This document walks you through how to run colonycounting\_v2 using this data. The script “example” will also run the example.

The first thing to know is that all of the code was written so that it could run on multiple folders. Each of the folders can contain raw images from more than one scan, but those images CANNOT be separated into subfolders.

**If you want to analyze multiple folders of scan(s):**

1. Collect the folders with images you want to analyze.
   1. Create a cell array where each entry is the complete path to the folder.
2. Stitch the scans.
   1. Run “colonycounting\_v2.stitch\_all\_scans”.
   2. You will be prompted to enter the number of rows and columns making up each scan.
   3. You will be prompted to align the images for each scan.
   4. The script will stitch each scan (this will take some time).

1. Segment the colonies.
2. Count the cells.

**If you want to analyze a single folder of scan(s):**

1. Collect the folders with images you want to analyze.
   1. Create a cell array where the only entry is the complete path to the folder.
   2. Or, change MATLAB’s working directory to the folder.
2. Stitch the scans.

1. Segment the colonies.
2. Count the cells.