ColFeatures

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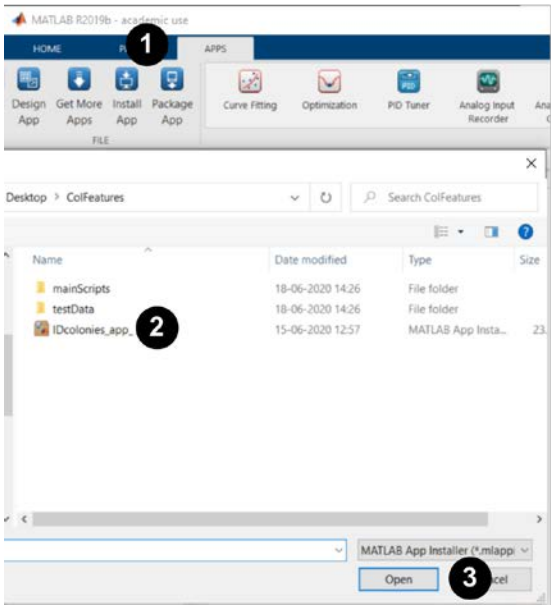
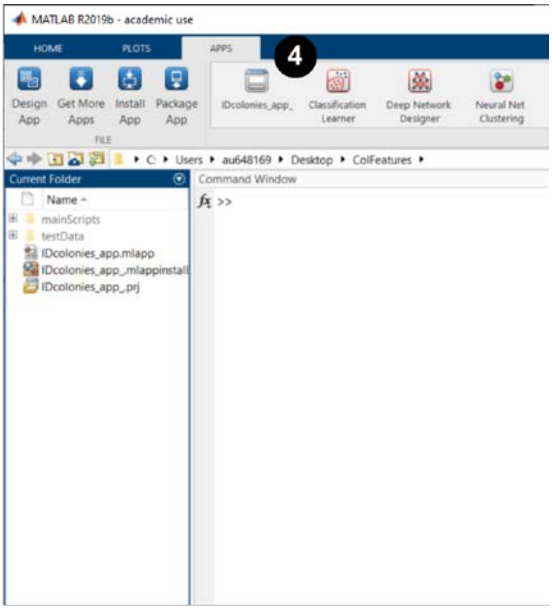
GUI interface

Installation

You need to have MATLAB installed in your computer as well as the Image Processing Toolbox and the Signal Processing Toolbox. We were using 2019 version. For installation, after downloading the different files go to Apps and click on 'Install App' **(1)**, browse the ColFeatures folder and select the MATLAB App Installation file **(2)**, then open the file **(3)**. After this the GUI interface will appear as an app in your APPS panel **(4)**.

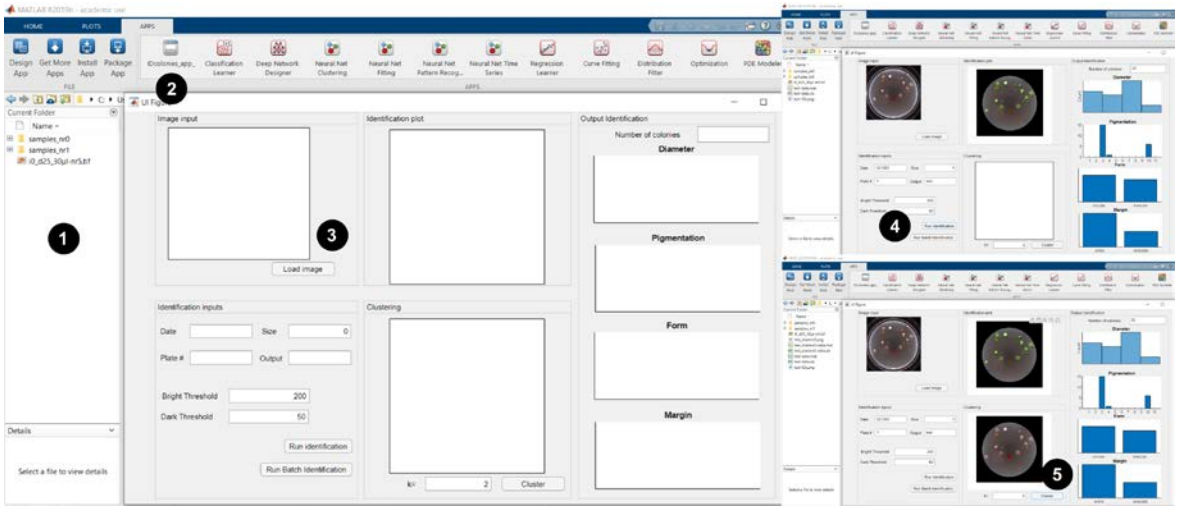




Usage

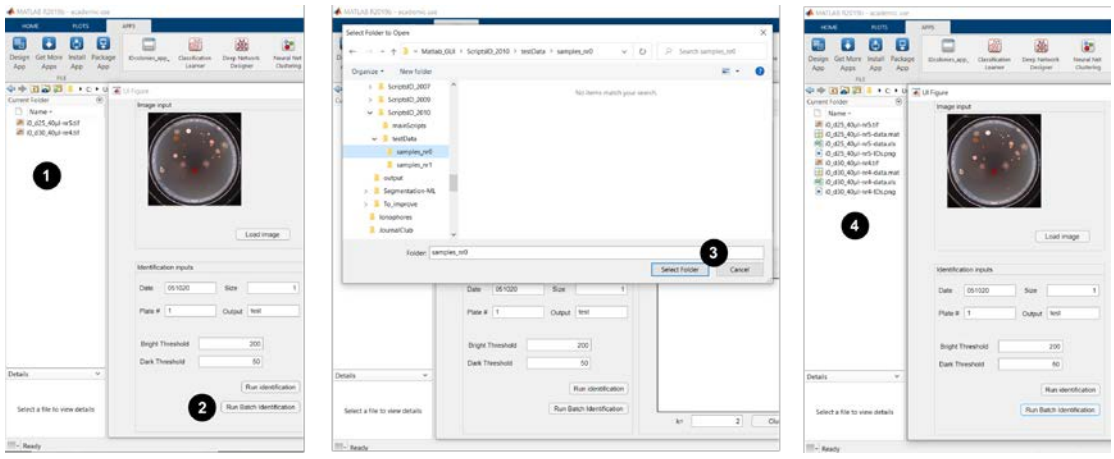
Single .tif file

Once installed, it is ready to be used. The first step is to go to the folder (do not forget to add the folder to the path) where you have your data, remember the GUI only works with .tif files **(1)**. Once in your folder, click on the App: *IDcolonies_app_* **(2)**, the App will open right away. On the App, click on **Load image** and select the image to analyze **(3)**, provide also de inputs for the fields: *Date, Plate #, Size (of the plate to analyze: 0 for 85 mm plates or 1 for 150 mm plates) and Name (of the Output Files)*. One can also modify the threshold values for the segmentation step: *Bright threshold and Dark Threshold.* After clicking on *Run identification* **(4)** the App will show your image output and some of the metrics. You can either stop here or also try the *Cluster* option, after providing the number of clusters to partition your data and clicking in *Cluster* **(5)** the App will show how the colonies were clustered. In each step, output files will be generated and stored in your main folder.



Batch

Once you have found the right parameters to analyze a batch of images with similar properties one can run the batch option. As a first step, in the MATLAB ***Current Folder*** you have to go inside the folder where all the images for batch analysis are saved (1). Go back to the App and click on **Run Batch Identification**, a window will open where you can select the folder where you have your data (2). After clicking on **Select Folder** (3) a script will run in the background, once finished you will see all the output files in the ***Current Folder*** (4) panel in MATLAB.

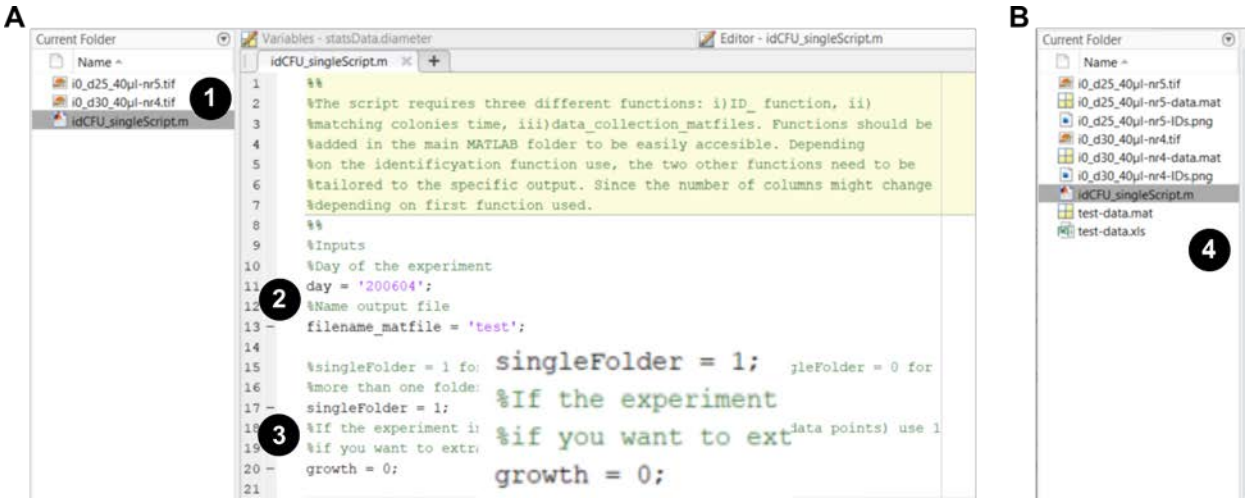


Batch analysis (scripting)

Download the MATLAB scripts IDcfu_Final, dataCollection_Final, dataCollectionGrowth_Final and matchColonies_Final, save them in your MATLAB folder. Also download the idCFU_singleScript and depending on the analysis you will need to save in in specific locations.

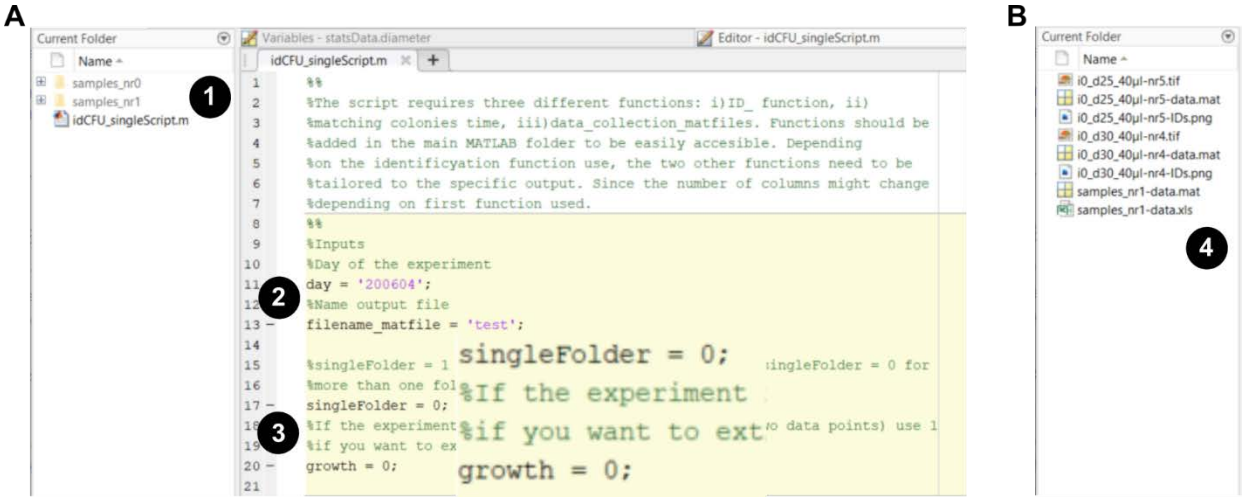
One folder analysis

In this case, you are only interested in analyzing a set of images in a single folder. You need to save the idCFU_singleScript in the same folder as your images (1). Provide the required inputs (2) and set the decision flags as follows: **single_Folder = 1 and growth = 0 (3)**. After this you only need to run the script and three different types of files will be generated (4).



Multiple folders analysis

There is also an option to analyze multiple folders at once. For this case, you need to save the idCFU_singleScript in the core folder, which subfolders are the ones to be processed (1). It is important that the subfolders are numbered, such as **nr0, nr1** and so for. The script requires the pattern **"nr"** to go into each subfolder. Provide the required inputs (2) and set the decision flags as follows: **single_Folder = 0 and growth = 0 (3)**. After this you only need to run the script and three different types of files will be generated in each folder (4).



Multiple folders analysis and growth rate calculation

When analyzing multiple folders, we can also obtain apparent growth rate based on two pictures taken at different time points. One has to be careful to have a way to make sure that the colony centroids will not change much, in our case, we found it useful to draw a line in one side of the plate and also mark a line on the tray to take pictures. For this case, you need to save the idCFU_singleScript in the core folder, which subfolders are the ones to be processed (1). It is important that the subfolders are numbered, such as **nr0, nr1** and so for. The script requires the pattern **"nr"** to go into each subfolder. Provide the required inputs (2) and set the decision flags as follows: **single_Folder = 0 and growth = 0 (3)**. After this you only need to run the script and three different types of files will be generated in each folder. This option will also generate a final data frame where all the data points from each folder will be saved (4).