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FIRST PERSON

First person – Sara Rolfe

First Person is a series of interviews with the first authors of a selection of papers published in Biology Open, helping researchers promote themselves alongside their papers. Sara Rolfe is first author on 'Deep learning enabled multi-organ segmentation of mouse embryos', published in BiO. Sara is a Research Scientist in the lab of Murat Maga at Seattle Children's Research Institute, investigating quantifying morphology from 3D images, automated phenotyping, and open image science.

Sara Rolfe

Describe your scientific journey and your current research focus

I am a computer scientist specialising in collaborations with clinicians and biological researchers to develop novel methods and open-source toolkits for conducting biomedical image analysis. My research has focused on building algorithms to measure, localise, and classify asymmetry and abnormal morphology in 3D images. In my doctoral work, I developed a computational approach to quantify shape change during fetal growth in animal models. I completed a post-doctoral fellowship working with clinicians and researchers at Seattle Children's Research Institute where I developed methods to evaluate surgical outcomes by measuring subtle asymmetries in facial images and examined connections between normally occurring facial asymmetry and genetic factors.

How would you explain the main finding of your paper?

MEMOS, our deep learning-powered segmentation module, provides a fully open-source workflow for segmenting 50 anatomical regions in scans of fetal mice generated by the NIH Common Fund Knockout Mouse Phenotyping Program (KOMP2). This dataset is a rich and publicly available resource for researchers exploring genotype/phenotype interactions. Our workflow provides significant improvements in speed and accessibility over comparable methods.

What are the potential implications of this finding for your field of research?

Segmentation is a crucial step in making biological sense from images. For high-resolution 3D images, this step typically requires significant manual labor or high-powered computational systems that can pose barriers to research. The MEMOS module provides a segmentation workflow that will help make the KOMP2 database more accessible. In addition, we provided the first publicly available pre-trained model for fetal mouse segmentation as a resource for researchers working with similar datasets.

"…we provided the first publicly available pre-trained model for fetal mouse segmentation as a resource for researchers working with similar datasets."

Which part of this research project was the most rewarding?

Seeing the MEMOS module deployed in our lab to improve our segmentation workflows was very rewarding and I look forward supporting its use by other research groups.

What do you enjoy most about being an early-career researcher?

This stage of my career has allowed me to actively support open, reproducible imaging research. As imaging science advances, access to imaging equipment, hardware and software tools, and programming expertise can pose challenges, especially for research questions requiring a large number of images. I really enjoy that a core aspect of my current role is producing freely available toolkits for images analysis that are used by researchers with a variety of backgrounds to help drive the field forward!

What piece of advice would you give to the next generation of researchers?

Figure out what energizes you most in your research and use that to guide your career moves.

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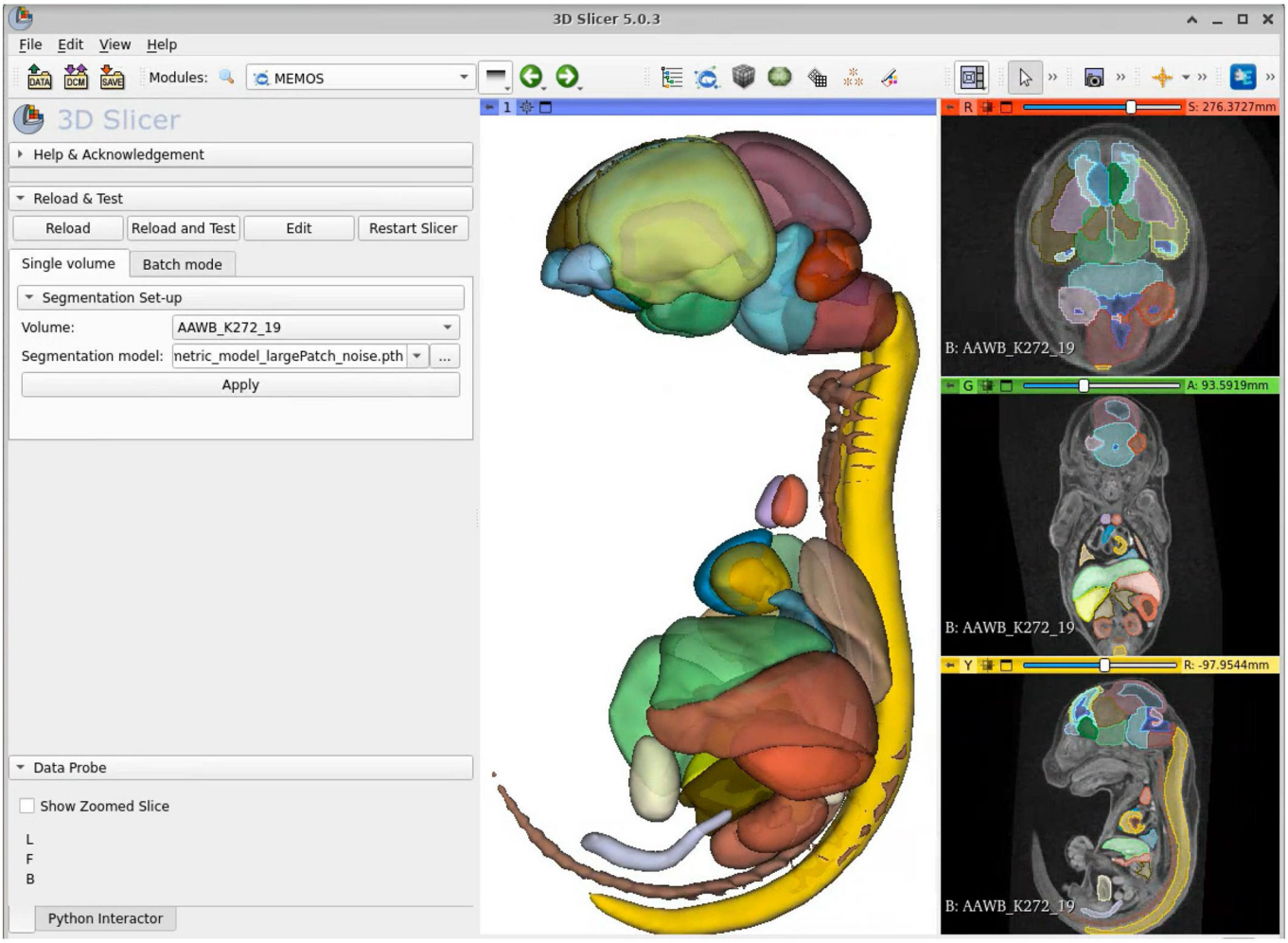

The MEMOS module interface for open-source, deep learning-powered segmentation of fetal mouse scans.

What's next for you?

In our paper, we introduce MEMOS as a general tool for fetal mouse segmentation. Next up, I will be generalising MEMOS to accommodate more variability including anatomy, mouse strains, and imaging sources. I am currently using the segmentations produced by the MEMOS workflow to do dense phenotyping of anatomical abnormality and asymmetry in the KOMP2 dataset.

Reference

Rolfe, S. M., Whikehart, S. M. and Maga, A. M. (2023). Deep learning enabled multi-organ segmentation of mouse embryos. *Biol. Open* **12**, bio059698. doi:10.1242/bio.059698