

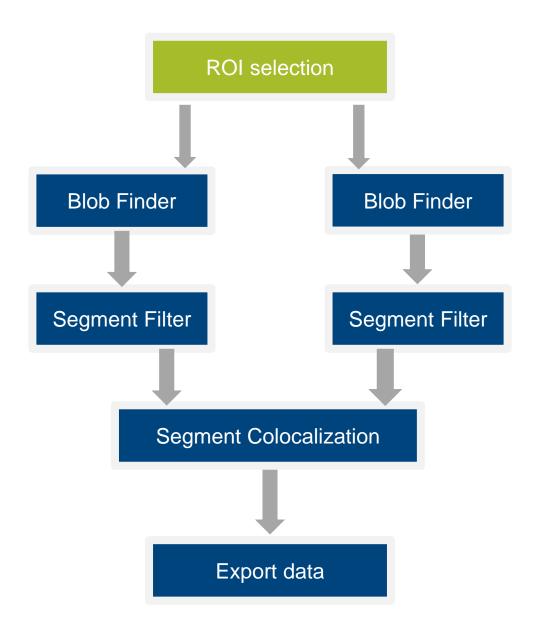


## CELLS/PARTICLES COMPARTMENTALIZATION

«Cells or Particles compartmentalization»

The pipeline purpose is to detect objects, falling in two different classes, using Blob Finder operators. The detected objects are compared to find partial or total overlap conditions. It can be applied to Cells, Nuclei or any kind of small particles.

# Arivis Vision4D Pipeline example «Cells or Particles compartmentalization» Working Flowchart:





## Arivis Vision4D Pipeline example

In order to run the pipeline described here below, please download the demo dataset according to the following instruction.

## Step 1.

Click on the below link to access to the Arivis downloading demo dataset's area.



arivis Vision 4D-Demo Data-Sample Pipelines - Detect Structures.zip file is saved on the download folder.



## Step 2.

Create a new folder on your local disk.

Move the ZIP file from the download folder inside it.



## Step 3.

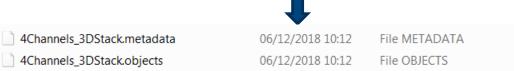
4Channels\_3DStack

## UnZip the file:

arivis Vision 4D-Demo Data-Sample Pipelines - Detect Structures.zip.

arivisVision4D-DemoData-SamplePipelin... 10/12/2018 07:39

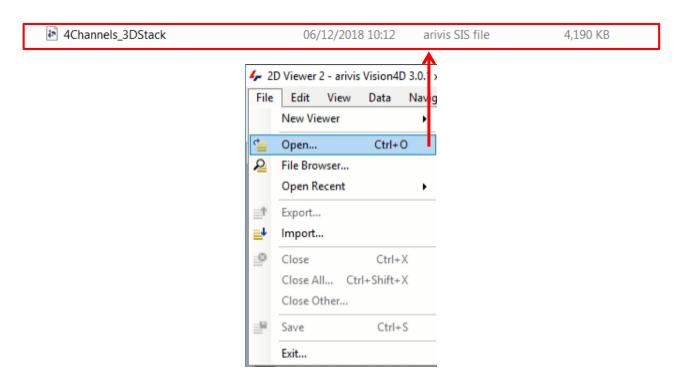
Three files are now available in the folder.



06/12/2018 10:12

arivis SIS file

Step 4.
Open the SIS file on Vision4D.





4 KB

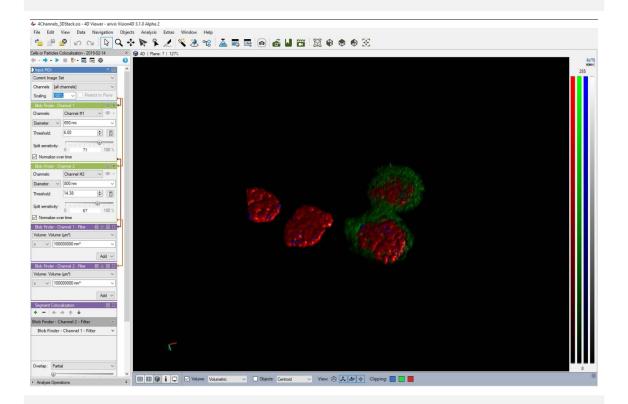
108 KB

4,190 KB

## The dataset is visualized in the V4D viewing area.

#### TIPS:

The dataset is visualized according to the current rendering setting parameters. Please refer to the *User Manual* for more details about how to set or modify the rendering options.



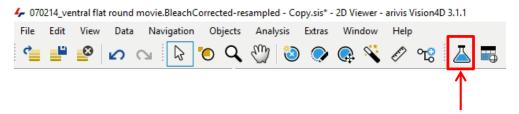
#### **DETAILS:**

The dataset is a multidimensional, discrete, representation of your real sample volume. It can be structured as a Z series of planes (eg Optical sectioning) of multiple channels (dyes) in a temporal sequence of time points (located in several spatial positions). Usually the dataset shows a single experimental situation ( a complete experiment can be composed by several dataset). The datasets are available as graphic files saved in plenty of graphic formats (standard formats as well as proprietary formats)

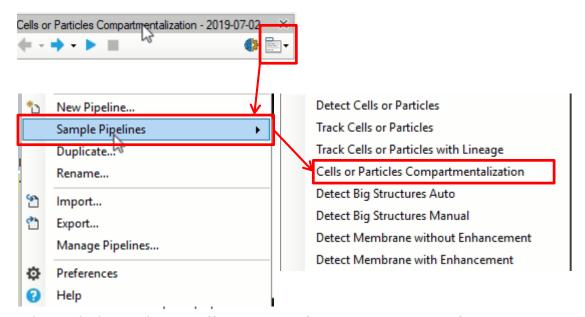


### Step 5.

## Activate the «Cells or Particles comparmentalization » pipeline.



If not already done, open the Analysis panel



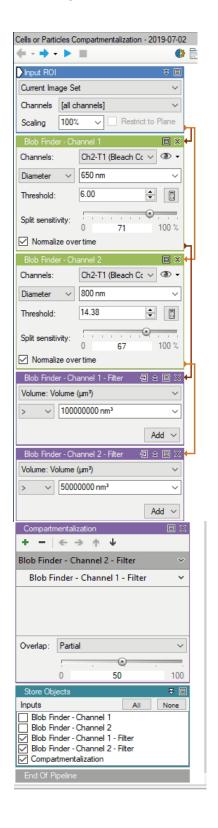
Then click on the «*Cells or Particles comparmentalization*» item.

#### **TIPS:**

The active Pipeline, if any, will be replaced by the new one. Please refer to the *User Manual* for more details about how to export a pipeline.



## The «Pipeline Template - Cells or Particles comparmentalization » pipeline operators layout.



### 1. Region Of Interest:

This operator allows the region of interest (ROI) selection. ROI defines the dataset subarea that will be processed and analyzed by the pipeline.

#### 2. Blobs Finder:

Automatic small objects detection algorithm. It uses a local treshold method.

- 3. <u>Segment Filter</u>
  Allows the blob filtering based on multiple parameters selection.
- Segment
   comparmentalization
   The detected objects are compared to find partial or total overlap conditions.
- 5. <u>Store Objects</u>
  Store the detected segments (TAG) in the active dataset.



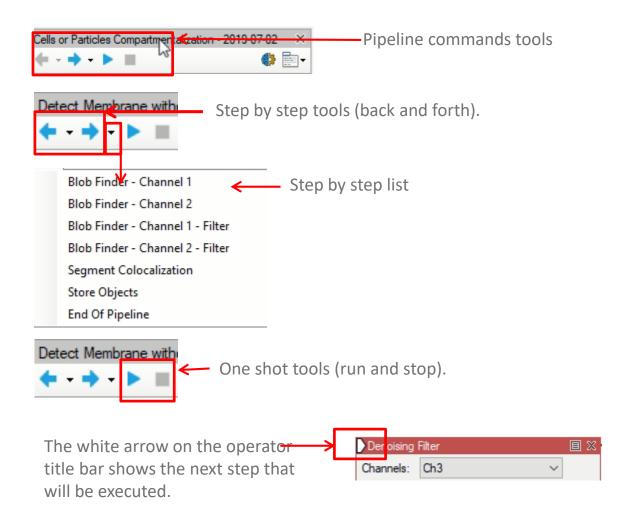
## Step 6.

## Execute the «Cells or Particles comparmentalization» pipeline.

#### TIPS:

The pipeline can be executed as single shot or step by step. Step by step method allows to run and undo a single *Operation*. Single shot method runs all the pipeline in one task (no stop until the pipeline execution ends).

Either the arrow buttons or the *Operation* list can be used to run both methods.



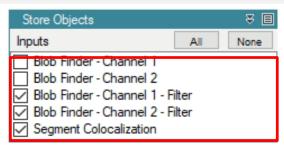
## Step 7.

## View the results

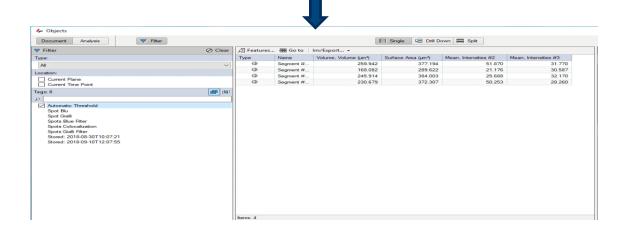
#### TIPS:

Results (segments and measurements) will be stored in the dataset only if the *Store Objects* operator has been correctly set.

Please tick appropriately the option as shown below before complete the pipeline execution.



Selected TAGs measurements are now visible in the data table



#### TIPS:

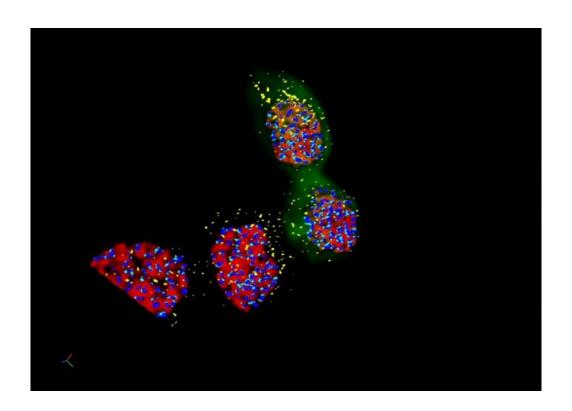
If the data table is not already visible, please click on the related icon to open it.





View the results.

Segments can be visualized either in 2D as well as 4D according to the currently set options.



#### TIPS:

Please refer to the *User Manual* for more details about how to visualize segments on the dataset.



## Arivis Vision4D Pipeline example

The «*Cells or Particles comparmentalization*» pipeline can be modified to be adapted to your datasets.

All the pipeline parameters must be set according to your dataset features.

#### TIPS:

Before starting to modify the Pipeline layout, switch the Viewing area from 4D to 2D view mode.

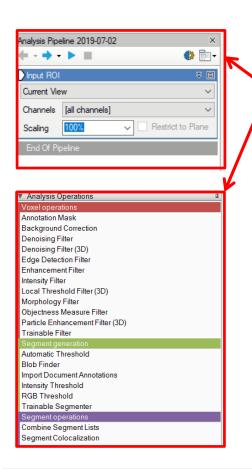
During analysis setup, the Operator preview mode is only available in 2D mode. Once the segments have been generated, you can switch back to 4D view mode.



#### TIPS:

Please refer to the *User Manual* for more details about how to switch the Viewing Area from 4D to 2D view mode.





#### **DETAILS:**

The Analysis Pipeline panel consists of two main areas. The Pipeline sequence area and the analysis operations list area.

#### TIPS:

Please refer to <u>Addendum A</u> for more details about how to add or remove an *Operator* to the current Pipeline

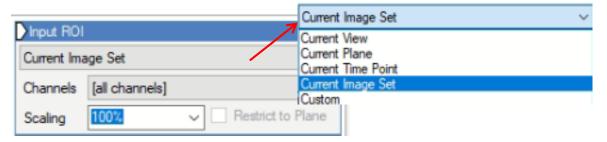
#### **DETAILS:**

Analysis Pipeline protocol is executed from top to bottom of the pipeline. The Operations must be added to the Pipeline in the correct order.



## Step A.

How to set the ROI operator



Processing & Analysis target options:

#### a. Current View

Only the selected Z plane and the visualized area in the viewer are processed.

#### b. <u>Current Plane</u>

Only the selected Z plane is processed regardless to the visualized area (real XY pixel size).

#### c. Current Time Point

The selected time point is entirely processed (all Z planes and the real XY pixel size)

#### d. Current Image Set

The complete dataset (XYZ and time) is processed.

#### e. Custom

Allows a detailed selection of each parameters.

#### **DETAILS:**

Use the Custom option during the pipeline setting and testing. Set a sub volume (XY, Planes, Time Points, channels) of your dataset on which perform the trial. This will speedup the setting process.

#### TIPS:

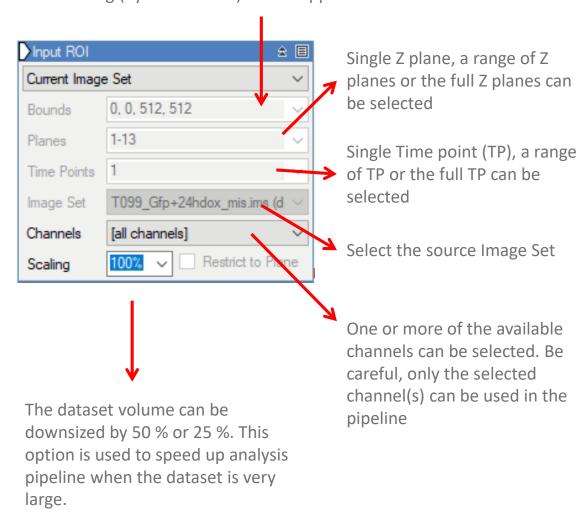
Please refer to the *User Manual* for more details about how to select the active Z plane and/or the active Time Point.



## Step A.

## How to set the **Input ROI** operator Custom option

The full XY size, the viewing area or a free area setting (by coordinates) can be applied

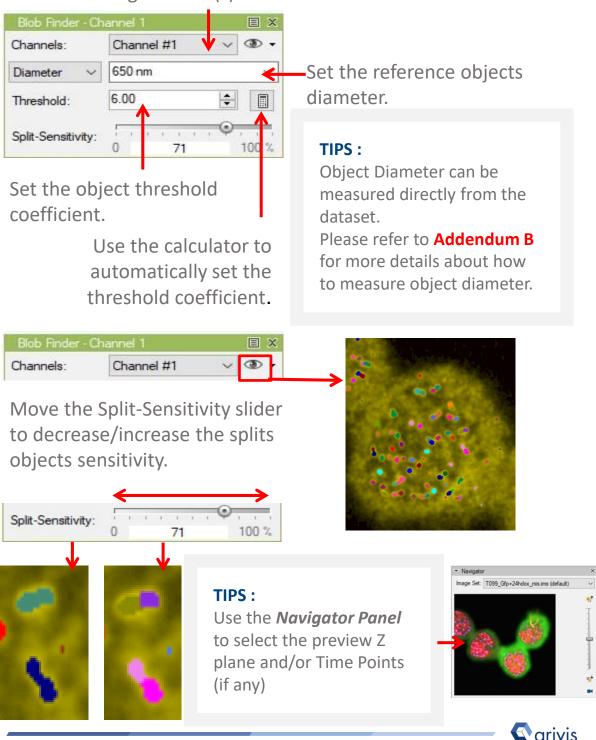




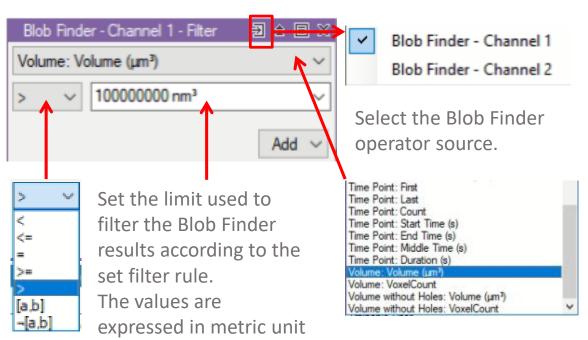
## Step B.

## How to set the **Blob Finder** operator

Select working Channel(s).

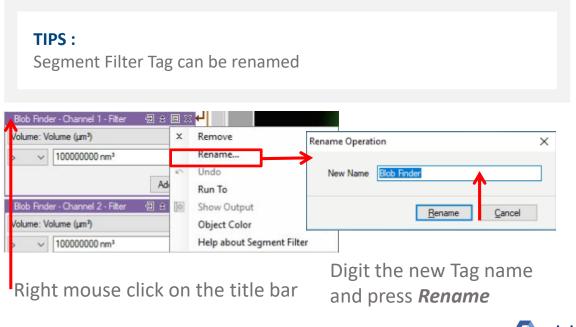


## Step C. How to set the **Segment Filter** operator



Select the filter rule.

Select the Feature to be used for filtering the blobs



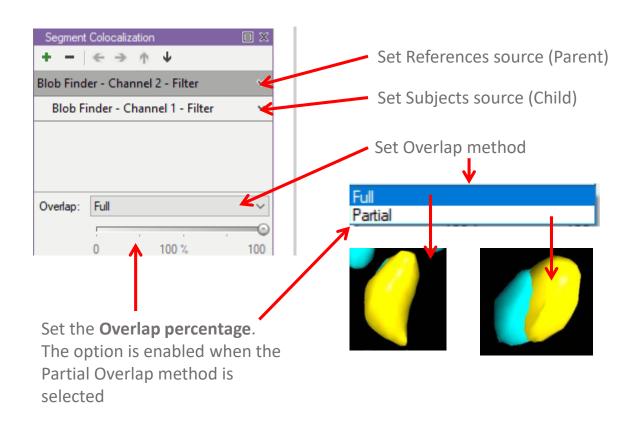
## Step D.

## How to set the **Segment** *comparmentalization* operator

#### **DETAILS:**

The **segment** *comparmentalization* operator compares the objects set as Subjects with the objects set as References.

The Operator find overlapped objects (partially or totally) according to the overlap method.

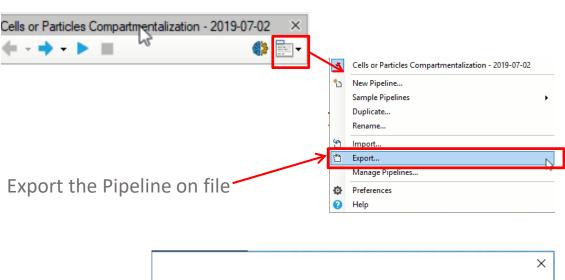


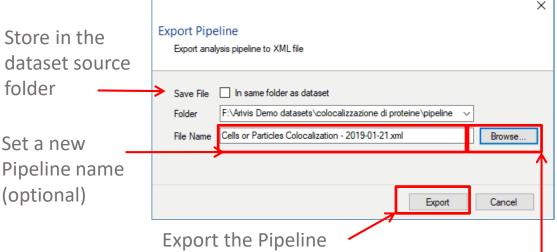


## Step E.

## How to export the modified Pipeline

Once you have finished your pipeline settings, according to your needs, the pipeline can be exported on disk. Exporting the pipeline on file allows you to run it with different datasets.





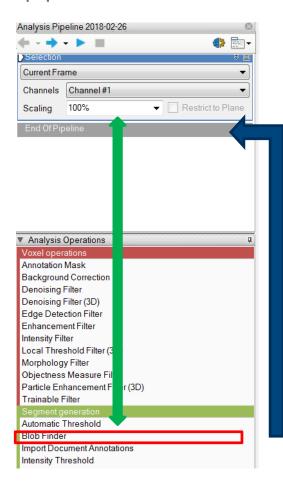
Browse the destination folder



### **Addendum A:**

How to add or remove an *Operator* from the

pipeline.





The *Operators* can be added to Pipeline in two ways

1. Double click on the **Operator** you wish to add to the current Pipeline.

The operator will be inserted at the end of the group of operations to which it belongs. Voxel Operations are positioned before the Segment generation meanwhile Store operations are put always at the end of the Pipeline.

2. Drag and drop the *Operator* you wish to add to the current Pipeline.

The *Operator* will be automatically inserted in any place within the group of operations to which it belongs. The *Operator* cannot be added during the Pipeline execution

To remove an Operator from the Pipeline, press the X button located in the right side of the operator title bar.

#### TIPS:

Please refer to the *User Manual* for more details about how to add a new *Operator* to the current Pipeline.

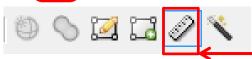


## **Addendum B:**

How to measure Object diameter

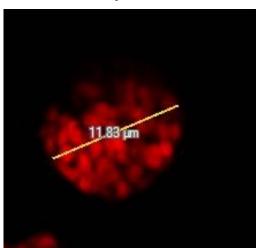


Switch to 2D view mode.

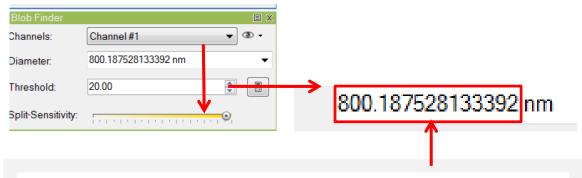


Press the Ruler icon in the **Shortcut toolbar panel**.

- 1. Move the mouse cursor (it shows a little ruler instead of the standard arrow) on one side of the structure you want to measure.
- 2. Keeping the left mouse button down, draw a line over the structure diameter.
  Once the mouse button is released, the distance measured is shown over the image.



3. Take note of this number and digit it in the *Diameter Box* 



#### TIPS:

Before write down the diameter in the Box, select from the list the right metric unit you want to use.

Then digit the measure without delete the unit in the box

