

# Example project: blob segmentation

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## 1. Description

This project segments the blobs example from ImageJ

## 2. Utilized nodes

Name	Description	Signature
<b>Auto threshold 2D</b>	Applies an auto-thresholding algorithm. If higher-dimensional data is provided, the filter is applied to each 2D slice.  This algorithm groups the incoming data based on the annotations. Those groups can consist of one data item per slot.	<i>(Image (8 bit) Input) -&gt; (Image (mask) Output)</i>
<b>Compartment output</b>	Output of a compartment	<i>() -&gt; ()</i>
<b>Extract ROI metadata as table</b>	Extracts the metadata (properties map) of each ROI and writes them into a table	<i>(ROI list Input) -&gt; (Results table Output)</i>
<b>File list</b>	Converts each provided path into file data.	<i>() -&gt; (File Filenames)</i>
<b>Find particles 2D</b>	Converts mask images into ROI by applying a connected components algorithm and generates measurements. Please note that this algorithm will always trace the external object boundaries and convert them into polygonal ROIs. This means that holes will be closed. This node requires a thresholded image as input and will extract measurements from the thresholded image. If you already have ROI available and want measurements, use 'Extract ROI statistics'. If higher-dimensional data is provided, the results are generated for each 2D slice.	<i>(Image (mask) Mask) -&gt; (ROI list ROI, Results table Measurements)</i>
<b>Import image</b>	Loads an image via the native ImageJ functions.	<i>(File Files) -&gt; (Image Image)</i>
<b>Set ROI metadata by statistics</b>	Sets ROI metadata by statistics.  This algorithm groups the incoming data based on the	<i>(ROI list ROI, Image Reference) -&gt; (</i>

<b>(expression)</b>	annotations. Those groups can consist of one data item per slot. Set overlay ROIs	<i>ROI list</i> Output)
<b>Set overlay</b>	This algorithm groups the incoming data based on the annotations. Those groups can consist of one data item per slot.	( <i>Image</i> Input, <i>ROI list</i> ROI) -> ( <i>Image</i> Output)

## 3. Dependencies

### 3.1. JIPipe extensions

Name	Version	Author(s)
<b>Filesystem types and algorithms</b>	1.81.0	Zoltán Cseresnyés*, Ruman Gerst*, Marc Thilo Figge#
<b>Standard table operations</b>	1.81.0	Zoltán Cseresnyés*, Ruman Gerst*, Marc Thilo Figge#
<b>ImageJ algorithms</b>	1.81.0	Zoltán Cseresnyés*, Ruman Gerst*, Marc Thilo Figge#
<b>Strings</b>	1.81.0	Zoltán Cseresnyés*, Ruman Gerst*, Marc Thilo Figge#
<b>Compartment management</b>	1.81.0	Zoltán Cseresnyés*, Ruman Gerst*, Marc Thilo Figge#
<b>Forms</b>	1.81.0	Zoltán Cseresnyés*, Ruman Gerst*, Marc Thilo Figge#
<b>Core</b>	1.81.0	Zoltán Cseresnyés*, Ruman Gerst*, Marc Thilo Figge#
<b>ImageJ integration</b>	1.81.0	Zoltán Cseresnyés*, Ruman Gerst*, Marc Thilo Figge#

### 3.2. ImageJ update sites

Name	URL
<b>IJPB-plugins</b>	<a href="https://sites.imagej.net/IJPB-plugins/">https://sites.imagej.net/IJPB-plugins/</a>
<b>ImageScience</b>	<a href="https://sites.imagej.net/ImageScience/">https://sites.imagej.net/ImageScience/</a>

## 4. Citations (dependencies)

- ImageScience by Erik Meijering. <https://imagescience.org/meijering/software/imagescience/>
- Steger, C., 1998. An unbiased detector of curvilinear structures. IEEE Transactions on Pattern Analysis and Machine Intelligence, 20(2), pp.113–125.

- Legland, D.; Arganda-Carreras, I. & Andrey, P. (2016), "MorphoLibJ: integrated library and plugins for mathematical morphology with ImageJ", *Bioinformatics* (Oxford Univ Press) 32(22): 3532-3534, PMID 27412086, doi:10.1093/bioinformatics/btw413
- Papyrus Icon Theme: <https://github.com/PapyrusDevelopmentTeam/papyrus-icon-theme> (Licensed under GPL-3)
- Breeze Icons: <https://github.com/KDE/breeze-icons> (Licensed under LGPL-2.1)
- Melissa Linkert, Curtis T. Rueden, Chris Allan, Jean-Marie Burel, Will Moore, Andrew Patterson, Brian Loranger, Josh Moore, Carlos Neves, Donald MacDonald, Aleksandra Tarkowska, Caitlin Sticco, Emma Hill, Mike Rossner, Kevin W. Eliceiri, and Jason R. Swedlow (2010) Metadata matters: access to image data in the real world. *The Journal of Cell Biology* 189(5), 777-782
- Rueden, C., Schindelin, J., Hiner, M. & Eliceiri, K. (2016). *SciJava Common* [Software]. <https://scijava.org/>.
- RandomJ by Erik Meijering. <https://imagescience.org/meijering/software/randomj/>
- MTrackJ by Erik Meijering. <https://imagescience.org/meijering/software/mtrackj/>
- Schneider, C. A.; Rasband, W. S. & Eliceiri, K. W. (2012), "NIH Image to ImageJ: 25 years of image analysis", *Nature methods* 9(7): 671-675
- Gerst, R., Cseresnyés, Z. & Figge, M.T. JIPipe: visual batch processing for ImageJ. *Nat Methods* (2023). <https://doi.org/10.1038/s41592-022-01744-4>
- Schindelin, J.; Arganda-Carreras, I. & Frise, E. et al. (2012), "Fiji: an open-source platform for biological-image analysis", *Nature methods* 9(7): 676-682, PMID 22743772, doi: 10.1038/nmeth.2019
- FeatureJ by Erik Meijering. <http://imagescience.org/meijering/software/featurej/>
- Rueden, C. T.; Schindelin, J. & Hiner, M. C. et al. (2017), "ImageJ2: ImageJ for the next generation of scientific image data", *BMC Bioinformatics* 18:529
- Blobs image: <https://imagej.nih.gov/ij/images/blobs.gif>
- Eliceiri K. V., Berthold M. R., Goldberg I. G., Ibanez L., Manjunath B. S., Martone M. E., Murphy R. F., Peng H., Plant A. L., Roysam B., Stuurmann N., Swedlow J.R., Tomancak P., Carpenter A. E. (2012) *Biological Imaging Software Tools Nature Methods* 9(7), 697-710

## 5. Pipeline text description

### 5.1. Compartment C1 "Main"

#### 5.1.1. Node #1 "File list" of type "File list"

- The parameter item #1 of "Files" (file-names) is set to **"blobs.gif"**

#### 5.1.2. Node #2 "Import image" of type "Import image"

- Input "Files" of node #2 receives data from output "FileNames" of node #1
- The parameter "Remove LUT" (remove-lut) is set to **true**

#### 5.1.3. Node #3 "Auto threshold 2D" of type "Auto threshold 2D"

- Input "Input" of node #3 receives data from output "Image" of node #2
- The parameter "Method" (method) is set to **"Moments"**

#### 5.1.4. Node #4 "Find particles 2D" of type "Find particles 2D"

- Input "Mask" of node #4 receives data from output "Output" of node #3
- The parameter "Extracted measurements" (measurements) is set to {"values": ["Centroid", "Area", "PixelValueMinMax"], "collapsed": true}

#### **5.1.5. Node #5 "Set ROI metadata by statistics (expression)" of type "Set ROI metadata by statistics (expression)"**

- Input "ROI" of node #5 receives data from output "ROI" of node #4
- The parameter item #1 of "Generated metadata" (metadata-generators) is set to **value = Area, key = "Area"**
- The parameter item #2 of "Generated metadata" (metadata-generators) is set to **value = AVG(all.Area), key = "MeanArea"**

#### **5.1.6. Node #6 "Set overlay" of type "Set overlay"**

- Input "Input" of node #6 receives data from output "Image" of node #2
- Input "ROI" of node #6 receives data from output "ROI" of node #4

#### **5.1.7. Node #7 "Extract ROI metadata as table" of type "Extract ROI metadata as table"**

- Input "Input" of node #7 receives data from output "Output" of node #5

#### **5.1.8. Node #8 "Main output" of type "Compartment output"**

- Input "Data" of node #8 receives data from output "Output" of node #6