



Protocols

Graphical programming for Icy

a.k.a. programming, for the rest of us

Foreword: Reproducible Research

- Quote: "Results aren't much if they can't be reproduced!"
(your boss, your reviewers, your colleagues, you!)

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[...] Image quantification was carefully conducted using Photoshop. [...]

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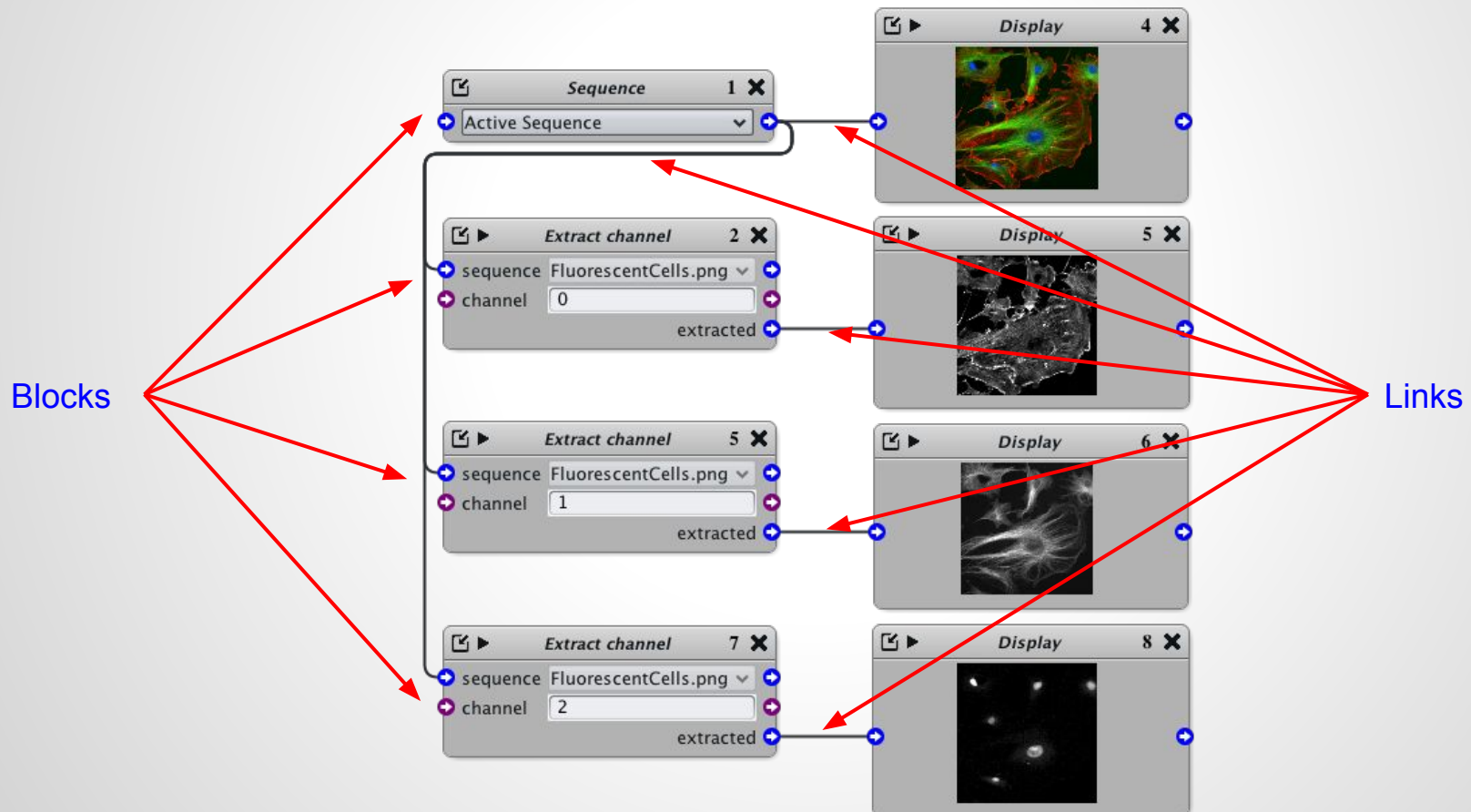
Foreword: Reproducible Research

- Quote: "Results aren't much if they can't be reproduced!"
- Fact: Most journals now **reject** papers without proper quantification
- Conclusion: Image quantification is a protocol in its on right...
- Icy makes these protocols easy to read / write / use / adapt
 - **Design** a protocol once, run on thousands of images
 - **Upload** your protocol and share with the world (within publications)
 - **Download** other protocols, run them out-of-the-box
 - **Extend** any protocol to meet your needs and share/publish again

all in just a few clicks, no programming knowledge required.

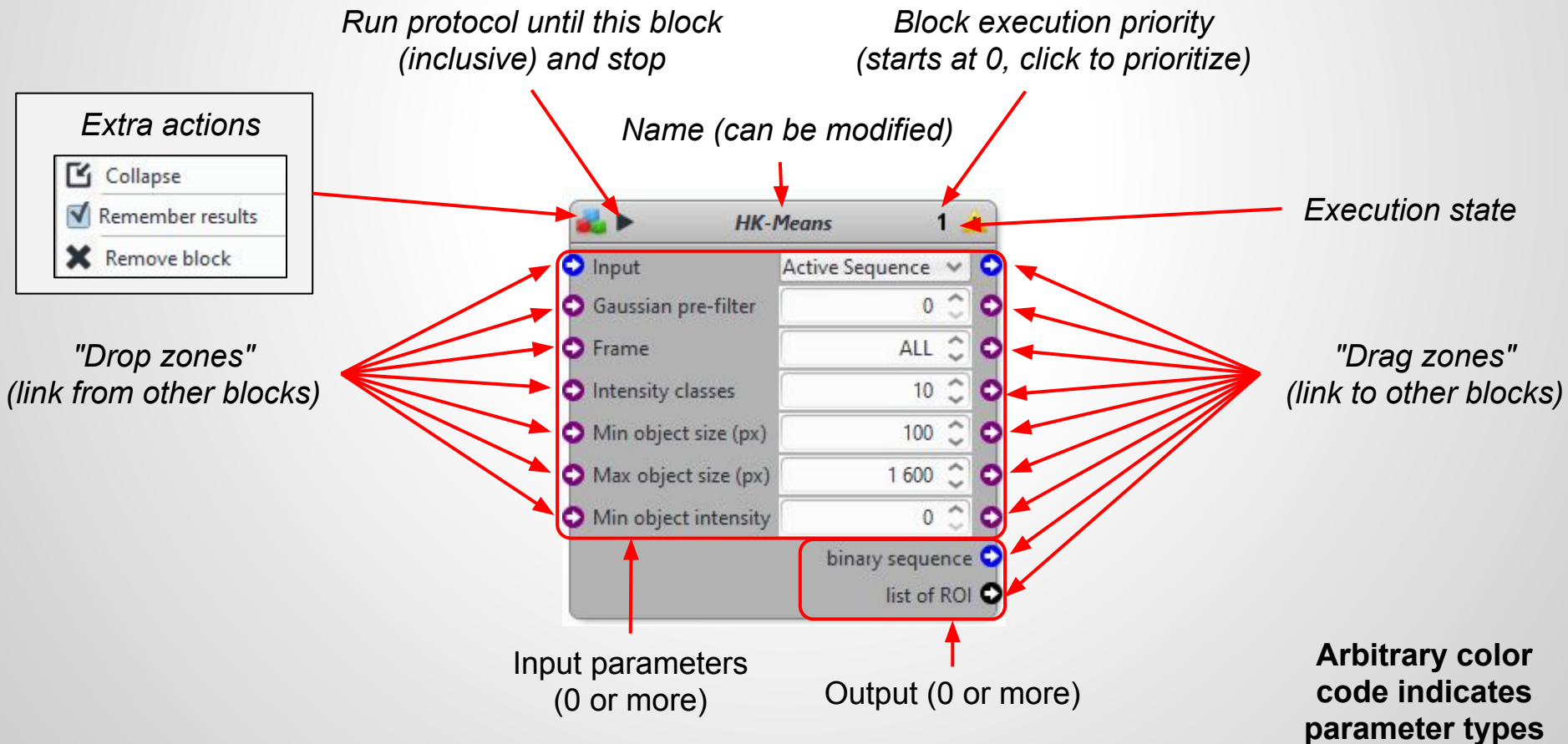
Protocols in Icy

- A protocol is a workflow linking processing blocks together



Protocols in Icy

- Standardised design: all blocks look the same
- Strong modularity: one block = one task



Protocols in Icy

- The protocols editor: <http://icy.bioimageanalysis.org/plugin/Protocols>

The screenshot shows the 'Protocols editor (Blocks engine v.5.1)' window. The interface includes a menu bar with 'New', 'Load', 'Save', 'Save as...', 'Embed', 'Run', and 'Reset'. A search bar on the left contains the text 'seq'. Below the search bar is a list of blocks matching the search, including 'Adaptive histogram equalize', 'Add ROI to sequence', 'Anisotropic Filter', 'C-CRAFT', 'Create sequence', 'Crop 5D', 'Crop sequence', and 'Crop sequence to ROI'. A detailed view of the 'Crop 5D' block is shown at the bottom left, with its public description: 'Select a portion of a sequence in all 5 dimensions (XYZCT)'. The main workspace displays a workflow with blocks: 'Sequence 1' (Active Sequence), 'Get file name 2' (Sequence: neurones, Folder: checked, Extension: checked), and two 'Display' blocks. The first 'Display' block shows a 3D visualization of neurons. The second 'Display' block shows the file path 'D:/Stephane/Pictures/bio/tiff/3D_C/neurone'. The status bar at the bottom indicates 'The workflow executed successfully (total running time: 0.0 seconds)'. Red arrows point from text labels to specific UI elements: 'New protocol' to the 'New' button, 'Open a protocol' to the 'Load' button, 'Save / Save as...' to the 'Save' and 'Save as...' buttons, 'Embed protocol inside a batch loop' to the 'Embed' button, 'Start / Stop the protocol' to the 'Run' button, 'Right click into the workspace to insert a block in the current protocol' to the workspace area, 'Search block by name' to the search bar, 'Blocks matching current search. Just drag and drop the block in the workspace to add it.' to the block list, 'Documentation of selected block' to the 'Crop 5D' block details, 'Opened protocol(s)' to the 'Sequence 1' block, 'Workspace' to the main workspace area, and 'Status bar' to the bottom status bar.

New protocol

Open a protocol

Save / Save as...

Embed protocol inside a batch loop

Start / Stop the protocol

Right click into the workspace to insert a block in the current protocol

Search block by name

Blocks matching current search. Just drag and drop the block in the workspace to add it.

Documentation of selected block

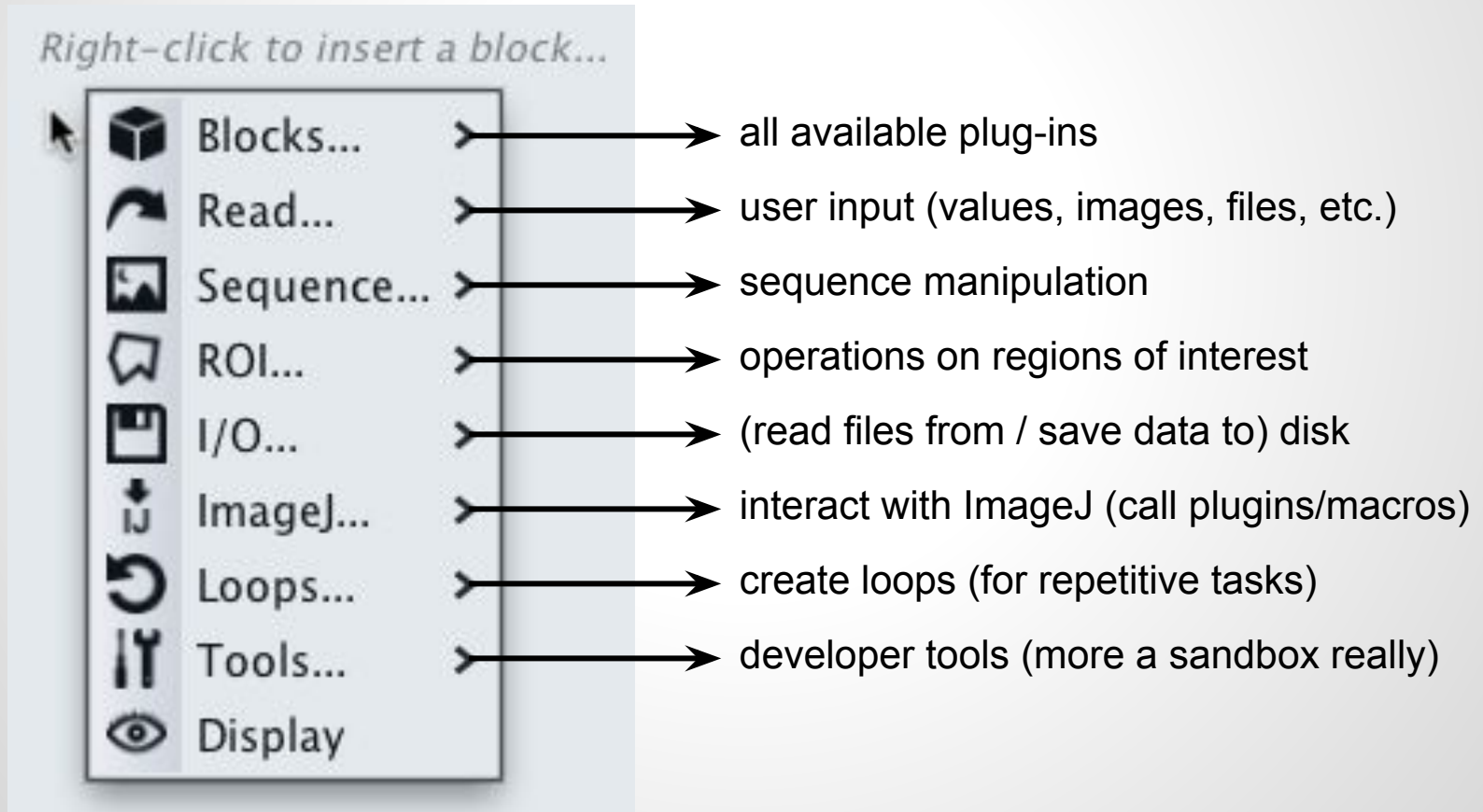
Opened protocol(s)

Workspace

Status bar

Protocols in Icy

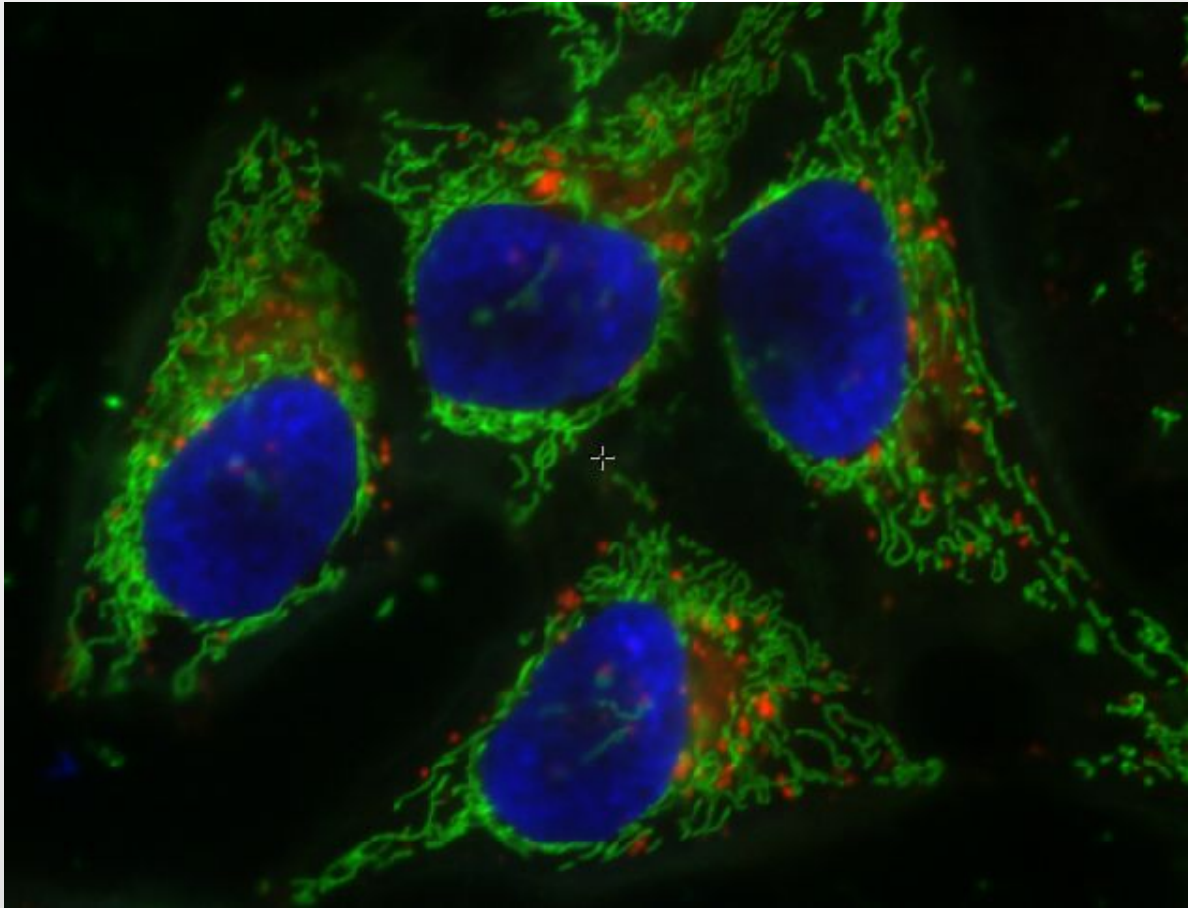
- Blocks are organised by groups



More ideas on how to tidy things up? Let us know!

Protocols in Icy

- Question: how would you find the nuclei in this image?



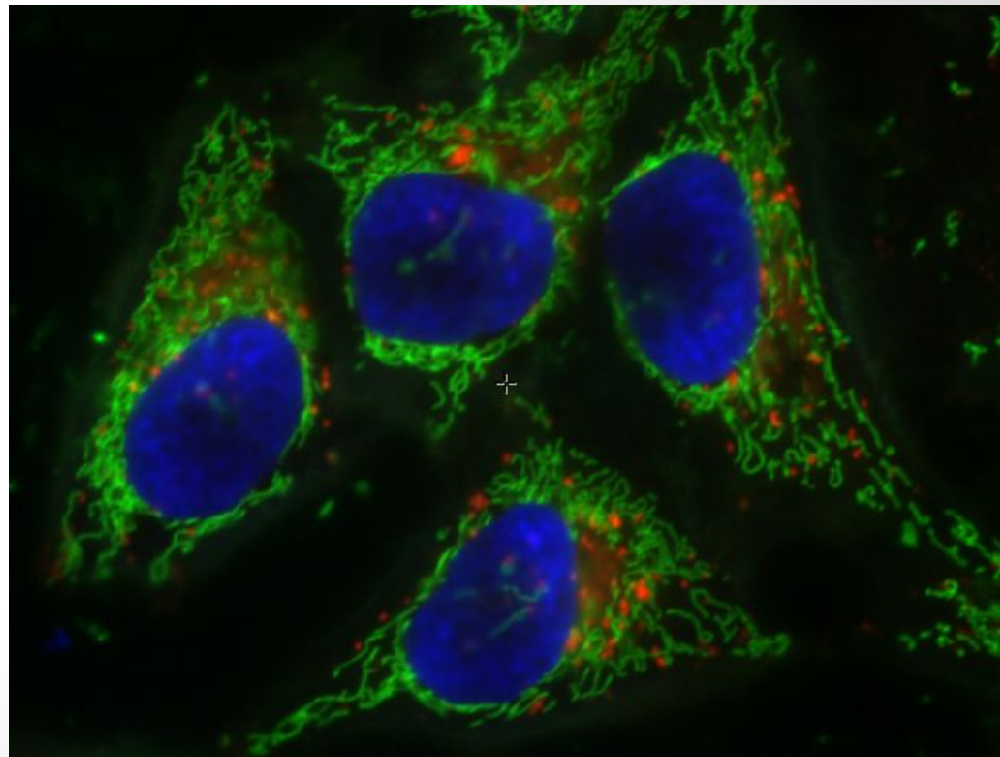
Protocols in Icy

- Question: how would you find the nuclei in this image?

Outline:

1. Extract the channel of interest
2. Clean the data
3. Find an intensity threshold
4. Threshold the image
5. Extract the regions of interest
6. Quantify

(notice how generic this outline is...)



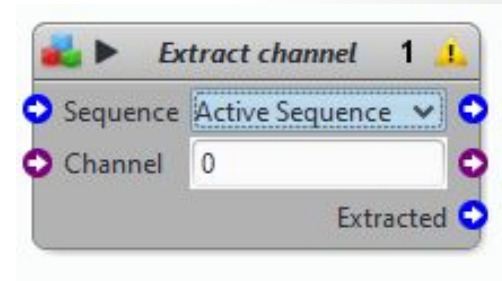
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Menu: Sequence > Extract Channel



NOTE: channel index starts at 0...

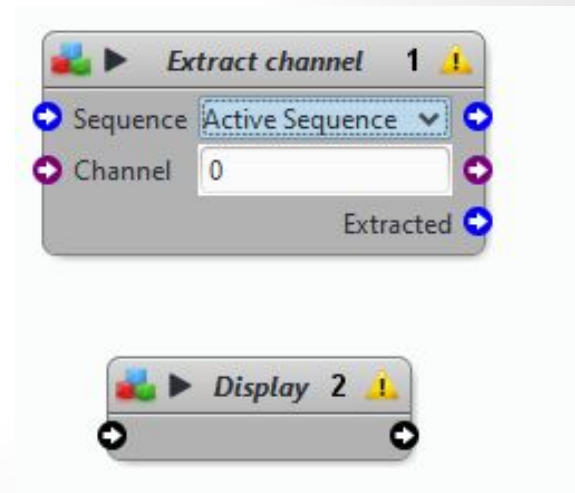
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NOTE: adding a Display box is helpful to see what we are doing !

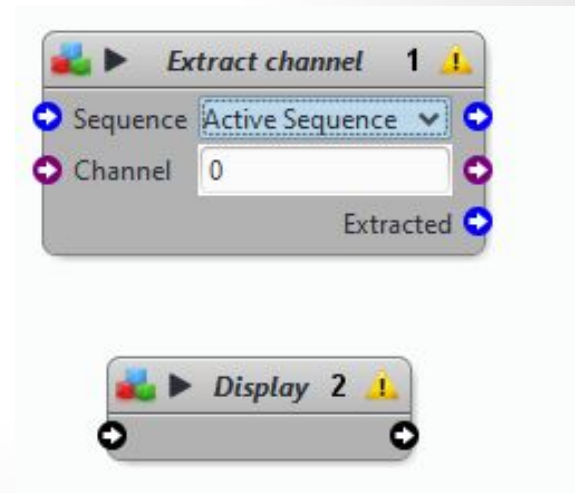
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We connect blocks by dragging Output on Input. Let's see that !

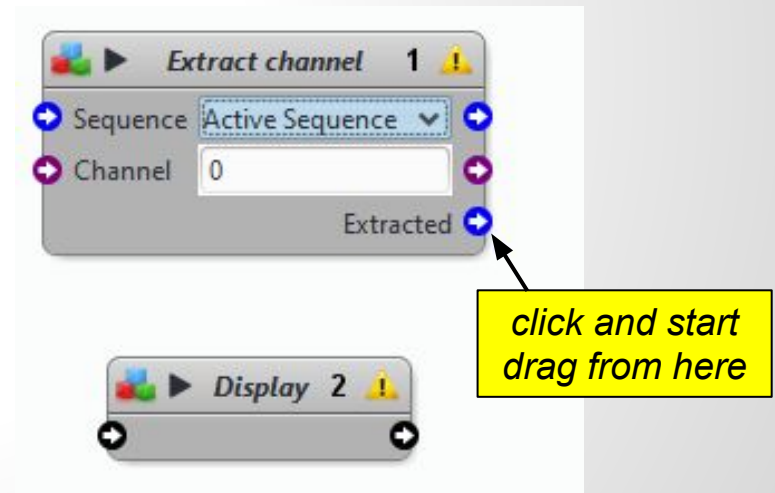
Protocols in Icy

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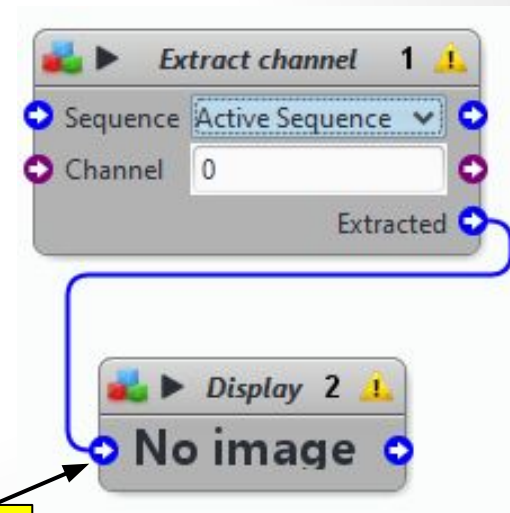
Protocols in Icy

- Question: how would you find the nuclei in this image?

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release here

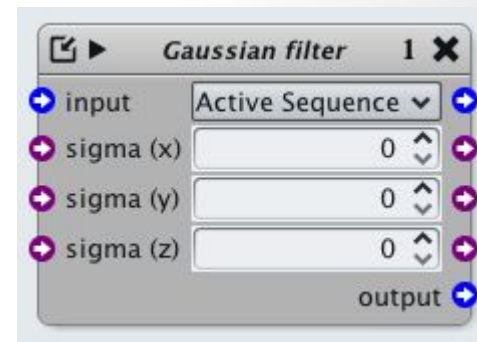
Protocols in Icy

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Menu: Blocks > Gaussian Filter



Diffuses the intensity contained in each pixel (i.e. makes the image look blurry)

*Adapt the diffusion to the image noise
Too much diffusion: edges fade away!*

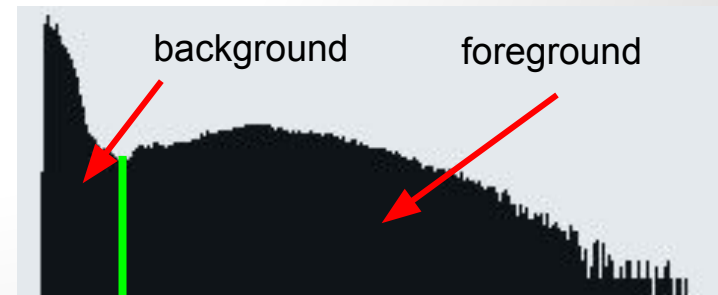
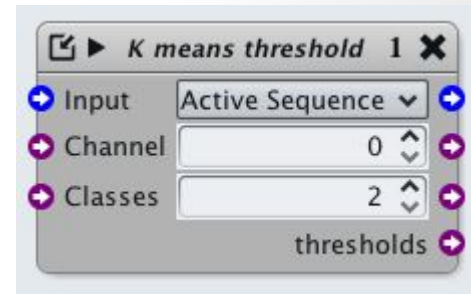
Protocols in Icy

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Menu: Blocks > KMeans Threshold



Finds the optimal separation(s) between the histogram modes (i.e. intensity classes)

2 modes => 1 threshold (3 => 2, etc.)

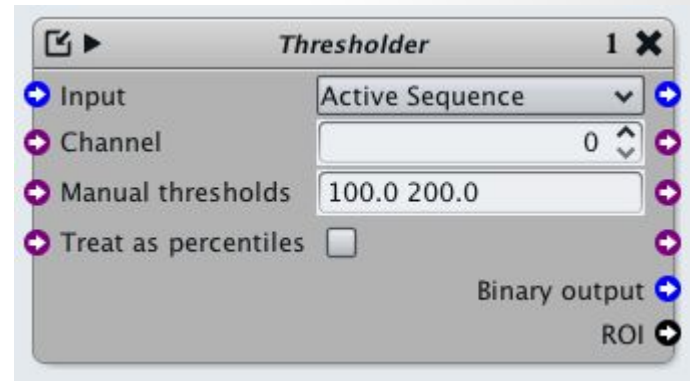
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Menu: Blocks > Thresholder



Creates a labeled image by classifying pixel intensities according to the threshold(s)

1 threshold => [0;1] (binary) image

2 thresholds => [0;1;2] (labeled) image

etc.

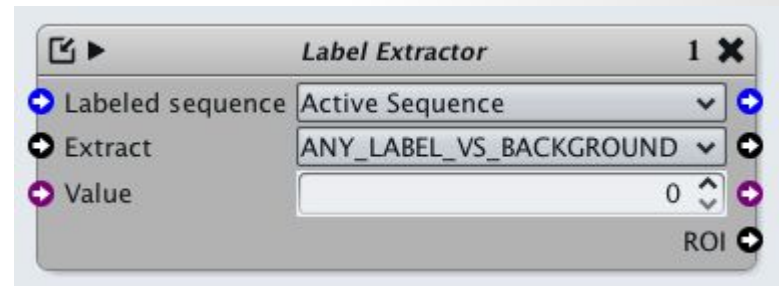
Protocols in Icy

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Menu: Blocks > Label Extractor



Extracts objects from a labeled image using connected component analysis

Protocols in Icy

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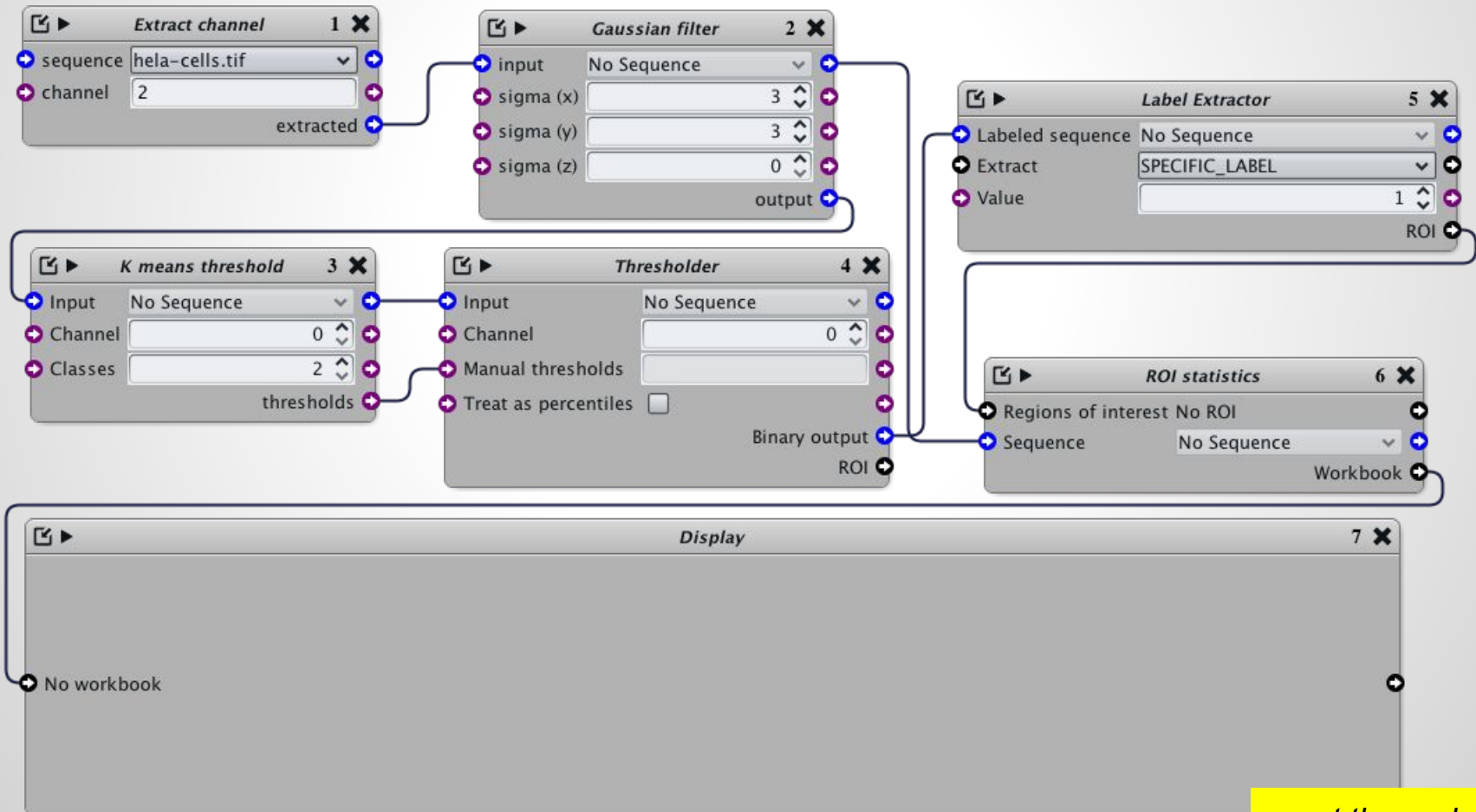
Menu: ROI > ROI Statistics



Calculates size, dimensions, intensity statistics, etc.

Protocols in Icy

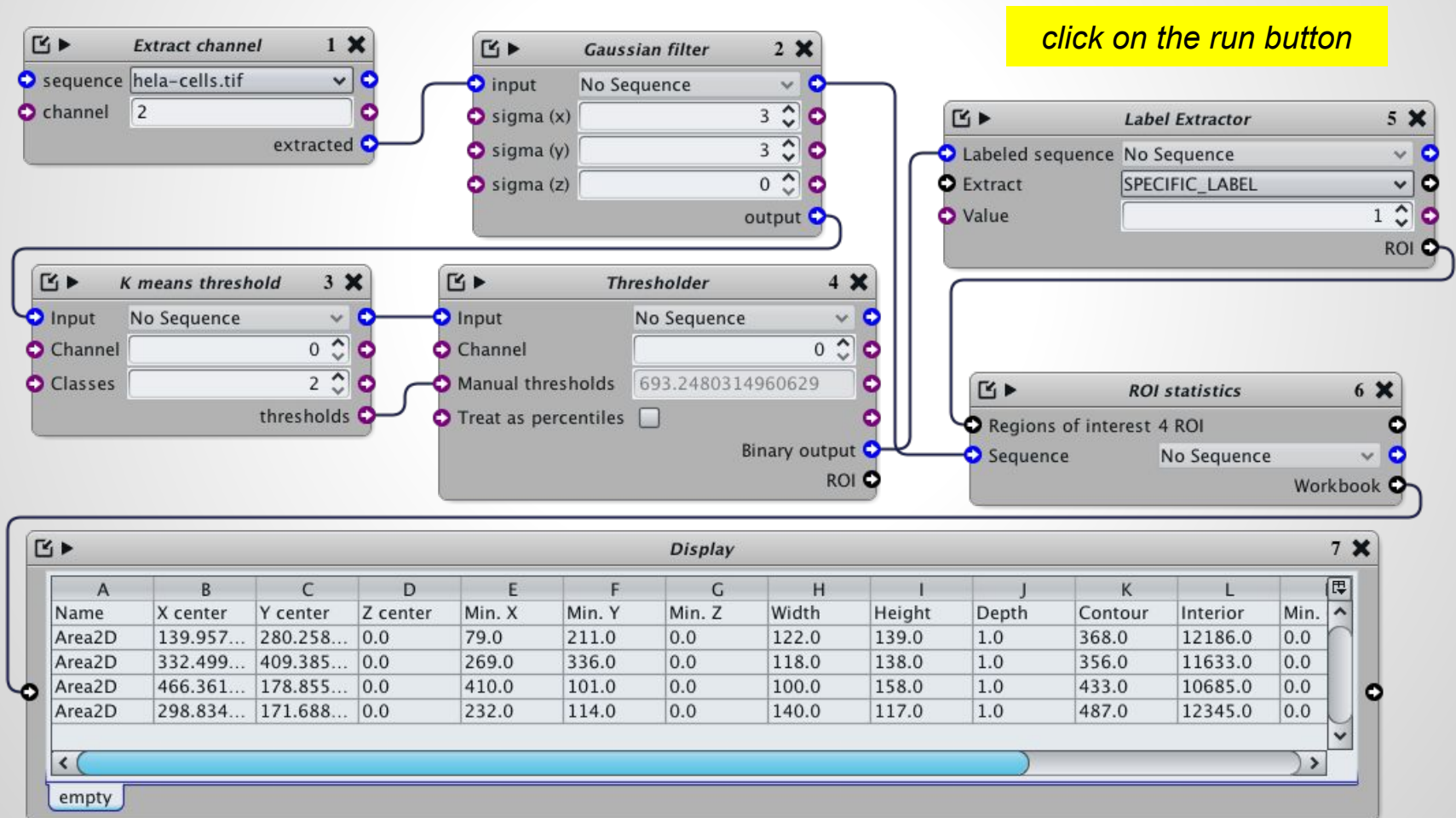
- Question: how would you find the nuclei in this image?



at the end...

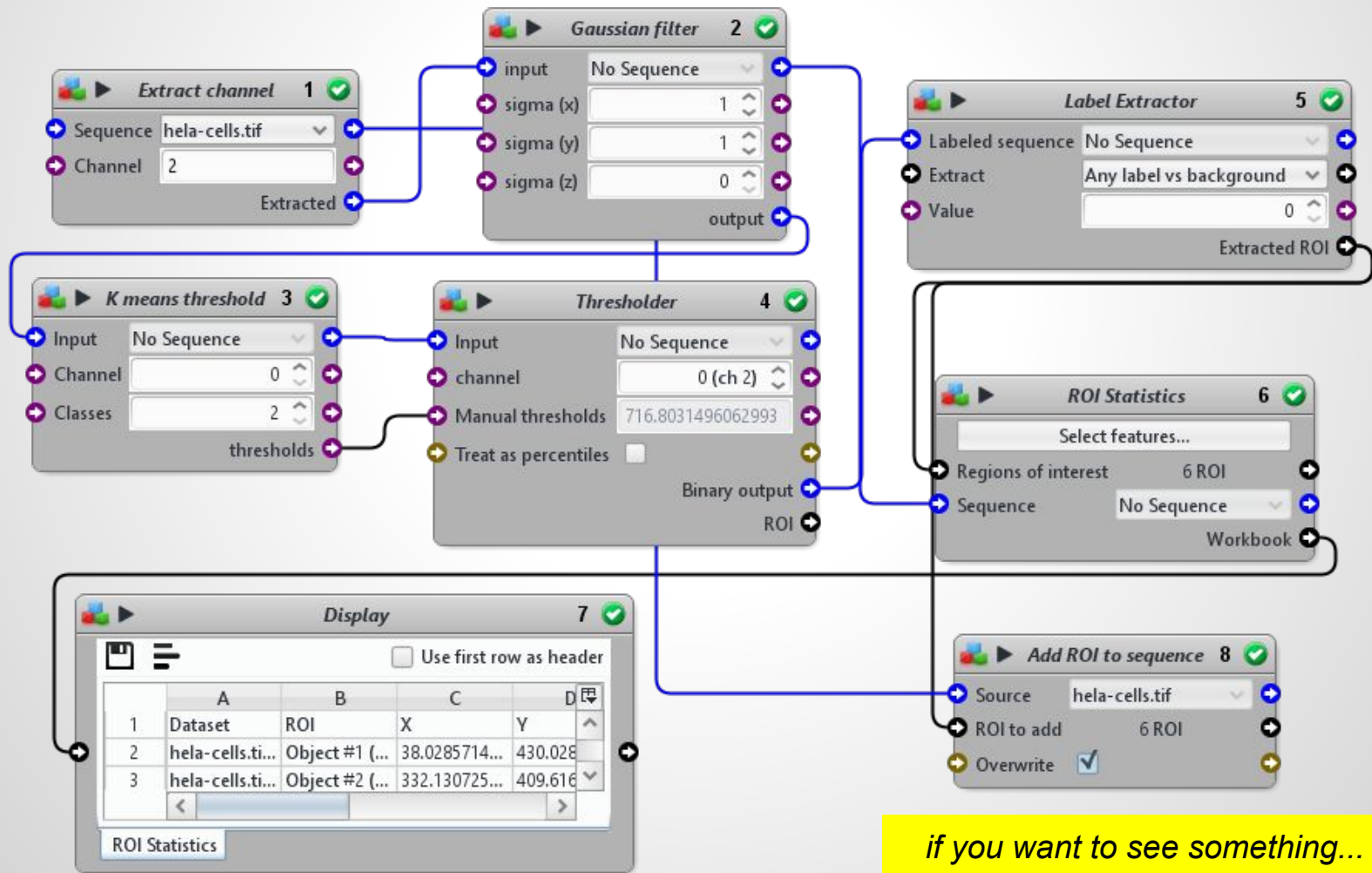
Protocols in Icy

- Question: how would you find the nuclei in this image?



Protocols in Icy

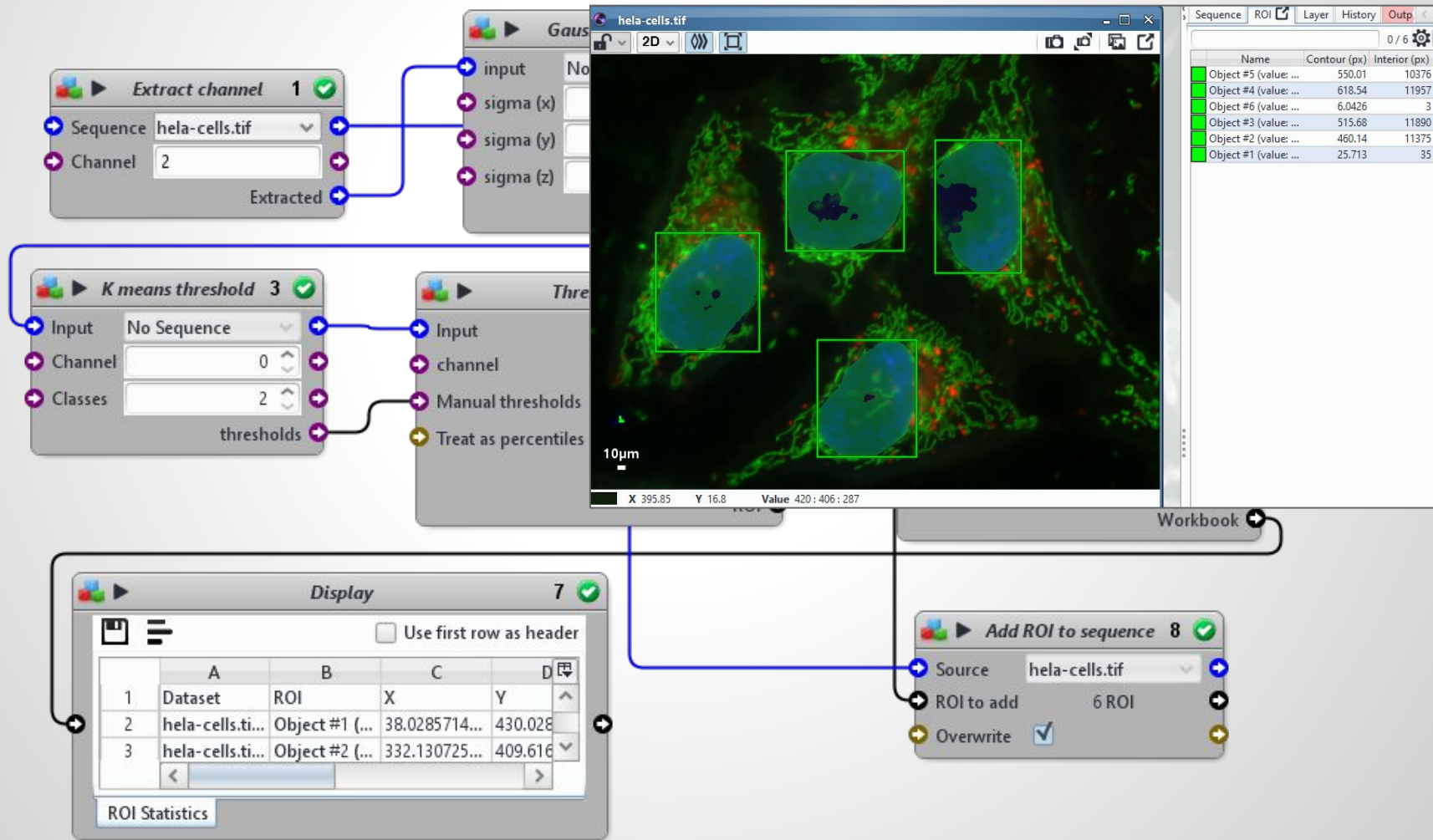
- Question: how would you find the nuclei in this image?



if you want to see something...

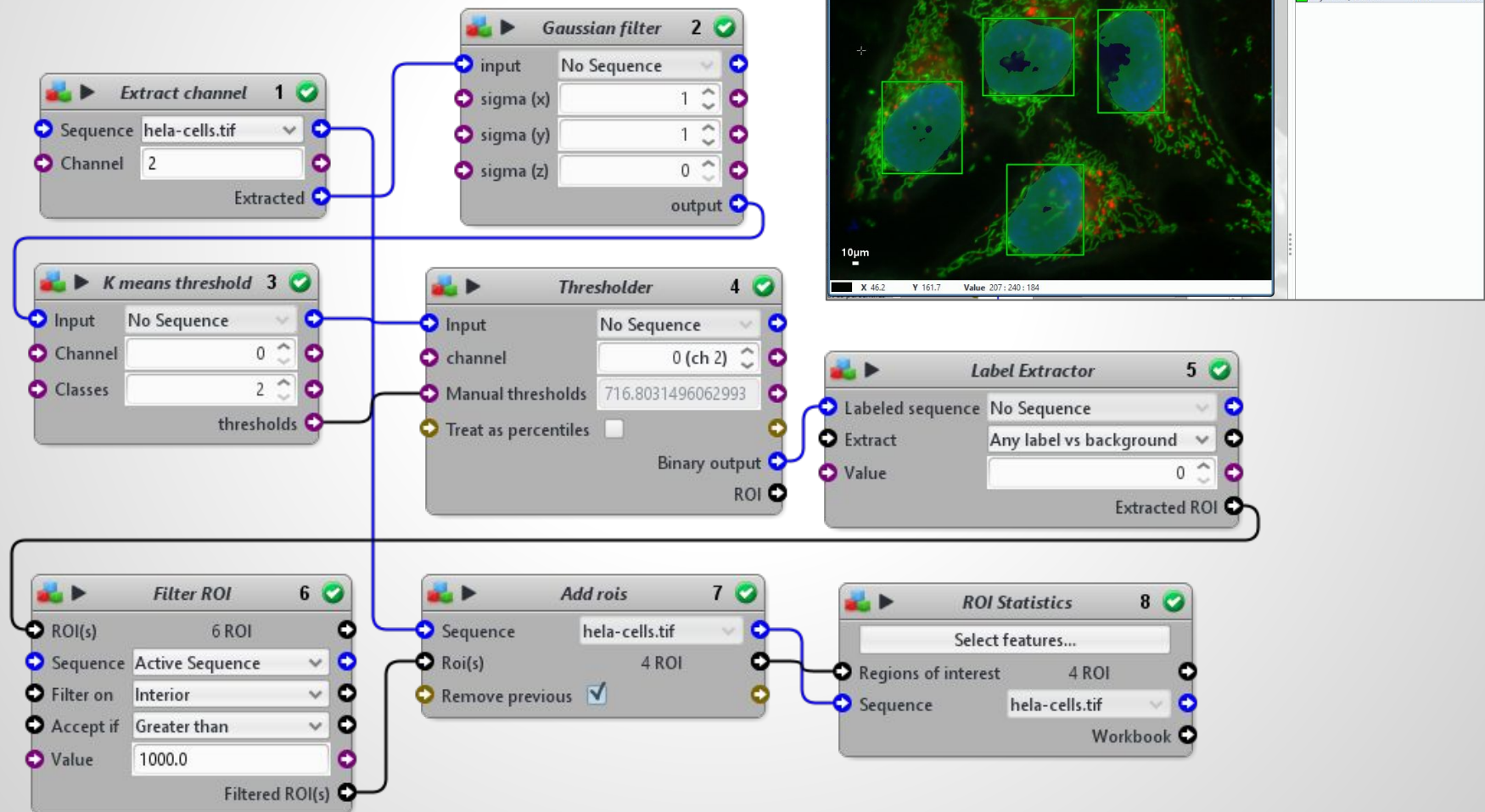
Protocols in Icy

Improving the results - what we can do ?



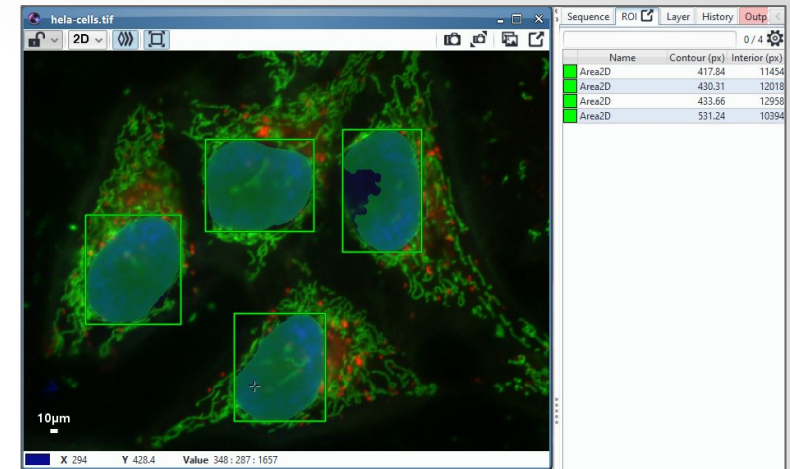
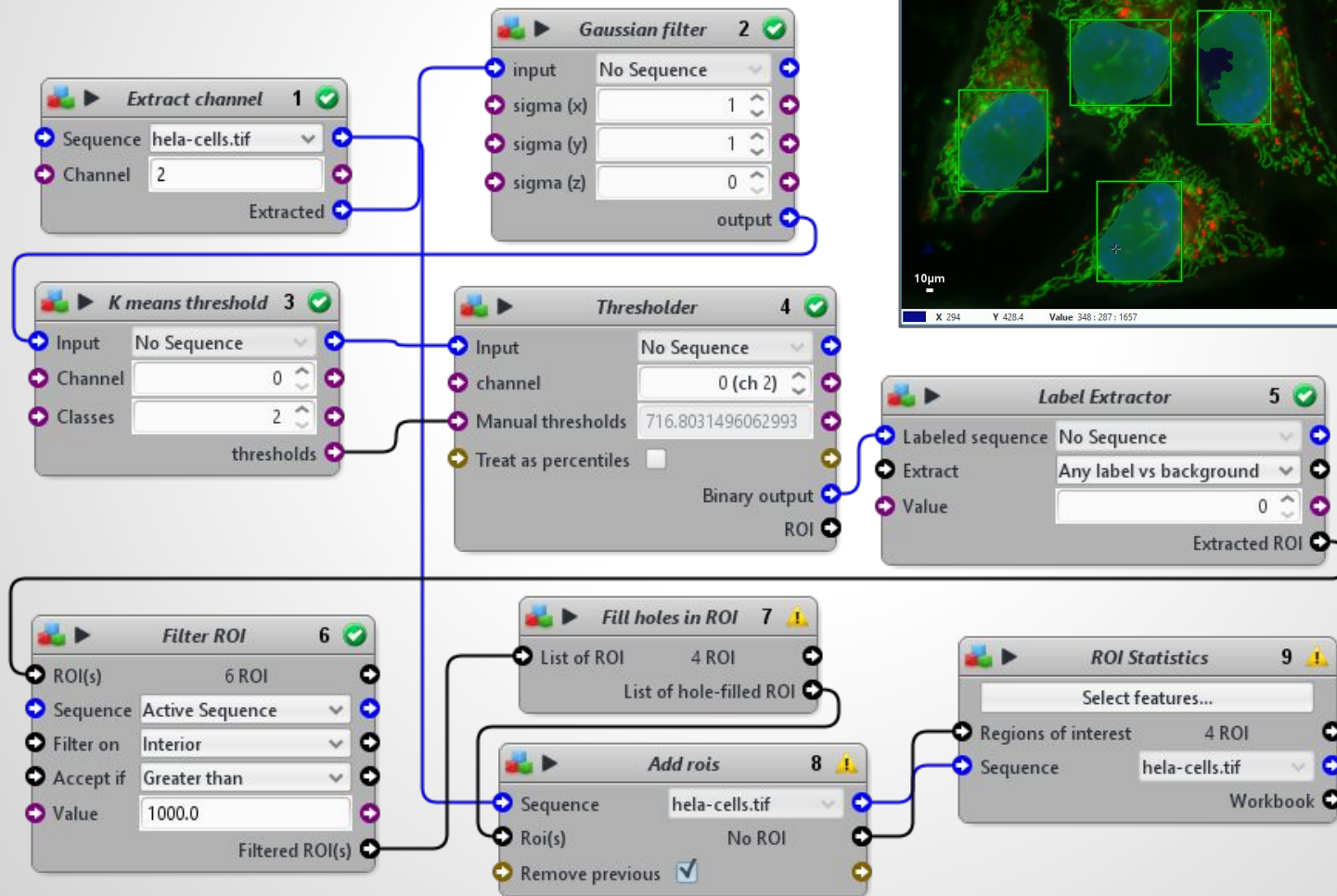
Protocols in Icy

Improving the results - filtering ROI



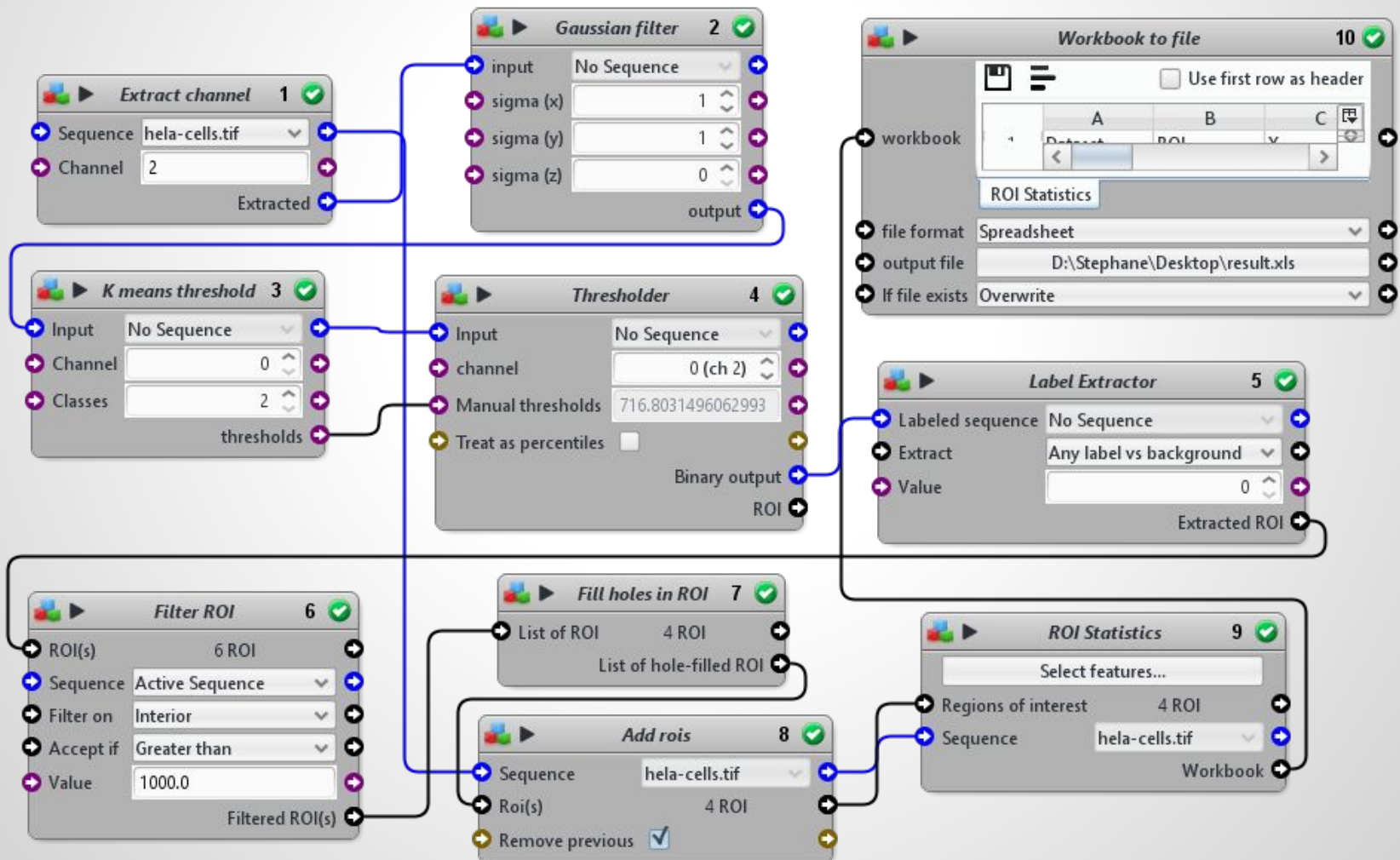
Protocols in Icy

Improving the results - filling holes



Protocols in Icy

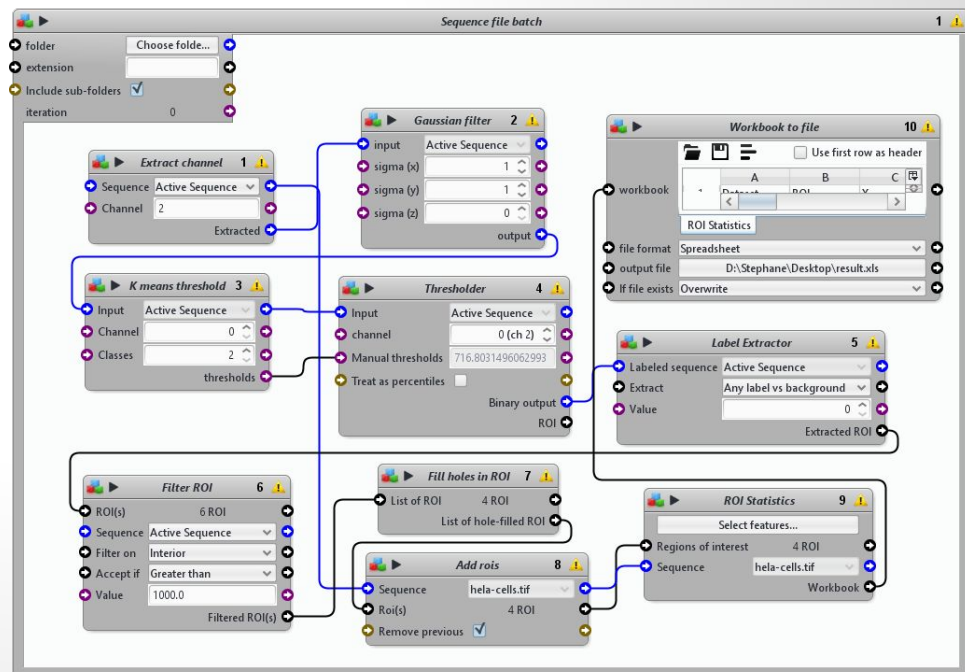
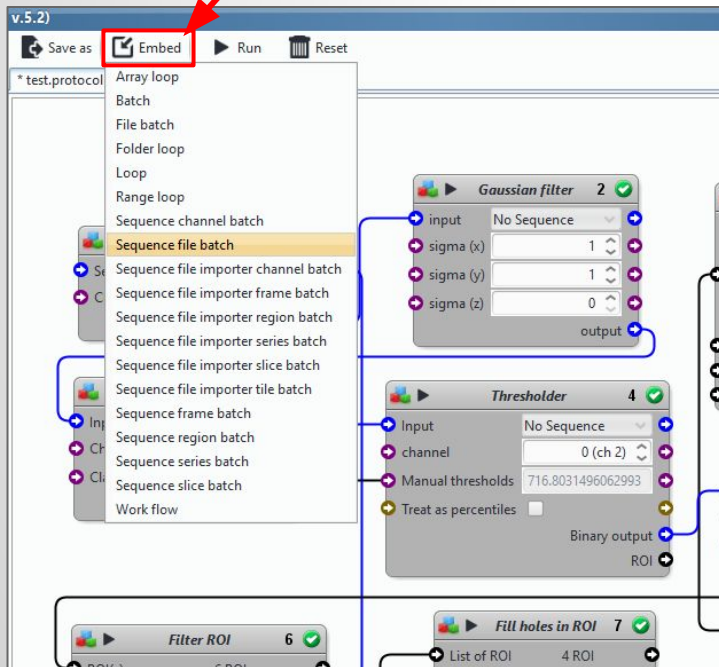
Then save your statistics on disk !



Protocols in Icy

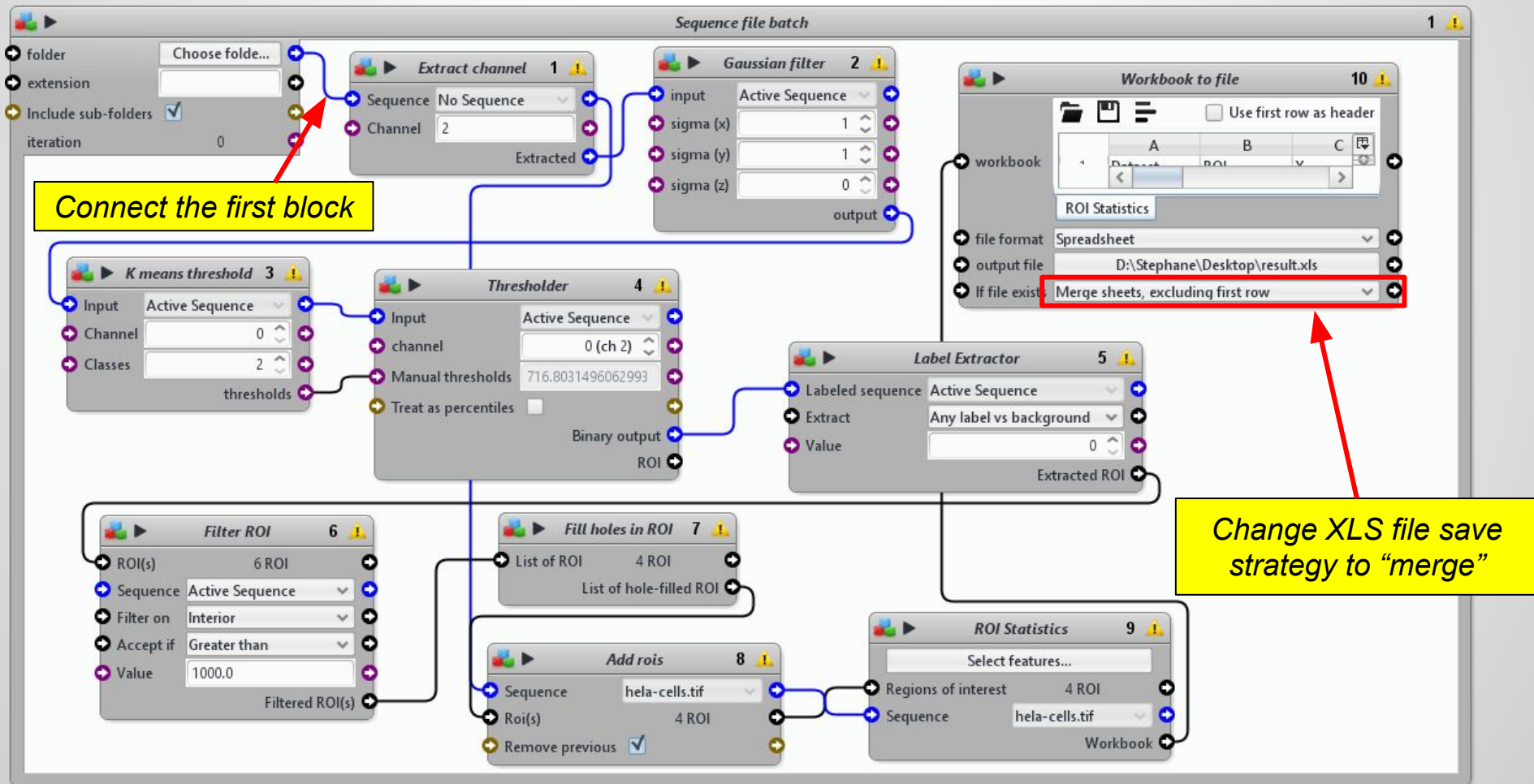
- How about batch processing ?

*Embed your protocol inside a
Sequence File Batch box*



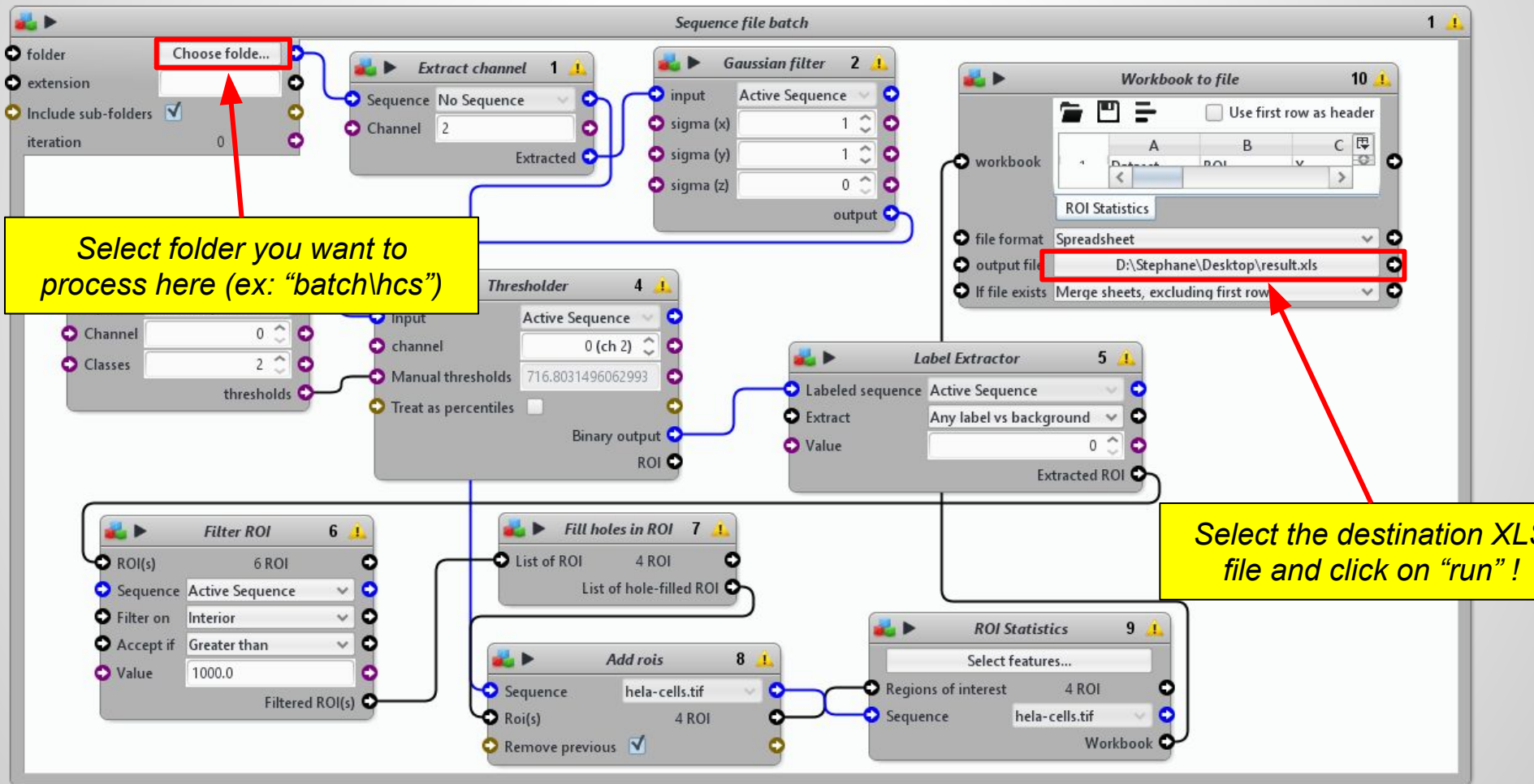
Protocols in Icy

- How about batch processing ?



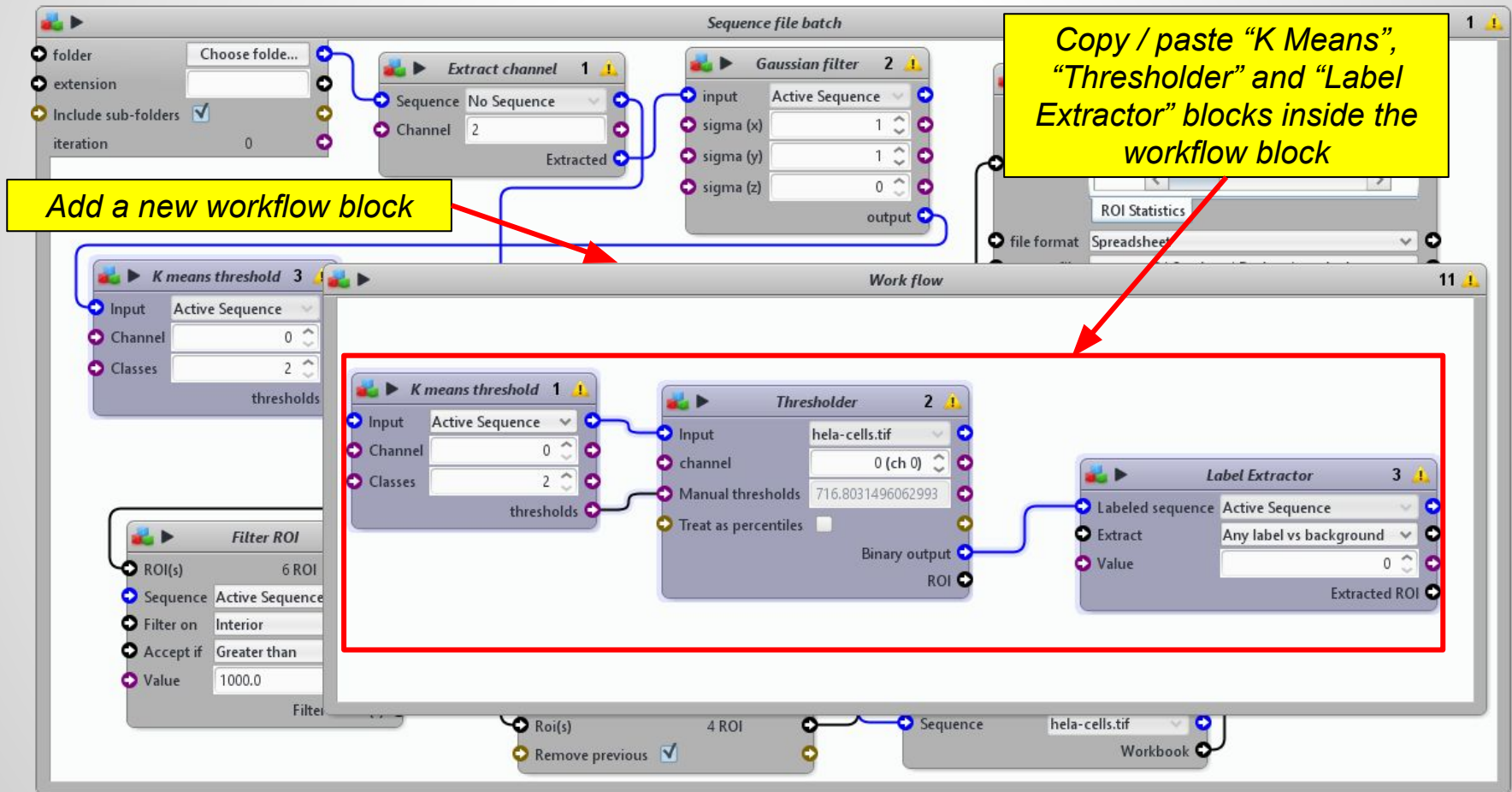
Protocols in Icy

- How about batch processing ?



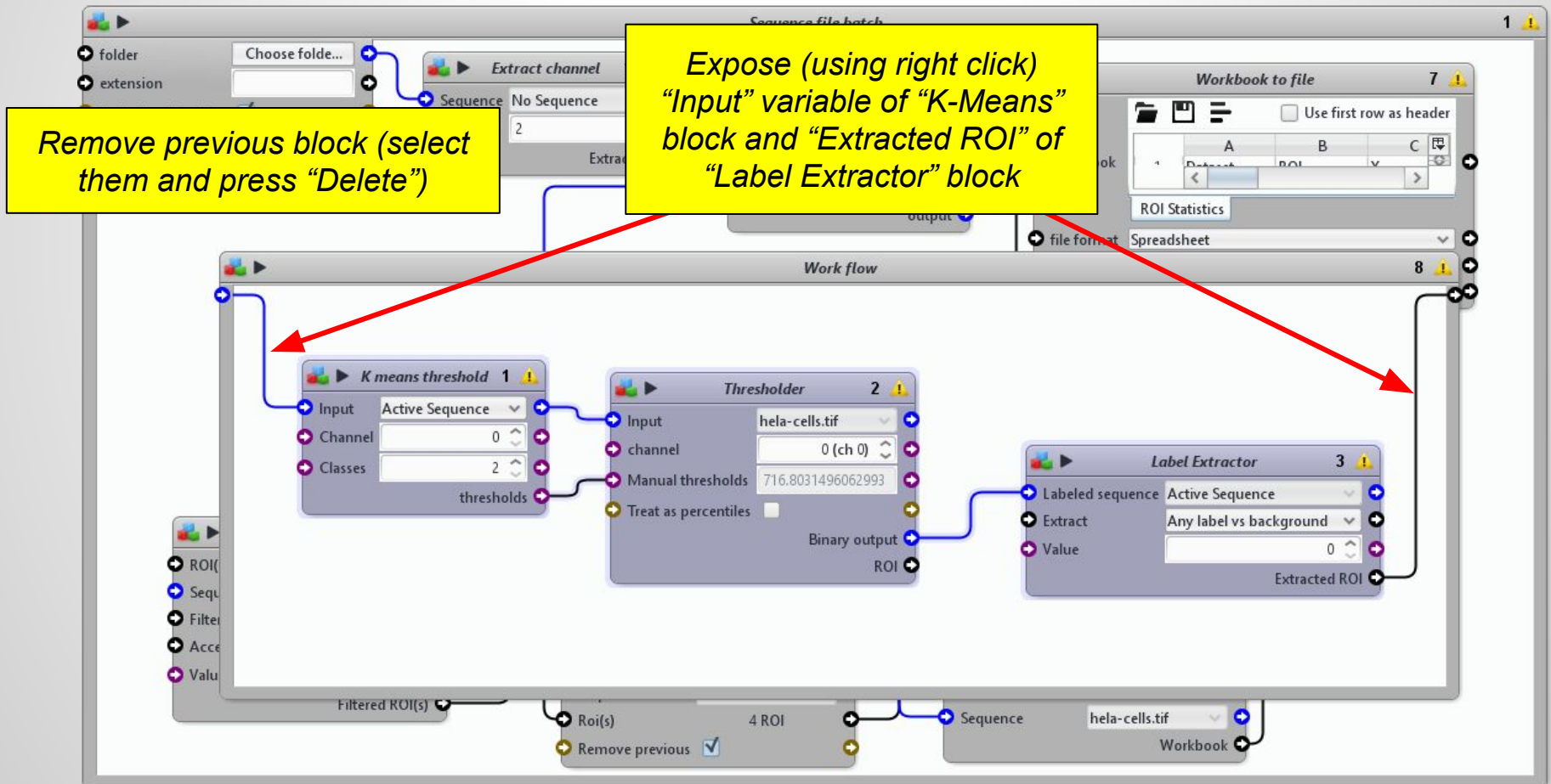
Protocols in Icy

- Make your protocol nicer: build your own block with “workflow” !



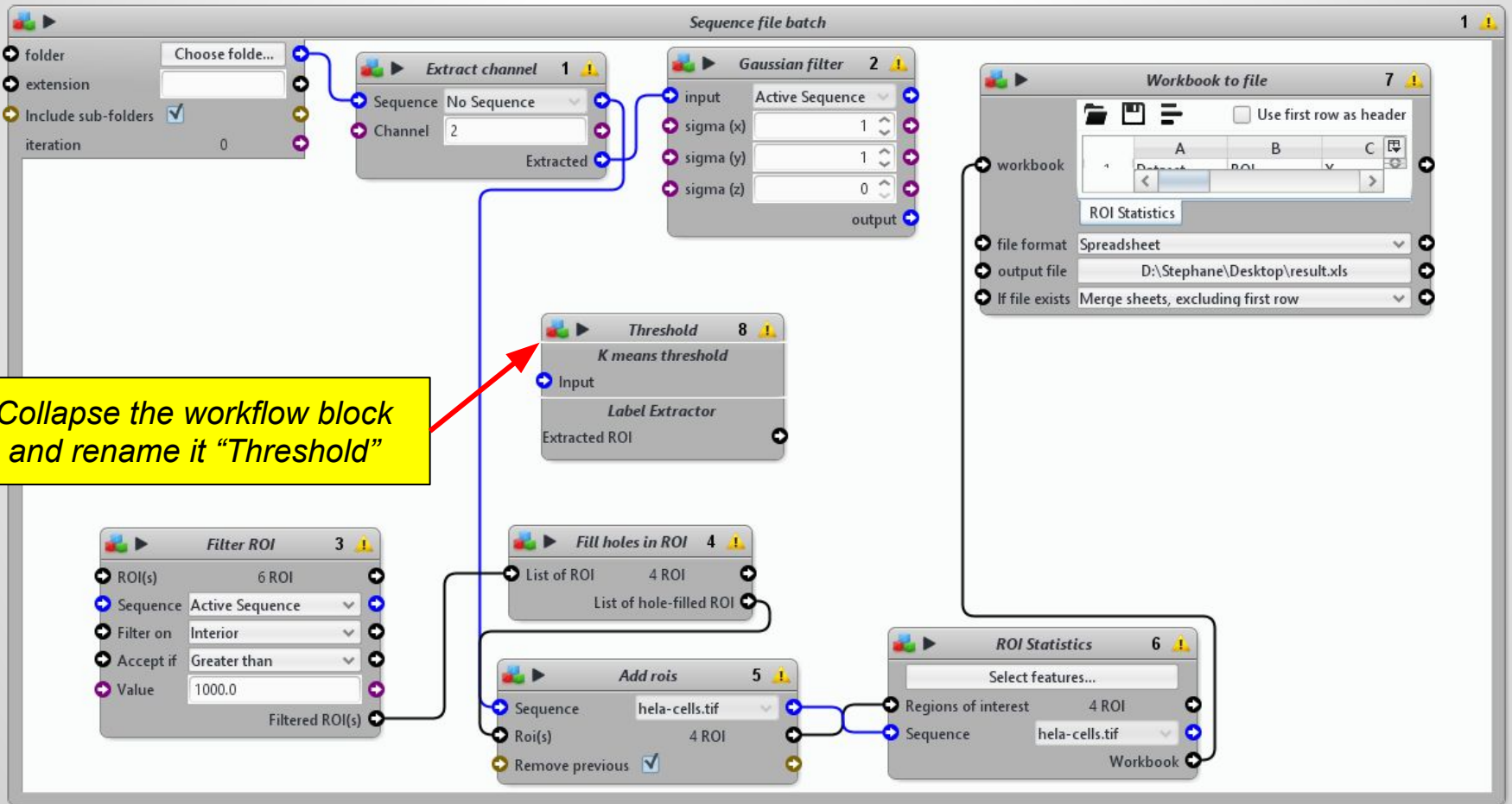
Protocols in Icy

- Make your protocol nicer: build your own block with “workflow” !



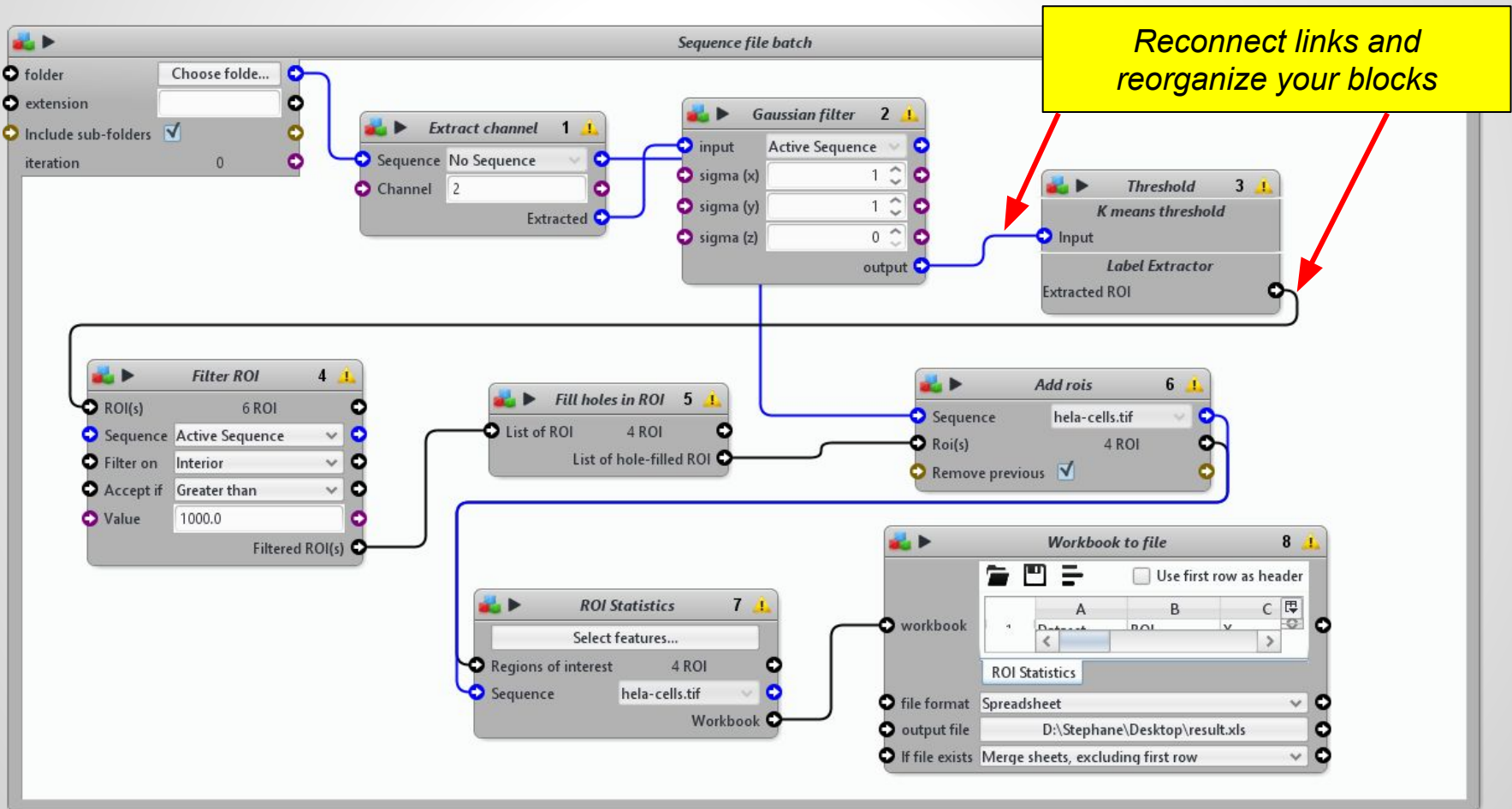
Protocols in Icy

- Make your protocol nicer: build your own block with “*workflow*” !



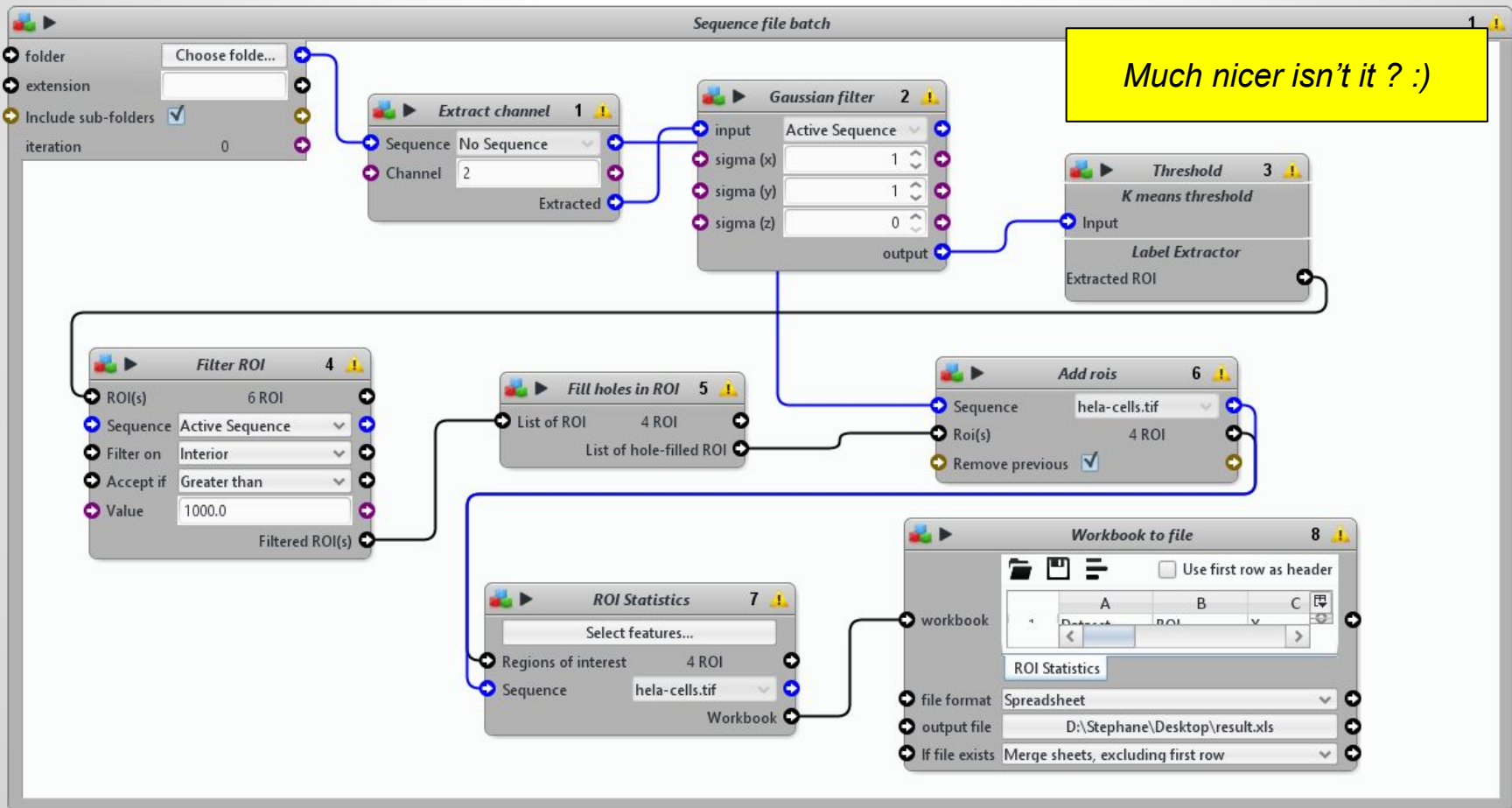
Protocols in Icy

- Make your protocol nicer: build your own block with “workflow” !



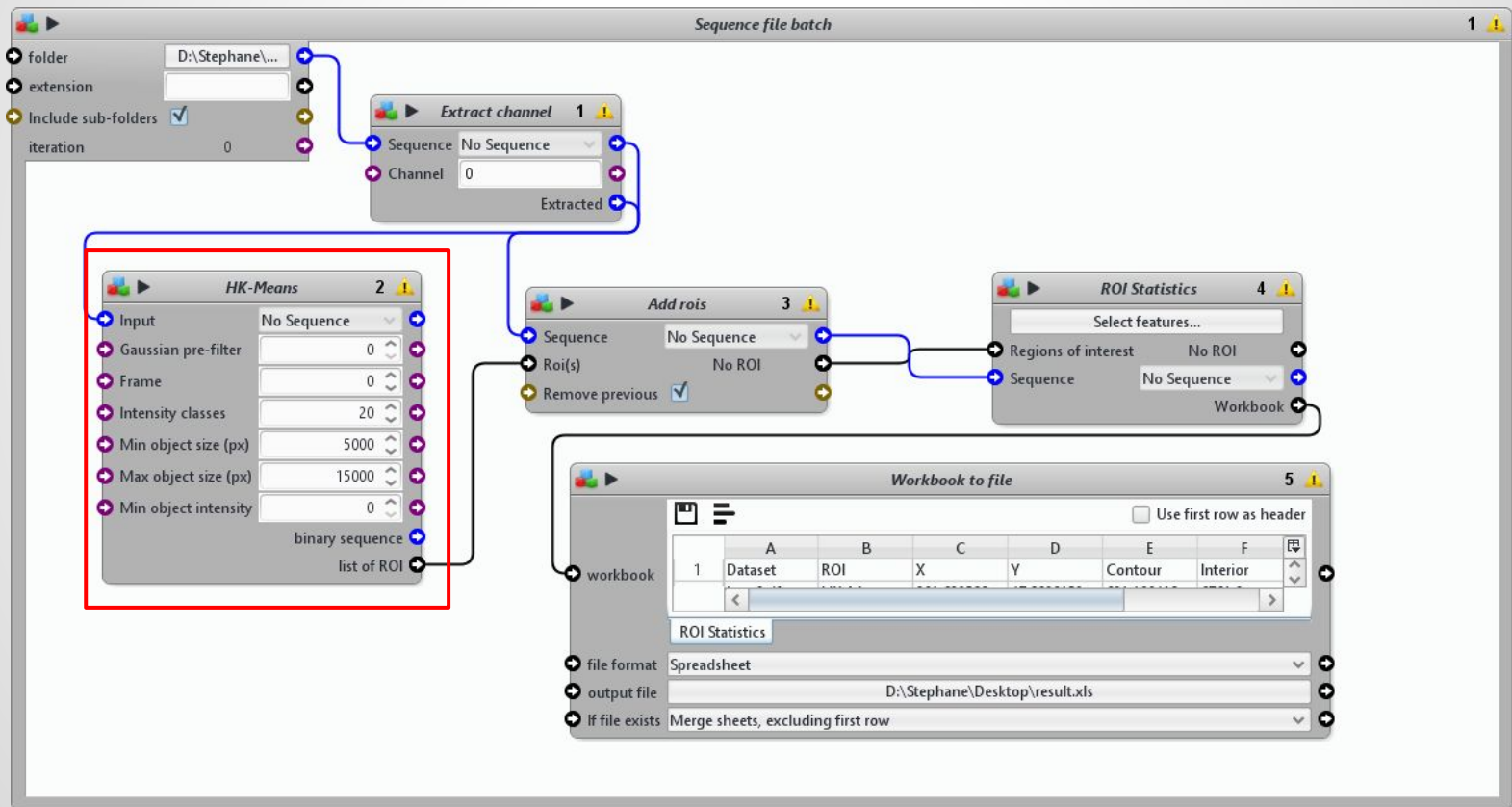
Protocols in Icy

- Make your protocol nicer: build your own block with “workflow” !



Protocols in Icy

- Make your protocol nicer: you can also better tool ;)



Protocols in Icy

- Most plugins have their corresponding Block
- What if the one you need isn't there (yet)?
 - #1: Leave a comment on the plug-in's page online

The screenshot displays the Icy website interface for the 'KMeans Color Quantization' plugin. The sidebar on the left contains navigation links: 'SHORT DESCRIPTION', 'DOCUMENTATION', '1 REVIEW', 'DEPENDENCIES', and 'CHANGELOG', along with social media icons. The main content area features a section titled 'This resource needs' with two plugin recommendations: 'MaskEditor' and 'NHerve Toolbox', both by Nicolas Hervé. Below this is a section titled 'One review on "KMeans Color Quantization"' showing a user's comment and a star rating. A prominent yellow box with the text 'Leave a comment & rating' is overlaid on the review section. At the bottom, there are buttons for 'LEAVE A REVIEW' and 'VIEW FULL CHANGELOG'.

PLUGIN
KMeans Color Quantization
Nicolas Hervé
Publication ID: ICY-411F1

SHORT DESCRIPTION
DOCUMENTATION
1 REVIEW
DEPENDENCIES
CHANGELOG

This resource needs

MaskEditor
Nicolas Hervé
PLUGIN

NHerve Toolbox
Nicolas Hervé
PLUGIN

One review on "KMeans Color Quantization"

Hi! very nice plugin, i was wondering if it was possible to call it in block editor?
NOVEMBER 24, 2012
RATED
★★★★☆
REPLY EDIT

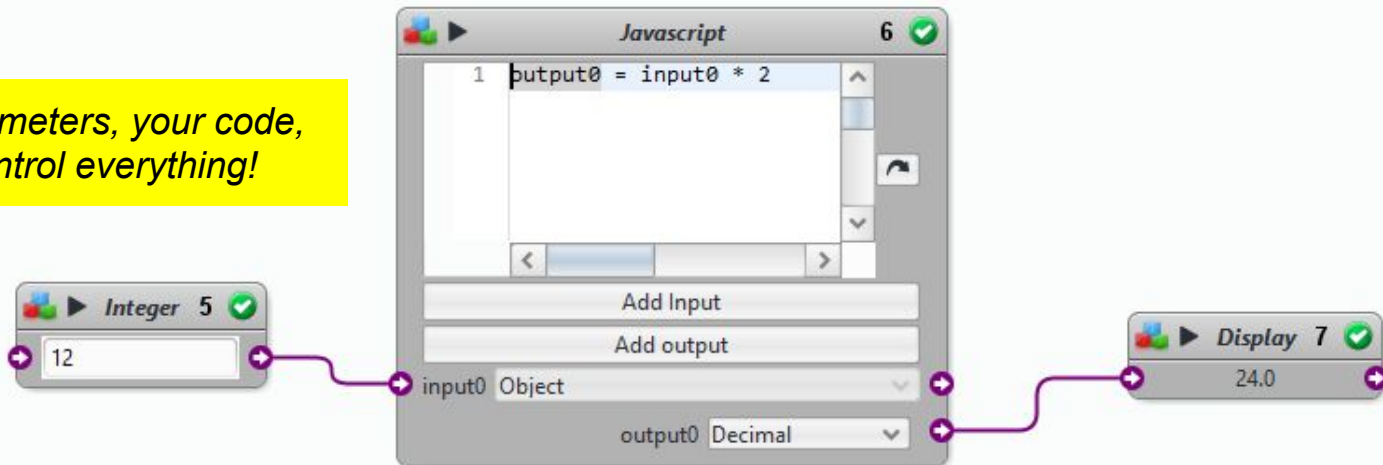
Leave a comment & rating

LEAVE A REVIEW VIEW FULL CHANGELOG

Protocols in Icy

- Most plugins have their corresponding Block
- What if the one you need isn't there (yet)?
 - #1: Leave a comment on the plug-in's page online
 - #2: The "DIY" (Do It Yourself) approach

Your parameters, your code, you control everything!



Protocols in Icy

- Protocols can be used in *headless* mode (command line) !
See the plugin documentation to get more information about it:
<http://icy.bioimageanalysis.org/plugin/protocols/>

And our protocol is ready. Here comes the magic spell:

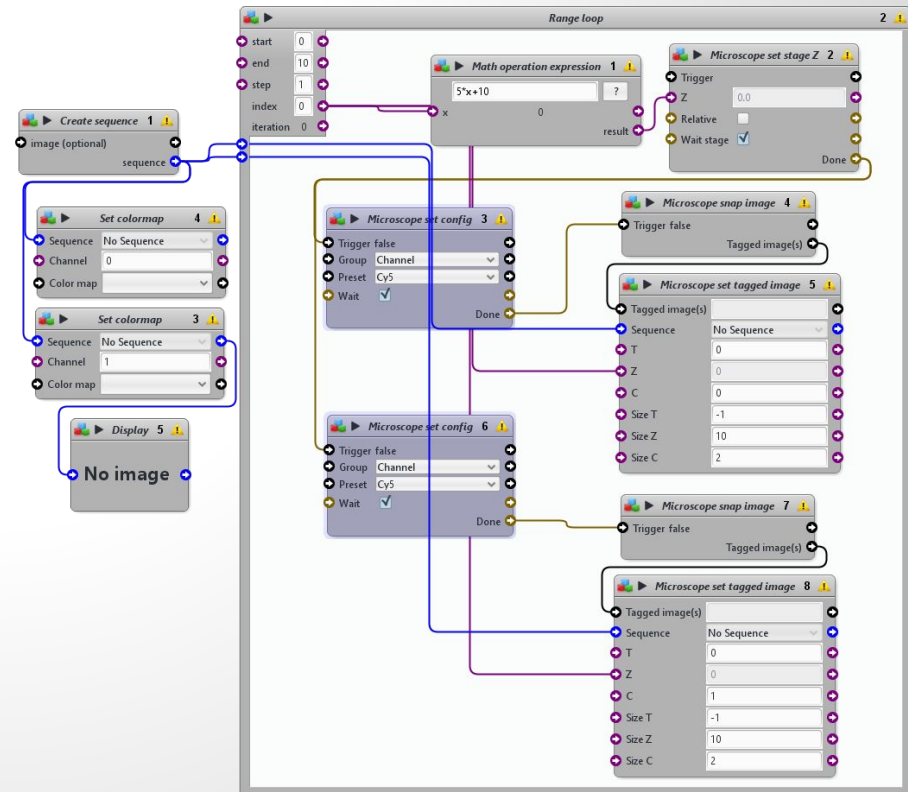
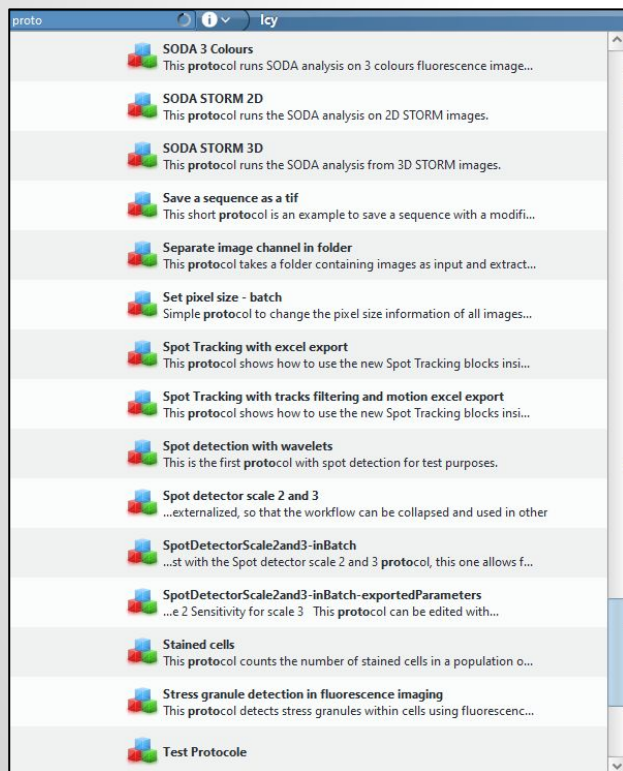
```
icy.sh -hl -x plugins.adufour.protocols.Protocols protocol=/my/great.protocol input1=/my  
/inputFile output1=/my/outputFile
```

Let's briefly analyse this line:

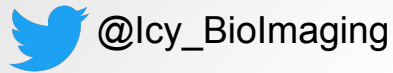
- icy.sh is the Icy startup command (NB: replace by icy.exe on windows; you can also generically use "java -jar icy.jar" instead)
- "-hl" is short for "headless", which means icy will run on the command line and no graphical interface will appear
- "-x" tells icy to run a specific plugin at startup (this plugin is "Protocols", as you might have guessed)
- "protocol=..." indicates the path to the protocol file to run
- "input1=..." and "output1=..." are used to pass all the necessary parameters to the protocol, using the IDs specified above.

Protocols in Icy

A good way to learn: use online protocols and adapt them to your needs !



Keep in touch !



Support forum

<http://icy.bioimageanalysis.org/support>

Image Analysis Hub Open Desk

Every other Thursday 9h30-12h30

Pasteur - François Jacob Building

<https://research.pasteur.fr/en/news/image-analysis-opendesk/>

Don't forget to cite and acknowledge us :)

