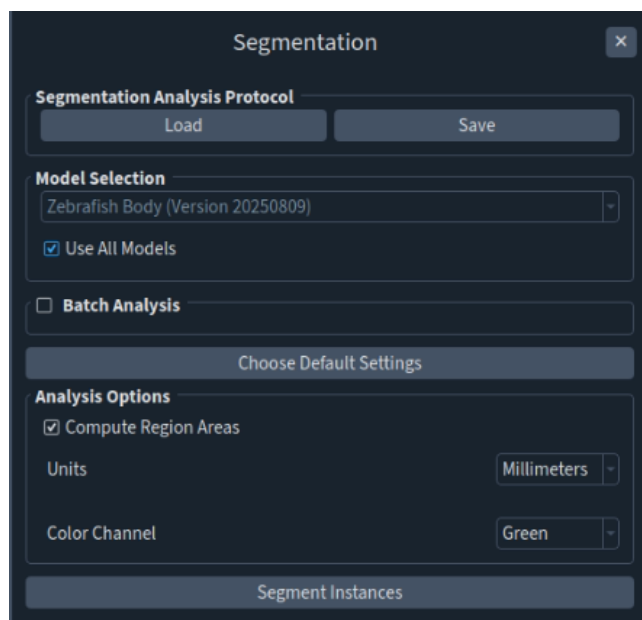
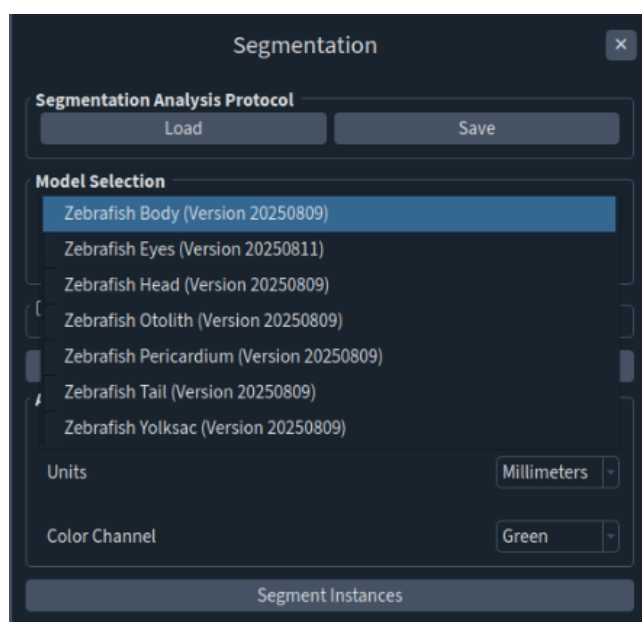


Zebrafish Morphology and Segmentation - BrightField

The Ramona MCAM supports fully automated segmentation of zebrafish from both single-frame and stack datasets. Users can choose from seven segmentation models—body, eyes, otolith, pericardium, tail, and yolk sac—or apply all models simultaneously. The analysis produces a CSV file containing the measured area for each selected model. For additional details on the underlying mechanics of the segmentation workflow, please refer to the MCAM User Manual.



Step	Function
1	Acquire an XYZ-stack dataset using the XYZ-stack acquisition mode described above.
2	Open the dataset in the MCAM Viewer by double clicking on the metadata.nc file or drag-and-dropping it into the viewer.
3	Go to Analysis > Zebrafish > Segmentation to open the segmentation panel.
4	Select a segmentation model specific to the current segmentation task from the model selection menu.
5	If you would like to compute region areas, check "Compute Region Areas" .
6	Select an SI unit for exported values. "Millimeters" is selected by default.
7	Click "Segment Instances" to run the analysis.
8	Results are output to a new directory with the same name as the analyzed dataset with "_segmentation_results" appended.
9	Segmentation visualizations are displayed in the MCAM Viewer.