Using Graph Theory to Describe Vascular Networks

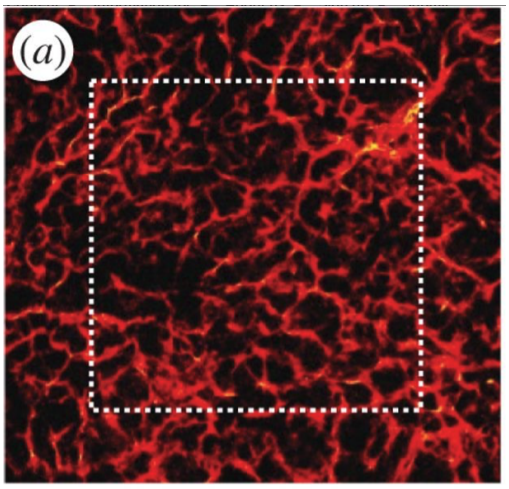
Background

The vascular network is the network of different types of blood vessels such as arteries, capillaries and veins through which blood flows through our bodies. How these blood vessels grow plays an important role in processes such as embryonal as well as tumour development as blood needs to reach every part of the tissue to deliver oxygen and discard waste products.

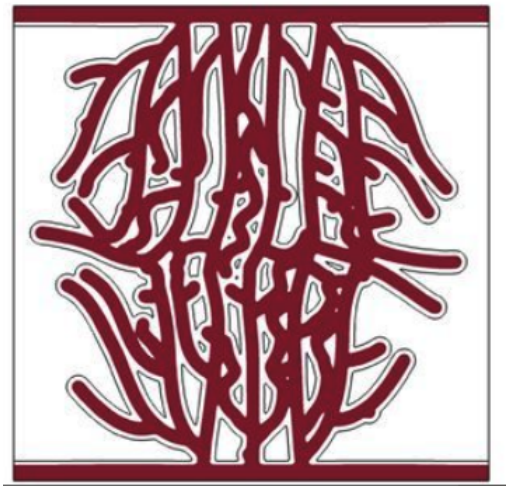
Specifically for tumour development, angiogenesis describes the formation of new blood vessels from already existing ones. Once these new blood vessels reach the tumour, this starts a critical new phase of tumour development which we want to understand better. To promote this understanding, different mathematical and computational models exist that simulate the angiogenic process, however, it is difficult to quantify how well the vascular networks generated by these models function compared to the networks found in vivo or in vitro experiments as we can see in Figure 1.

Project aim

The aim of the project is to find graph representations of vascular networks so we can use graph theory to describe the network. The idea is to set branching points as nodes and connecting vessels between these points as edges to get a graph representation of the network. This can obviously done by hand for individual pictures but within the project, we want to find a way to automate this step of generating a graph from an input picture of a vascular network. Then, using graph theory to describe the graphs, we can compare both simulated and real-life networks to determine if different models result in realistically-generated networks with similar amounts and ways of branching.



(a) Figure 1(a) from [2] showing in vivo capillary growth in a tumour.



(b) Figure 5(e) from [2] showing a simulated vascular network.

Figure 1: Comparison between in vivo and simulated vascular networks can be difficult to quantify.

Project Suggestion

The first and probably biggest step in the project is to find graph representations of modelling results and in vivo or in vitro pictures similar to what has been done in [1]. After that, you should find different ways to quantify the growth of the network, e.g. the amount of branching or finding different efficiency measures, where you can determine which features are the most relevant and should be included in quantifying the general structure of the different vascular networks. One example of this is the distance-weighted efficiency of the network

$$E = \frac{1}{n(n-1)} \sum_{\substack{i,j \in [1,n], \\ i \neq j}} \frac{1}{d(i,j)}$$

where n is the number of vertices in the graph and $d(i,j)$ is the distance of the shortest path between vertices i and j as used in [1].

These first two steps are the bulk of the project but after you have achieved these, you can choose to investigate other aspects of the vascular networks as well. Depending on interest, you could for example investigate how individual cells move during angiogenesis and if this affects the quantified network or inspect what role tip cell movement plays in the generated networks [3].

Contact person

Gesina Menz, gesina.menz@it.uu.se

References

[1] Vilanova, G., Colominas, I., Gomez, H. *Computational Modeling of Tumor-Induced Angiogenesis.* Archives of Computational Methods in Engineering, 24(4), 1071–1102. 2017. doi: `https://doi.org/10.1007/s11831-016-9199-7`

[2] Vilanova, G., Colominas, I., Gomez, H. *A mathematical model of tumour angiogenesis: growth, regression and regrowth.* J. R. Soc. Interface. 14: 20160918. doi: `https://doi.org/10.1098/rsif.2016.0918`

[3] Boas, S. E. M., Merks, R. M. H. *Tip cell overtaking occurs as a side effect of sprouting in computational models of angiogenesis.* BMC Systems Biology, 9(1). 2015. doi: `https://doi.org/10.1186/s12918-015-0230-7`