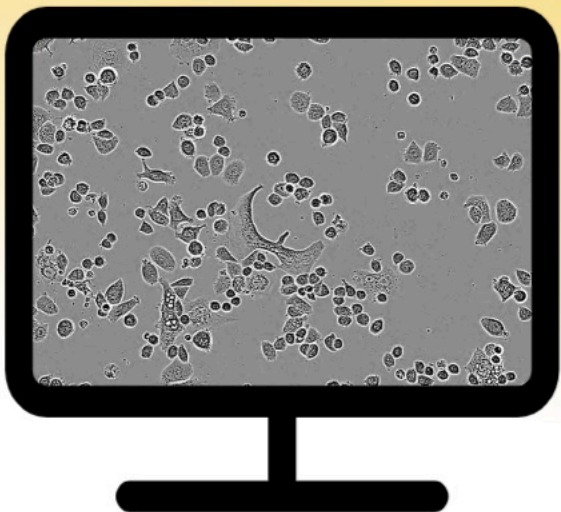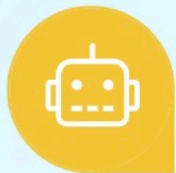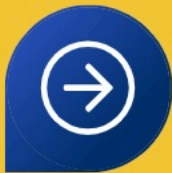# Multires-ML Microscopy

## User Guide

# How
## CellApp Helps

**Aims to make medical image analysis accessible to non-technical users without expertise in complex machine learning methods.**

## Guide
## Overview

**This guide will provide detailed instructions on the run through of the CellApp from the initial upload to data exports.**
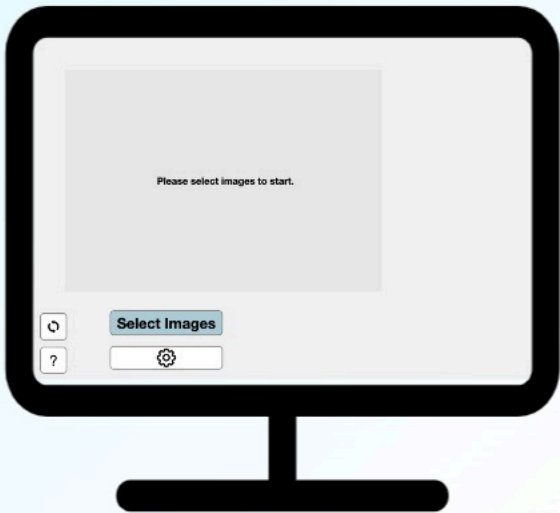
# Step 1. Upload Images

**01** Pressing the Select Images button, allows the desired images to be selected for analysis.

**02** Note that only image files are accepted (jpg, png, tiff, etc.).

**03** If a file with an invalid format is selected, an error message will appear.

Please select images to start.

↻

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Select Images

⚙

# Step 2. Segmentation

**01** After uploading, a preview of the selected images and the Segment button appears. Pressing this button initiates the segmentation process.

**02** Segmentation masks are continuously updated and displayed for the user to visualise the segmentation process. The progress bar indicates the progress on the image dataset and the pause button stops the segmentation.
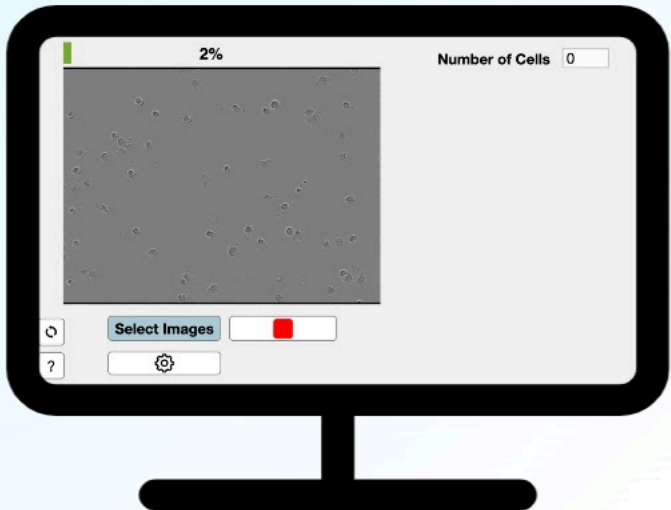
# Step 3. Analysis

**01** Visualise the data by selecting variables from the drop-down menus. This plots any two variables against each other or a histogram of only one variable against Frequency.

**02** Choose to also analyse data across all images of the dataset or for individual images using the toggle switch. The user can navigate between the images with the arrow buttons or, alternatively, select the relevant image from a list.
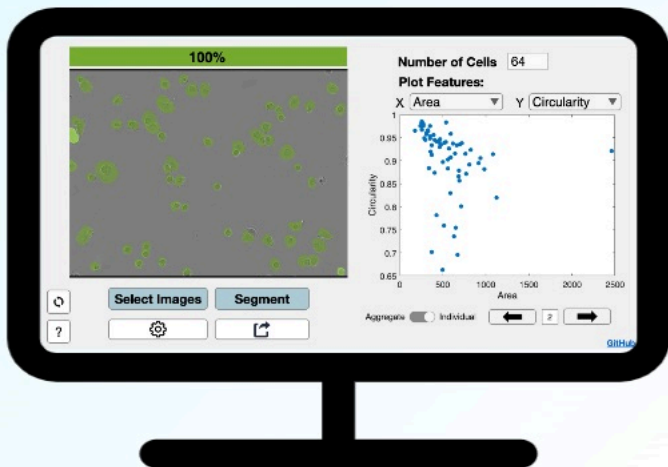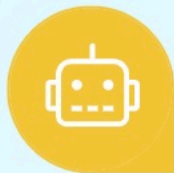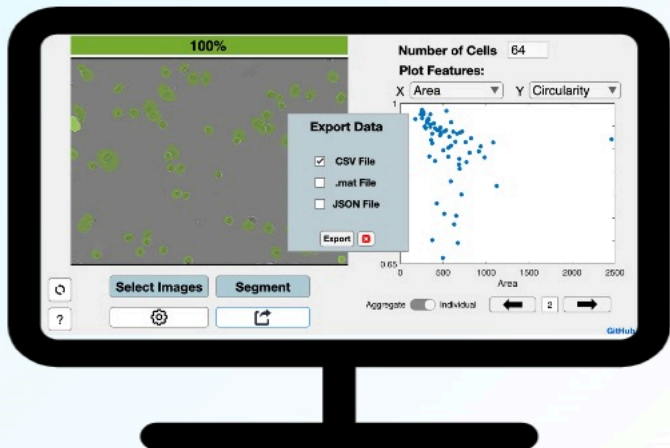
# Step 4. Exports

**01**

Export the results to a chosen folder by pressing the export button. Options include:
- CSV file
- MAT file
- JSON file

**02**

Note: MAT and JSON files contain additional data, including the raw images and instance segmentation masks. The mask segmentations are output in Tagged Image File Format (TIFF).

# Advanced Settings

**Presets: (Default, Conservative, Relaxed)**
Altering parameters impacts the false positive and negative rates of cell segmentation. These parameters can be manually adjusted by the user before each segmentation run.

**DWT Level and Threshold:**
Higher number of levels remove higher of high frequency noise, whereas lower levels retain more frequency information. Note: A 10% threshold will retain only the largest 10% detail coefficients and remove the rest.

**Confidence Threshold:**
Predictions under the confidence threshold will not be outputted. Therefore, this metric has the most direct impact on the conservativeness of the model's predictions. This metric is set to 50% by default.

**Maximum Proposals:**
Limit set to the number of region proposals that can be made. This can ensure more consistent computation times across images, at the expense of reducing recall as fewer proposals are considered.
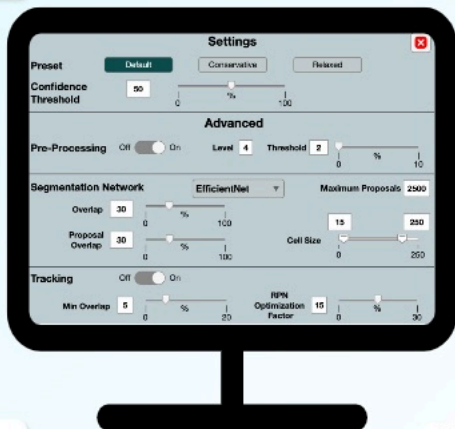
**Min IoU Threshold:**
This is the minimum amount of overlap two objects must have between frames so that it is tracked.

## Settings ✕

Preset | Default | Conservative | Relaxed

Confidence Threshold | 50 | % | 100

### Advanced

Pre-Processing | Off ⬤ On | Level 4 | Threshold 2 | % | 10

Segmentation Network | EfficientNet ▼ | Maximum Proposals 2500

Overlap | 30 | % | 100

Proposal Overlap | 30 | % | 100

Cell Size | 15 | 250 | 0 | 250

Tracking | Off ⬤ On

Min Overlap | 5 | % | 20

RPN Optimization Factor | 15 | % | 30

**Overlaps:**
If two detections have an overlap greater than this value (measured by IoU), then only the most confident one is shown.
If two proposals have an overlap greater than this value (measured by IoU), then the less confident one is discarded.

**Object Size:**
Predictions whose bounding box falls outside this range are discarded.

**RPN Optimisation Factor:**
This value determines the extent to which the number of region proposals are reduced by filtering out those that differ from the previous frame. The higher this value, the more proposals will be discarded.