Rigaku

EPISODE 04

IMAGE PROCESSING WORKSHOP

*Companion eBook*

# IMAGE PROCESSING USING DRAGONFLY

*Presenter: Angela Criswell*

# You'll learn:

In previous workshops, we covered how to use ImageJ for image processing and morphological operations. In this workshop, you will learn how to perform similar techniques using the Dragonfly software offered by Object Research Systems, Inc.

Dragonfly is a commercial software package offering many useful features. It is available for free for non-commercial use, or a license can be purchased for commercial use. There are also options available for cloud computing and storage. To try the software, you can also download a free trial copy.

Here is the recording of the workshop.

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# PRESENTERS

*Presenter: Angela Criswell*
*Senior Scientist*

Angela holds a PhD from Rice University and has been with Rigaku for 20 years. She started in the Macromolecular Crystallography Applications lab focusing on X-ray techniques to study structural biology. She has gained expertise in a number of X-ray methods in her tenure at Rigaku, including small angle X-ray scattering and X-ray computed tomography. Angela likes working with customers to find the best fit for their samples while addressing their specific experimental questions.

*Co-presenter: Aya Takase*
*Director of X-ray Imaging*

Aya holds a PhD in engineering from Osaka University and a MA in physics from Tokyo University of Science and has been with Rigaku for 24 years. She started in the X-ray Diffraction Application Lab and transitioned to X-ray Imaging in 2017. Her goal: Help non-expert X-ray users achieve expert results with less time and effort. She has worked on many projects designing automated and user-friendly X-ray instruments and analysis software. She is very passionate about helping people learn more about X-rays and working with X-ray users to solve their specific problems.

*Host: Tom Concolino*
*Sales Manager*

Tom holds a PhD in Chemistry from Mississippi State University and has been with Rigaku for 20 years. He started out in the Small Molecule Crystallography Applications Lab before transitioning to the sales team in 2002. He has been on the front lines helping clients save on time, cost, and effort while pushing forward to support the never-ending need to innovate and explore new materials and structures. From academia to mining to pharmaceutical research, Tom has learned the value of bringing a fresh perspective to each customer application while utilizing his vast experience to collaborate on the best fit solution for each and every customer.

# 1

# Benefits of commercial software

The ultimate goal of X-ray micro computed tomography (micro-CT) data analysis is to quantify features we observe in CT images. And there are a wide variety of software packages available for analysis of CT data. In previous workshops of this series, we focused an open-access software package, ImageJ. In this workshop, we will switch gears to focus on commercial options for CT data analysis.

There are many commercial tools for CT data analysis and it can be difficult to find out which is the right one for you based on the type of analysis you need and your software budget. Luckily, many software manufacturers offer free trials so that you can test ride their software with your data. Additionally, there are some tools to guide you as to what's available.

Before you can select the best tool for you, you must first know what types of analyses you'll need to perform for your CT data. Then, you'll want to explore the features of the programs to see if they will fit your needs. This web page lists commonly used software ant the various features they provide.

This blog article lists the best software for different types of analysis needs and might help you choose the right one for your research.

In this workshop, we'll focus specifically on Dragonfly. We use this program often because it handles most of the materials and life science CT image analysis needs. You can learn more about Dragonfly from this blog article, which covers typically asked questions like: What does it do? What are the computer requirements? What are the pros and cons of Dragonfly? What type of license do I need?

Though Dragonfly doesn't offer the advantage of being open-source, it makes up with many benefits over ImageJ. Specifically, Dragonfly performs computations much faster and uses GPU for many computations. There are licensing options to use cloud computing and storage with Dragonfly so you don't need to have a supercomputer in your lab. Additionally, Dragonfly has some great tools for segmentation including a powerful segmentation wizard to quickly assign voxels to ROIs. Finally, Dragonfly is under constant development and training is readily available. We especially like the Dragonfly Daily Playlist on youtube that contains around forty 30-minute tutorial videos that start from installation and take you all the way to complex tasks, for example Deep Learning segmentation.

# 2 Dragonfly hands-on exercises

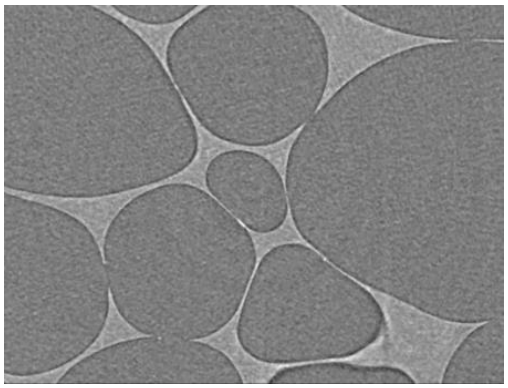
Hands-on exercises help us understand how various tools can be used to process images and refine our segmentation results.

In this section, we will use the Dragonfly to show how to perform image filtering and use morphological operations.

If you are new to Dragonfly, watch this Dragonfly Daily series presented by Mike Marsh.

## Image Denoising

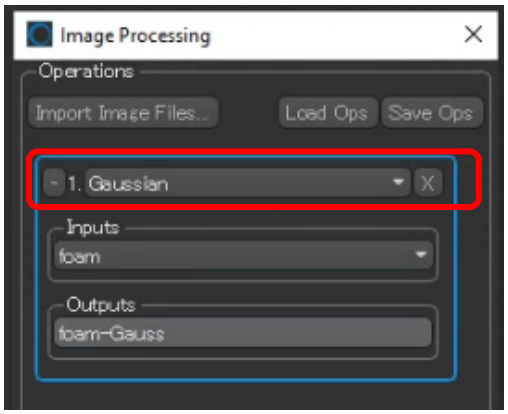
Let's look at a few image filters that are available in Dragonfly.



**Original binary image**: CT cross section of a foam material. 565 x 565 pixels, 1.06 microns/pixel, 8-bit grayscale

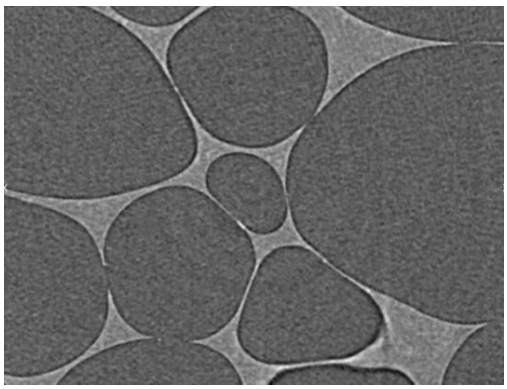
### Gaussian filter

Open the Image processing tool by clicking Workflows → Image Filtering. Select the Gaussian option from the Operation drop-down list and select "foam" as Inputs.

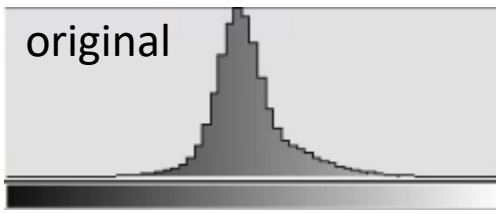


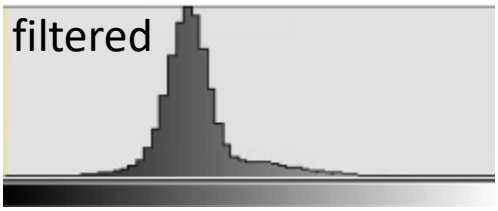

Try different options for kernel size and standard deviation.


### 1. Kernel 3 , Std Dev 1.0



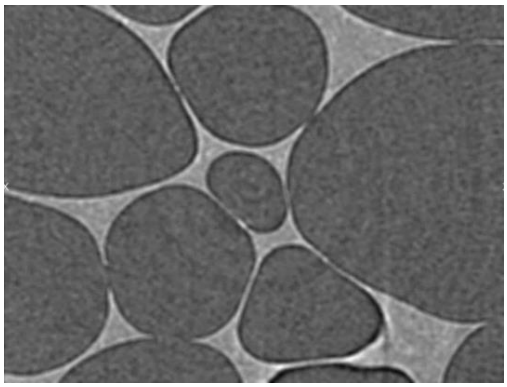
Compare the filtered image to the original one. Also, compare the original histogram to the filtered image histogram. Are there separate peaks for polymer and foam?



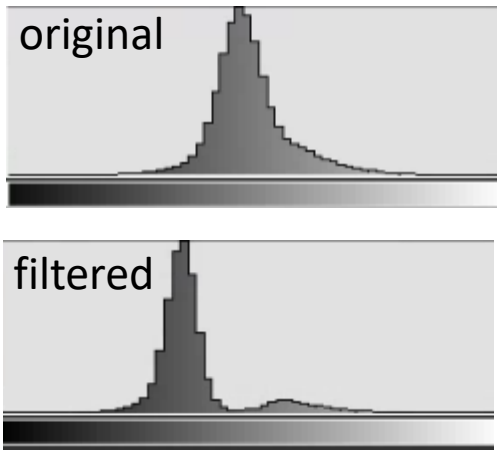



Try different values for kernel size and standard deviation and compare images.

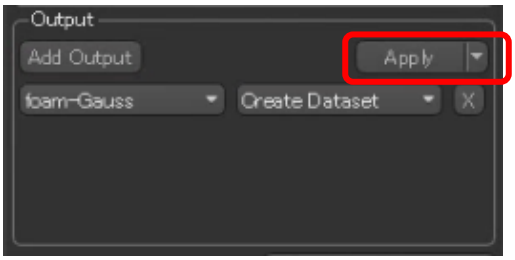
**Kernel 7 , Std Dev 5.0**



Notice the reduced noise level using higher kernel and std dev values and the peaks for polymer and foam are separated in histograms (see below).




Once you have decided on the appropriate values, apply the filter and output a new image stack by clicking ‘Apply’. Make sure that ‘Create Dataset’ is selected in the drop-down list so that you don’t overwrite original data.

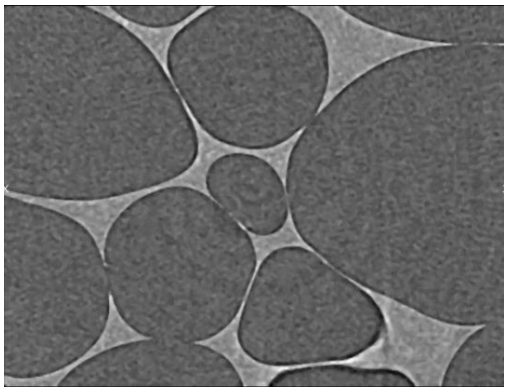



**Median filter**

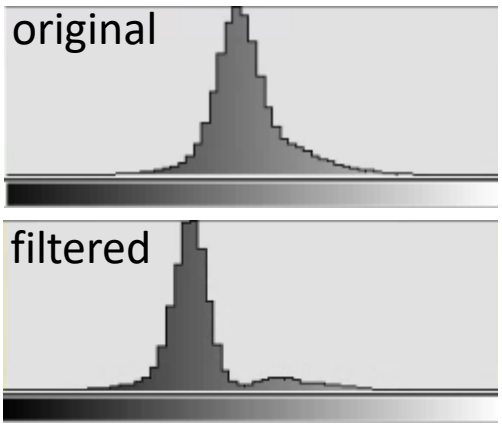
Now let’s try the median filter. Select the Median option from the Operation drop-down list and select “foam” as Inputs.

Try different options for kernel size and shape.

### Kernel 7 , shape ‘circle’



Compare the filtered image to the original. Do the thin sections of foam between voids retain their shape? How does that compare when you use shape ‘square’? Also, remember to compare the original and filtered image histograms.



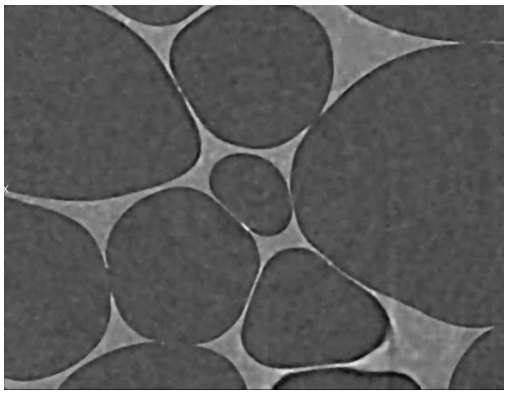

To create a new dataset with the best value, click the ‘Apply’ button in the Output group.

### tv_Chambolle filter

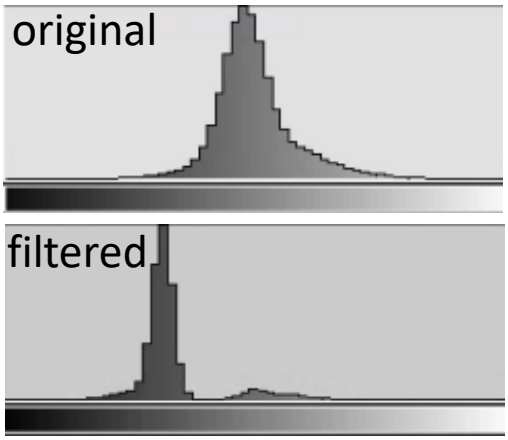
Now let’s try the total variation Chambolle (tv_Chambolle) filter. Select tv_Chambolle from the Operation drop-down list and select “foam” as Inputs.

Try different options for weight.


### Weight 0.1000



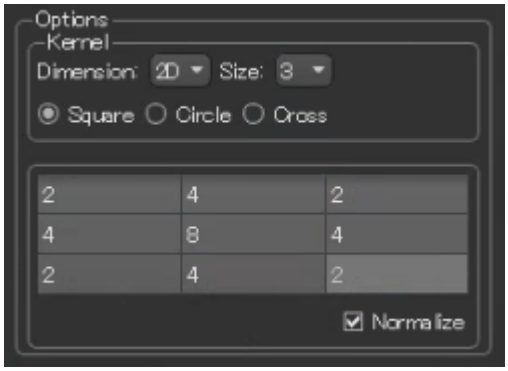
How does that compare to the original? Compare the original and filtered image histograms.



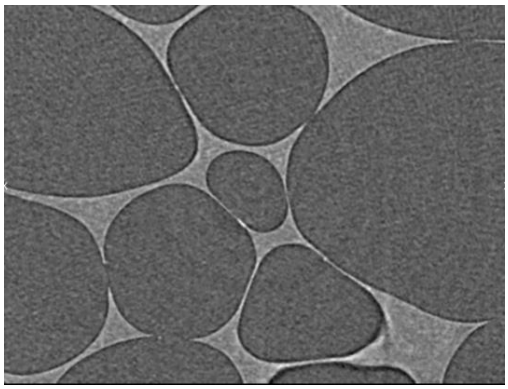
Try larger weight values, for example 0.5 and higher, and compare. Once you've selected an ideal value, you can create a new dataset with the best value by clicking the 'Apply' button in the Output group.

### Editable filter

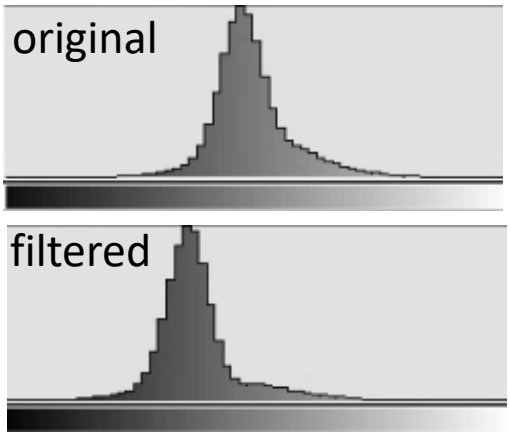
If you would like to create your own filter and select kernel matrices values, try the Editable filter by selecting 'Convolution' from the Operation drop-down list and select "foam" as inputs.




Then, select kernel size and shape and enter values you want to use for the matrix. In this example, we'll use a weighted average filter with the above shown values. Enter the same values and calculate a preview.



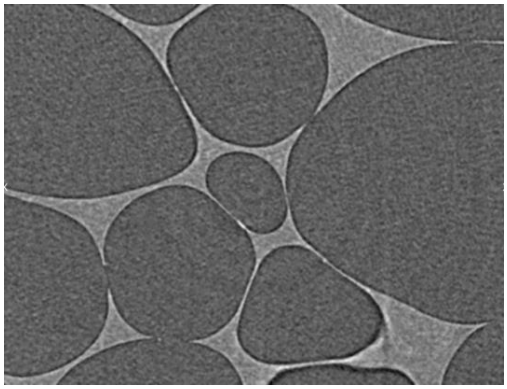
How does the filtered image compare to the original? Compare the original and filtered image histograms.



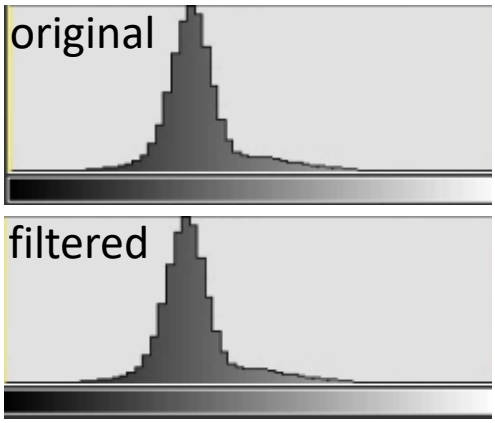

### Unsharp

Now let's try the 'unsharp' sharpening filter. Select the unsharp option from the Operation drop-down list and select "foam-Gauss" as Inputs to see if the borders smeared by the Gaussian filter can be sharpened.

### Kernel 5 std dev 0.1, unsharp 1.0



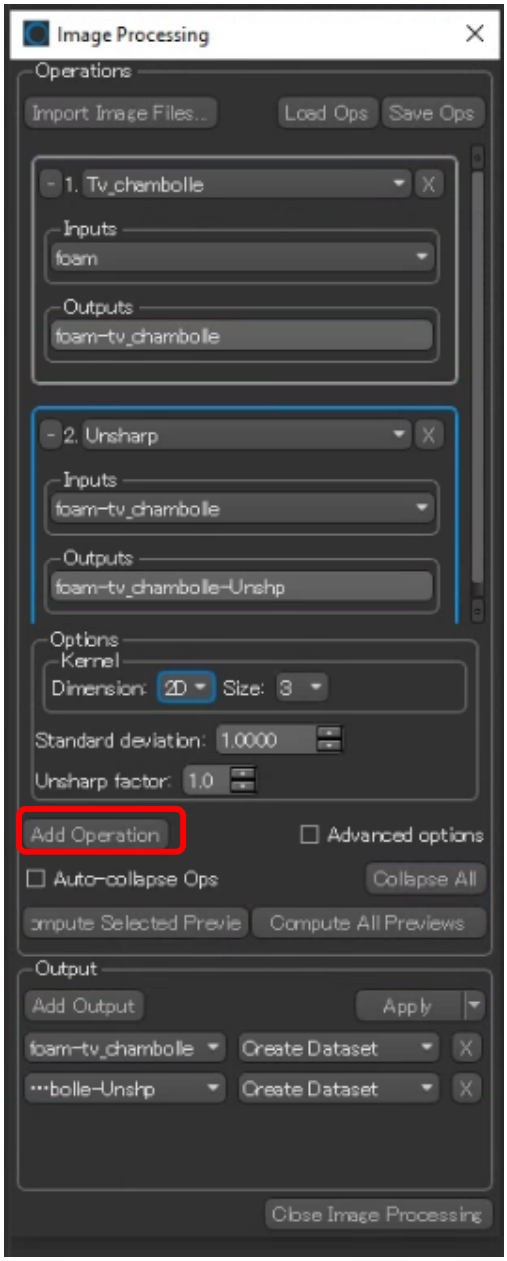
Compare the image and histogram to the original.




Notice unsharp does not affect the histogram much.

### Multiple Operations

Dragonfly offers the benefit that multiple operations can be run in sequence easily. To add a second, or sequential operation, click ‘Add  Operation’ (see red rectangle on right). Now you have two operations.

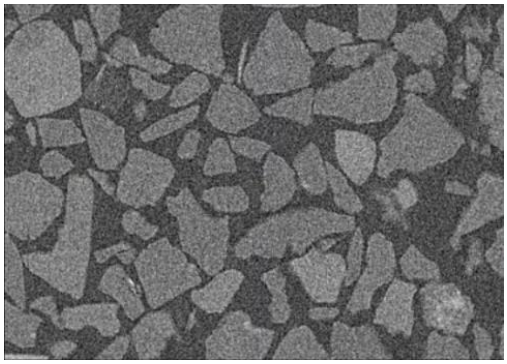



Choose which operations you want to run sequentially from the drop-down lists.

On your own, test combinations of operations. You can apply and save output datasets for one or both operations combined.

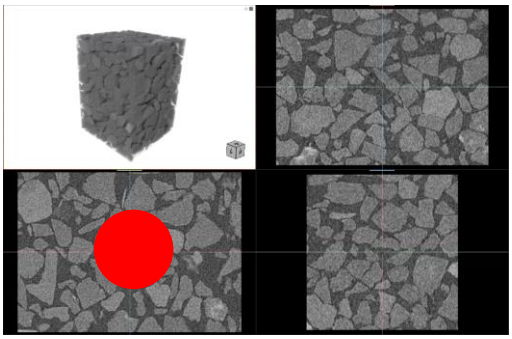
## Thresholding and Morphology Operations

Now let's have a look at how to perform threshold segmentation and clean up ROIs using  morphological operations in Dragonfly.

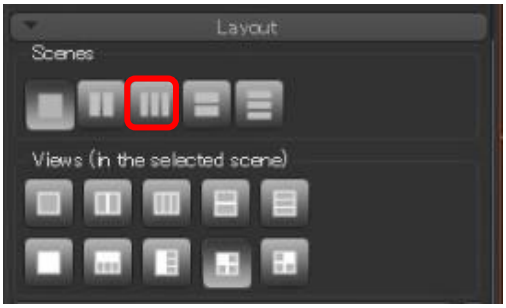


**Original binary image**: CT image of sandstone. 436 x 311 x 319 pixels, 5.18 microns/pixel, 16-bit grayscale

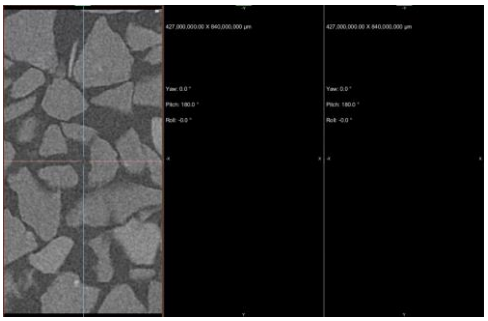
First, let's zoom in on the bottom left cross-section image by double-clicking on the bottom left display window (double-click on panel with red dot).



Then, let's prepare to view 3 results side-by-side. To do this, click the 3 panels button in the Layout -> Views (see red rectangle below).

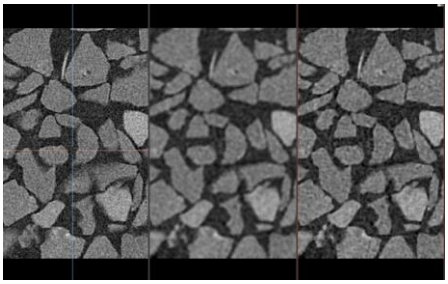



Your display should now look like this.



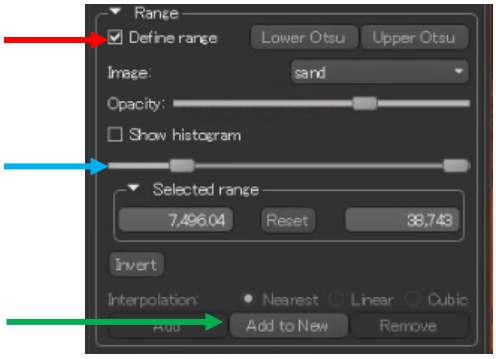
Click the middle black area and then turn on the eye beside 'sand-Gauss' CT data. Then, click the right black area and turn on the eye beside 'Sand-Med' CT data.

Your display should now look like this with three images are displayed side-by-side cross-sections.

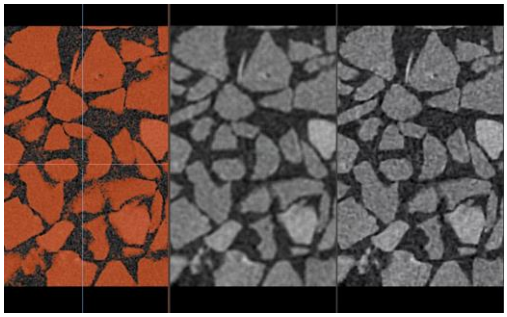



**Thresholding**

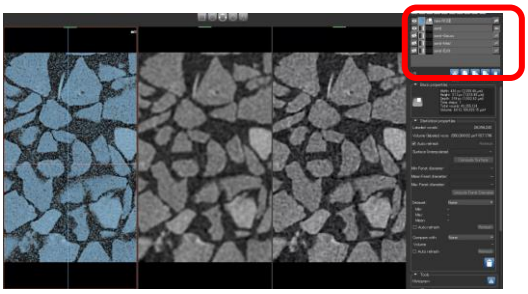
Click on the left data (1) and click the Segment tab. Click ‘Define range’ check box in the ‘Range’ group (red arrow).




Threshold by clicking Upper Otsu and label the sand phase red. You can adjust the threshold with slide bar (blue arrow).



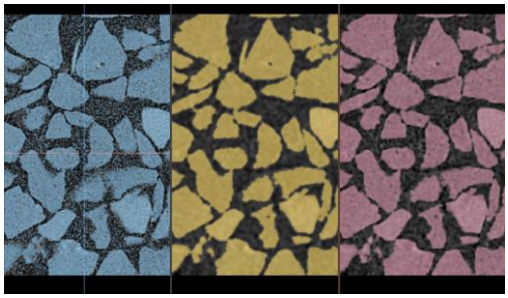
Click the ‘Add to New’ button to save this ROI (green arrow). Then, uncheck ‘Define range’ check box (red arrow).



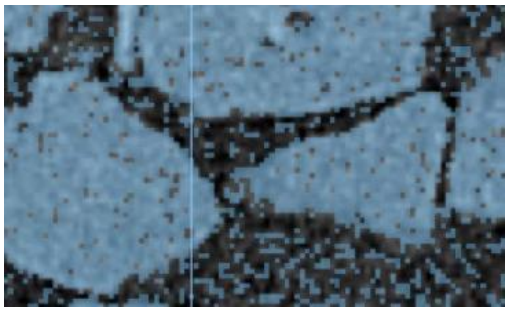
You now have a new sand ROI in the Data list. You can rename it by double-clicking the new ROI name in Data Properties and entering a different value. This is the ‘sand’ original data.

Now, repeat the same procedure with the other panels (2, 3) to threshold and save new ROIs for Gaussian and Median filtered data.

You should have something like the picture on the top left of the next page.



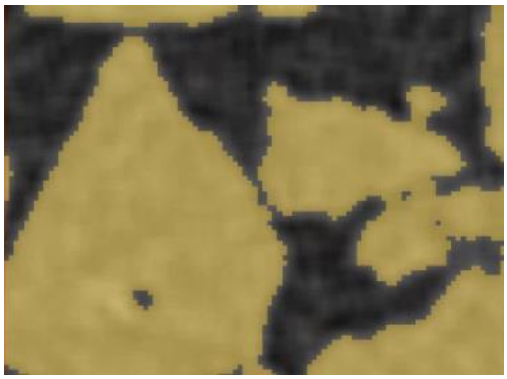
Compare thresholding results among the three. Notice that labelling is incorrect for some of the rock phase, especially for the original noisy data.



**Morphology Operations**

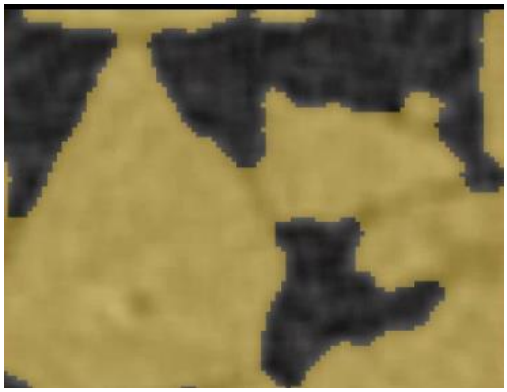
Let's use some morphological operations and improve segmentation results. For example, click the middle panel (sand-Gauss data), then click row with corresponding to this ROI in the Data Properties list.

Here's a before image.



Then, click the Close button in the 'Morphological operations' group.

Here's an after image.

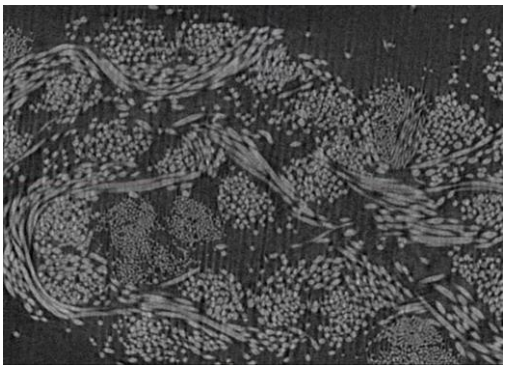


You see that some holes are now filled, but space between sand grains is incorrectly labeled.

Change the kernel size to test its effect. On your own, test different operations and decide which ROIs can be corrected most easily and with which operations?

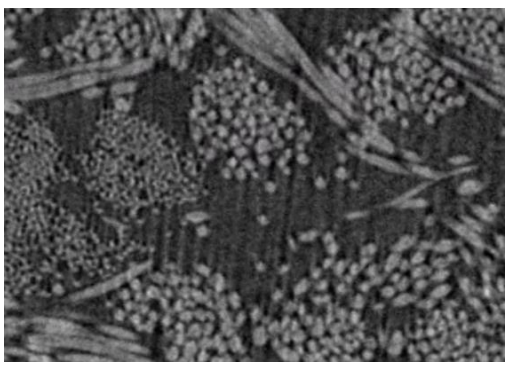
## Artifact Correction

For our last exercise, we will investigate how to destripe vertical artifacts using the denim data.

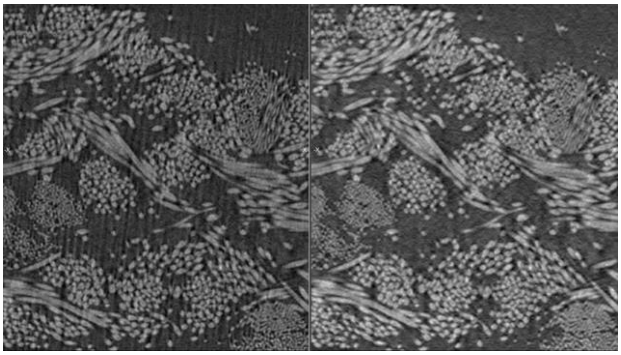


**Original binary image**: CT image of denim. 694 x 500 x 199 pixels, 4.08 microns/pixel, 8-bit grayscale

First, let's zoom in on the bottom left cross-section image by double-clicking on the bottom left display window. Then, hold the middle mouse down and drag the mouse towards you to see the stripes better.



Open the Image Processing panel by clicking on Workflows -> Image filtering. Then, select 'Vertical Destriping' from the Operations list and 'denim' as Inputs. To review results of the filter, click the button to compute a preview.



Notice the improvement in the image on the right. The stripes are not as visible as in the original image on the left. This filter is very effective in destriping.

# ABOUT THE TOOL

## Dragonfly

Dragonfly is a software platform for scientific image processing developed and distributed by Object Research Systems (ORS). Dragonfly can process CT images to extract quantitative information about various objects and materials. In addition to CT, it can treat various 2D/3D/4D scientific images, including data from correlative and hyperspectral imaging systems, SEM, FIB-SEM, ion beam, and confocal microscopy.

You can learn more about Dragonfly from this link:

https://www.theobjects.com

# Takeaways

There are many software tools  for performing image processing, segmentation and data analysis for CT data. The price for these packages varies from free to $100K, depending on the software and added features set included.

Here, we shared some information about the Dragonfly package and the image processing tools it offers. For more information about other available packages, read our free "Analysis Software" blog article

## LET'S LEARN TOGETHER

Many people have learned what X-ray computed tomography (CT) is, how it works, and where it can be helpful in our webinar and workshop series. All recordings, application examples, a publication list, and blog articles are available at imaging.rigaku.com.

Subscribe to the email updates to stay informed about new articles, recommended publications and books, and upcoming learning events.

**CONTACT US**

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