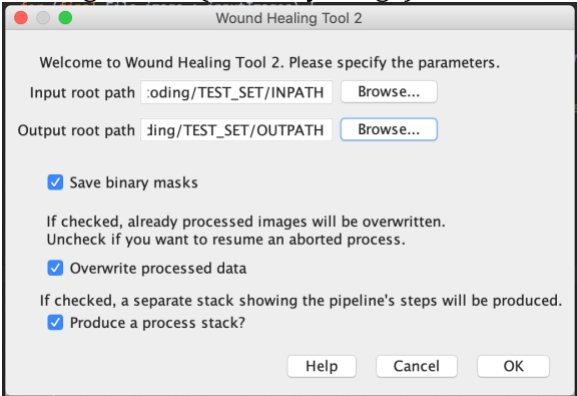


Design & Specification

Project:	Biological Image Segmentation
Team:	Nurzhan Sakenov, Bekzhan Kaspakov, Madiyar Katranov
What the System Does	
<p>The system consists of two modules. The first one allows users to perform image segmentation of Wound Healing Assay imaging datasets using a fixed pipeline. The second allows users to customize the segmentation algorithm via a graph-based interface.</p>	
How the User Interacts with the System	
<p>Use Case 1: Segment a loaded dataset Actor: a microbiologist Precondition: the actor must have a WHA imaging dataset loaded in FIJI Postcondition: the actor will have a set of binary masks outputted to the screen Main Scenario: the actor clicks on the plugin button, then confirms segmentation of a loaded dataset. The actor can provide the parameters for segmentation. Extensions: the actor can check the checkbox for “progress stacks”, which will result in outputting the whole segmentation progress in a single stack (for every image).</p> <p>Use Case 2: Segment a dataset in a directory Actor: a microbiologist Precondition: the actor must have a WHA imaging dataset in a root folder of folders (one folder per dataset) Postcondition: the actor will have a set of binary masks saved in a directory mirroring the structure of the input directory Main Scenario: the actor provides the directory of the dataset, as well as the output directory. The actor can provide the parameters for segmentation. Extensions: the actor can check the checkbox for “progress stacks”, which will result in outputting the whole segmentation progress in a single stack (for every image).</p>	
	

Use Case 3: Segment a dataset using a custom algorithm

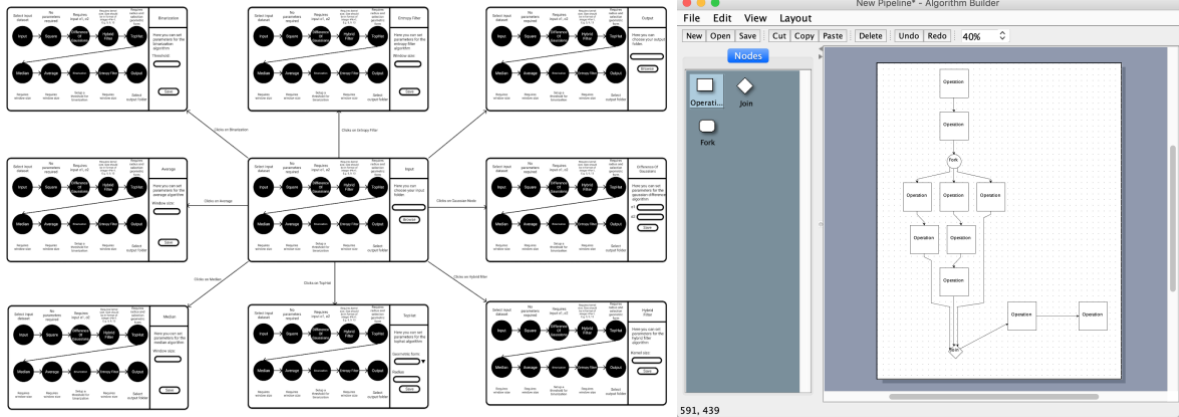
Actor: a microbiologist

Precondition: the actor must have a WHA imaging dataset

Postcondition: the actor will have a set of binary masks either in memory or saved to the hard drive

Main Scenario: the actor launches the graph-based tool, where they construct the graph (each node is a step in the algorithm customizable with parameters), then launches the segmentation

Extensions: if the graph is not a valid pipeline, an error will be shown.



Performance Requirements

The accuracy of the segmentation is usually evaluated visually/subjectively by a microbiologist, but that is not a quantifiable metric. To quantify the accuracy, we may try comparing the automatically segmented images to images segmented by hand (probably via the Hamming Distance of the two binary images). In terms of time, an “average” biologist can segment a wound healing image by hand in about 45 seconds. There could be about 4TB of images of about 8 MB each in a dataset. The algorithm must process an image in no worse than 45 seconds. Our implementation will hopefully be significantly better than this. Furthermore, we may compare our tool to some legacy tools.