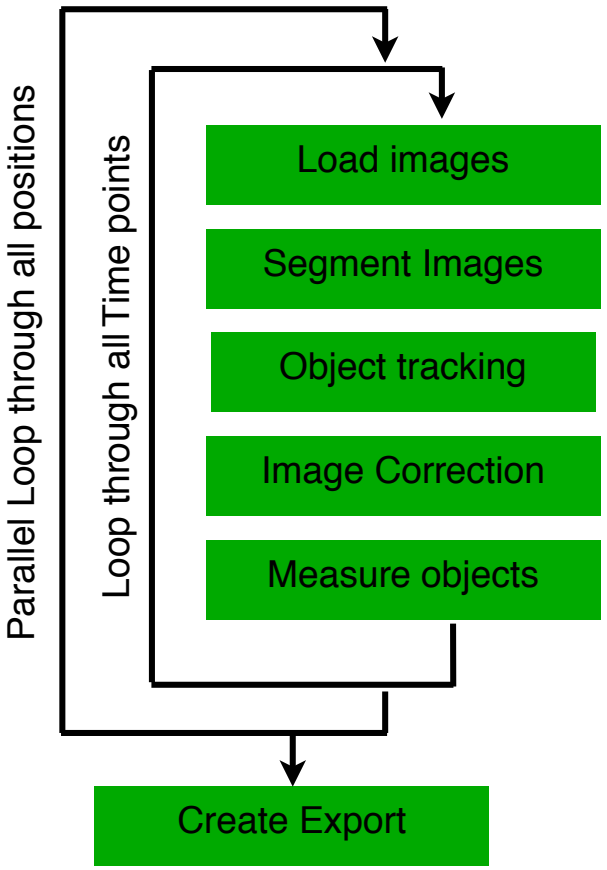
YeastQuant 7 to 9

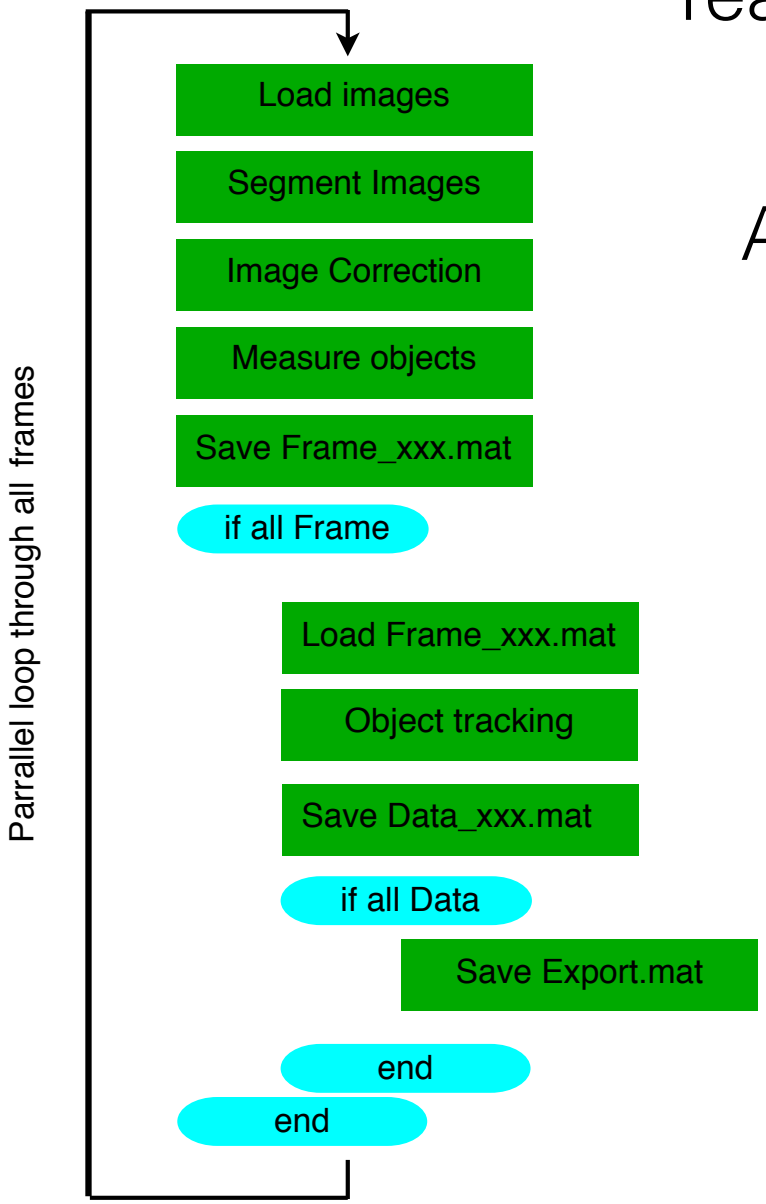


All positions are analyzed in parallel

For an analysis with 10 XY positions and 15 Time points
10 parallel processes

Export Files created when All positions are processed

YeastQuant X



All frames are analyzed in parallel

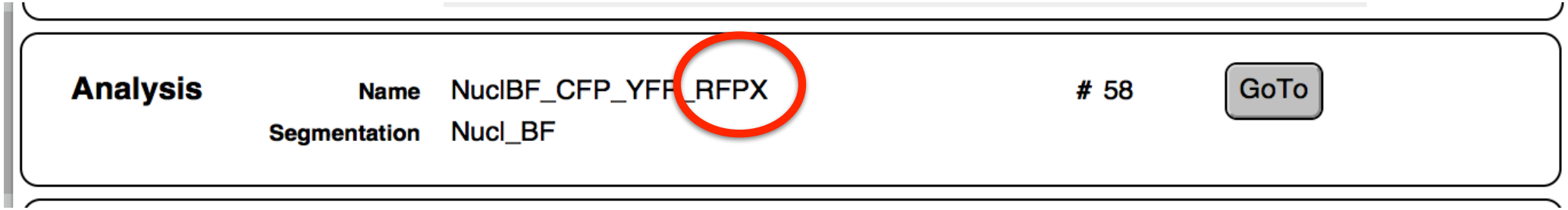
For an analysis with 10 XY positions and 15 Time points
150 parallel processes

Export Files created as soon as all Data.mat from one experiment are present

Database entries

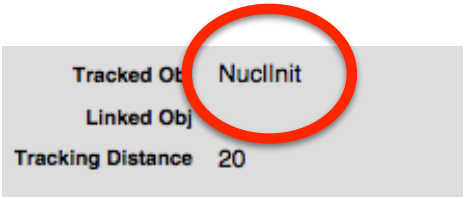
Same as before

BUT special analysis sheet

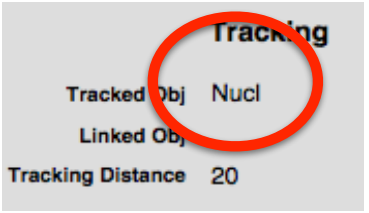


Main difference in analysis sheet:

YQ v9



YQ X



Analysis preparation for signaling server

Same as before!
but:

Simpler call of prepare analysis

```
VarCell = PrepareAnalysis([2125:2127], 'Linux')
```

Platform

ExpNum number

removed one level of cell to structure to VarCell

YQ v9

```
VarCell{1}{1}.Analysis.xyz
```

YQ X

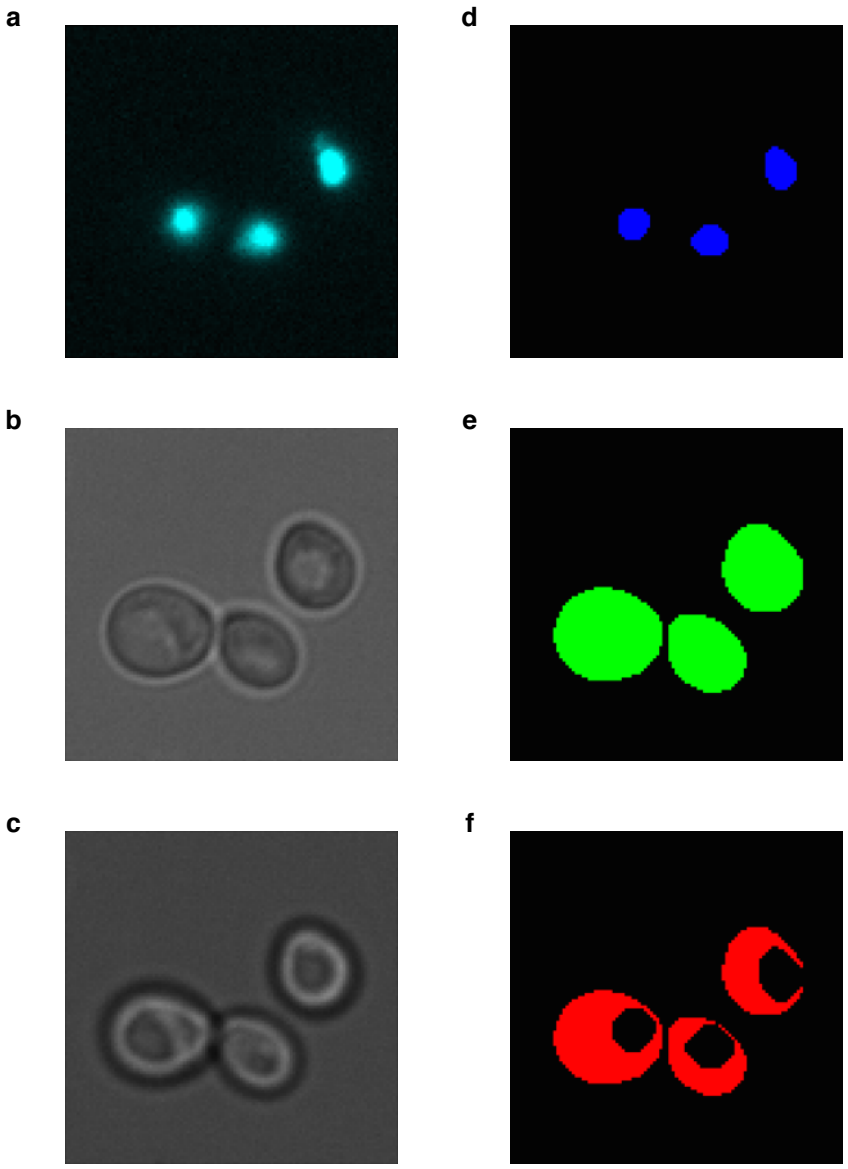
```
VarCell{1}.Analysis.xyz
```

Running the analysis on Signaling server

Start screen!
Start Matlab
load VarCell
Run ParallelFrameAnalysis

Main function: ParallelFrameAnalysis

```
function ParallelFrameAnalysis(VarCell, OverWrite)
%Overwrite = -1: Prepare only the VarFrame data
%OverWrite = 0: Perform segmentation only on missing Frame.mat files
%OverWrite = 1: Delete Data.mat file and reprocess the export file
%OverWrite = 2: Delete Frame.mat file and re-do the segmentation
```



Supplementary Figure 2: Image segmentation process using YeastQuant
a. - b. - c. Microscopy images used for the segmentation: histone tag CFP (**a**), bright field image in the focal plane (**b**), and out of focus bright field image (**c**, z=-2.5µm).
d. - e. - f. Different objects are defined by the segmentation process. First, the Nucleus is characterized using the CFP image (**d**). The two bright field images are used to find the cell contour and define the Cell object (**e**). Then, the Nucleus object, enlarged by 2 pixels, is subtracted to the Cell object, to define the Cytoplasm object (**f**).

Secondary object

Border definition:

get border pixels

Size = N
Expand inside object by N # of pixels

Size = N.M
Expand inside object by N # of pixels
Expand outside object by M # of pixels

Perimeter definition

get border pixels

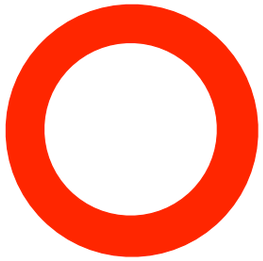
Circle definition

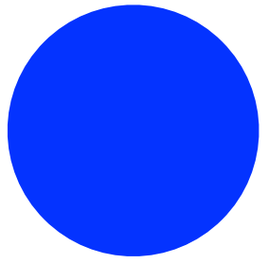
Match circle on cell shape
Size argument is not used

Intensity image not required for those object definitions

Expand small objects

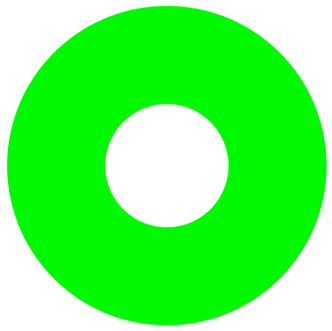
BORDER



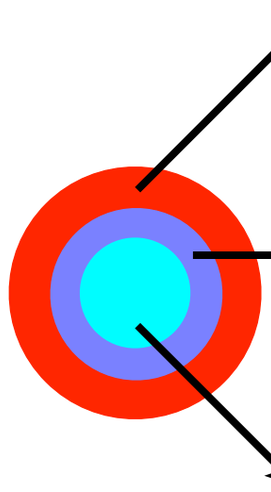


CELL

Grow small object by N pixels



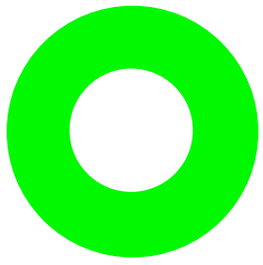
Border



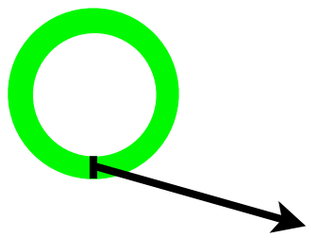
Rim (4 pix wide)

Cyto (should fill the entire cell middle, 5 pix away from Border so should not overlap with the Rim)

Exclude pixels outside large object



Exclude pix from small object with added border B



= N-B