Elliptical Fourier Analysis of Tumoroid Morphology using High Resolution Episcopic Microscopy

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BACKGROUND

- Quantifying tumour shape is important as tumour shape could influence tumour progression. It has been suggested that cell shape changes can promote breast cancer progression [1].
- Shape quantification bypasses verbal descriptions' limitations (vocabulary, complexity) and enables all information pertaining to shape to be captured.
- Greater knowledge of factors influencing tumour shape, and how this influences metastasis could translate into new, effective therapeutics.

AIMS

- To develop a method to extract and reconstruct the 2D tumour morphology from a HREM dataset.

METHODS

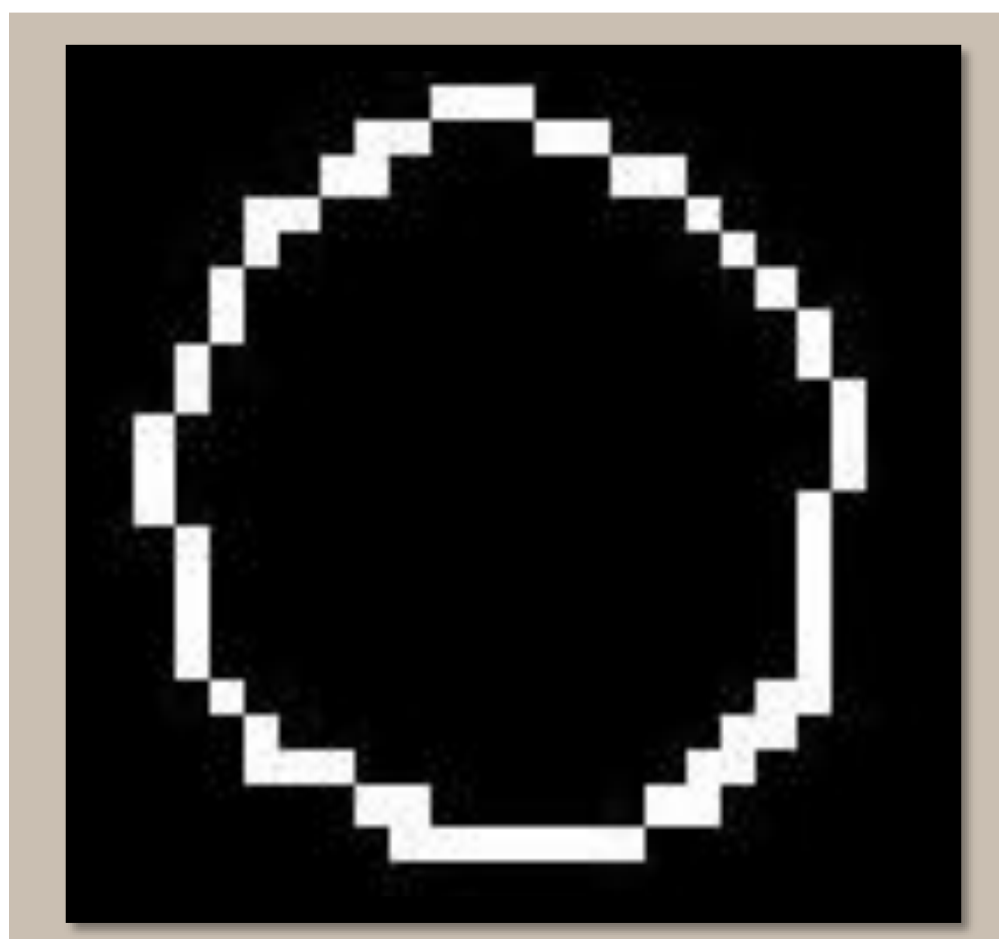

Figure 1: *Tumoroid outline extracted using the Canny method*

Figure 2: *Radii intersecting boundary to produce sample points*

- Tumoroid data segmented and random slice chosen.
- Using MATLAB and the Canny method, the outline was extracted. Equiangularly spaced radii emanating from the centroid and intersecting the boundary were produced.
- Elliptical Fourier analysis (EFA) was performed on intersection points and the shape reconstructed.
- Reconstructions were done with 3, 50 and the number of maximum harmonics, n, (determined by the Nyquist frequency) to see any change in the reconstruction.
- The number of reconstruction points varied to: 50, 200, 500 and 1000.

RESULTS

- Increasing the harmonics used resulted in the shape incorporating more corners and straight edges.
- With the number of reconstruction points ≥ 200, the outline shape was almost identical.
- The residual between the outline and reconstructed shape (with n harmonics and 200 reconstruction points) was: $4.0040\mu m$.

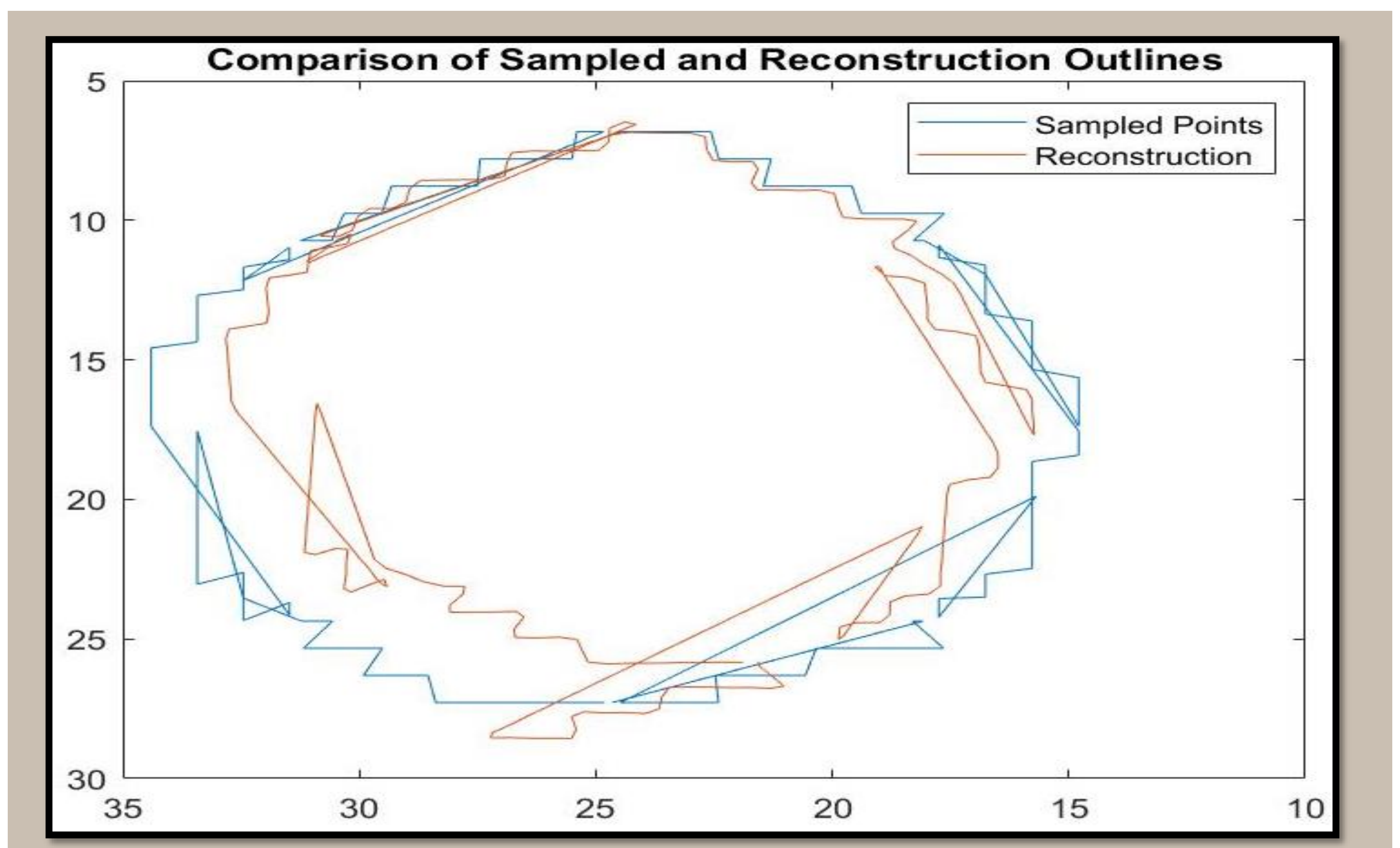

Figure 3: *Comparison of the sampled and reconstructed outlines using the maximum number of harmonics, and the same number of reconstruction and sampled points*

CONCLUSIONS

- Overall, EFA resulted in an accurate representation of the outline shape, with the major difference being size, whilst outline differences were subtler.
- In the future, this method will be extended to 3D tumoroids.
- More consideration will be given to dealing with overlapping regions to prevent the loss of data that occurred with the strategy employed here

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REFERENCES

[1] H. Z. Sailem and C. Bakal, "Identification of clinically predictive metagenes that encode components of a network coupling cell shape to transcription by image-omics.," *Genome Research,* vol. 27, no. 2, pp. 196-207, 2017.

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