

Multi-component analysis of X-ray Computed Tomography datasets

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Outline

1 Data collection and compromising artefacts

2 Data preparation

3 Pore analysis

4 Pore filtering

5 Recipe creation and application



Data courtesy of Dr. Shengchuan Wu, Southwest Jiaotong University

Data collection and compromising artefacts

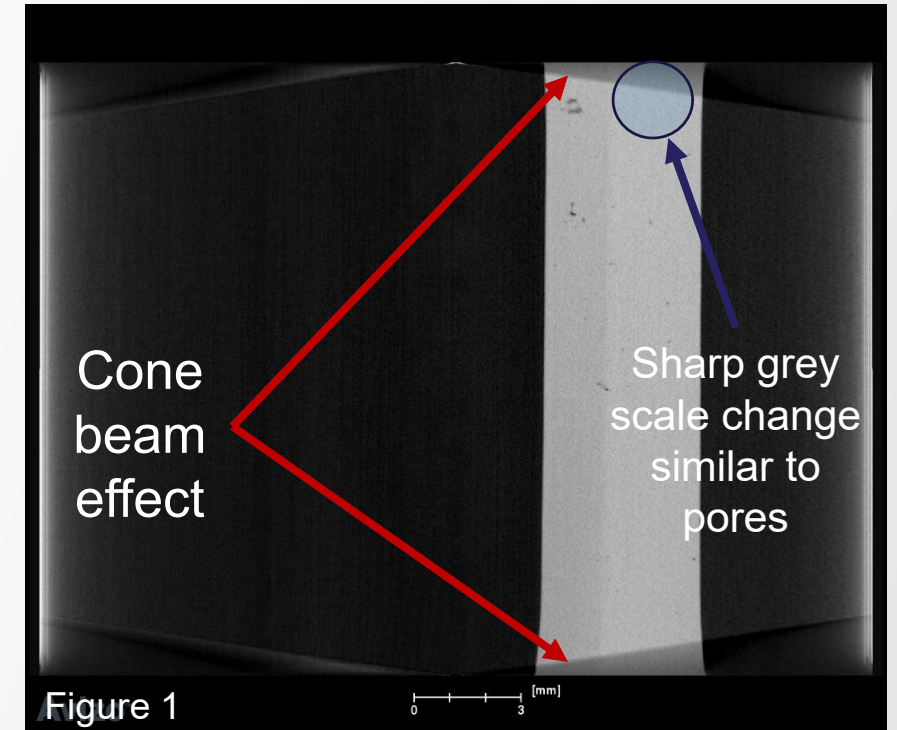
Introduction

In the analysis of engineering components using X-ray CT the inability to produce consistent results and to automate analysis routines usually originates from the acquisition of poor data. This in turn results in the data having to be manually corrected. However appropriate specimen setup prior to scanning can overcome most of the barriers to automating data analysis. The following examples are common problems when analyzing X-ray CT data and can be either corrected or removed from the final reconstructed volume.

Data collection and compromising artefacts

Cone beam effect

The cone beam effect in laboratory based X-ray CT is a common problem that originates from the X-ray source aperture window. During reconstruction the sections of the object close to edge will come in and out of the projections depending upon their position during the scan resulting in the effect shown above. The cone beam effect results in a sharp greyscale change in the image that can make it appear as a different phase. In this example it is similar to the porosity in the test piece. The cone beam effect can be minimised by moving the detector further away from the source or moving the specimen towards the detector. However the cone beam effect can never be truly eliminated and the best solution is to remove the upper and lower reconstructed Ortho Slices slices during the reconstruction stage.



Data collection and compromising artefacts

Streak artefacts

Streak artefacts are caused by the features not correctly aligning during the reconstruction process. There are three main causes:

1. The samples have moved during the scan. This is usually when samples have been glued to a stand and the glue has not been given enough time to set. The other main cause is the mounting of the specimen on a foam base that sags over time. To eliminate these causes it is best to mount specimens at least 24hrs prior to scanning.
2. The use of fly scans is common when there are time restraints for scanning. During a fly scan the sample is continuously rotated during the radiograph acquisition. This can sometimes result in a slight misalignment of the radiographs resulting in streaks although this is usually seen along flat edges. This effect is usually minor and to eliminate it completely it is better to use a step scan. A more significant issue relating to fly scan reconstructions is the presence of ring artefacts that are difficult and time consuming to remove in post processing. Therefore if feature segmentation and analysis are required then it is recommended to use a step scan with ring artefact dithering.
3. If the rotation stage on the X-ray CT scanner is damaged this will result in misaligned radiographs resulting in streak artefacts in the final reconstruction as well as the doubling or blurring of feature edges.

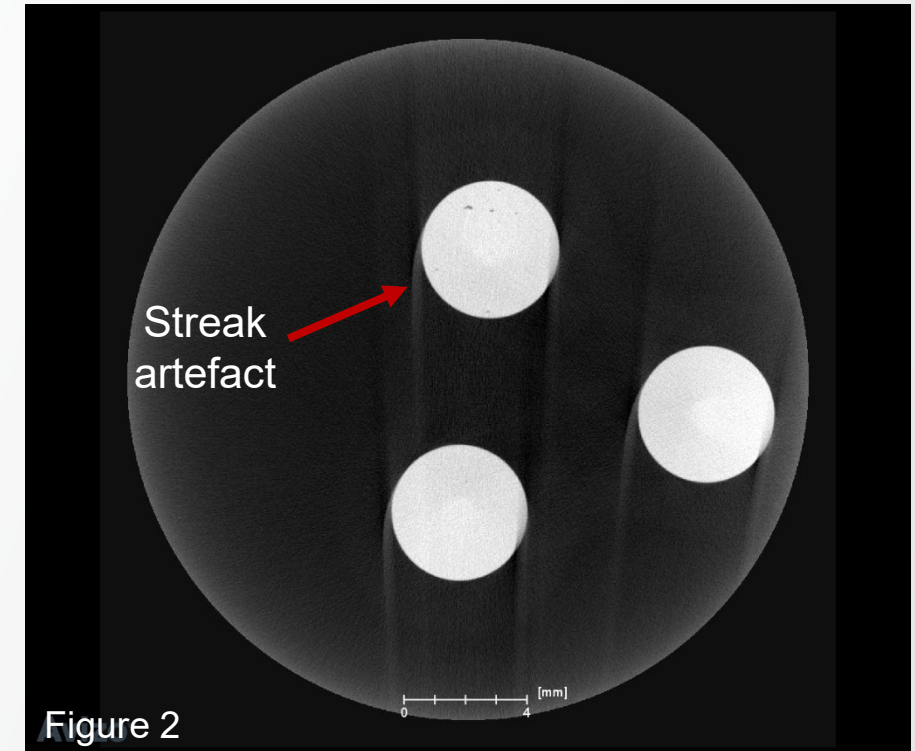
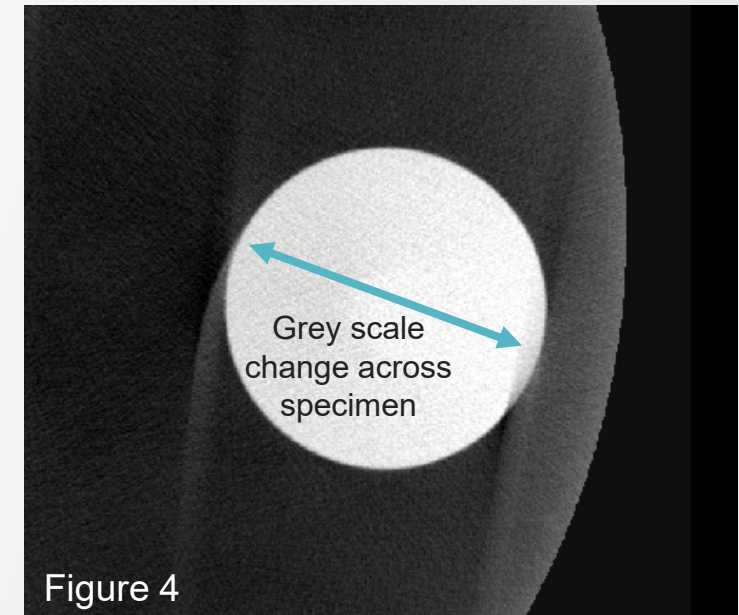
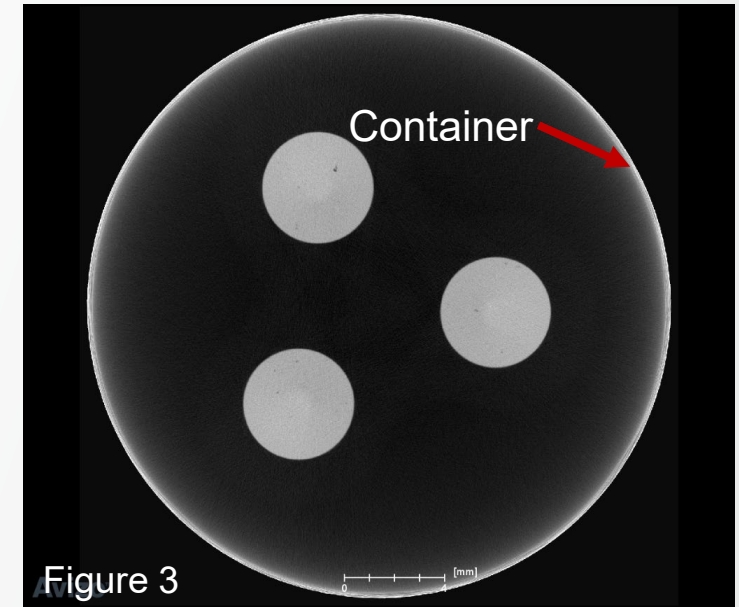


Figure 2

Data collection and compromising artefacts

Beam hardening

For cylinder shaped specimens that are placed in the centre of rotation the effect of beam hardening is relatively easy to correct during post processing. But it is common practice to scan multiple specimens in a single scan in order to save time as shown in Figure 3. A sufficient X-ray filter on the X-ray source can minimise beam hardening corrections in post processing, however samples may be set in a case for transport or as an alternative method of reducing beam hardening. In this case specimens should be located centrally within the container (Figure 3) with a sufficient distance from the container wall to produce a flat grey scale profile during analysis. If a specimen is located too close to the container wall (Figure 4) then the grey scale profile across the specimen will be non uniform. The addition of the outer container in the final reconstruction will also complicate post processing resulting in the need for additional steps to eliminate this feature!



Data collection and compromising artefacts

Saving the reconstruction output

Typical X-ray CT reconstructions are produced in 32, 16 and 8bit and the dynamic range can be outputted in full, percentile or a selected range. Care should be taken when selecting the outputted files since this can result in a significant loss of information that will affect the ability to post process the data. Figure 5 is an example of a poorly selected output file where automated analysis was not possible.

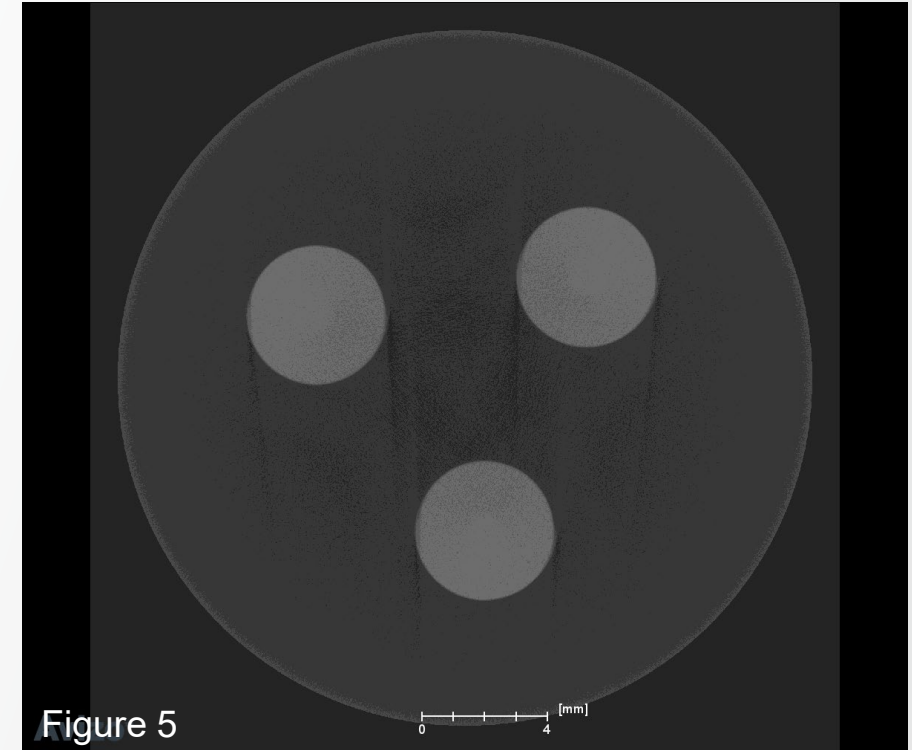


Figure 5

Data collection and compromising artefacts

Conclusion

For the analysis of multiple components in a single X-ray CT dataset the artefacts shown above should be avoided. Figure 6 shows a prime example of a dataset that can have the post processing stages automated to extract information regarding each of the barbell samples. In this dataset the important features are:

1. Samples are positioned equidistant from the centre of rotation
2. The container wall has been removed during the reconstruction process. This reduces the reconstructed volume size making data loading faster and removes the need for a complicating post-processing step to remove this feature later.
3. The top and bottom slices were removed during the reconstruction stage to eliminate the cone beam artefact.
4. The reconstruction output file shows a clean image. In this case the greyscale range was a percentage value and the file was a 16bit vol. file for ease of data selection rather than the more cumbersome tif. stack.

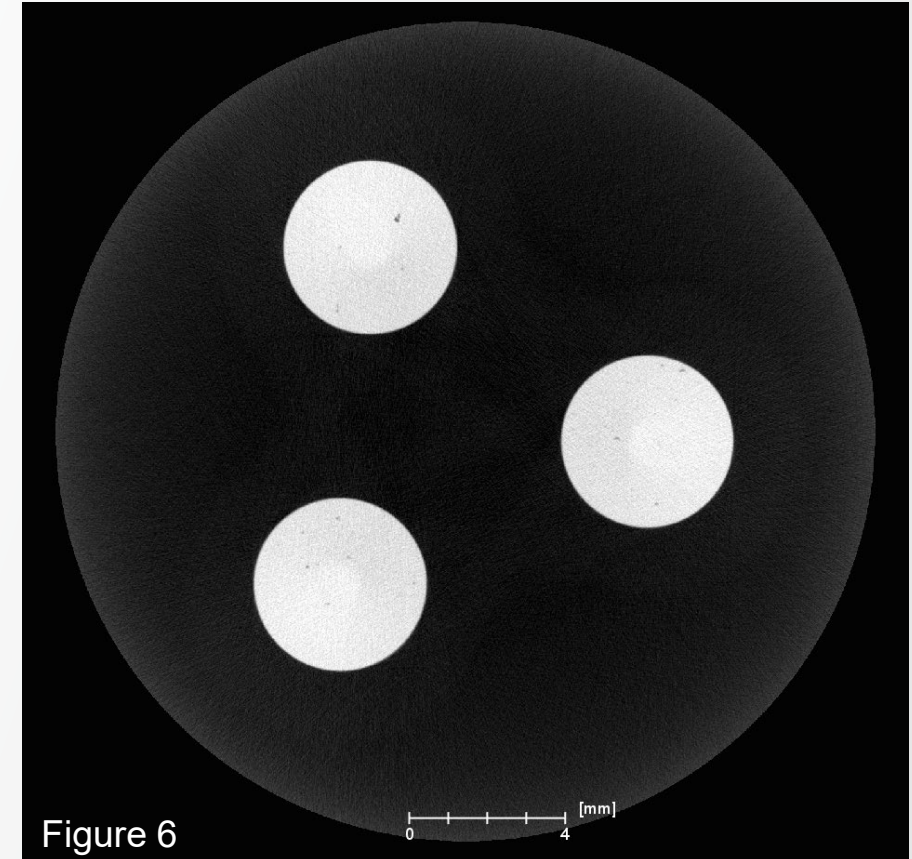


Figure 6

Thermo Scientific™ Avizo™ Software tools useful for this analysis

In Avizo Software there are a wide range of tools and it is possible to achieve similar results using a number of different tool combinations. In this example, because the data is a clean and artefact free, image filters are not required since their use would in information loss. Instead an analysis filter has been used to remove features associated with noise in the latter stages.

A short list of the tools used is as follows:

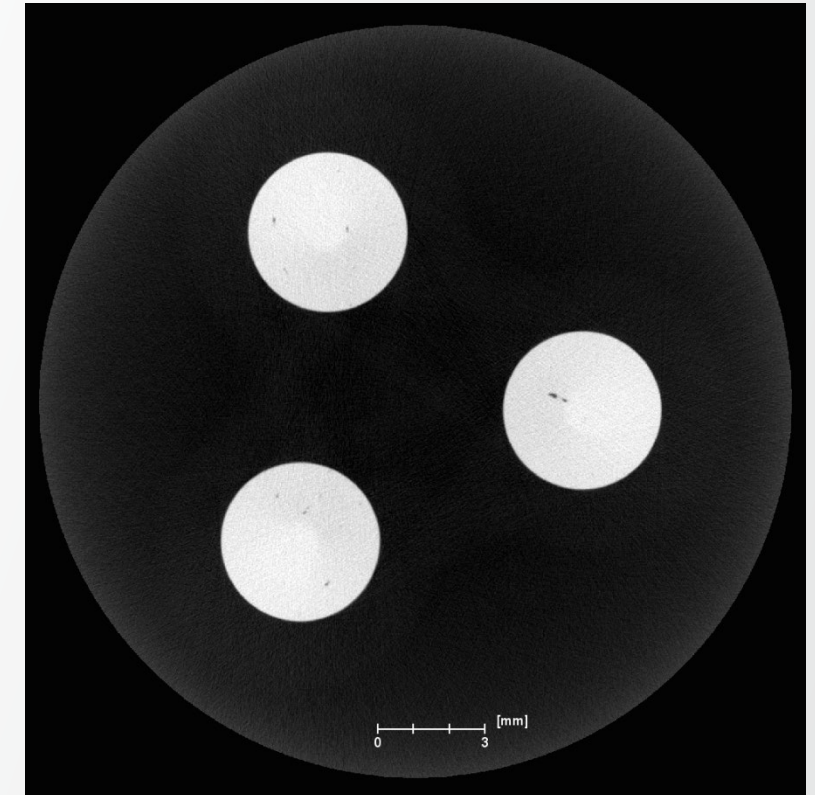
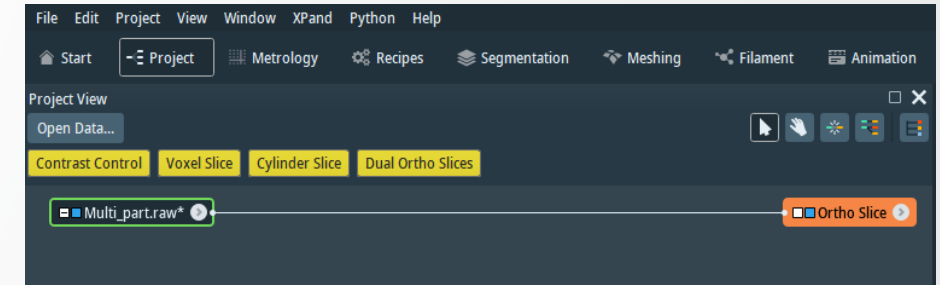
- Arithmetic: combining and separating volumes
- Mask: isolating components in the data for individual analysis
- Closing by reconstruction: removing internal features in order to produce a mask
- Closing: this is an alternative to “closing by reconstruction” which results in a shorter processing time and has been used in this example
- Border kill: a very useful tool for separating the internal porosity within an object from the air volume outside of the component
- Label analysis: used initially in this study to identify each component and used in combination with the “mask” tool to isolate the component. Once the component was isolated and the internal porosity identified the label analysis tool was used to extract pore information
- Analysis filter: this tool is useful for separating data into specific groups. In this example the analysis filter was applied to the porosity measurements to remove pores that were below the spatial resolution of the scan and were therefore considered indistinguishable from background noise

Data preparation

Initial check of the test data

An initial check of the test data is an essential first step to ensure the data is free from ring artefacts or those mentioned in chapter 1.

The simplest method is to scroll through the **Ortho Slices** initially along the xy direction and then either the xz or yz orientations. If the data is artefact free then it is likely that the X-ray setup is producing clean and artefact free data and the reconstruction stage is cutting out any remnant effects of the cone beam artefact. Therefore assuming the same criteria are used then subsequent datasets should display the same quality and will be amenable to automated analysis.



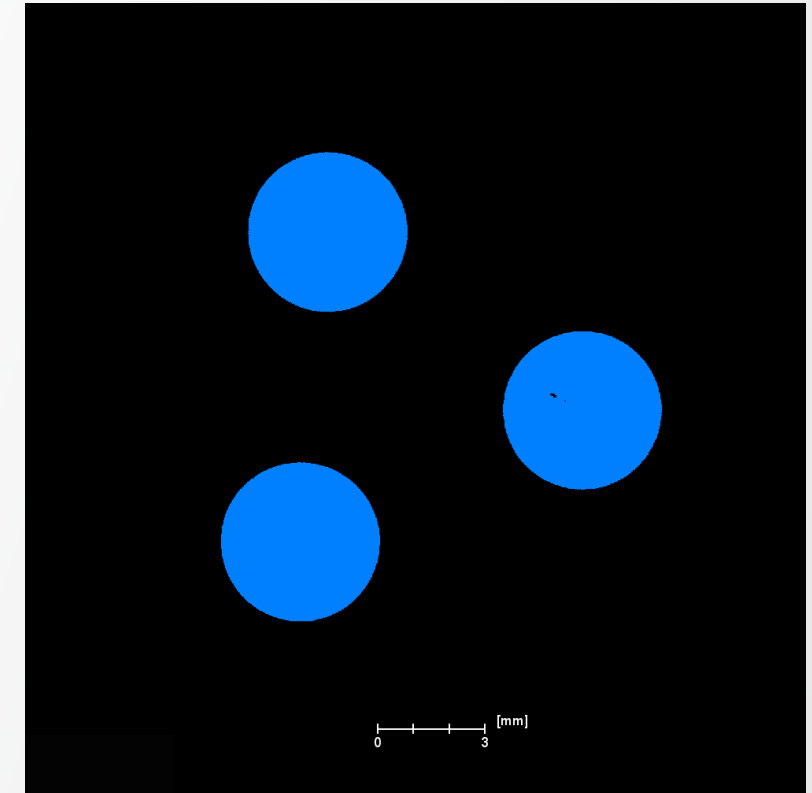
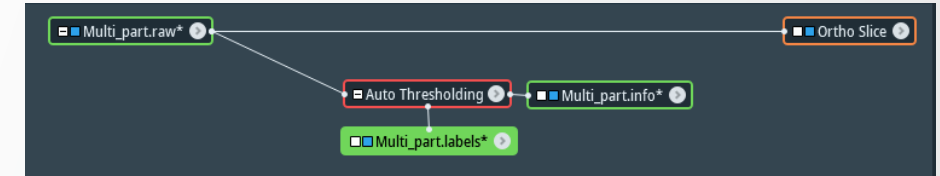
Data preparation

Thresholding the metal components

Within the data set, three separate components can be seen and these will need to be separated for further analysis.

The first step here is to segment each of the components. This can be done automatically using a number of the segmentation binarization tools.

Since the dataset only contains the metal specimens and air, the **Auto Thresholding** module provides a fast effective segmentation that faithfully follows the component/air boundary.

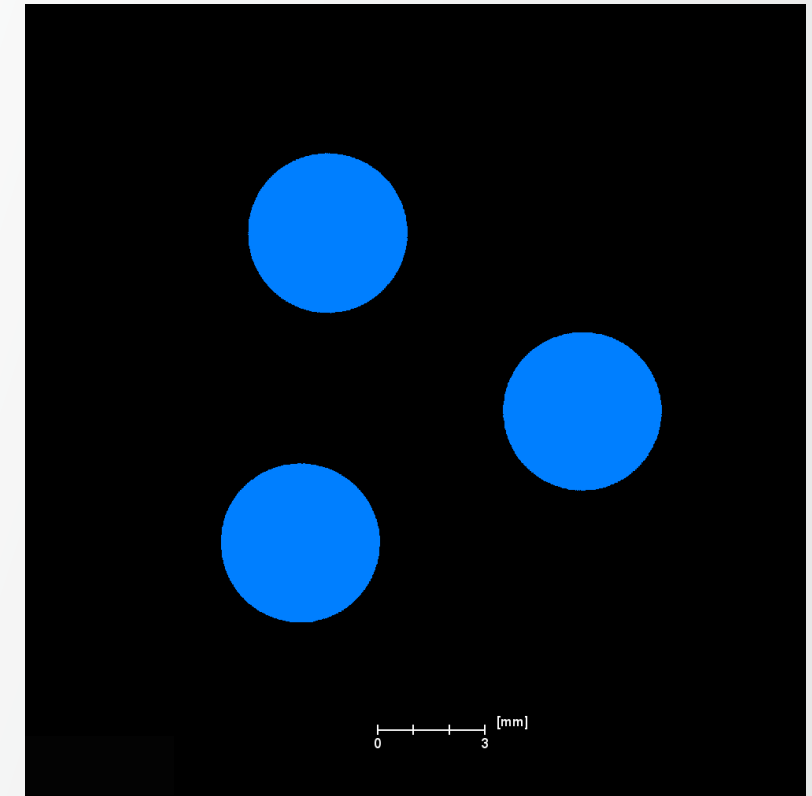
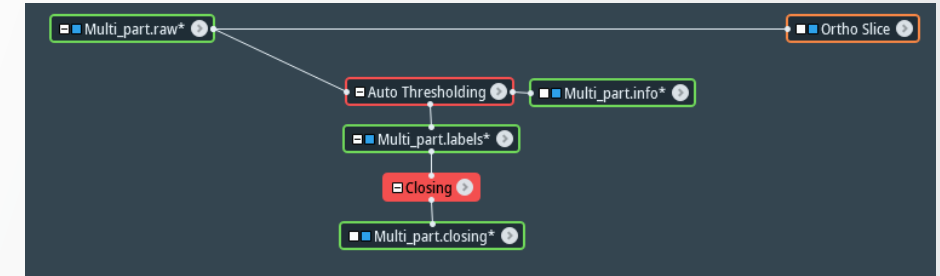


Data preparation

Filling the pores in

Although the segmentation accurately followed the component surface, internal porosity will not have been filled in. For the analysis of the porosity of each component at the later stages it is important to fill these pores in. The modules **Closing** and **Closing by Reconstruction** are useful tools for removing internal features within the segmented volumes whilst retaining the accuracy of the outer geometry.

It is important to understand the upper limits to the pore sizes within the components when selecting the closing parameters. More information on how Closing and Closing by Reconstruction modules work can be found by clicking on the information links.

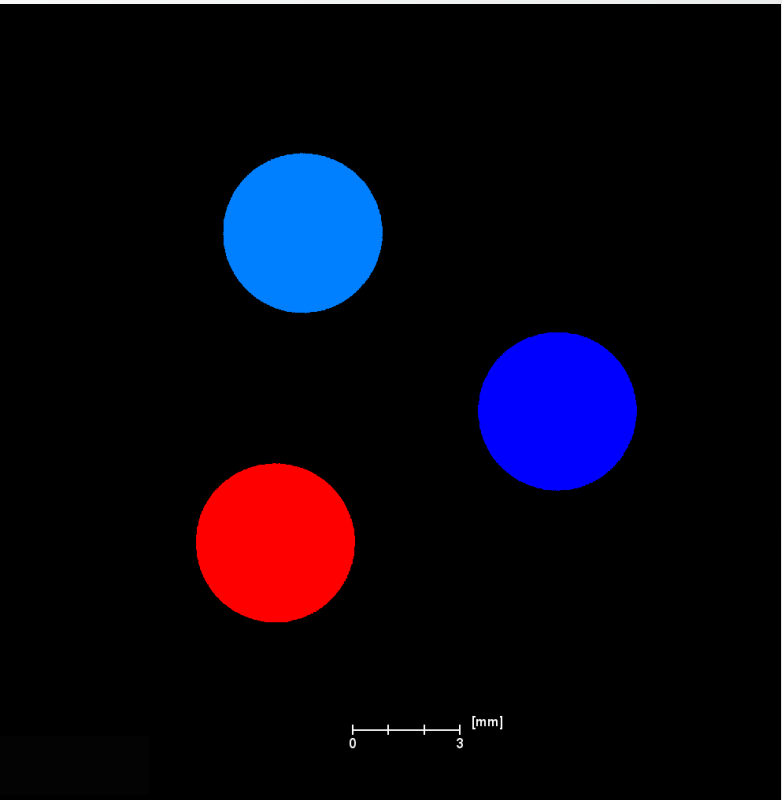
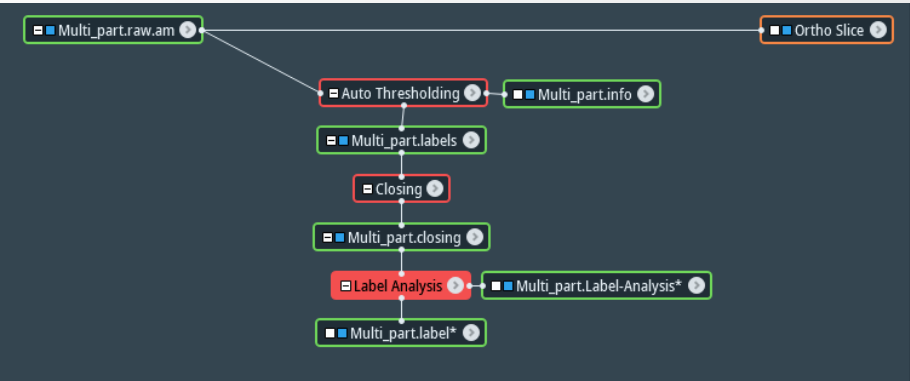
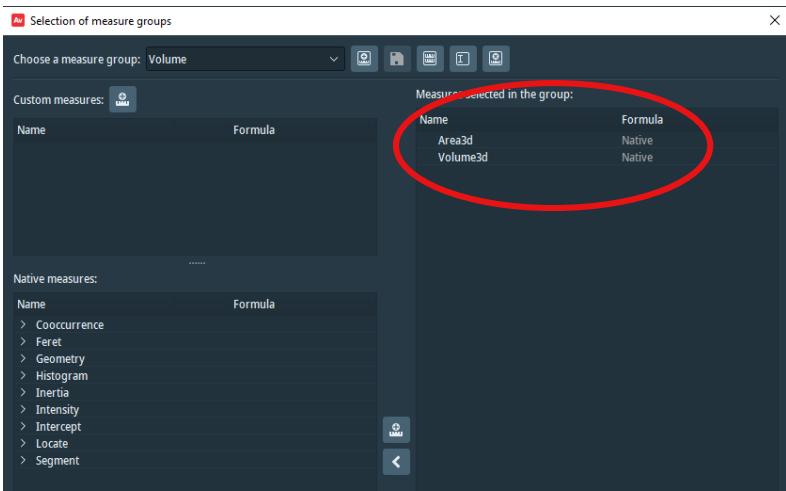


Data preparation

Separating each component

The **Label Analysis** module is a very useful tool for separating each of the components. In this case it is useful to generate information such as the surface area and volume since this information may be useful for later comparisons.

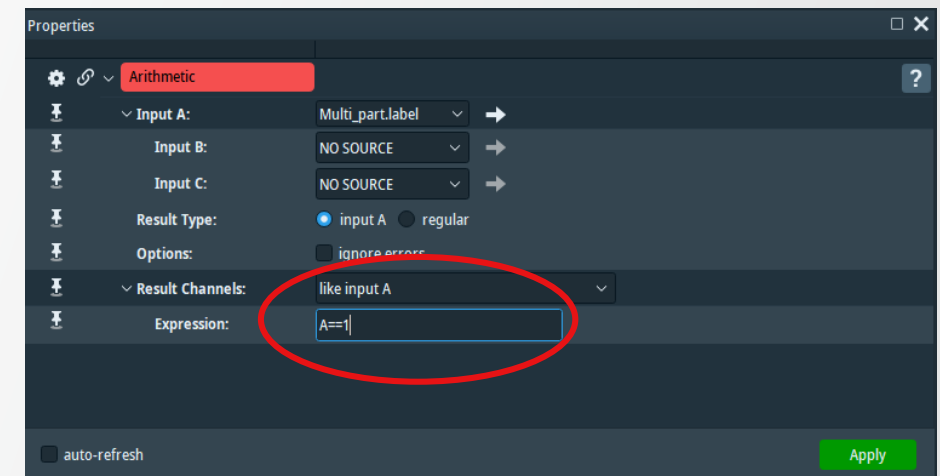
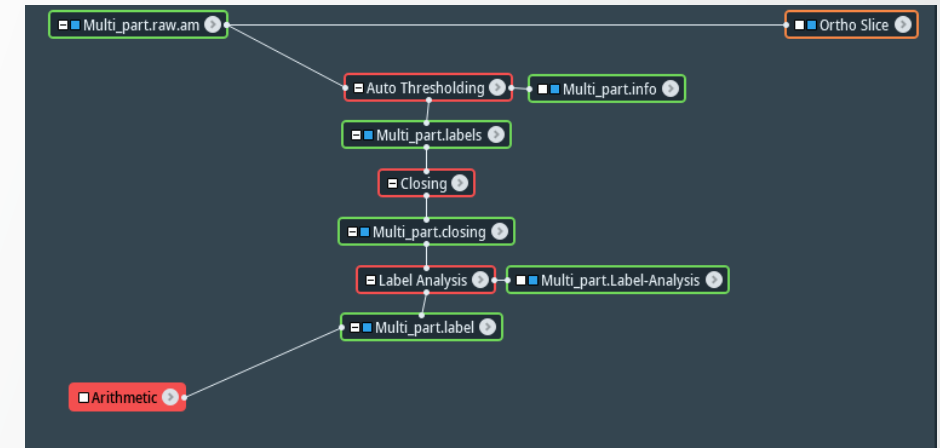
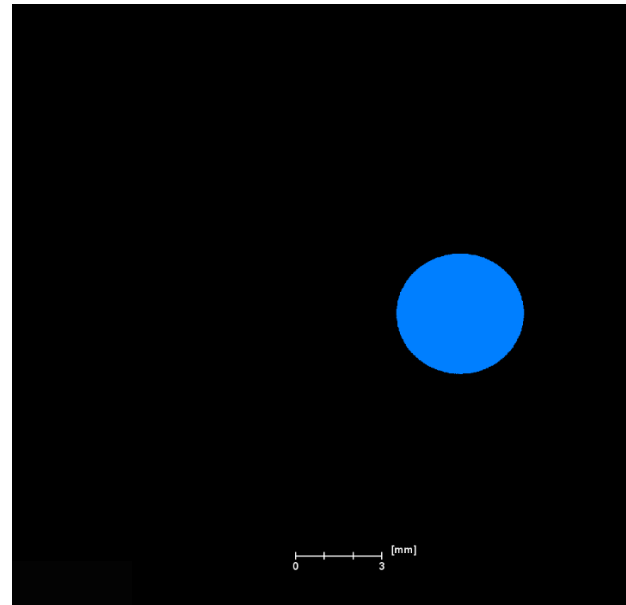
Because each component is physically separated in the scan the Label Analysis we will assign each component a number which is associated with a colour. In this case an 8bit colour scheme is used where 1, 2 and 3 are shown as light blue, dark blue and red respectively. This is important in the next step in separating the components.



Data preparation

Isolating each component

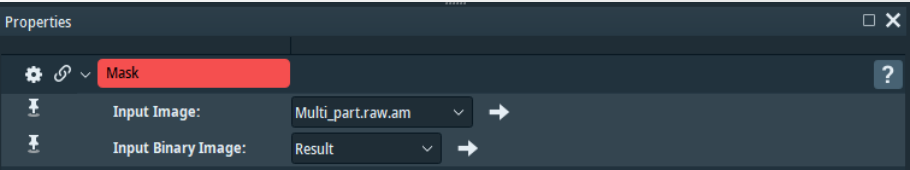
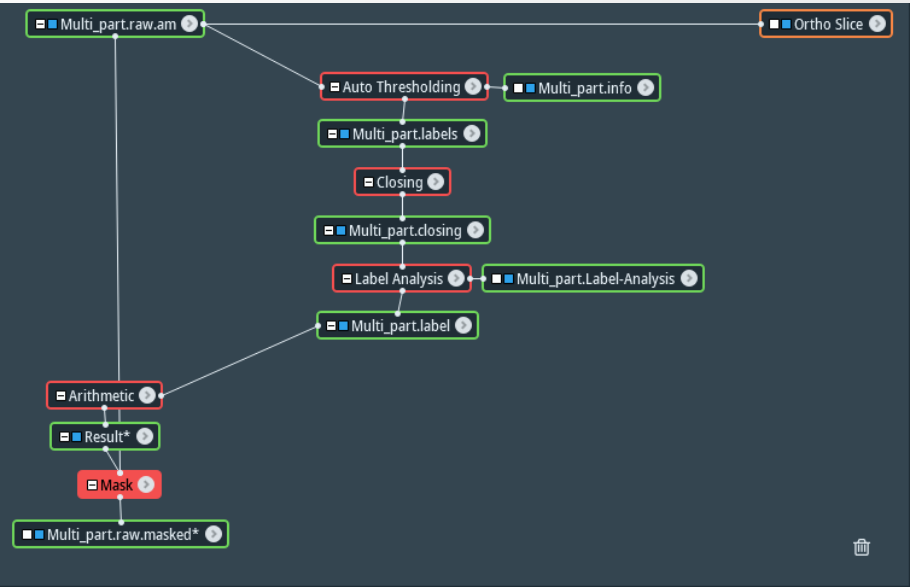
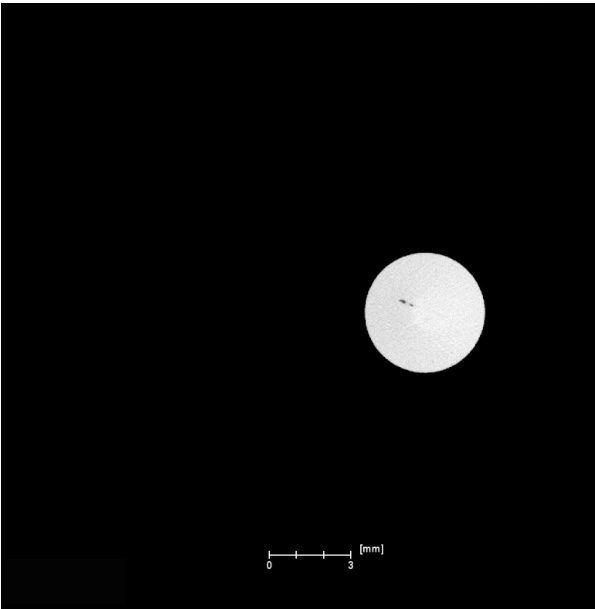
The Label Analysis tool has effectively separated each of the components, however they are still part of the same volume making an automated porosity analysis difficult. The **Arithmetic** module can be used to separate each component into its own separate volume. Using the expression $A==1$ the Arithmetic module can be used to separate component 1 as shown here.



Data preparation

Separating each component of the original data

The resultant label from the Arithmetic step can now be used as a **Mask** to separate the component raw data from the original volume as shown here.



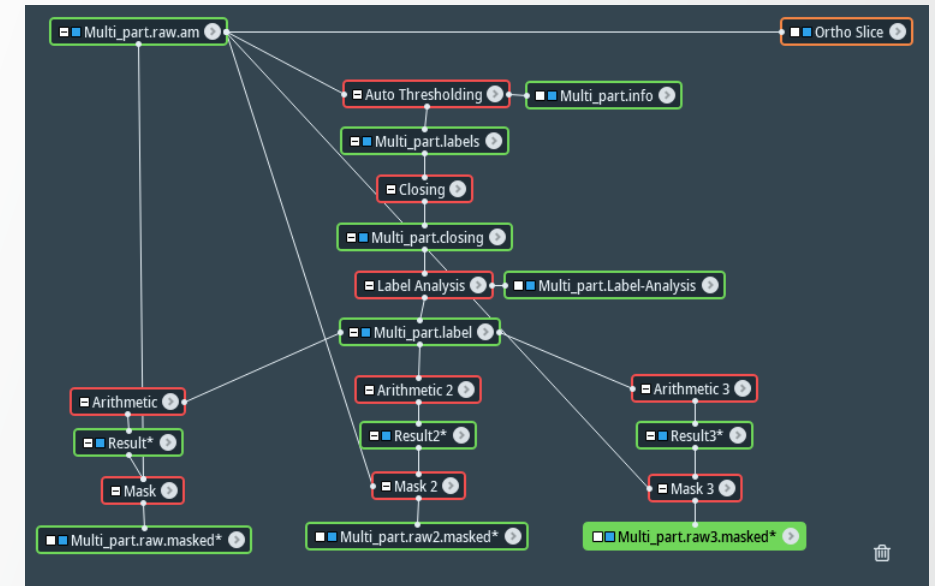
Data preparation

Repeating the process for each component

The process shown above can now be repeated using the Arithmetic and Mask modules to separate components 2 and 3.

Remember that the expression used to separate components 2 and 3 in Arithmetic will be $A==2$ and $A==3$ respectively.

At this stage the project file will start to appear very complex and it is advisable to break the analysis into clear lines as shown here.

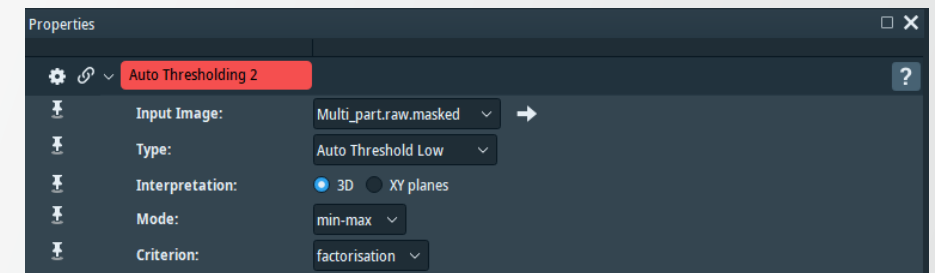
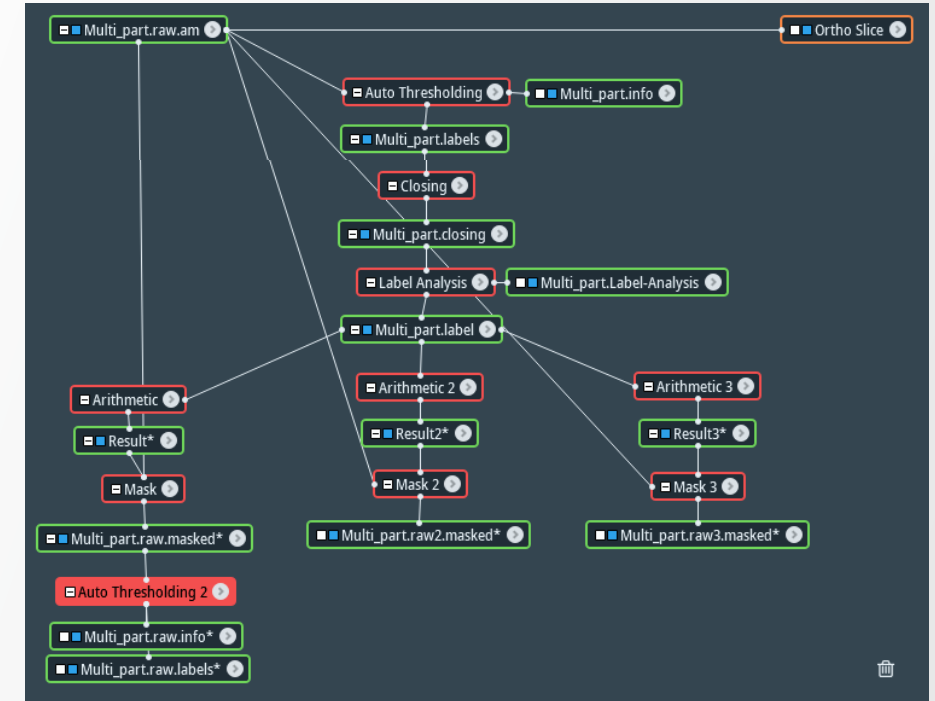


Pore analysis

Segmenting the pores – step 1/2

In the previous stage the raw volumes for each component were separated into three distinct volumes. This makes it possible to analyse the porosity of each component separately.

The first step is to segment the porosity in the first component as shown here. As previously described, any of the binarization segmentation tools could be used and in this example the **Auto Thresholding** module has been used since it gave the most faithful representation of the porosity in this study. Remember that to segment the pores the “Auto Thresholding Low” option must be selected.



Pore analysis

Segmenting the pores – step 2/2

The Auto Thresholding accurately segments the pores within the component volume, however it also selects all the voxels outside of the component (Figure 1).

To remove the voxels associated with the exterior the module **Border Kill** can be used. This function removes all the selected voxels that are in contact with the volume border. Since the internal pores are separated, these will be unaffected as shown in Figure 2.

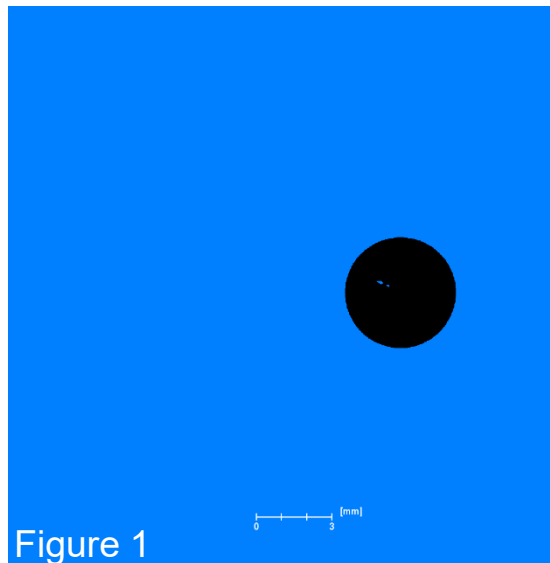


Figure 1

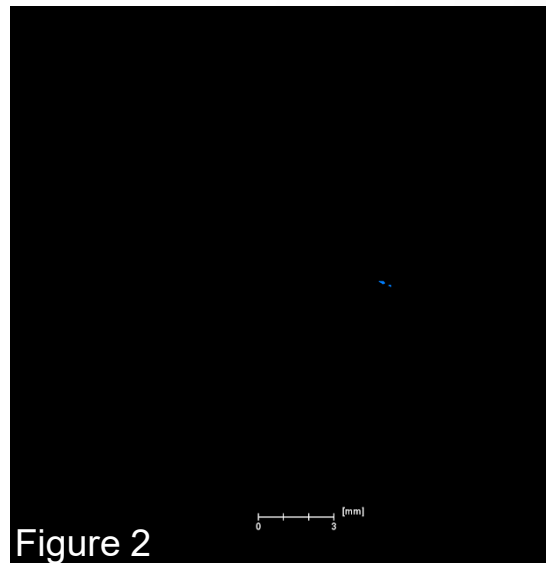
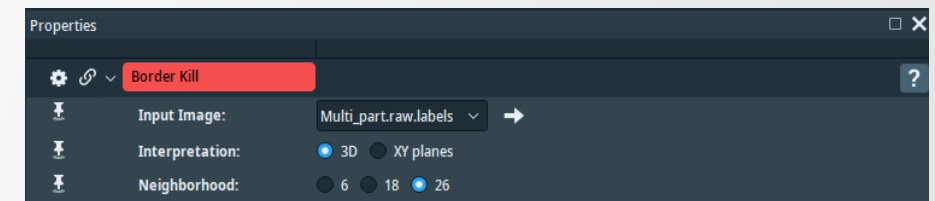
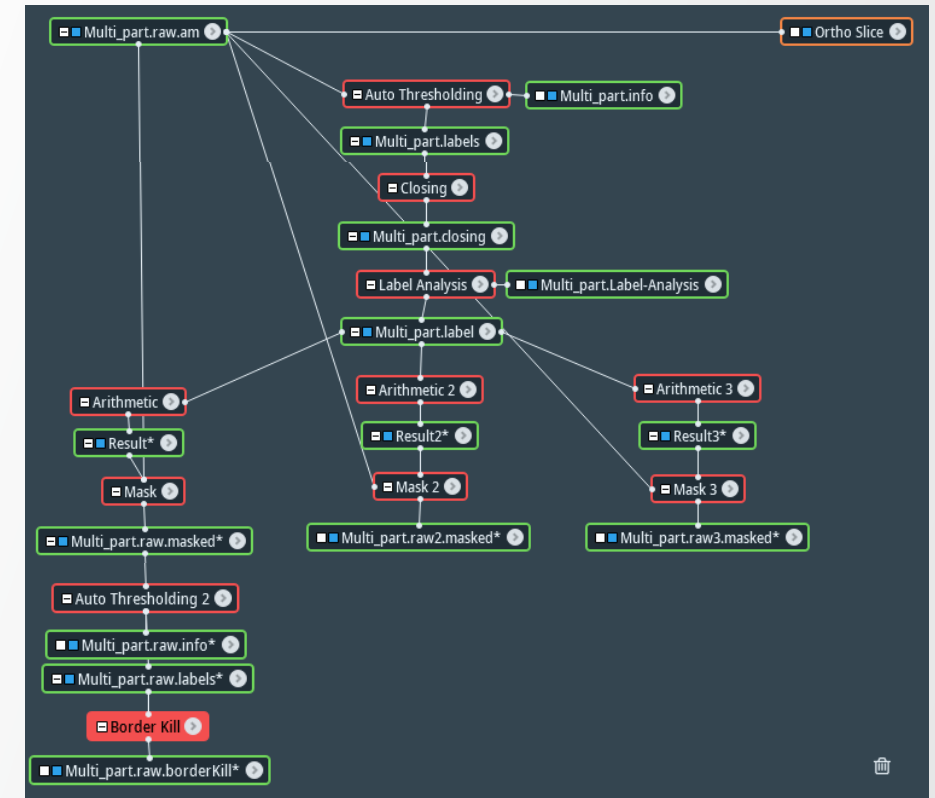
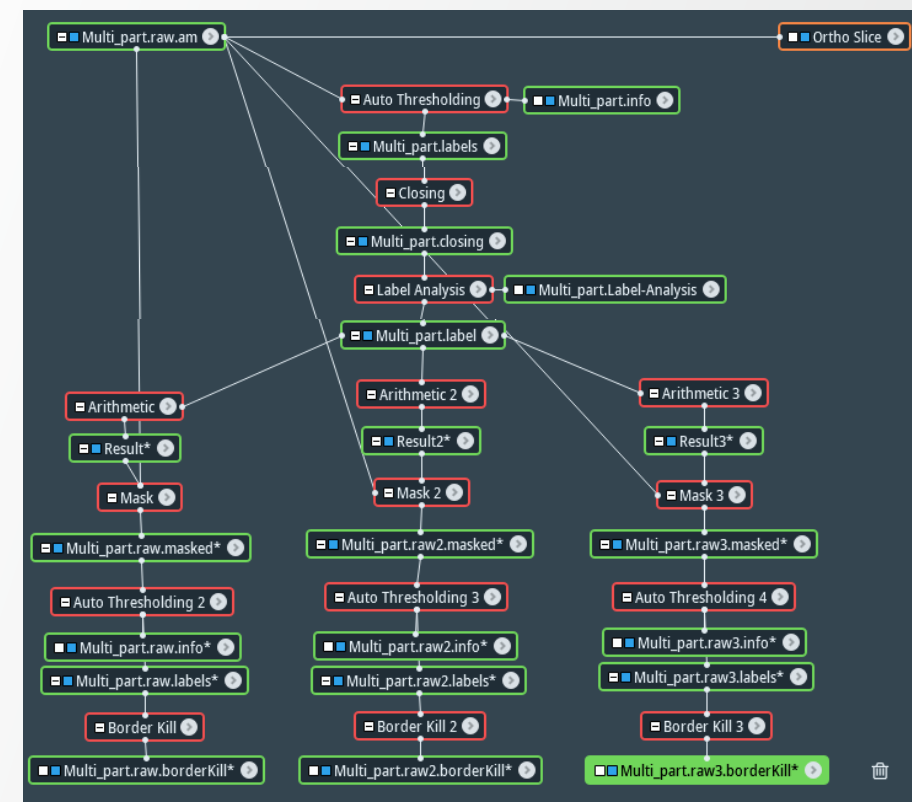


Figure 2



By repeating steps of Auto Thresholding and Border Kill, the porosity in components 2 and 3 can then be segmented using the steps above as shown here.



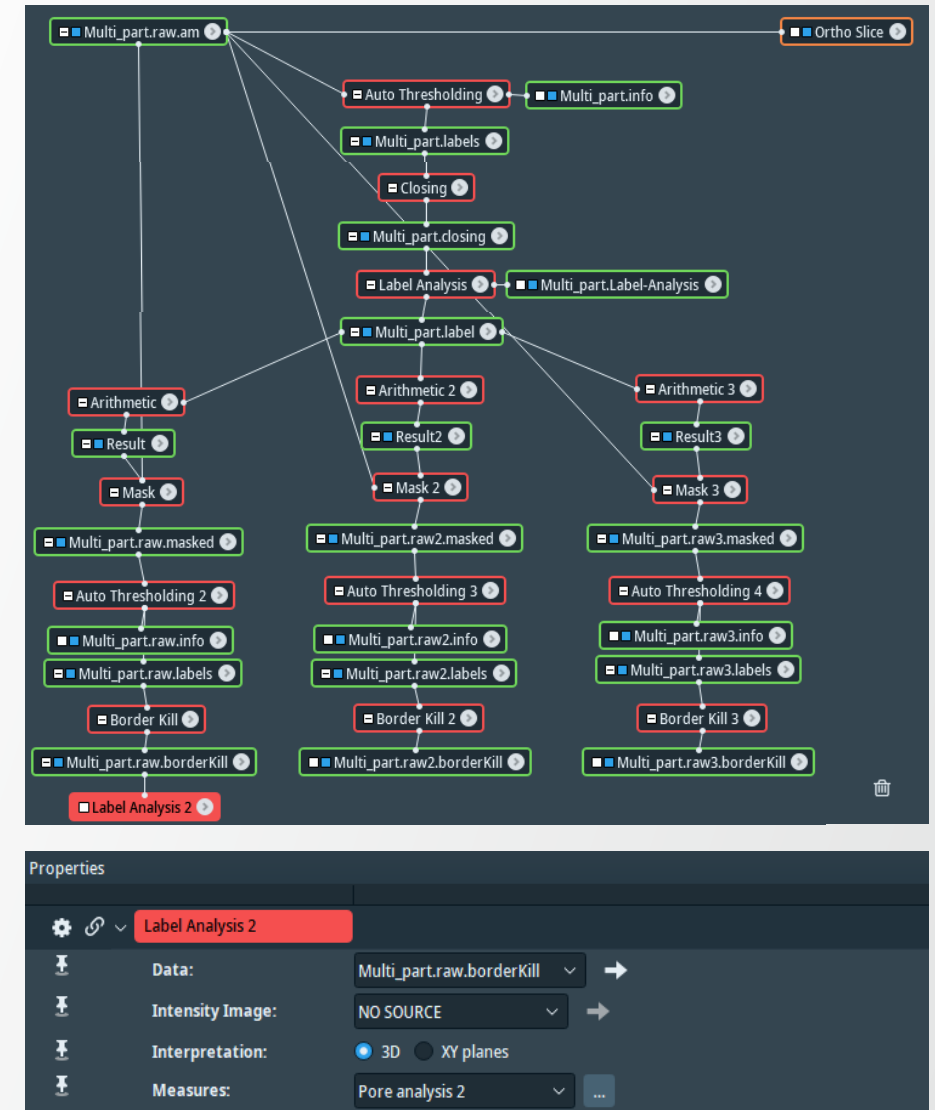
Pore analysis

Pore analysis and measurements

Once the segmented pores have been isolated it is now possible to analyse them using **Label Analysis**. The Label Analysis module contains a wide range of measures but in this example the following measures will be taken:

- Volume3D is a useful quantification of the pore size
- Ferret shape3D for characterising the general shape
- Orientation Phi and Theta for comparing preferred orientation
- BaryCentre X,Y & Z for pore coordinates
- BoundingBox Dx, Dy & Dz for filtering by size

Information on how customised measures can be created in Label Analysis can be found on the information tab. Once the Label Analysis has completed, an analysis label field and information tab are created.



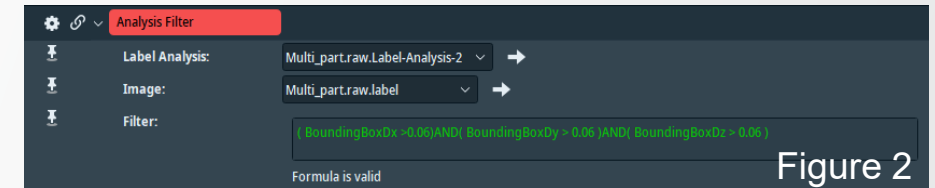
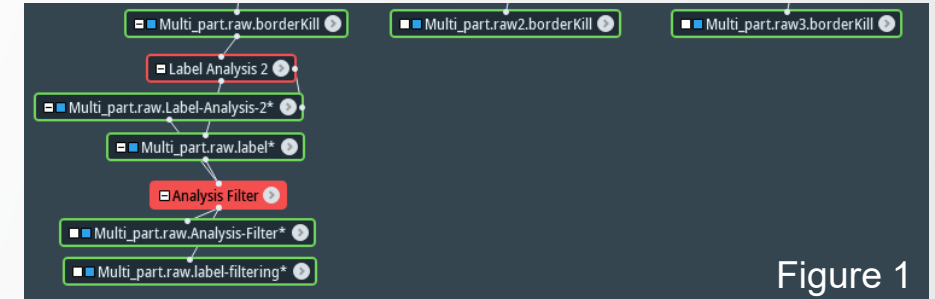
Pore filtering

Filtering pores above spatial resolution

In X-ray CT volumes, image noise is a significant problem. Usually image noise is removed by adding a image filtering step. Although image filters are excellent tools for improving the segmentation stage they do result in data loss. Therefore for quantitative analysis, it is better to collect as higher quality X-ray CT data as possible.

In the worked example, the spatial resolution of the X-ray CT data was measured as 60 microns using a spatial target. Therefore any features below 60 microns cannot be verified as true features and could be considered as image noise.

The **Analysis Filter** module can be used to remove features below 60 microns. The BoundingBoxDx, BoundingBoxDy and BoundingBoxDz were used in the expression in Figure 2. The Analysis Filter then outputs a new label showing only pores above 60 microns.



Pore filtering

Filtering pores above spatial resolution

The Label Analysis and Analysis Filter can then be applied to components 2 and 3 to extract the associated pore data.



Recipe creation and application

Automating the process with a recipe

We have now analysed the porosity in each of the three components, and we have done this manually, which can take a long time. To speed this up we can automate the process by creating a recipe.

More information about recipe creation can be found in the dedicated “Creating recipes to automate workflow automation” section of Avizo Software documentation and in our tutorial videos.