Analyzing branching shapes with cycle matching and signed distance persistent homology

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Tubular and membranous shapes appear in many important biomedical applications. Their branching morphologies, modelled by interactions and diseases, inform us on biological systems. I propose to generate them with the “curvatubes" model (Song (2021)), and analyze them using two approaches based on persistent homology.

Cycle matching, as proposed by Reani & Bobrowski (2021), detects “true" cycles in resampled data, by comparing spaces through image-persistence (Cohen-Steiner *et al.* (2009)). Using Ripser-image (Bauer & Schmahl (2022)), I will discuss how to analyze vascular images directly while bypassing any sophisticated segmentation.

Alternatively, branching surfaces can be analyzed by computing the persistent homology on the sublevel filtration of a signed distance function. This has been used for porous media (Herring *et al.* (2019); Moon *et al.* (2019)) and is related to discrete Morse theory (Robins *et al.* (2011); Delgado-Friedrichs *et al.* (2015)). I will show how to interpret these persistence diagrams as describing “shape textures".

Both approaches are tested on synthetic shapes generated by “curvatubes", as well as on proprietary images of bone marrow vasculature, remodelled in acute myeloid leukaemia. This research is carried out in collaboration with Anthea Monod and Inés Garcia Redondo (maths); Dominique Bonnet and Antoniana Batsivari (biology).

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