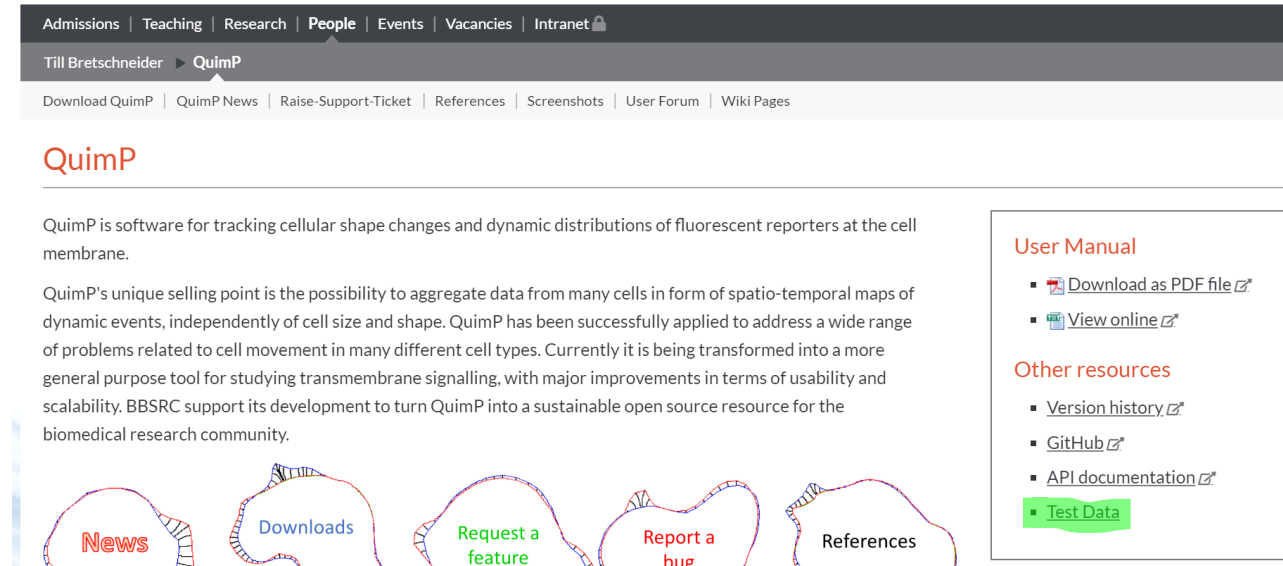


warwick.ac.uk/quimp

- <https://github.com/CellDynamics/QuimP> - issue tracker, source code
- <https://github.com/CellDynamics/QuimP-Python> - Python notebook with integration examples

Workshop files

- warwick.ac.uk/quimp/test_data
- Download:
 - [Example Analysis \(single cell\)](#)



The screenshot shows the QuimP website homepage. At the top is a navigation bar with links for Admissions, Teaching, Research, People, Events, Vacancies, and Intranet. Below this is a sub-navigation bar for Till Bretschneider, with a dropdown menu for QuimP. A secondary navigation bar contains links for Download QuimP, QuimP News, Raise-Support-Ticket, References, Screenshots, User Forum, and Wiki Pages. The main heading is "QuimP". The text describes QuimP as software for tracking cellular shape changes and dynamic distributions of fluorescent reporters at the cell membrane. It highlights the software's unique selling point: the ability to aggregate data from many cells into spatio-temporal maps of dynamic events, independent of cell size and shape. It also mentions that QuimP has been successfully applied to address a wide range of problems related to cell movement in many different cell types and is currently being transformed into a more general purpose tool for studying transmembrane signalling, with major improvements in terms of usability and scalability. BBSRC support is mentioned as a key factor in turning QuimP into a sustainable open source resource for the biomedical research community. At the bottom, there are five icons representing different sections: News, Downloads, Request a feature, Report a bug, and References. On the right side, there is a sidebar with a "User Manual" section containing links for "Download as PDF file" and "View online". Below that is an "Other resources" section with links for "Version history", "GitHub", and "API documentation". A green button labeled "Test Data" is also present in the sidebar.

Admissions | Teaching | Research | People | Events | Vacancies | Intranet

Till Bretschneider ▾ QuimP

Download QuimP | QuimP News | Raise-Support-Ticket | References | Screenshots | User Forum | Wiki Pages

QuimP

QuimP is software for tracking cellular shape changes and dynamic distributions of fluorescent reporters at the cell membrane.

QuimP's unique selling point is the possibility to aggregate data from many cells in form of spatio-temporal maps of dynamic events, independently of cell size and shape. QuimP has been successfully applied to address a wide range of problems related to cell movement in many different cell types. Currently it is being transformed into a more general purpose tool for studying transmembrane signalling, with major improvements in terms of usability and scalability. BBSRC support its development to turn QuimP into a sustainable open source resource for the biomedical research community.

News Downloads Request a feature Report a bug References

User Manual

- [Download as PDF file](#)
- [View online](#)

Other resources

- [Version history](#)
- [GitHub](#)
- [API documentation](#)

[Test Data](#)

Installation

The screenshot displays the ImageJ Update Manager interface. It features a main window titled 'ImageJ Update Manager' and two overlapping 'Manage update sites' dialog boxes.

The background dialog, titled 'Manage update sites', contains a table with the following columns: 'A...' (checkbox), 'Name', 'URL', and 'Host'. The 'QuimP' entry is selected with a checkmark.

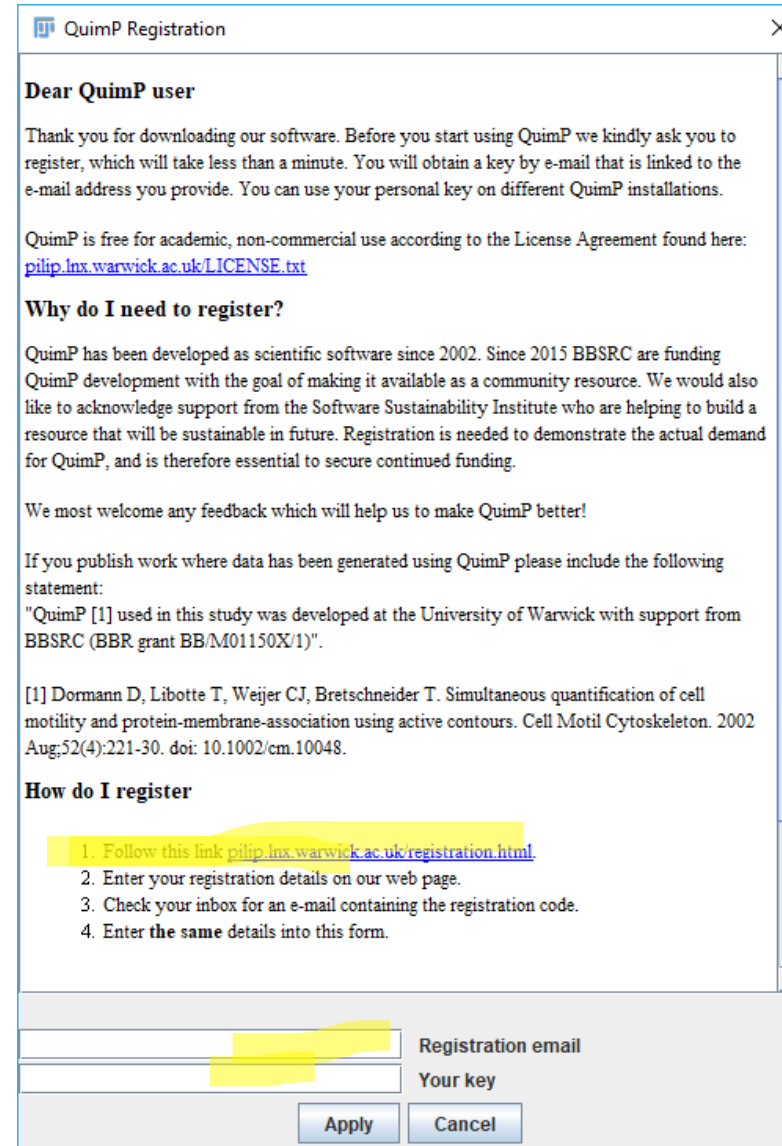
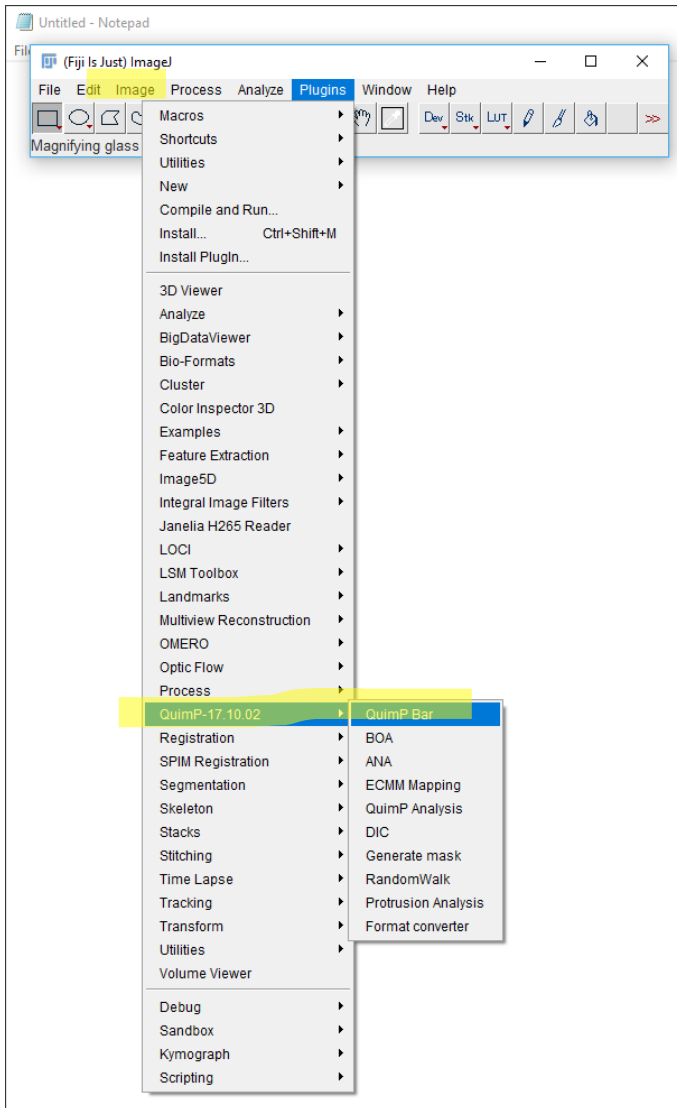
A...	Name	URL	Host
<input type="checkbox"/>	OMERO 5.1	http://sites.imagej.net/OMERO-5.1/	
<input type="checkbox"/>	OMERO 5.2	http://sites.imagej.net/OMERO-5.2/	
<input type="checkbox"/>	OpenSPIM	http://openspim.org/update/	
<input type="checkbox"/>	OPTIMISME	http://sites.imagej.net/Dbenielli/plugins/	
<input type="checkbox"/>	Oxford Oncology	http://sites.imagej.net/MicroscopyOncologyOxford/	
<input type="checkbox"/>	ParticleSizer	http://sites.imagej.net/Ndef-psizer/	
<input type="checkbox"/>	Pendent Drop	http://sites.imagej.net/Daerr/	
<input type="checkbox"/>	PET-CT	http://sites.imagej.net/Ilan/	
<input type="checkbox"/>	PHANTAST	http://sites.imagej.net/Nicjac/	
<input type="checkbox"/>	PhotonImaging	http://sites.imagej.net/PhotonImaging/	
<input type="checkbox"/>	PillarTracker	http://sites.imagej.net/PillarTracker/	
<input type="checkbox"/>	PTBIOP	http://biop.epfl.ch/Fiji-Update/	
<input type="checkbox"/>	Quantixed	http://sites.imagej.net/Quantixed/	
<input checked="" type="checkbox"/>	QuimP	http://pilip.lnx.warwick.ac.uk/quimp-update-site/	
<input type="checkbox"/>	Radial Symmetry	http://sites.imagej.net/Milkyklim/	
<input type="checkbox"/>	RadialIntensityProfile	http://sites.imagej.net/PTschaikner/	
<input type="checkbox"/>	ResultsToExcel	http://sites.imagej.net/ResultsToExcel/	
<input type="checkbox"/>	RT-Multiview-Deconvoluti...	http://sites.imagej.net/RT-Multiview-Deconvolution/	
<input type="checkbox"/>	Sceptical Physiologist	http://sites.imagej.net/Scepticalphysiologist/	
<input type="checkbox"/>	SCF MPI CBG	http://sites.imagej.net/SCF-MPI-CBG/	
<input type="checkbox"/>	ScientiFig	http://sites.imagej.net/Aigouy/	
<input type="checkbox"/>	Scientifig-deprecated	http://sites.imagej.net/SF-Deprecated-Legacy/	
<input type="checkbox"/>	Scijava Jupyter Kernel	http://sites.imagej.net/Scijava-jupyter-kernel/	
<input type="checkbox"/>	SIMcheck	http://downloads.micron.ox.ac.uk/fiji_update/SIMc	

The foreground dialog, also titled 'Manage update sites', contains a table with columns: 'A...' (checkbox), 'Name', and 'URL'. The 'ImageJ', 'Fiji', and 'Java-8' entries are selected with checkmarks.

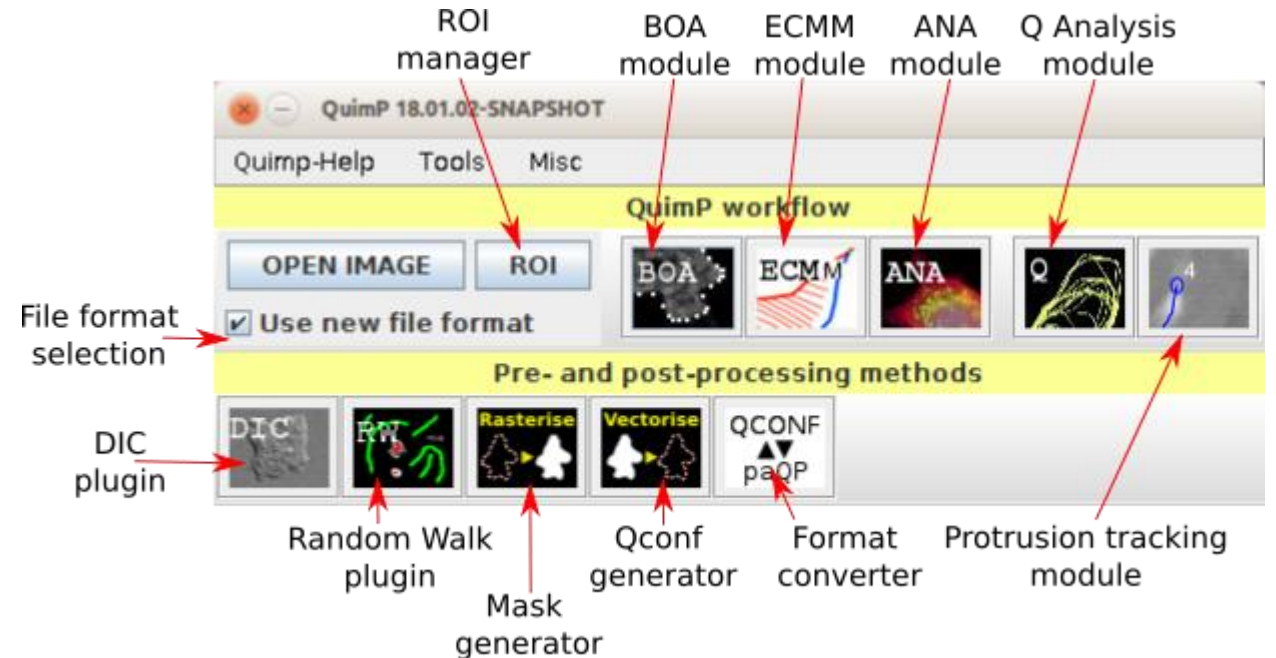
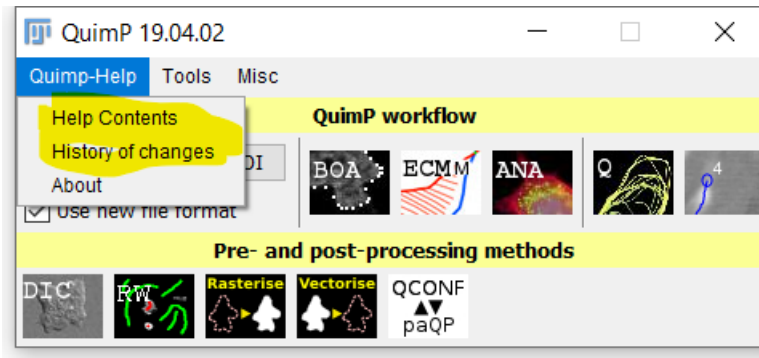
A...	Name	URL
<input checked="" type="checkbox"/>	ImageJ	http://update.imagej.net/
<input checked="" type="checkbox"/>	Fiji	http://update.fiji.sc/
<input checked="" type="checkbox"/>	Java-8	http://sites.imagej.net/Java-8/
<input type="checkbox"/>	2015-Conference	http://sites.imagej.net/2015-Conference/
<input type="checkbox"/>	3D ImageJ Suite	http://sites.imagej.net/Tboudier/
<input type="checkbox"/>	Angiogenesis	http://sites.imagej.net/Angiogenesis/
<input type="checkbox"/>	AngioTool	http://sites.imagej.net/AngioTool/
<input type="checkbox"/>	Archipelago	http://sites.imagej.net/Lindsey/

At the bottom of the background dialog are buttons: 'Add my site', 'Add update site', 'Remove', and 'Close'. At the bottom of the foreground dialog are buttons: 'Apply changes', 'Advanced mode', and 'Cancel'. A yellow highlight is present on the 'Manage update sites' button in the bottom left corner of the main window.

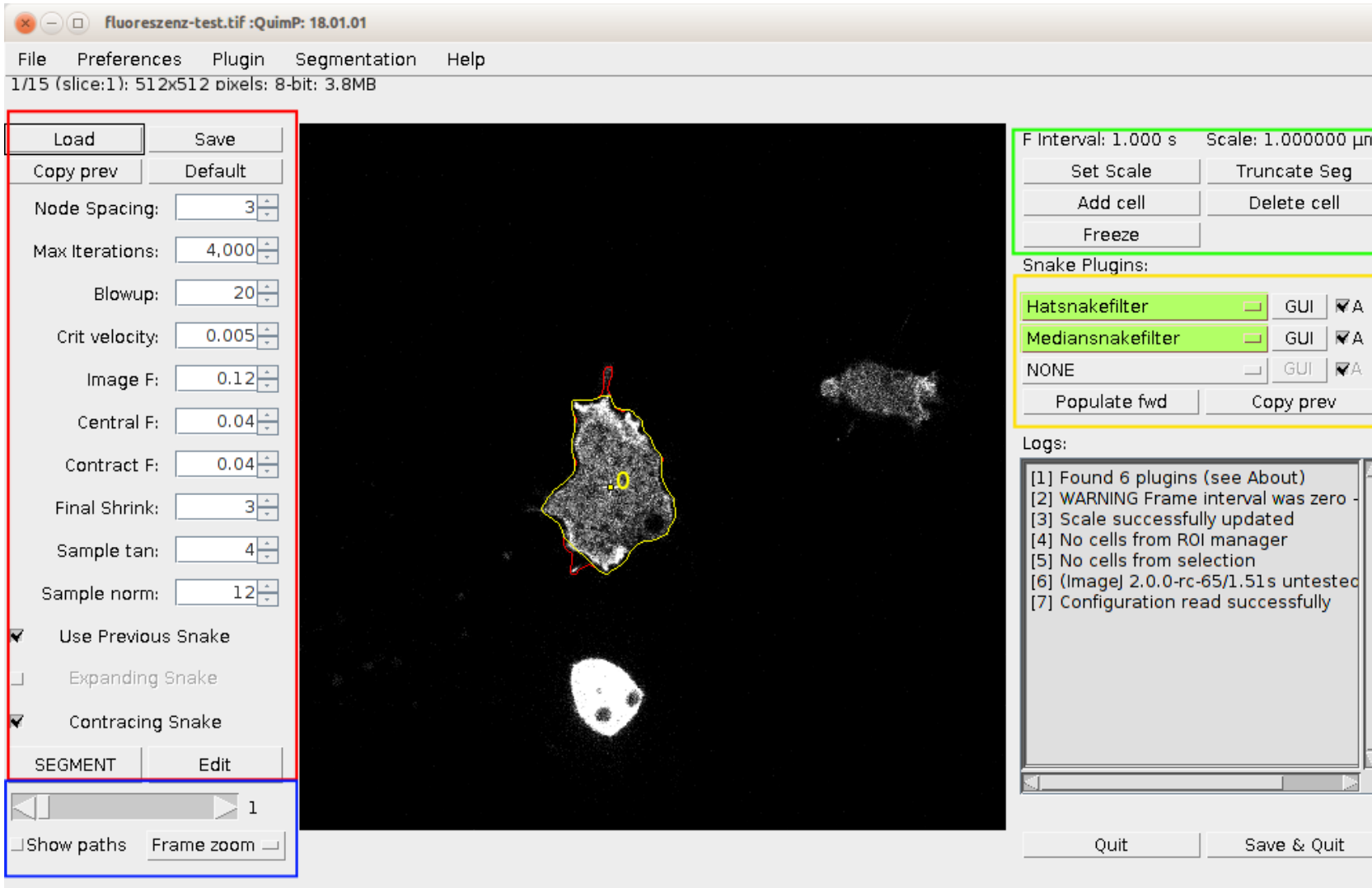
First run



Looking around



BOA - Basic segmentation



- Red: segmentation parameters
- Blue: controls for navigating through frames in a time series and for zooming cells visible in the current frame.
- Green: tools for manual editing of contours.
- Yellow: access to cell contour postprocessing filters (described in section [7.3](#)).

(User Manual, chapter 7)

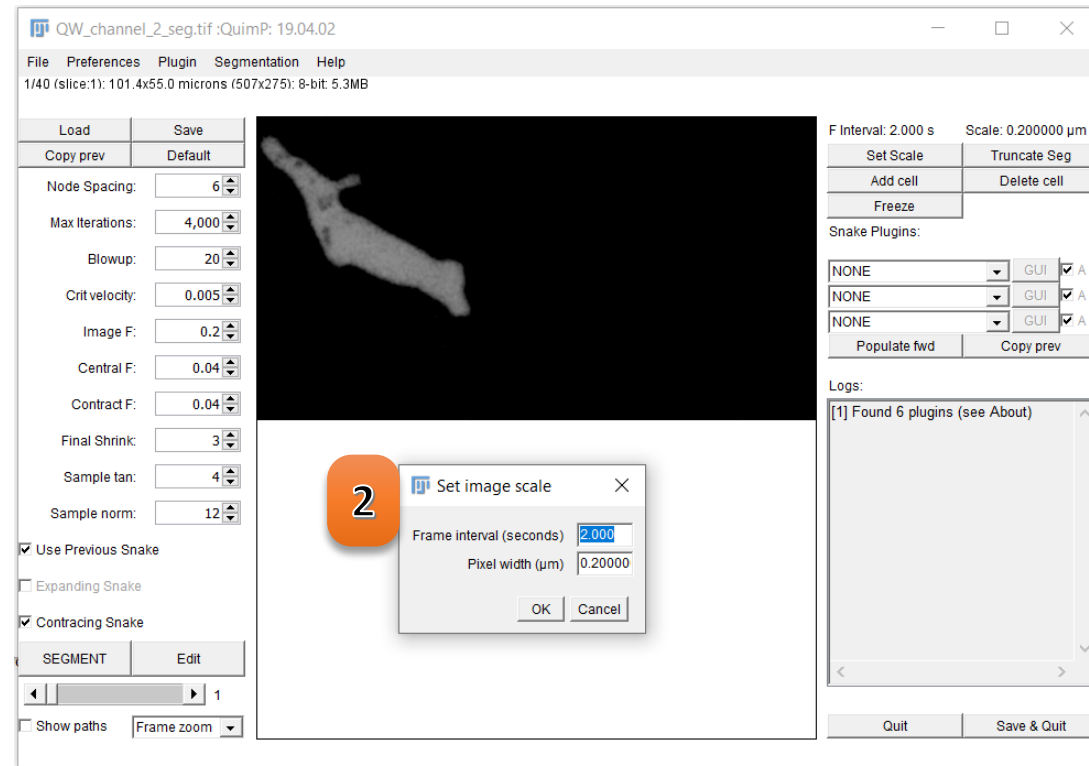
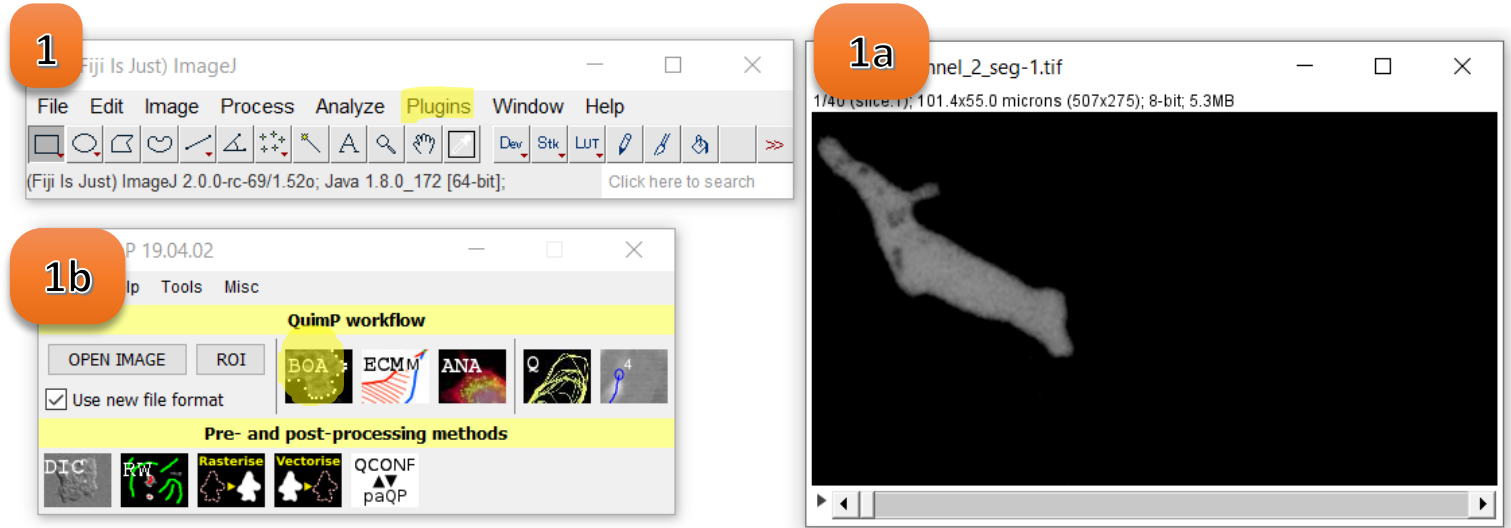
Walkthrough example

- The folder *QuimP_walkthrough* contains 4 tiff image sequences which you can analyse [1].
 - *QW_channel_1_actin.tif* - Actin label. Image and has been background corrected and contrast enhanced.
 - *QW_channel_2_neg.tif* - Negative stain. The cell appears as a shadow on a bright background, which has then been inverted.
 - *QW_channel_2_seg.tif* - For segmentation we shall use the negative stain channel. A 1 pixel Gaussian blur has been applied, the background removed, and contrast enhanced.
 - *QW_channel_2_talA.tif* – simulated talA label from corresponding binary mask by GAN network
 - *Segmentation.tif* - Already segmented image - will not be used in this tutorial.

[1] Images are courtesy of Evgeny Zatulovskiy, Rob Kay Group, MRC Laboratory of Molecular Biology

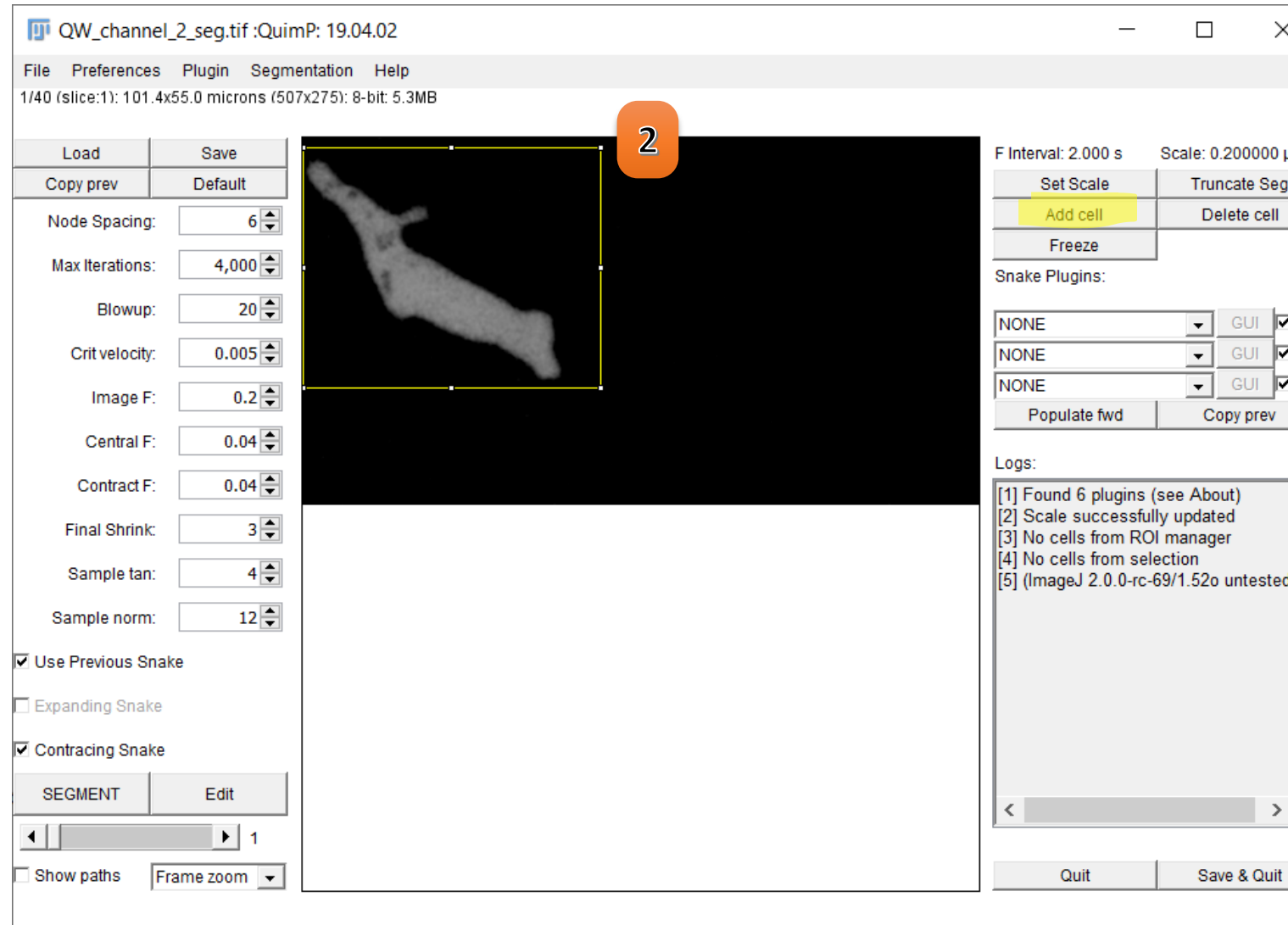
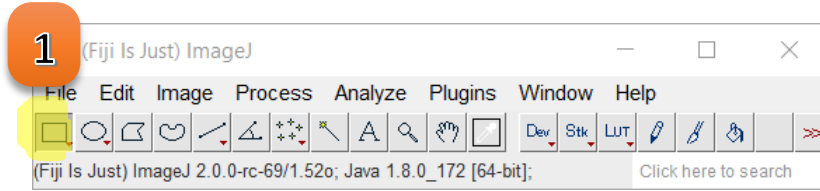
BOA

1. Open ImageJ and launch the QuimP bar [*Plugins* → *QuimP* → *QuimPBar*].
 - a) Open the image *QW_channel_2_seg.tif*.
 - b) Launch BOA from the QuimP bar.
2. At the prompt check the scale is correct (2 second frame interval, pixel width 0.2 microns).



BOA

1. Using the polygon selection tool,
2. create a selection encompassing the cell. This can be very rough. Click *Add cell*.



BOA

1. Adjust the parameters to get a good segmentation (default are fine).
2. Click *SEGMENT* and wait for completion.
3. Scroll through the sequence to check the segmentation result using either the scroll bar or mouse wheel. The segmentation should have completed to the last frame.

The screenshot displays the BOA software interface. The title bar reads "QW_channel_2_seg.tif :QuimP: 19.04.02". The menu bar includes "File", "Preferences", "Plugin", "Segmentation", and "Help". The status bar shows "40/40 (slice:196): 101.4x55.0 microns (507x275): 8-bit: 5.3MB".

The left panel contains a table with "Load" and "Save" columns, and "Copy prev" and "Default" sub-columns. Below this are various parameters with spinners: Node Spacing (6), Max Iterations (4,000), Blowup (20), Crit velocity (0.005), Image (0.2), Central F (0.04), Contract F (0.04), Final Shrink (3), Sample tan (4), and Sample norm (12). There are also checkboxes for "Use Previous Snake", "Expanding Snake", and "Contracting Snake". At the bottom of this panel are buttons for "SEGMENT" (highlighted in cyan) and "Edit".

The central image window shows a grayscale image of a cell with a yellow outline. A small yellow circle with the number "1" is overlaid on the image.

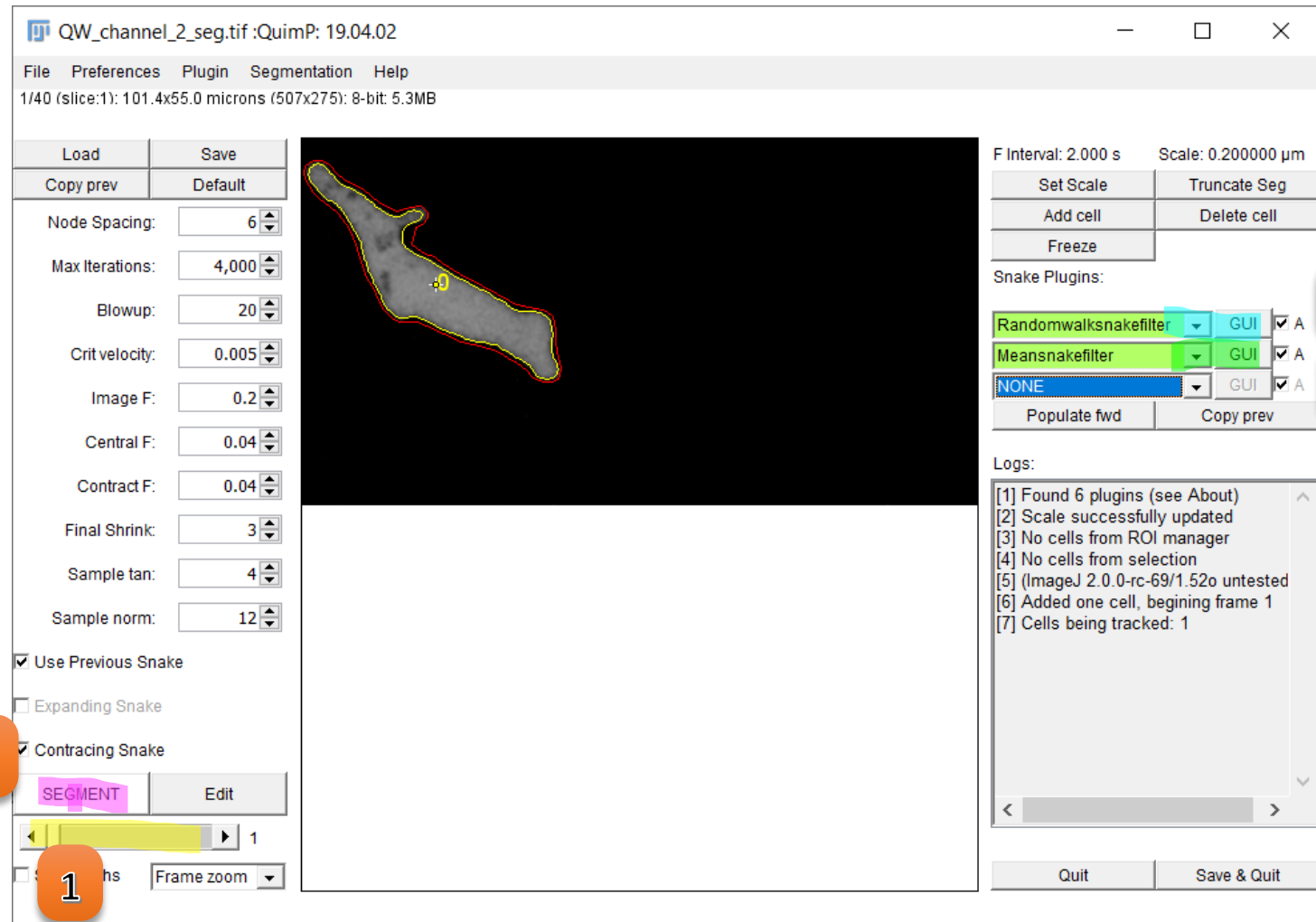
The right panel has a "Snake Plugins" section with three rows, each with a "NONE" dropdown, a "GUI" checkbox, and an "A" checkbox. Below this are "Populate fwd" and "Copy prev" buttons. The "Logs" section contains a list of messages: [1] Found 6 plugins (see About), [2] Scale successfully updated, [3] No cells from ROI manager, [4] No cells from selection, [5] (ImageJ 2.0.0-rc-69/1.52o untested), [6] Added one cell, beginning frame 1, [7] Cells being tracked: 1. At the bottom of the right panel are "Quit" and "Save & Quit" buttons.

Three orange circles with numbers 1, 2, and 3 are overlaid on the interface. Circle 1 is on the "Image" parameter. Circle 2 is on the "SEGMENT" button. Circle 3 is on the green scroll bar in the bottom panel.

BOA

We can try to improve segmentation in concave regions by using Random Walk plugin.

1. Scroll to the first frame
2. Select RandomWalkFilter in plugin selector at first position. Current view will be updated.
3. Select MeansnakeFilter at second slot. Current view will be updated.
4. Click SEGMENT and wait until segmentation finishes.
5. Scroll through the sequence to check the segmentation result.



BOA

1. Click *Save&Quit* – the QCONF file will be created.
2. This file can be loaded back to BOA if needed

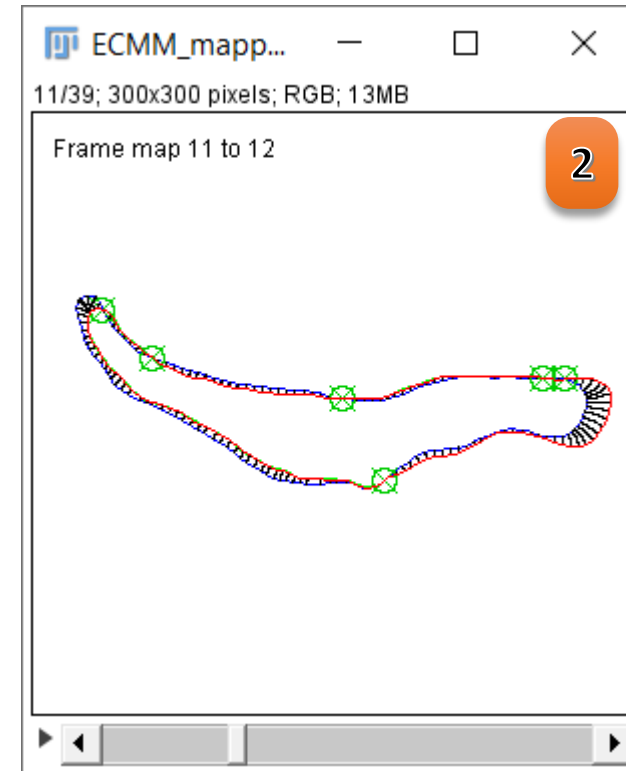
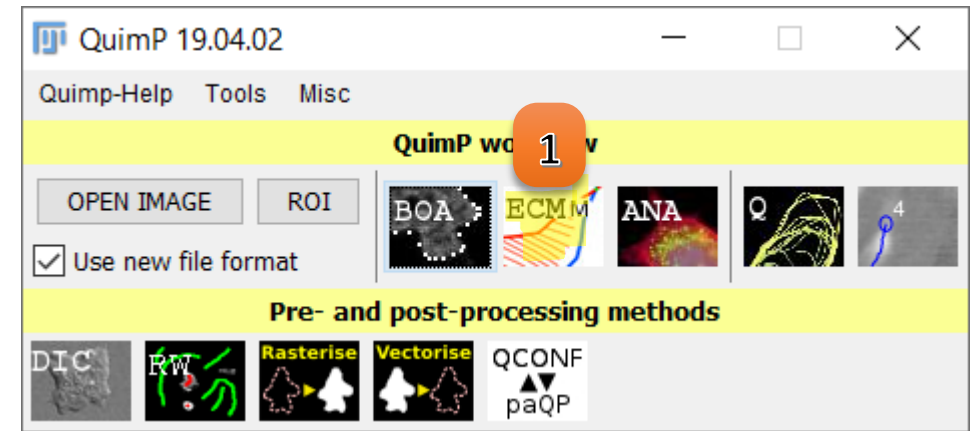
2

The screenshot shows the BOA software interface. The main window displays a grayscale image of a cell with a red and yellow outline. The interface includes a menu bar (File, Preferences, Plugin, Segmentation, Help), a status bar (1/40 (slice:1): 101.4x55.0 microns (507x275): 8-bit: 5.3MB), and several control panels. On the left, there are sliders for Node Spacing (6), Max Iterations (4,000), Blowup (20), Crit velocity (0.005), Image F (0.2), Central F (0.04), Contract F (0.04), Final Shrink (3), Sample tan (4), and Sample norm (12). Below these are checkboxes for 'Use Previous Snake', 'Expanding Snake', and 'Contracting Snake'. At the bottom left, there are 'SEGMENT' and 'Edit' buttons, a frame navigation bar showing '1', and a 'Show paths' checkbox with a 'Frame zoom' dropdown. On the right, there are buttons for 'Set Scale', 'Truncate Seg', 'Add cell', 'Delete cell', and 'Freeze'. Below these are 'Snake Plugins' with dropdowns for 'Randomwalksnakefilter', 'Meanssnakefilter', and 'NONE', each with a 'GUI' checkbox. At the bottom right, there is a 'Logs' panel with a list of messages: '[1] Found 6 plugins (see About)', '[2] Scale successfully updated', '[3] No cells from ROI manager', '[4] No cells from selection', '[5] (ImageJ 2.0.0-rc-69/1.52o untested', '[6] Added one cell, beginning frame 1', and '[7] Cells being tracked: 1'. At the very bottom right, there are 'Quit' and 'Save & Quit' buttons.

1

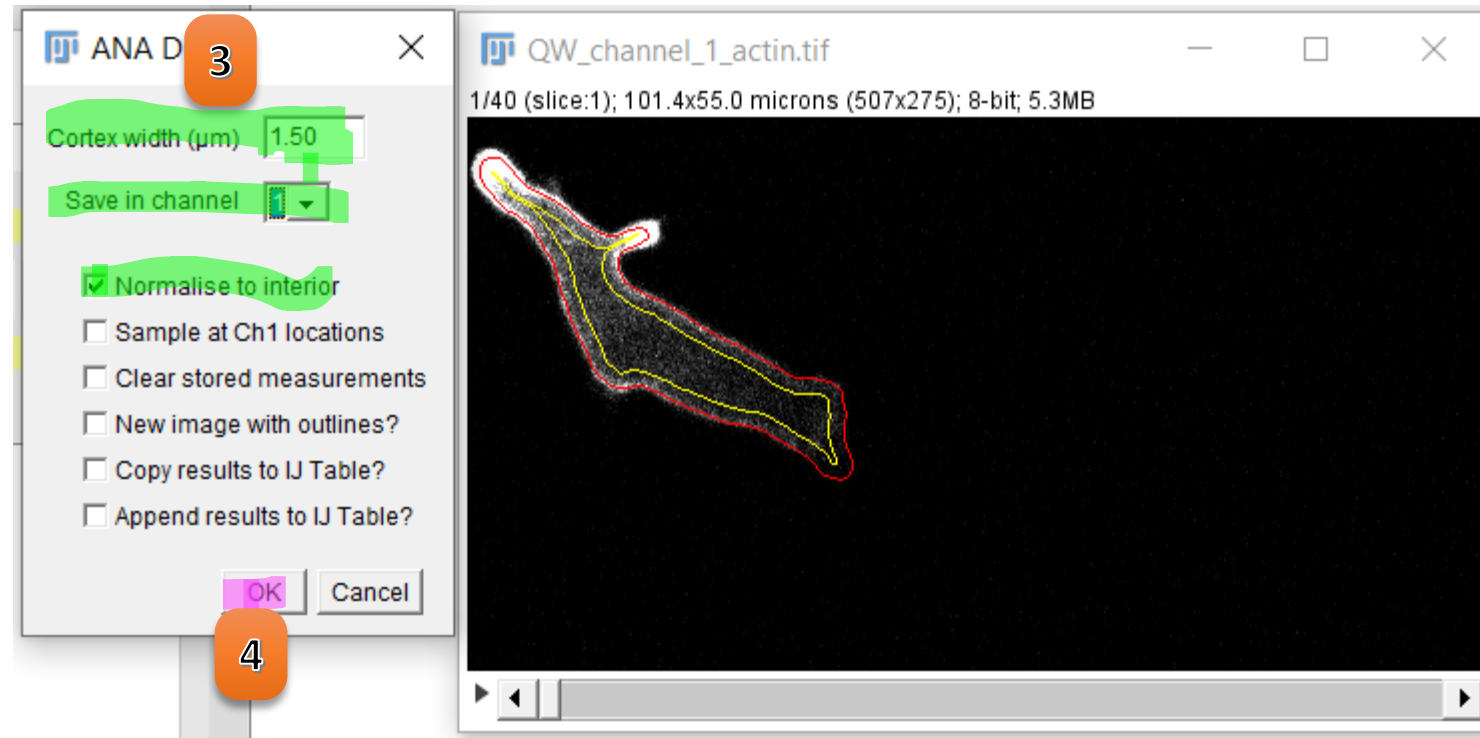
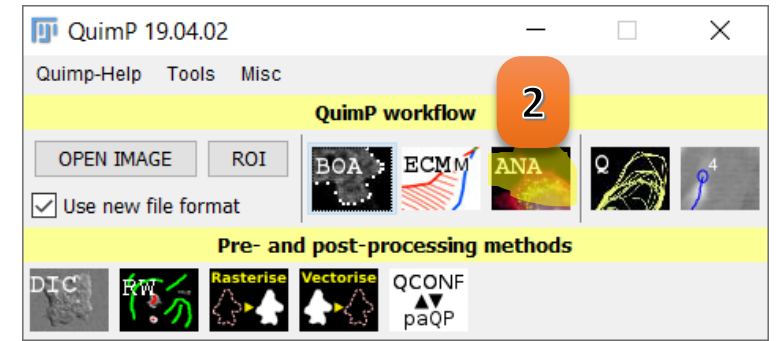
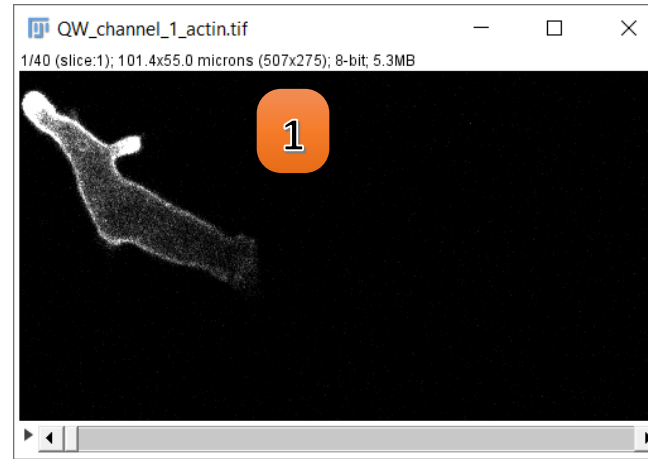
ECMM

1. Launch the ECMM plugin from the QuimpP bar. It does not require an image. When prompted, locate the QuimpP parameter file (*QCONF*) you just created.
2. ECMM will run. You can view the result and close the image.



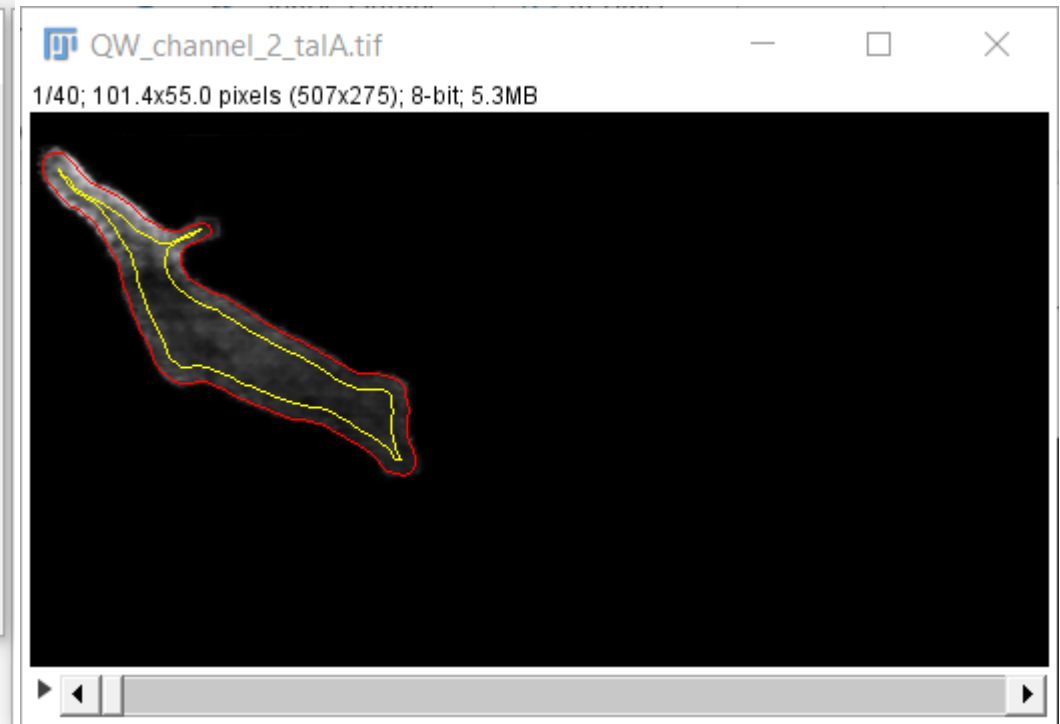
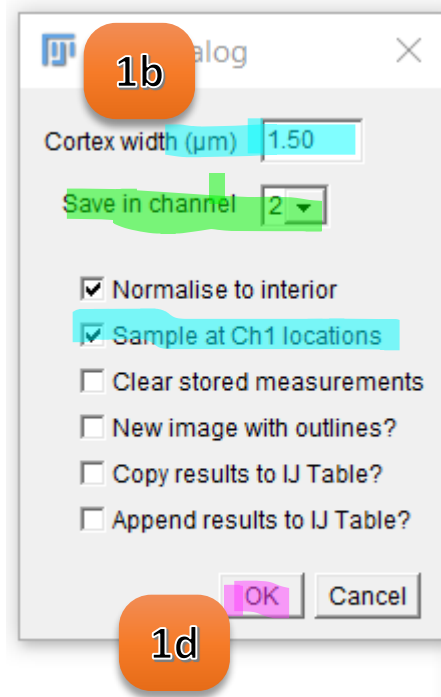
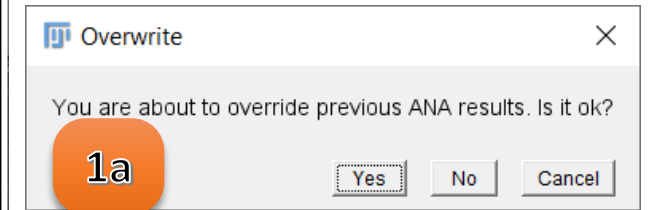
ANA

1. Open the image *QW_channel_1_actin.tif*.
2. With it in focus, launch the ANA plugin, and again select your parameter file.
3. Choose a sensible cortex width (e.g. 1.5 microns). Make sure 'save in channel' is set to 1, and normalise to interior is ticked.
4. Click *ok*. When complete, ANA will show the sample locations for the last frame.



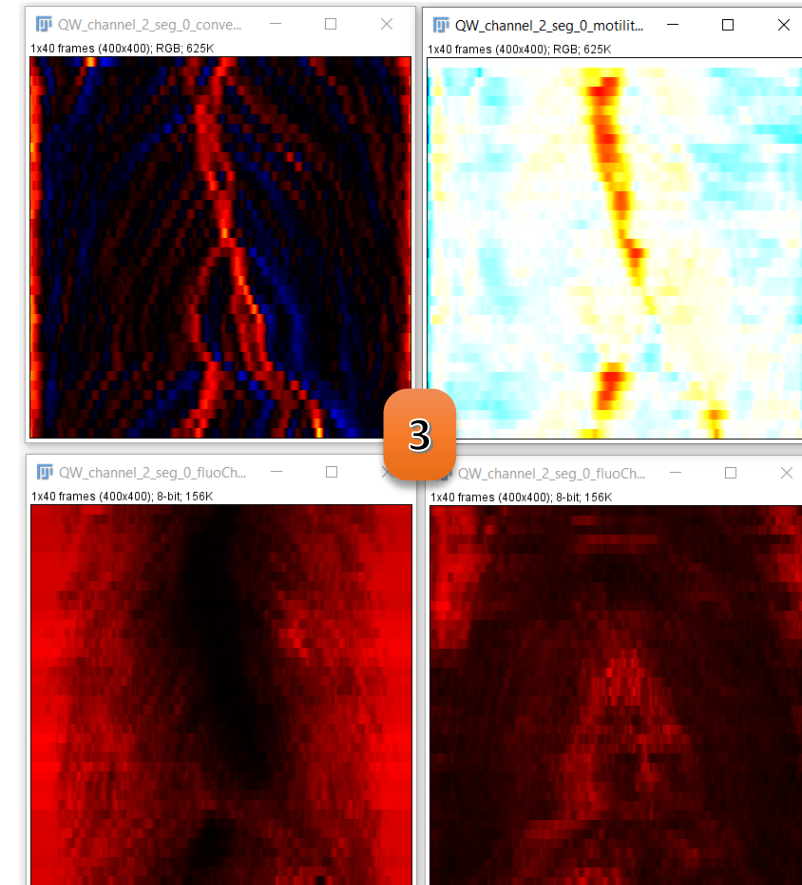
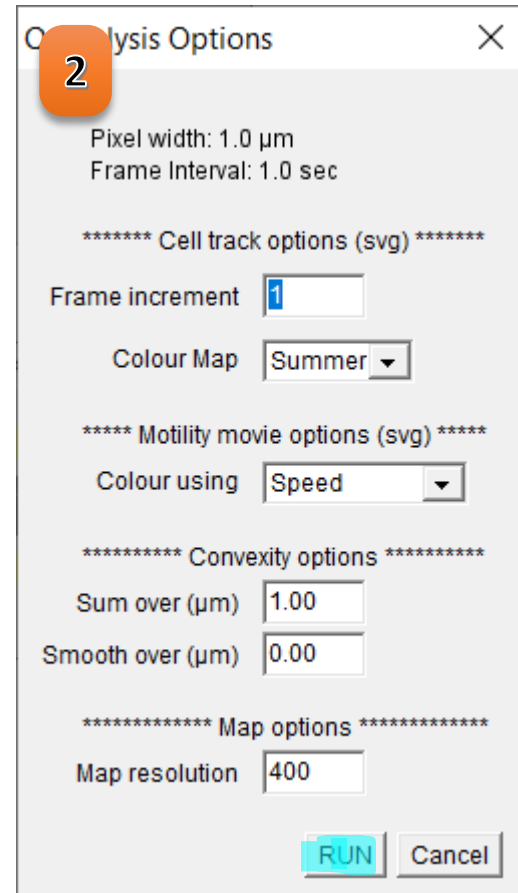
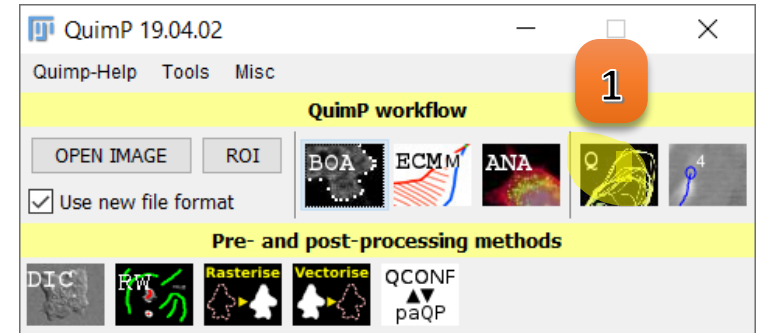
ANA

1. Close *QW_channel_1_actin.tif*, and open *QW_channel_2_talA.tif*.
2. We will record another channel for good measure. Repeat the last step, but with the channel 2 image, this time storing data in channel 2 (which is the default).
 - a) Run ANA, select your parameter file and answer **Yes** on dialog box that appeared
 - b) Tick *Sample at Ch1 locations*. ANA will now use the same sample points as computed for channel 1 (useful if you want to compute ratios between channels).
 - c) Make sure that second channel is selected.
 - d) Click *ok*. When complete, ANA will show the sample locations for the last frame.



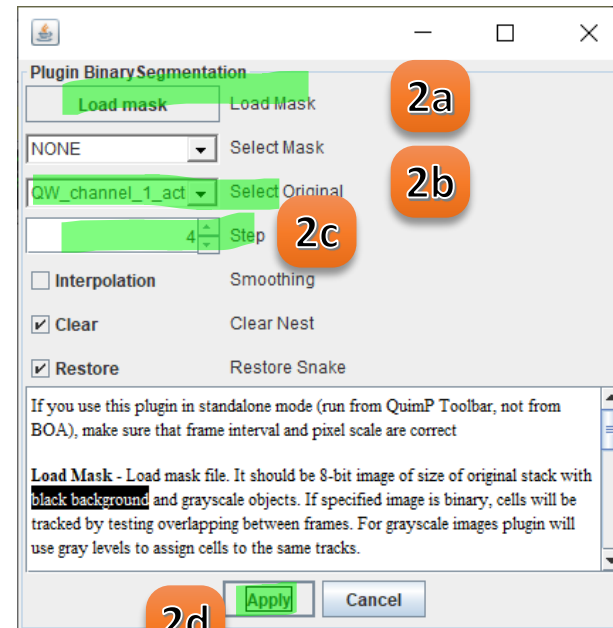
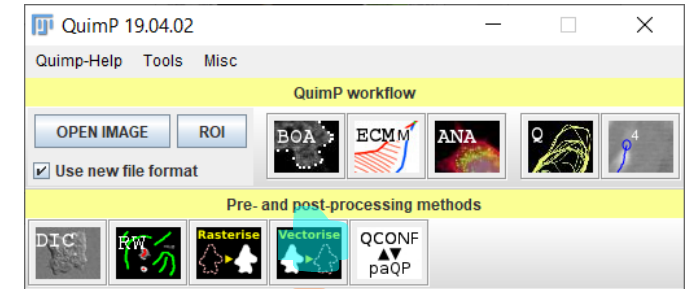
Q-Analysis

1. Launch the Q Analysis plugin
2. Check your scale is what you expect at the top of the parameter window. We will use all the current defaults, so click *RUN*. Inspect your maps, all of which are automatically saved to disk.
 - a) again choose your parameter file.
3. The displayed images have been scaled to cover the colour space. The raw values have been saved as text file, with the extension *.maQP* (e.g. *QTest_0_fluoCh1.maQP*). You can view them in ImageJ by opening them via [*File- > Import- > TextImage...*].
 - a) Note that latest versions of QuimP store these files inside *QCONF* configuration file. One can retrieve them by using Format Converter (see [section 14](#) of User Manual).
 - b) Investigate other files created in current folder



Advanced topics - external segmentation

- You can use your favourite segmentation package and still be able to work with QuimP workflow
 1. Open original image - *QW_channel_1_actin.tif*
 2. Select *Vectorise* plugin from QuimP
 - a) Click *Load Mask* and select binary file *Segmentation.tif*
 - b) Select original image in *Select Original*
 - c) Set sampling to 4
 - d) Click *Apply* – new *QCONF* file will be created that can be processed by *ECMM* and other modules.



Advanced topics - macros

- All modules can be called from macro apart from BOA and Protrusion Analysis.
- But if you use external segmentation, the full workflow can be scripted
- Have a look at *QuimP_walkthrough.ijm* example. You need to adjust paths in lines 11, 13, 15 and 29 to make it working on your computer.

```
QuimP_walkthrough.ijm
1  /**
2  * Exemplary macro running full QuimP analysis.
3  *
4  * Require already segmented image.
5  *
6  * Modify paths before use.
7  */
8
9  // define where to save main configuration file. It will be shared among QuimP modules.
10 // Any other file generated by QuimP will be saved in this folder as well
11 qconfOutput = "C:/Users/baniu/Downloads/experiment.QCONF"
12 // open segmented image, you can use any other segmentation software to obtain masks
13 open("C:/Users/baniu/OneDrive - University of Warwick/Documents/QuimP workshop/QuimP_walkthrough/Segmentation.tif")
14 // open original image
15 open("C:/Users/baniu/OneDrive - University of Warwick/Documents/QuimP workshop/QuimP_walkthrough/QW_channel_1_actin.tif")
16
17 // 1) perform conversion from mask to QCONF file. This step corresponds to saving segmentation in BOA
18 run("Generate Qconf", "opts={options:{ +
19     "select_mask:Segmentation.tif," + // name of the mask image (nod ID)
20     "select_original:QW_channel_1_actin.tif," + // name of the image or path here
21     "step:4.0,smoothing:true}," + // step stands for density of nodes, step=1 means each pixel of mask will be mapped to
22     "maskFileName:", + // alternatively path to mask file
23     "paramFile:("+qconfOutput+")}");
24
25 // 2) run ECMM analysis on configuration file
26 run("ECMM Mapping", "opts={paramFile:("+qconfOutput+")}");
27
28 // 3) run ANA analysis, we use only one channel
29 open("C:/Users/baniu/OneDrive - University of Warwick/Documents/QuimP workshop/QuimP_walkthrough/QW_channel_1_actin.tif"); // i
30 selectWindow("QW_channel_1_actin.tif");
31 run("ANA", "opts={plotOutlines:true,fluoResultTable:true,fluoResultTableAppend:false," + // configure displaying
32     "channel:0, userScale:5.0," + // set channel and cortex width (in um, pixel size from image will be used)
33     "normalise:true, sampleAtSame:false," +
34     "clearFlu:false," +
35     "paramFile:("+qconfOutput+")}");
36
37 // 4) run Q analysis
38 run("QuimP Analysis", "opts={trackColor:Summer," +
39     "outlinePlot:Speed," +
40     "sumCov:1.0,avgCov:0.0," +
41     "mapRes:400," +
42     "paramFile:("+qconfOutput+")}");
43
44 // 5) convert data to csv files and generate coordinates maps
45 run("Format converter", "opts={status:[ecmm:outlines,ecmm:centroid,map:coord,map:origin,map:ycoords,map:xcoords]," +
46     "areMultipleFiles:true," +
47     "paramFile:("+qconfOutput+")}");
```