

# Segmentation and organelle analysis: A computer exercise using CellProfiler

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## Background information:

The images in this experiment come from the [Broad Bioimage Benchmark Collection](#). They are fields of U2OS cells imaged in five channels (Cell Painting assay; see Gustafsdottir et al., 2013)

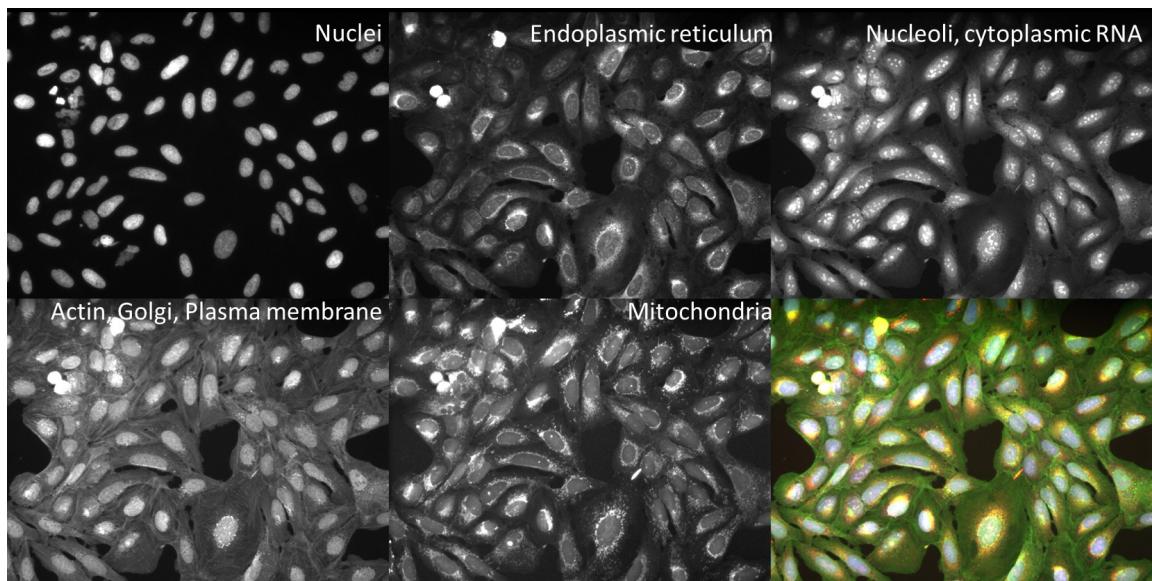


Figure 1: Images and channels from a Cell Painting assay.

## Goals of this exercise:

This exercise will give you practice finding segmentation parameters for larger “parent” objects (nucleus, cell, and cytoplasm) and show you ways to pull out smaller features in your image by segmenting organelles within the cells and nuclei. You will also be shown how to use RelateObjects so that you can relate the average counts, distances, and measurements of the smaller “child” organelles to their larger “parent” objects (i.e., cell and nucleus).

## Materials necessary for this exercise:

The images are contained in the **images** folder; these 50 images (10 sites imaged in 5 channels) represent 5 mock treated wells from a single 384 well plate experiment.

## Exercise instructions:

Read through the steps below and follow instructions where stated. Steps where you must figure out a solution are marked with **TO DO**.

## 1. Load starting pipeline (2 min)

- Start CellProfiler by double-clicking the desktop icon: 
- Drag and drop the ‘segmentation\_start.cppipe’ file into the ‘Analysis modules’ pane on the left.
- 2 modules should pop up.

## 2. Set up the input modules (10min)

The four input modules (Images, Metadata, NamesAndTypes, and Groups) are crucial for any CellProfiler pipeline because they define how images are loaded and organized in CellProfiler.

- Click on the ‘Images’ module in the top left corner of the CellProfiler window.
- Drag and drop the ‘images’ folder into the ‘Drop files and folders here’ pane. It should automatically populate. Notice that illumination correction images (with a file extension of ‘.npy’) are included in this data set.
- Notice that if the ‘Filter images?’ is set to ‘Images only’ the ‘.npy’ files appeared grey out.

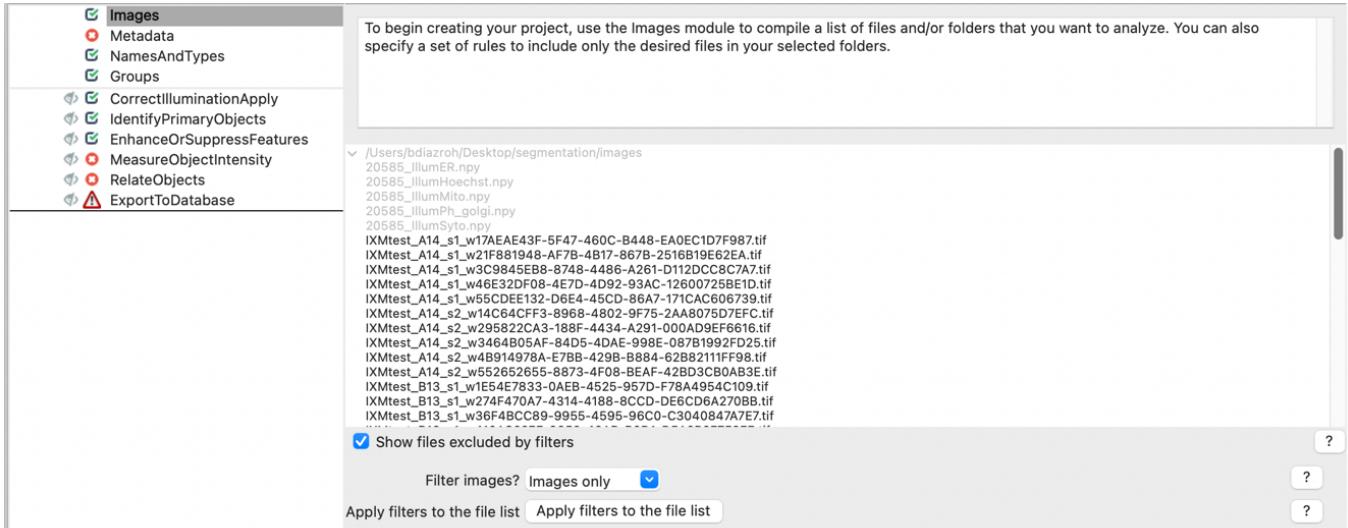


Figure 2: The Images module, grey out files will not be available for downstream modules

- TO DO: Change the filter to a custom filter to *include* the ‘.npy’ files.
- In the ‘Metadata’ module three metadata extraction methods should already be present and configured:
  - The first pulls Well, Site, and Channel metadata from all the image files except for the illumination correction functions.
  - The second pulls Plate metadata from the image folder.
  - The third pulls Plate metadata from the illumination correction functions.
- Click on the magnifying glass at the end of the regular expression box for each extraction method to see how it works.

- Return to the ‘Metadata’ module and press ‘Update’. You should now see several columns, look through them you should have 5 different channel numbers, 1 plate, 2 sites and 5 different wells.

The screenshot shows the 'Metadata' module interface. On the left, a sidebar lists modules: Images, **Metadata**, NamesAndTypes, and Groups. Below this are several configuration options: 'CorrectIlluminationApply' (checked), 'IdentifyPrimaryObjects' (checked), 'EnhanceOrSuppressFeatures' (checked), 'MeasureObjectIntensity' (unchecked), 'RelateObjects' (unchecked), and 'ExportToDatabase' (unchecked). The main area contains a descriptive text box about metadata extraction, an 'Extract metadata?' button set to 'Yes', and a 'Metadata extraction method' dropdown set to 'Extract from file/folder names'. A 'Metadata source' dropdown is set to 'File name'. A regular expression input field contains the pattern '(?P<Well>[A-P][0-9]{2})\_(?P<Site>[0-9])\_(?P<ChannelNumber>[0-9])'. Below these are two tabs: 'Extract metadata from Images matching a rule' (selected) and 'Extract metadata from Images matching a rule (Advanced)'. A table titled 'Found 55 rows' displays the extracted metadata. The columns are: Update, Path / URL, Series, Frame, ChannelNumber, FileLocation, Plate, Site, and Well. The table lists 13 rows of data, such as '/Users/bdiazr...5\_IllumER.npy' for row 1 and 'file:/Users/b...5\_IllumER.npy' for row 13. At the bottom are buttons for 'Output Settings', 'View Workspace', 'Start Test Mode', and 'Analyze Images'.

Update	Path / URL	Series	Frame	ChannelNumber	FileLocation	Plate	Site	Well
1	/Users/bdiazr...5_IllumER.npy	0	0		file:/Users/b...5_IllumER.npy	20585		
2	/Users/bdiazr...umHoechst.npy	0	0		file:/Users/b...umHoechst.npy	20585		
3	/Users/bdiazr...IllumMito.npy	0	0		file:/Users/b...IllumMito.npy	20585		
4	/Users/bdiazr...mPh_golgi.npy	0	0		file:/Users/b...mPh_golgi.npy	20585		
5	/Users/bdiazr...IllumSyto.npy	0	0		file:/Users/b...IllumSyto.npy	20585		
6	/Users/bdiazr...EC1D7F987.tif	0	0	1	file:/Users/b...EC1D7F987.tif	20585	1	A14
7	/Users/bdiazr...6B19E62EA.tif	0	0	2	file:/Users/b...6B19E62EA.tif	20585	1	A14
8	/Users/bdiazr...2DCC8C7A7.tif	0	0	3	file:/Users/b...2DCC8C7A7.tif	20585	1	A14
9	/Users/bdiazr...00725BE1D.tif	0	0	4	file:/Users/b...00725BE1D.tif	20585	1	A14
10	/Users/bdiazr...CAC606739.tif	0	0	5	file:/Users/b...CAC606739.tif	20585	1	A14
11	/Users/bdiazr...8075D7EFC.tif	0	0	1	file:/Users/b...8075D7EFC.tif	20585	2	A14
12	/Users/bdiazr...AD9EF6616.tif	0	0	2	file:/Users/b...AD9EF6616.tif	20585	2	A14
13	/Users/bdiazr...R10Q2F7D95.tif	n	n	3	file:/Users/b...R10Q2F7D95.tif	20585	2	A14

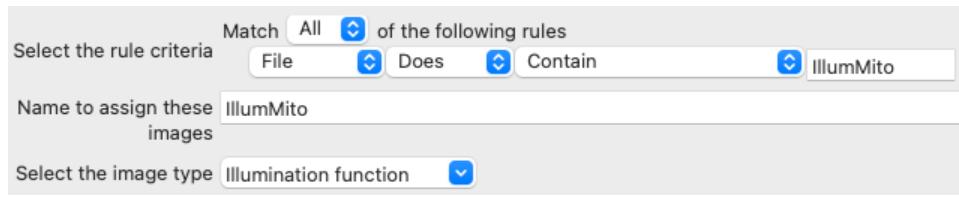
Figure 3: The Metadata module, columns in table correspond to metadata categories

- In the ‘NamesAndTypes’ module, we assign names to the images and configure image sets (i.e., all the different channels for a field of view). The channel mapping here is a bit complicated – we have a single set of illumination correction images (one ‘.npy’ file per channel) that map to each and every well and site. We will use the metadata we extracted in the previous module to make that association possible.
- The ‘NamesAndTypes’ module is fully configured already but scroll and look through the configuration to see the two different ways of mapping images to channel names that are demonstrated here. (There are several other ways to create correct mappings, but these may serve as a helpful example to refer to in your own work).
  - The ‘.tif’ image files are assigned a name by the Metadata extracted in the previous module (specifically ChannelNumber)

The screenshot shows the 'Image mapping' configuration interface. At the top, it says 'Match All 1 of the following rules'. Below this is a 'Select the rule criteria' section with a dropdown menu showing 'Metadata Does Have ChannelNumber matching 1'. Underneath are three dropdown menus: 'Name to assign these images' (set to 'OrigHoechst'), 'Select the image type' (set to 'Grayscale image'), and 'Set intensity range from' (set to 'Image metadata').

Figure 4: Image mapping using extracted metadata

- The ‘.npy’ illumination correction functions are assigned a name based on a unique string in the filename (such as ‘IllumER’)



*Figure 5: Image mapping using filename*

- As there is only one set of illumination correction functions for each entire plate, the image sets cannot simply be constructed by using ‘Image set matching’ as ‘Order’.
- Scroll to the bottom of the ‘NamesAndTypes’ to see how the image sets are constructed ‘Image set matching’ is set to ‘Metadata’
  - Each image channel is set to ‘Plate → Well → Site’.
  - Each illumination correction function is set to ‘Plate → (None) → (None)’

Image set matching method	Metadata	Plate	Plate	Plate	Plate	Plate	Plate	Plate	Plate	Plate	Plate	Plate	Plate	Plate	Plate
Match metadata		IllumER	IllumHoechst	IllumMito	IllumPh_golgi	IllumSyt0	OrigER	OrigHoechst	OrigMito	OrigPh_golgi	OrigSyt0				
		Plate	Plate	Plate	Plate	Plate	Plate	Plate	Plate	Plate	Plate	Plate	Plate	Plate	Plate
		(None)	(None)	(None)	(None)	(None)	(None)	(None)	(None)	(None)	(None)	(None)	(None)	(None)	(None)

*Figure 6: Image set matching using extracted metadata*

- For this exercise the ‘Groups’ module is not needed so it is set to ‘No’, this module can be useful when you have more than one plate, or different movies.
- For more information and examples on how to configure the Input modules we have created a blog and video tutorial that can be accessed here: <https://carpenter-singh-lab.broadinstitute.org/blog/input-modules-tutorial>.

### 3. Examine the output of the CorrectIlluminationApply module. (2min)

Since microscope objectives don’t typically have a completely uniform illumination pattern, applying an illumination correction function can help improve our segmentation and measurements by compensating for this. Pay close attention to the top of the field of view to see the greatest effect of correction.

- Enter test mode by clicking on the ‘Start Test Mode’ button at the bottom left corner of the window and hit ‘Step’ to run the CorrectIlluminationApply module.
- Briefly examine the output of the CorrectIlluminationApply module—you can see that the illumination correction functions show uneven illumination across the field of view.
- These functions were created by averaging and smoothing all 3456 images from this plate, so dim areas in the illumination correction function are areas of the field of view that are consistently dimmer across many images.

- Also note that while the illumination correction functions for each channel are similar, they aren't identical; each channel in your own experiments should therefore be illumination corrected independently.

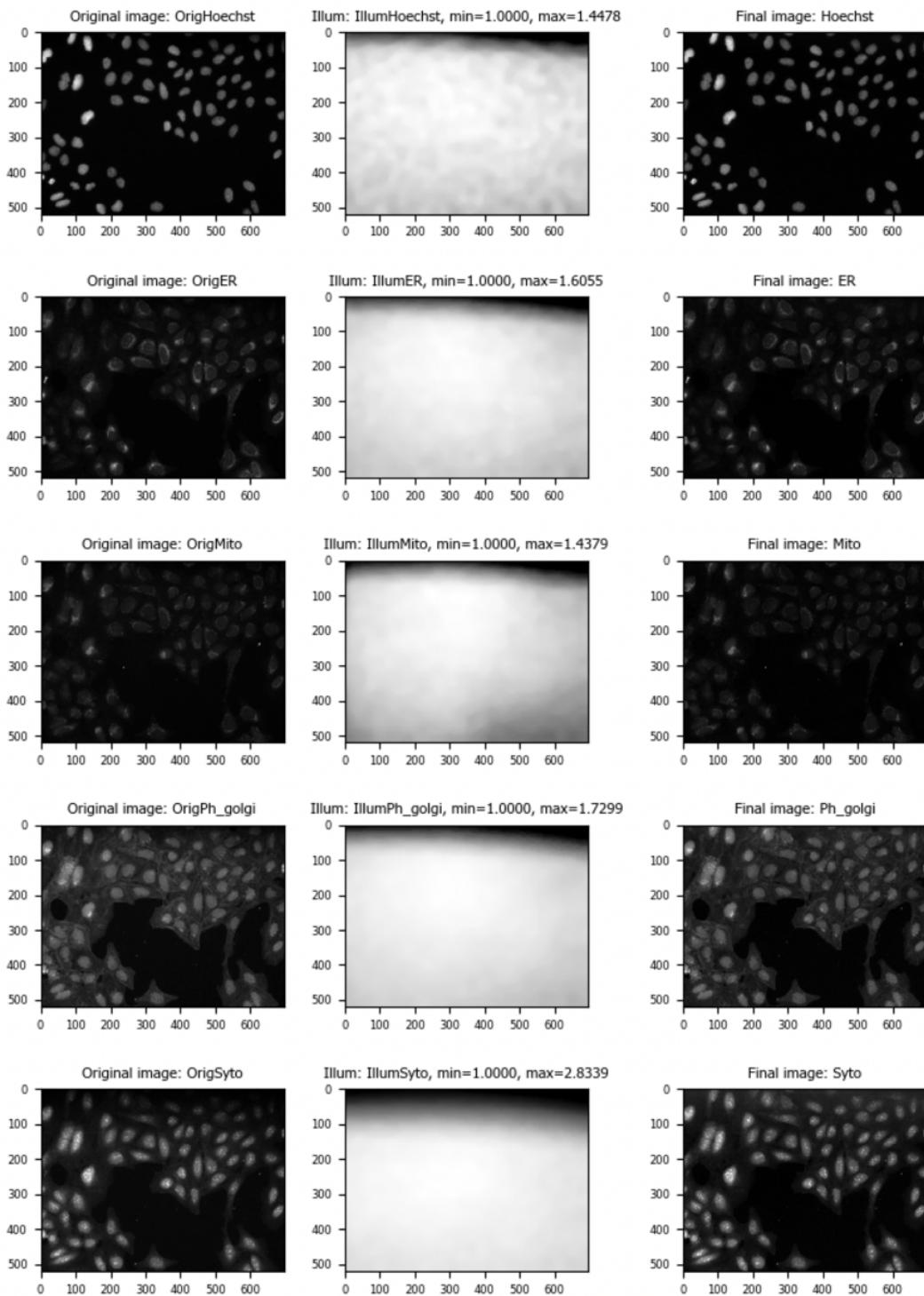


Figure 7: Application of the illumination correction function

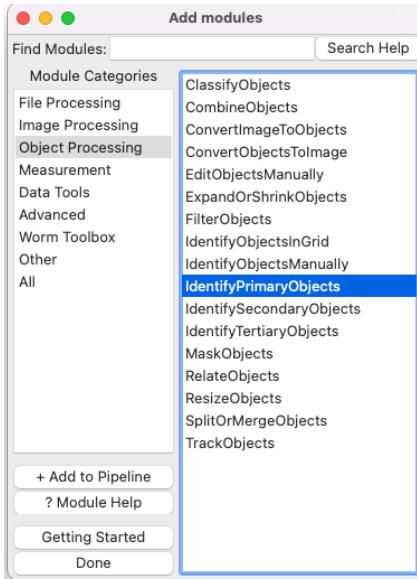
#### 4. IdentifyPrimaryObjects – Nuclei (10min)

Next, we'll take a first pass at identifying nuclei and cells in our initial image.

- After the CorrectIlluminationApply module, add an IdentifyPrimaryObjects module (from the 'Object

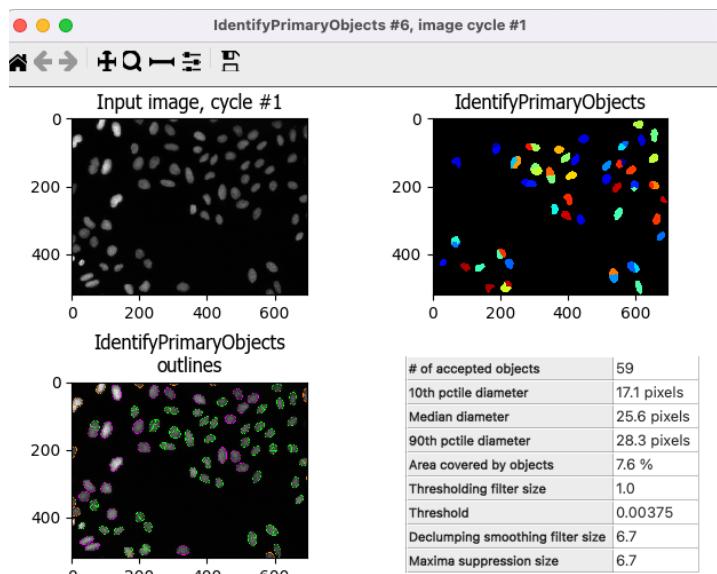
Processing' module category). Do this by clicking on the '+' sign in the bottom left corner of the CellProfiler window, which will pop up a small window called 'Add modules.'.

- Tip: You can also use the search bar at the top of the 'Add modules' window to search all modules by name.



*Figure 8: The Add modules window, modules are divided in categories based on their function*

- Create objects called Nuclei by segmenting on the Hoechst channel.
  - Select 'Hoechst' image as your input image from the drop-down menu.
  - Change the name of the output objects to 'Nuclei'.
- Hit 'Step' to run the module. How does your segmentation look?
- On the outlines display pane (bottom left) you can see three different colors; green is for accepted objects, orange for objects touching the border, and pink for objects outside the diameter range.
- On the table pane (bottom right) there is useful information that you can use to adjust your segmentation settings, like the median diameter, and the threshold.



*Figure 9: The IdentifyPrimaryObjects module output, you can use the information in this window to modify your segmentation parameters*

- Use the magnifying glass at the top of the window to zoom in on an area that was segmented poorly.
- **TO DO:** Improve your segmentation of nuclei:
  - Select ‘Yes’ for the ‘Use advance settings?’ option, then change some of the parameters:
    - Adjust the threshold method, may lead to better (or worse!) results.
    - Adjust the declumping settings.
  - Hit ‘Step’ to rerun and see how the changes affect the segmentation.
  - Adjust the segmentation parameters until you feel you’re ready to move on to identifying the cells around the nuclei; the identification should be good but doesn’t need to be perfect before you move on.

## 5. IdentifySecondaryObjects – Cells (5min)

- After the IdentifyPrimaryObjects, add an IdentifySecondaryObjects module.
- Create an object called Cells that is seeded on the Nuclei primary objects that you just created; select the Ph\_golgi image for your input image, nuclei for input objects and change the name to ‘Cells’.
- Hit ‘Step’ to run the module. How does your segmentation look?
- For this module the outline colors correspond to the object seed (green-nuclei) and the segmented objects (pink-cell)

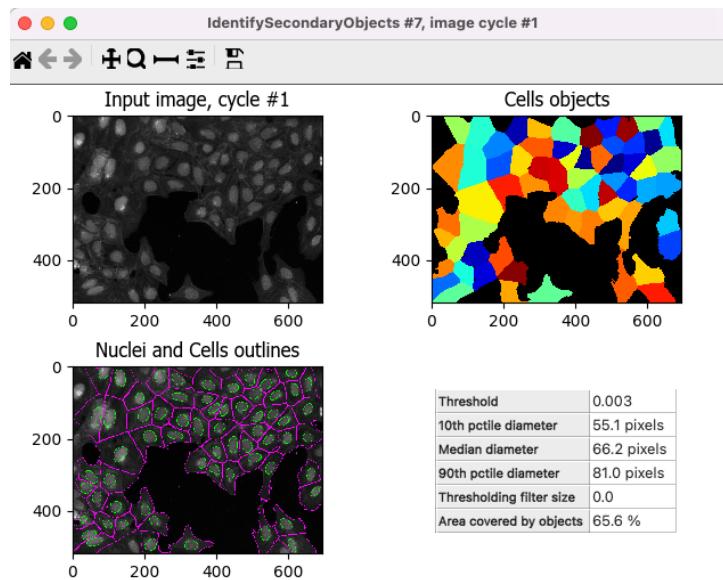


Figure 10: The IdentifySecondaryObjects module output

- **TO DO:** Improve cell segmentation
  - Examine the segmentation and adjust the segmentation parameters until you feel you’re ready to test them on another image; they don’t need to be perfect.
  - Adjust the threshold method.
  - Test the effects of using the various methods for identifying secondary objects (Propagation, Watershed-Image, Distance-N, etc) and, if using Propagation, the regularization factor.

## 6. Test the robustness of your segmentation parameters across images (5min)

It’s (relatively!) easy to come up with a good set of segmentation parameters for a single image however we aim to create a set of parameters that can segment cells on all the images on an experiment.

- To test the parameters, there are two options to change the image you are working on in Test Mode

- Click on the ‘Next Image Set’ at the bottom left corner, or
- Go to ‘Test’ on the top menu bar → Choose Image Set to bring up a list of the images in your experiment, select the image you want to test, and press the ‘OK’ button.
  - Tip: you can also use the Test menu to choose a random image set

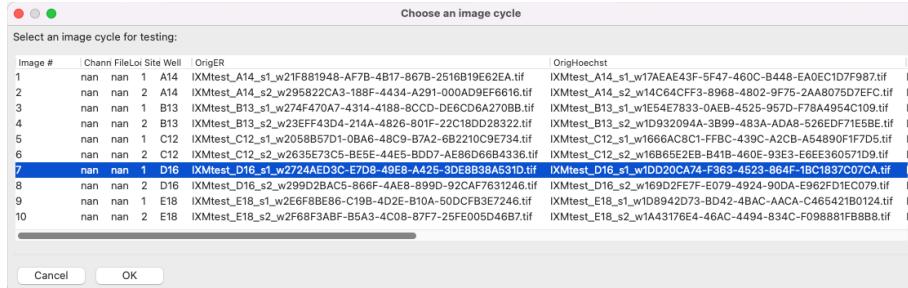


Figure 11: A section of the ‘Choose Image Set’ menu.

- Then run that image in test mode for your first 3 modules (through your IdentifySecondaryObjects step).
  - You can do it by clicking the step button, or
  - You can add a pause button on the module after IdentifySecondaryObjects and hit ‘Run’, this will run all modules before the pause.

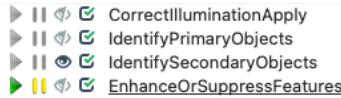


Figure 12: A section of the ‘Analysis modules’ pane.

- Examine the output – did your nuclear and cellular segmentation hold up compared to the first images you looked at?
- **● TO DO:** Adjust the parameters to get comparable results to the first image. Once your segmentation is good, try it on another image.

## 7. IdentifyTertiaryObjects- Cytoplasm (2min)

- After the IdentifySecondaryObjects module, add an IdentifyTertiaryObjects module.
- Create an object called Cytoplasm using the Cell and Nuclei objects you’ve created.
  - Select the larger and smaller identified objects from the drop-down menu.
  - Change the name of the objects to be identified.
  - ‘Shrink smaller object prior to subtraction?’ should both set to ‘No’.

## 8. Examine the steps used to segment the Nucleoli (15min)

So far, we have used untransformed images for object detection, but not all objects can be segmented from raw images. CellProfiler contains a variety of image processing modules that can aid segmentation. For this exercise, we will use two such modules, but there are other ones you can explore.

The next 3 modules have to do with the creation of the Nucleoli objects. Look at the output from each to see how the image is transformed to aid in segmentation.

- After the IdentifyTertiaryObjects module, add an EnhanceOrSuppressFeatures module.
- EnhanceOrSuppressFeatures is a module that helps enhance parts of an image- in this case, punctate objects or ‘Speckles’. As we are looking for nucleoli, we apply this to the RNA channel (Syto) image and call the output ‘FilteredRNA’.

## ● TO DO: Enhance nucleoli spots

- Change the input image from the drop-down menu to ‘Syto’
- Change the name of the output image to ‘FilteredRNA’
- Change the feature size to see how this affects the output and find a value that works well.
- See below for an example of results to aim for:

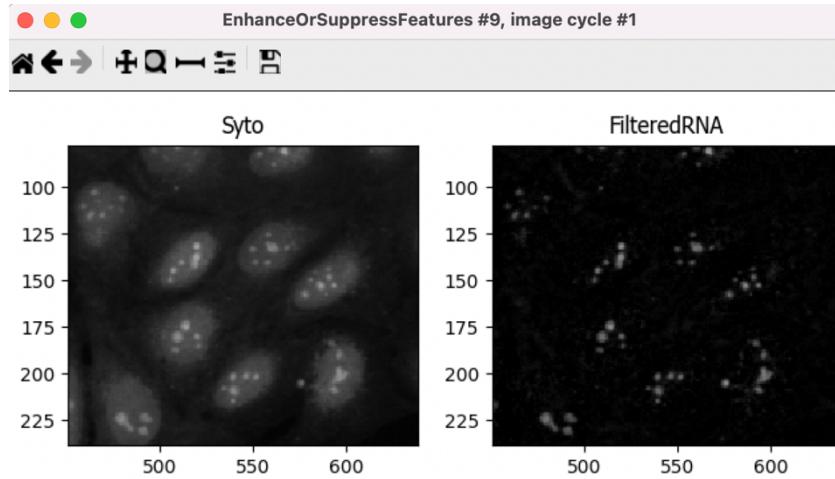


Figure 13. The EnhanceOrSuppress module output, enhancing the Syto image allows you to isolate nucleoli against the nucleoplasmic background signal.

- After the EnhanceOrSuppressFeatures module, add an MaskImage module.
  - MaskImage allows you to create a version of the ‘FilteredRNA’ image called ‘SytoNuclei’ where all the pixels except the ones you specify are set to an intensity of 0. In this case, we set to 0 any pixel not inside a nucleus. By doing this, we can decrease the likelihood of detecting cytoplasmic RNA dots.

## ● TO DO: Mask the RNA image to show only the ‘Nuclei’

- Change the input image from the drop-down menu to ‘FilteredRNA’
- Change the name of the output image to ‘SytoNuclei’
- Use the objects ‘Nuclei’ as the mask.
- See below for an example of results to aim for:

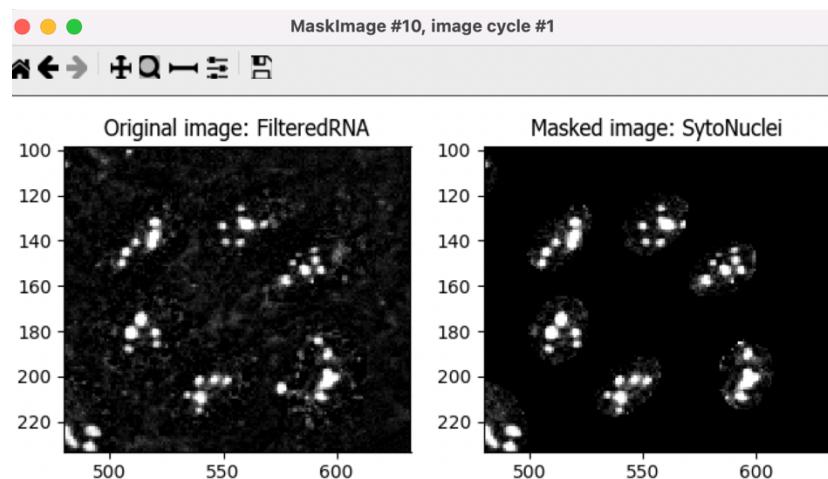


Figure 14. The MaskImage module output, the contrast was adjusted to show that the intensity of the pixels outside the nuclei are now set to 0.

- IdentifyPrimaryObjects is used to find the Nucleoli. This is a Primary object segmentation because we are not using another object as a seed (i.e., starting point), and are only segmenting based off the intensity in our ‘SytoNuclei’ image.

### ● TO DO: Segment nucleoli

- Change the input image from the drop-down menu to ‘SytoNuclei’
- Change the name of the objects to ‘Nucleoli’
- Adjust the segmentation parameters until you are satisfied with the segmentation results.

● TO DO: Add an ‘OverlayOutlines’ module at this point to overlay the identified nucleoli on the original Syto image to assure yourself that the segmentation not only matches the speckle enhanced ‘SytoNuclei’ image, but also looks accurate on the unprocessed image as well. This is not strictly necessary but can be a nice “sanity check”.

- Goal: display outlines of your nucleoli and your nuclei on the unprocessed ‘Syto’ image.
- Here’s an example of what that could look like (red=nuclei, green=nucleoli):
  - Tip: you can use a similar strategy to segment mitochondria using the ‘Mito’ channel

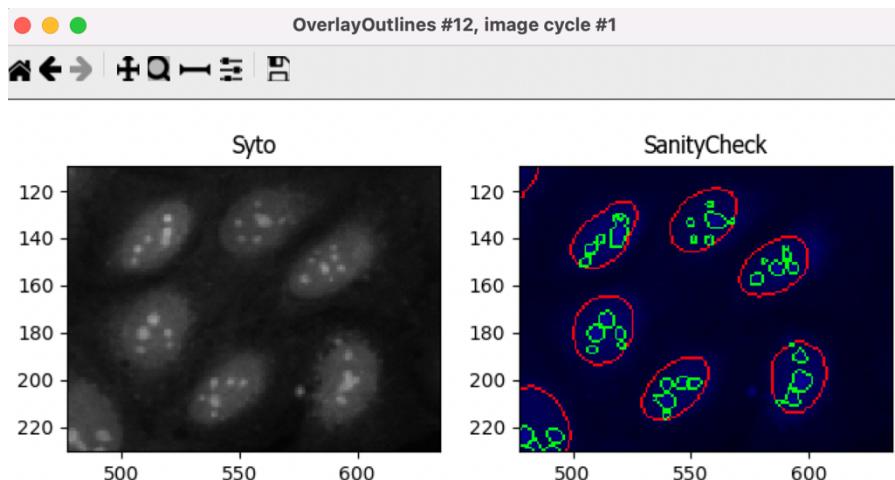


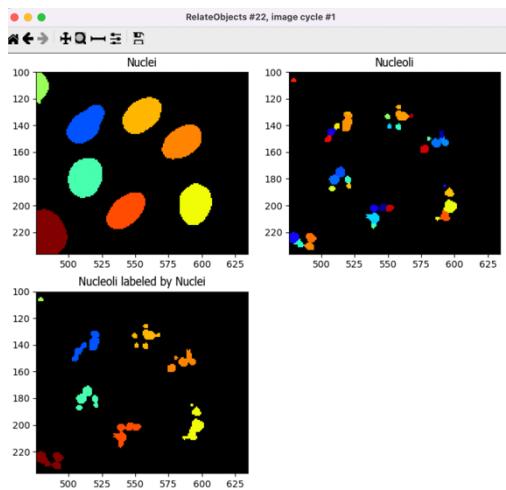
Figure 15. The OverlayOutlines module output, all detected nucleoli are within the nuclei.

### 9. ● TO DO: Add measurement modules to your pipeline (10min)

- After your segmentation of the nucleoli, add as many object measurement modules as you would like, we have added a MeasureObjectIntensity.
- Some suggested modules to add: MeasureObjectSizeShape, MeasureObjectIntensity, MeasureGranularity, MeasureObjectNeighbors.
- Which objects do you think would be valuable to measure with each of these modules? Which channels would you measure your objects in? For a typical Cell Painting experiment you would add as many measurements as possible, but that isn’t necessary here; however, do make sure every object gets at least some measurements. Note: While MeasureCorrelation, MeasureTexture, and MeasureObjectIntensityDistribution can produce valuable data for downstream profiling, they can be memory-intensive and/or slow so should not be added for this example pipeline in the interest of pipeline runtime.

## 10. RelateObjects (5min)

- ● **TO DO:** Add a RelateObjects module and configure it to relate ‘Nucleoli’ to ‘Nuclei’.



*Figure 17: The RelateObject module output.*

Relating the objects allows you to create per-parent means (e.g., for this cell, what is the average size of an individual mitochondrion) and calculate distances from the child objects to the edge and/or the center of the parent (e.g., how far is each nucleolus from the center of the nucleus).

## 11. Run the pipeline (optional)

- If you have time, add a ExportToSpreadsheet module at the end.
- Exit test mode.
- Click on ‘Output Settings’ button at the bottom left corner.
- Change the default output folder.
- Click on ‘Analyze Images’ button at the bottom left corner.
- Explore the spreadsheets created for each object.