Scripting in Icy

fast edition - creating batches
"A script is a program written for a software environment that automates the execution of tasks. The script benefits from a high level interface, much more accessible."
First Script

- Open the Script Editor plugin:
  - Search it with the SearchBar
  - (Install and) Run it by clicking on it
First Script

Menu Bar

One Tab per script

Lines

Text Field

Console Input

Run / Stop

Choose script language

Console output
Predefined features

- Open the sequence: hela-cells.tif

- Get the current Sequence:
  
  ```python
  seq = getSequence()
  ```
Display sequence information

- `seq = getSequence()
  name = seq.getName()
  println(name)

- Displays the name of the sequence.
Display sequence information

- `seq = getSequence()`
  `name = seq.getName()`
  `println(name)`

- Displays the name of the sequence.
Using Icy tools *(extractChannel.js)*

- Extract the channel containing the spots (channel 0)
Using Icy tools (extractChannel.js)

- All interesting methods for Sequence Operations are stored in the SequenceUtil.

```javascript
seq = getSequence()

SequenceUtil.
```
Using Icy tools *(extractChannel.js)*

- All interesting methods for Sequence Operations are stored in the SequenceUtil.

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seq = getSequence()
```

`SequenceUtil`.
Using Icy tools *(extractChannel.js)*

- All interesting methods for Sequence Operations are stored in the SequenceUtil.

```javascript
seq = getSequence()

SequenceUtil.extractChannel(seq, 0)
```

- The index always starts at "zero" and not "one".
Using Icy tools (extractChannel.js)

- Extract the channel containing the spots
Using Plugins  *(Auto Threshold.js)*

- Perform an Auto Threshold on the nuclei channel (channel 2)
Perform an auto threshold *(autothreshold.js)*

- KMeans is a probabilistic method that will compute thresholding values

```javascript
kmeans = KMeans.computeKMeansThresholds(seq, 2, 2, 255)
```
Perform an auto threshold *(autothreshold.js)*

- KMeans is a probabilistic method that will compute thresholding values

\[
kmeans = \text{KMeans.computeKMeansThresholds}(\text{seq}, 2, 2, 255)
\]

- Why two?
Perform an auto threshold (autothreshold.js)

- KMeans is a probabilistic method that will compute thresholding values

  \[
  \text{kmeans} = \text{KMeans.computeKMeansThresholds}(\text{seq}, 2, 2, 255)
  \]

- We want to separate the histogram in two parts.
Perform an auto threshold *(autothreshold.js)*

- KMeans is a probabilistic method that will compute thresholding values

\[
\text{kmeans} = \text{KMeans.computeKMeansThresholds}(\text{seq, 2, 2, 255})
\]

\[
\text{result} = \text{Thresholder.threshold}(\text{seq, 2, kmeans, false})
\]

\[
\text{result.setName(seq.getName() + " - thresholded")}
\]
Perform an auto threshold *(autothreshold.js)*

- KMeans is a probabilistic method that will compute thresholding values

```javascript
kmeans = KMeans.computeKMeansThresholds(seq, 2, 2, 255)
result = Thresholder.threshold(seq, 2, kmeans, false)
result.setName(seq.getName() + " - thresholded")
```

- the result is a sequence, that we can add into Icy with the “gui” variable:

```javascript
 gui.addSequence(result)
```
Using Plugins (Auto Threshold.js)

- Perform an Auto Threshold on the nuclei channel
Input / Output (openFile.js)

- Load a sequence

```javascript
f = FileDialog.open()

if (f == null) throw "User cancelled!"

loadedSequence = Loader.loadSequence(f)
```
Input / Output (saveFile.js)

- Save a sequence

```javascript
seq = getSequence()

f = FileDialog.save()

Saver.save(seq, f, true)
```
Auto threshold on a file

- Load a file, threshold it, save the result

```java
f = FileDialog.open()
seq = Loader.loadSequence(f)

kmeans = KMeans.computeKMeansThresholds(seq, 0, 2, 255)
result = Thresholder.threshold(seq, 0, kmeans, false)
result.setName(seq.getName() + " - thresholded")

f = FileDialog.save()
Saver.save(result, f, true)
```
Batch auto threshold\textsuperscript{(batchAutoThreshold.js)}

- Loop on a folder

```javascript
folderInput = FileDialog.openFolder()

files = folderInput.listFiles()

for (i = 0; i < files.length; ++i) {
    Loader.loadSequence(files[i])
}
```
Batch auto threshold (batchAutoThreshold.js)

```javascript
// will be either \ or / depending on your OS
sep = File.separator

// Folder containing the input to batch on
folderInput = FileDialog.openFolder()

if (folderInput == null)
    throw "User Cancelled."

// All the files contained inside the inputFolder
files = folderInput.listFiles()

// folder containing the result
folderOutput = FileDialog.openFolder()

if (folderOutput == null)
    throw "User Cancelled."

// fileName (a string) of the output, as a base for the files
fileName = folderOutput.getPath() + sep

// Loop on every file.
for (i = 0; i < files.length; i++) {
    seq = Loader.loadSequence(files[i])

    // computes the kmeans thresholds for automatic thresholding
    kmeans = KMeans.computeKMeansThresholds(seq, 0, 2, 255)

    // performs the threshold and put the result (a sequence) inside a variable
    result = Thresholder.threshold(seq, 0, kmeans, false)

    // create a file based on the original sequence name, to which
    // is added .kmeans.
    outputFile = new File(fileName + seq.getName() + ".kmeans.tif")

    // Save the resulting sequence to the file
    Saver.save(result, outputFile)
}
```
Find scripts

- Scripts are available on the website:
  http://icy.bioimageanalysis.org/script/list

- You can download them:
  - Directly from the website
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● Add your future scripts on the website, and share them!