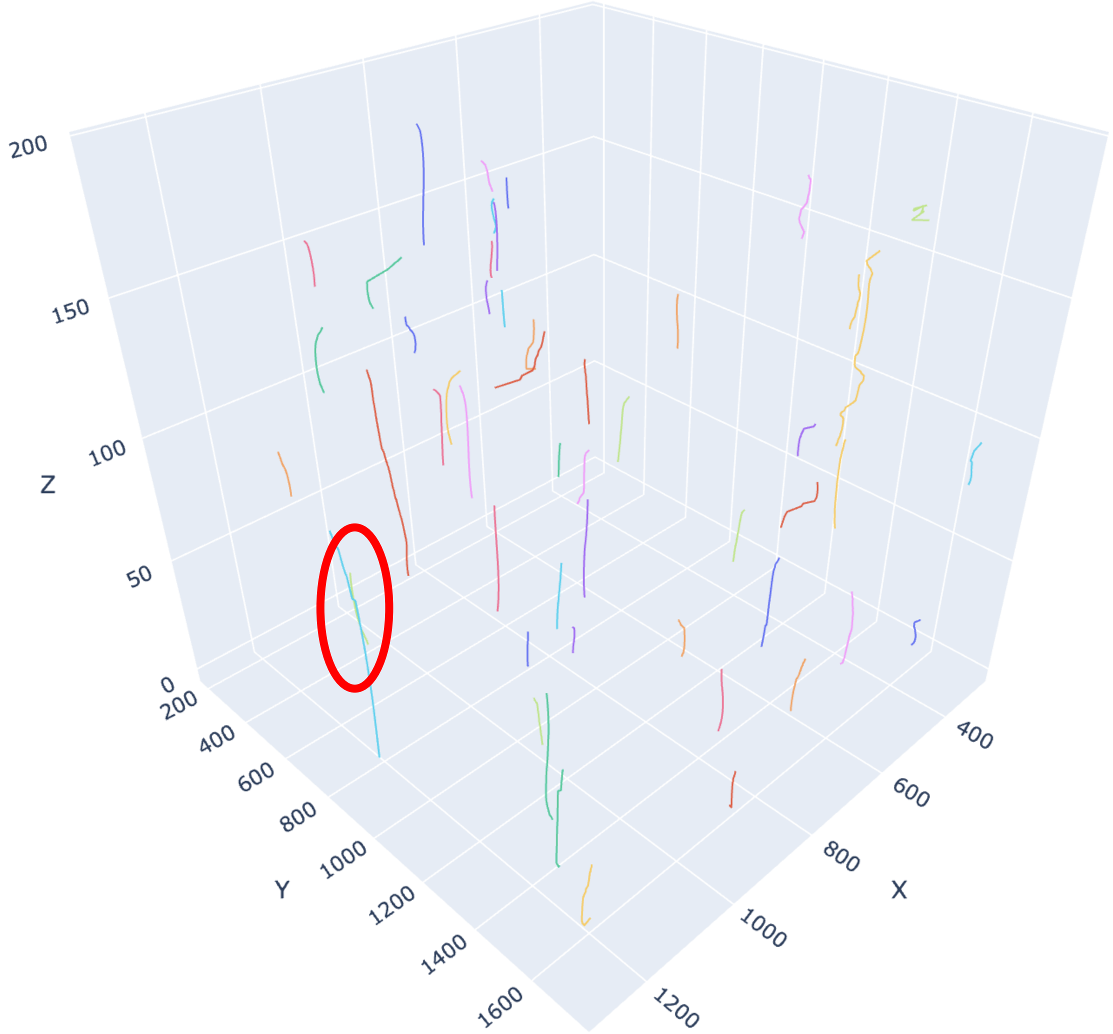
NL Registration, Feature selection

- Features are selected to ensure spread of features is sufficient for non-linear deformations (next step)
- Feature selection is determined by:
  - Ensuring there is space between the possible features
  - Prioritising either their length or smoothness
- Missing samples are interpolated between features



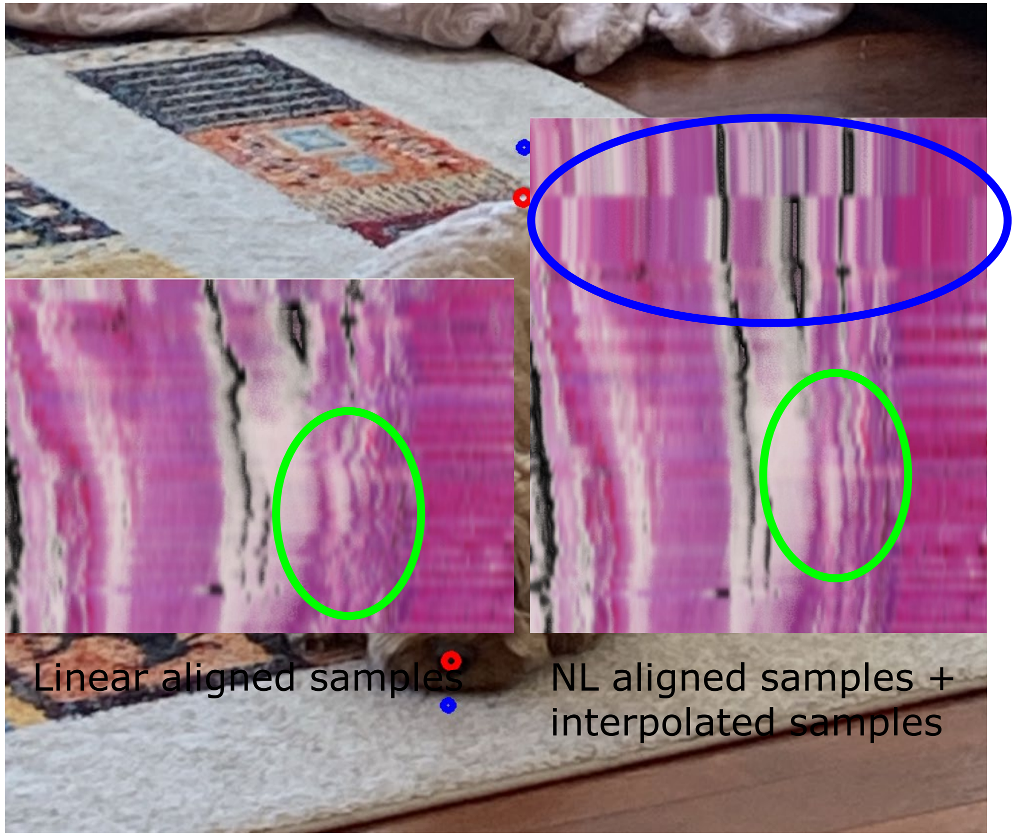
NL Registration, Feature smoothing

- Features in tissue progress smoothly (analogue)
- Features in digitised samples are discrete and sometimes non-continuous due to deformations
- Trajectory of samples is smoothed by a 3D cubic B-spline



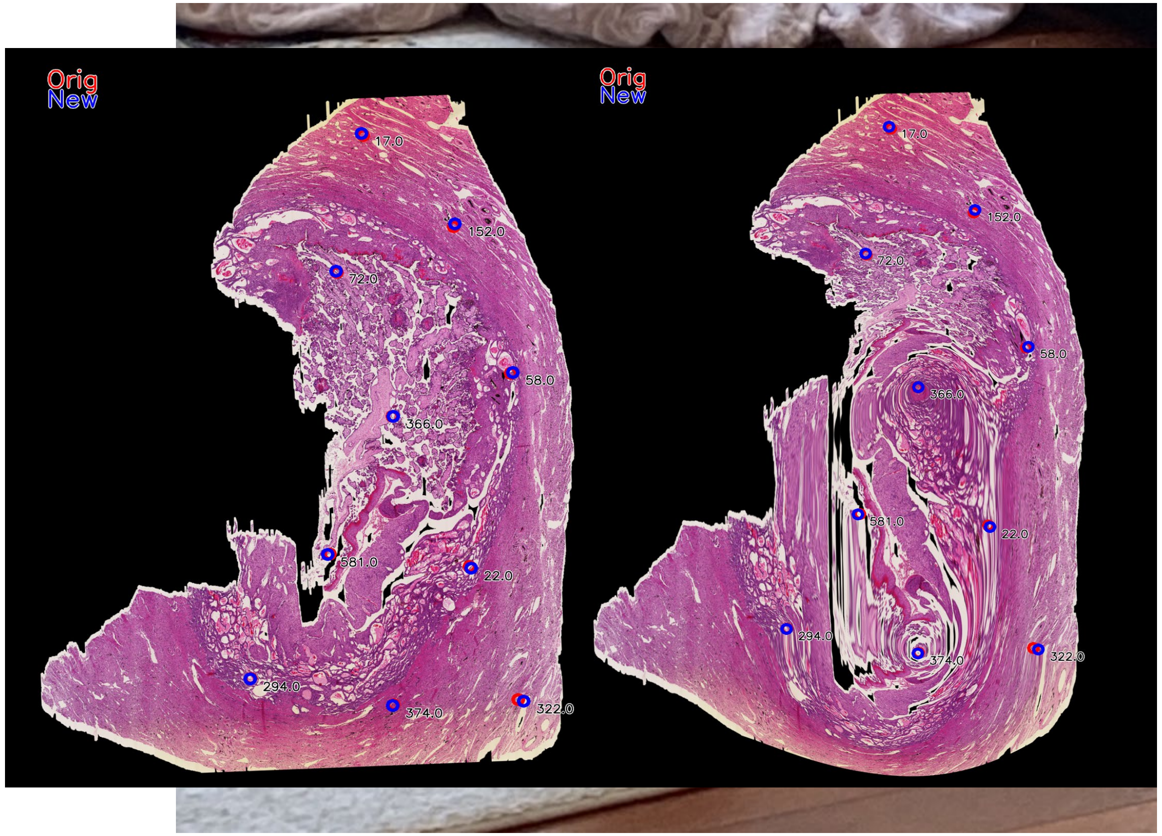
NL Registration, success

- Tissue with the smoothed feature trajectories, we can compensate for non-linear deformations
- Helps to create more biologically realistic visualisation
- Implemented by tensorflow_addons.image.sparse_image_warp

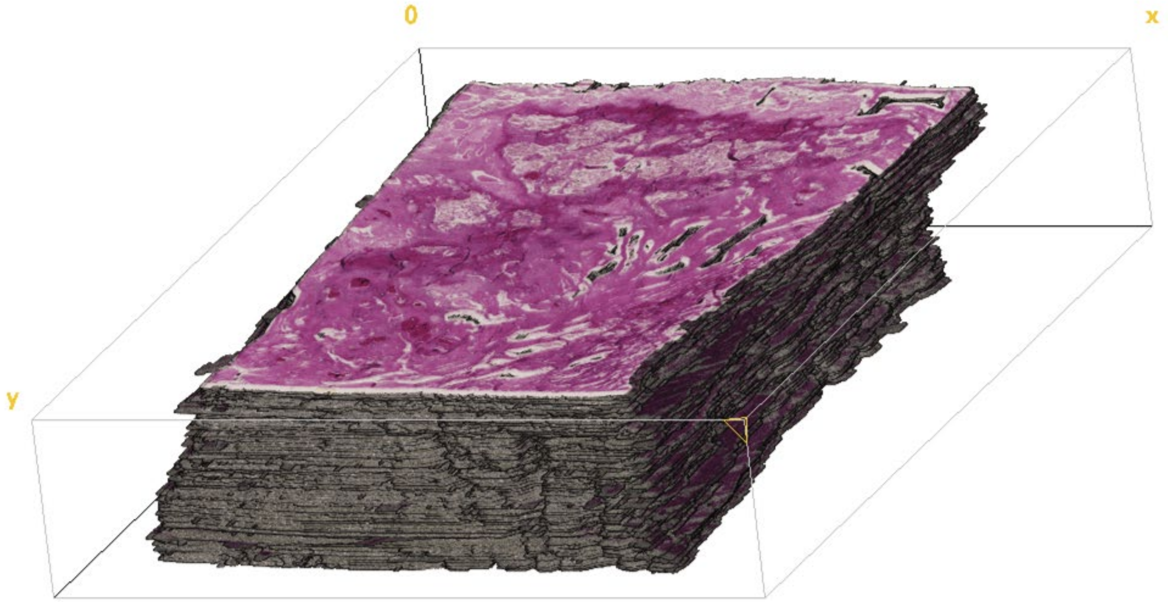


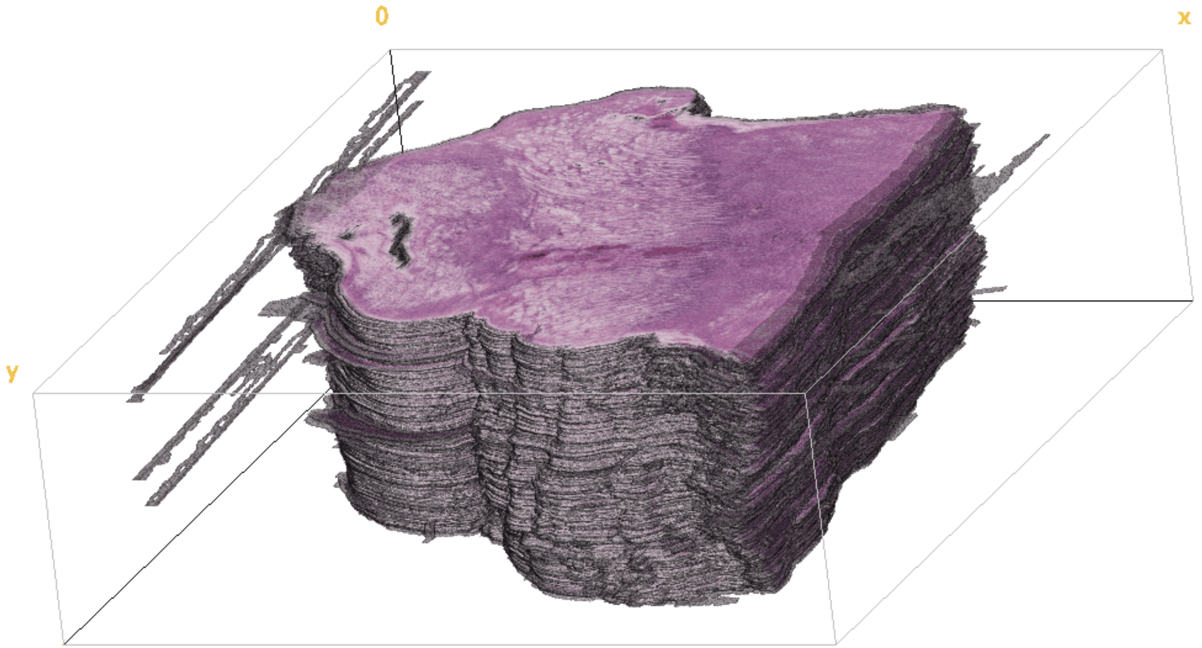
NL Registration, unsuccessful

- Works well for small deformations which are well-spaced apart
- Feature selection reduces the occurrence of "impossible" deformations
- Causes may be:
  - Incorrect feature tracking
  - Smoothing creates impossible situations
  - Interpolations are not constrained properly



Full registration



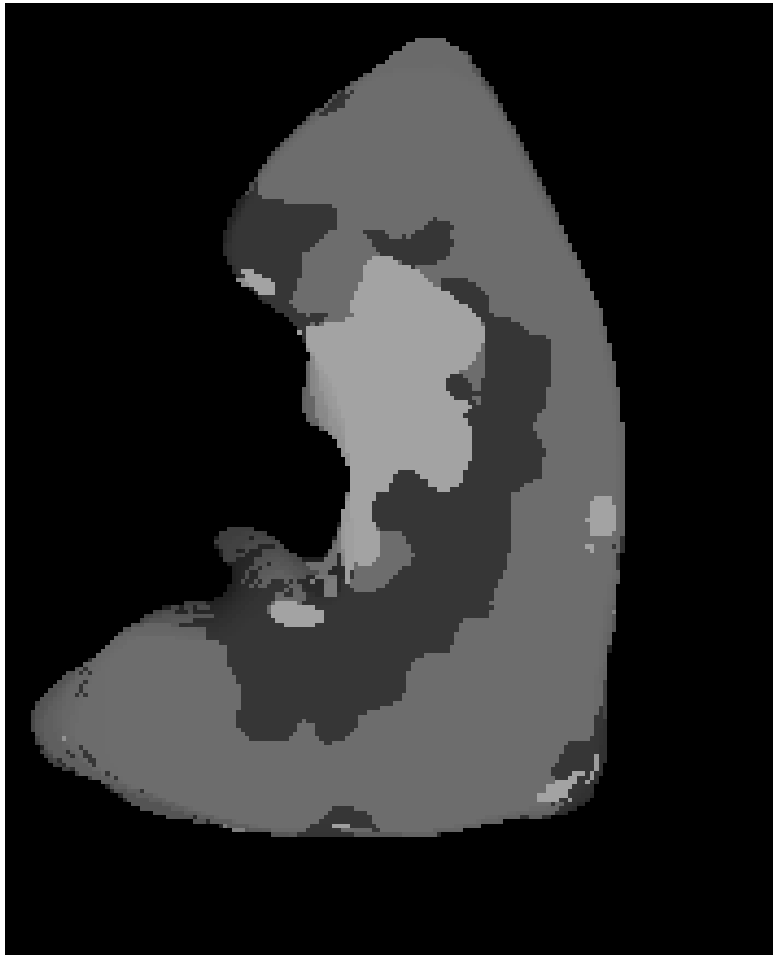


Segmentation

- Training data created by the tracked features already made

  two for the price of one

- Key tissue types: myometrium, decidua and villous tree
- Model created with imagenet pre-trained, Resnet101 network
- Similar results between models



Future work

- Segmentions with 3D convolutions
    - More accurate tissue type segmentation
    - Segment out the smaller structures
- Improved nonlinear deformations

Acknowledgements

- Alys, Jo, & Hanna
- Graham Burton, Centre for Trophoblast Research

MARSDEN FUND
TE PŪTEA RANGAHAU A MARSDEN

ROYAL SOCIETY
TE APĀRANGI

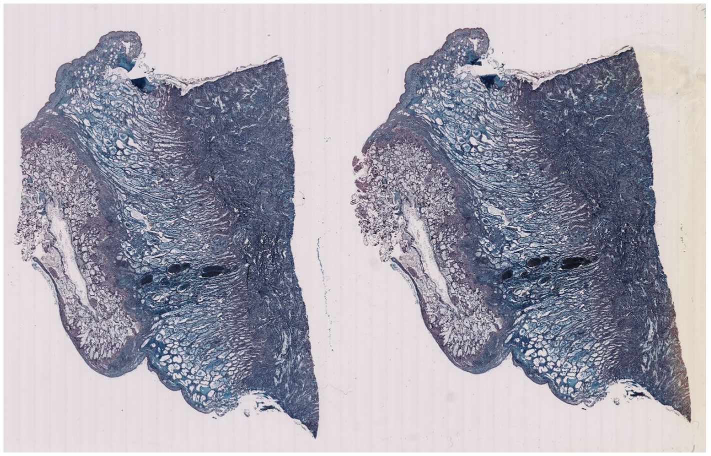
Thank you for listening

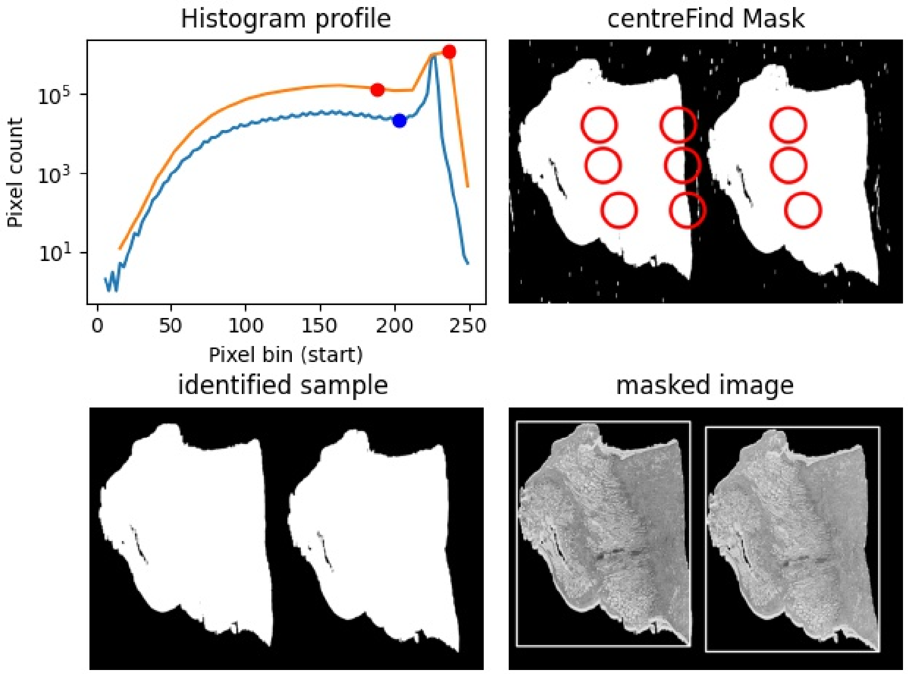
Any questions?

Specimen Extraction

- Samples are presented in their tissue blocks, often with multiple samples per block

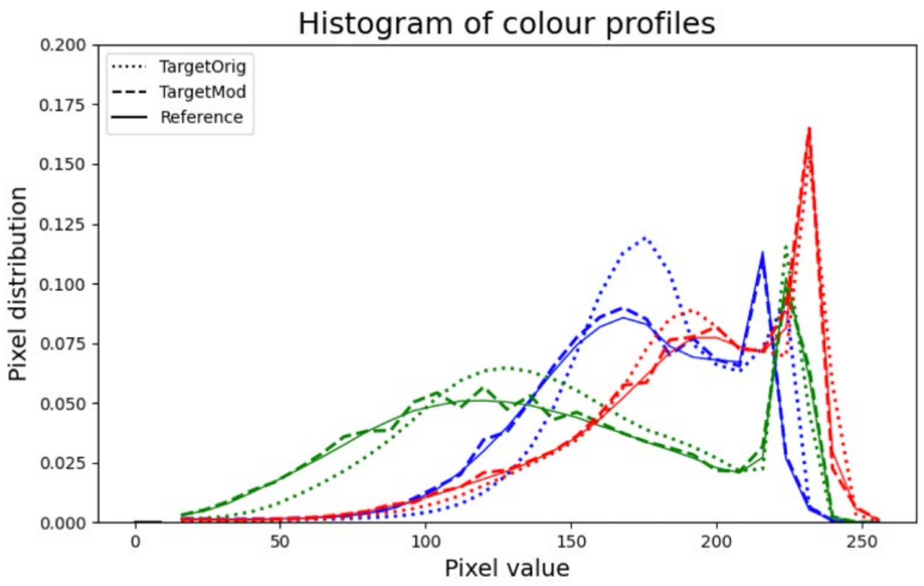
- Isolating samples critical for further processing
  a. Differentiate background from foreground
  b. Identify individual sample positions
  c. Extract individual samples
  d. Normalise colours

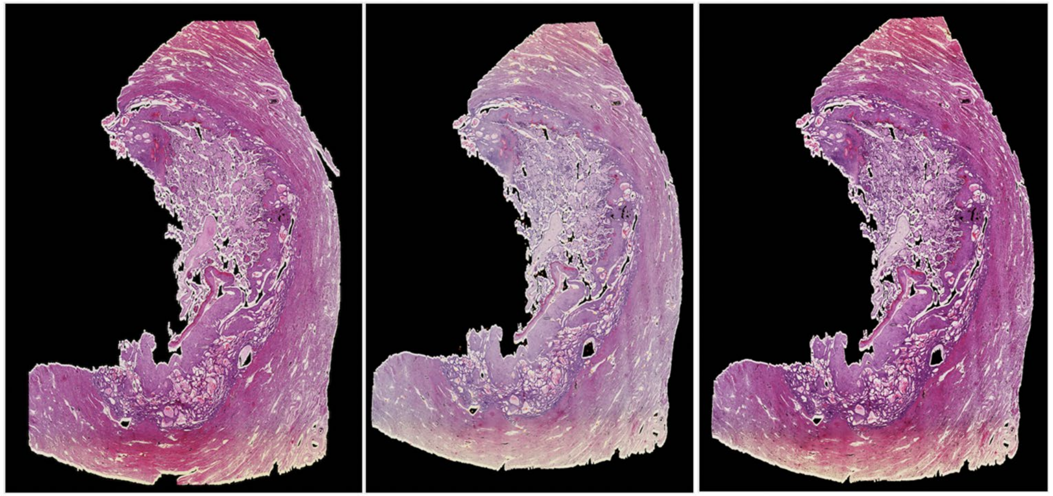




Colour correction

- Stains represent different cell structures
- Multiple stains used, hard to visualise and process stacked samples
- Normalise the colour distributions of each channel relative to a reference sample
- This method creates visual consistency





Reference image Target Original Target Modified