

Release Notes

GrainMapper3D™ 3.2

Non-destructive 3D Grain Mapping Solution for
Laboratory Diffraction Contrast Tomography



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Contents

GrainMapper3D

New Features and Product Enhancements	4
Revised Handling of Diffraction Images	4
New DCT Calibration	4
Absorption Data Replacement	4
Segmentation Spot Filters	5
Reconstruction	5
Grain Selection Filters	6
User Interface Changes	6

DCT Acquisition Wizard

New Features and Product Enhancements	9
Number of Projections	9
Importing Absorption Scan Recipes from Scout-and-Scan	9
Reduce Sample Rotations	10
Other Enhancements	11
User Interface Changes	11

GrainMapper3D Viewer

New Features and Product Enhancements	12
User Interface Changes	12

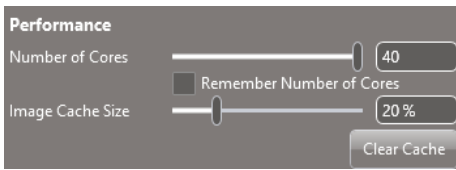
GrainMapper3D

New Features and Product Enhancements

Revised Handling of Diffraction Images

GrainMapper3D 3.2 enables handling project files of a size exceeding the physical memory of the workstation. This is achieved by loading and storing diffraction images on demand from or to disk and keeping them in memory only as long as applicable. This new mechanism greatly speeds up opening large project files as only data needed to display on screen is fetched. However, since the new mechanism is IO intensive, image processing related tasks such as importing DCT data or segmentation may perform slower when limited by the speed of the hard-drive. The **Image Cache Size** can be adjusted in the **Performance** section of the **Preferences** as described in [Table 1](#). Nevertheless, it is recommended to use the default value.

Table 1 New Image Cache Preference

Control	Function
	<p>Image Cache Size sets the percentage of how much of the total physical memory can be used as cache memory for DCPs. Increasing the image cache size may increase performance of image processing related tasks as less read/write operations may be necessary, but can cause use of swap memory instead. Press Clear Cache to free up memory occupied by unused DCPs.</p>

New DCT Calibration

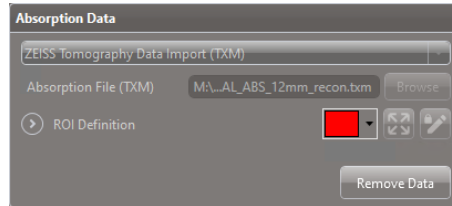
The Xnovo Engineering Tools used by your field service engineer to perform the DCT Calibration on your microscope have been completely revised. The new DCT Calibration carries over additional meta data in the tomography files utilized by the GrainMapper3D 3.2, which allows to enhance the reconstruction when using the Internal Calibration. The meta data are only partially backwards compatible with version GrainMapper3D 3.1. For optimal performance of GrainMapper3D 3.2, a new DCT Calibration has to be performed on your microscope with Xnovo Engineering Tools 3.2 by your field service engineer.

Absorption Data Replacement

It is now possible to **Remove Absorption Data** even after the imported data is persisted to disk, see [Figure 1](#). Click , if you need to remove the imported

data and replace it by another data set. It is only possible to remove the absorption data while no **Reconstruction** is present. Also, when importing absorption data the default histogram range has been adjusted for better contrast.

Figure 1 Remove Absorption Data

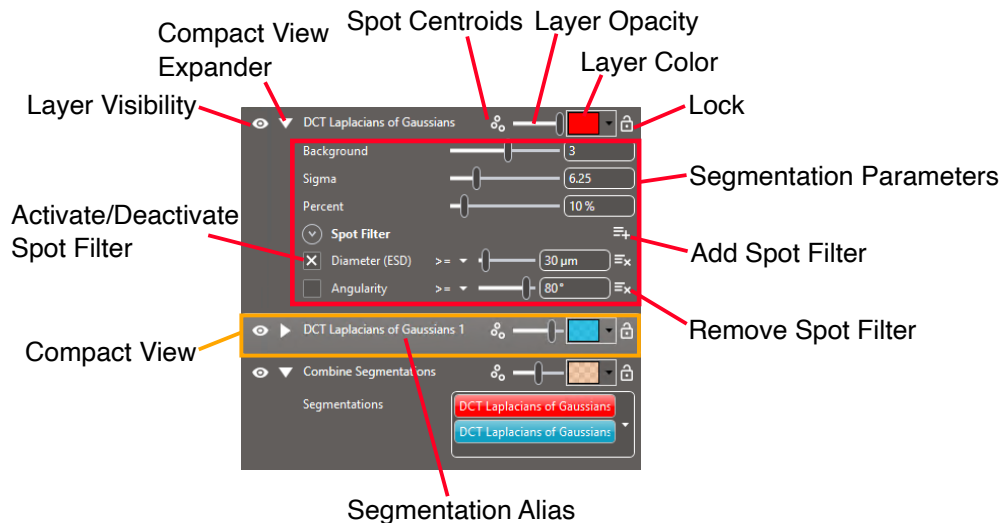


Segmentation Spot Filters

The Segmentation Tab now includes a check box to **Activate/Deactivate Spot Filters** (e.g. Spot Size, Angularity,...) for fast on/off switching to visually judge effect, see [Figure 2](#).

Under the **Add Spot Filter** list is now also the option to **Copy Filters** from other segmentations. A list of other segmentations is given and the user can select which one to copy filters from.

Figure 2 Activate-Deactivate Spot Filter



Reconstruction

For some data sets where reconstruction is very difficult and time consuming, the new release offers speed improvements in the range *15-30%*.


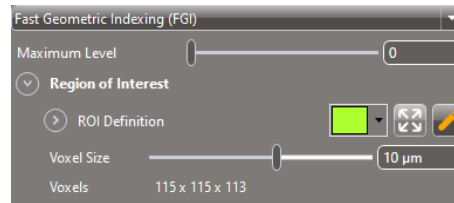
Volume Preset To select between **Preset Reconstruction Volumes**, press  next to the **ROI Definition** for preset ROI sizes and choose between either **Full Volume** or **Illuminated Volume**, see [Figure 3](#).

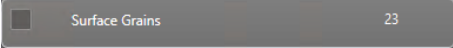

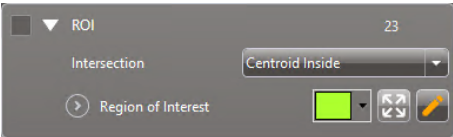
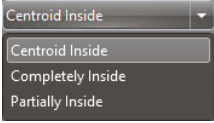
Figure 3 Reconstruction Volume



Grain Selection Filters

Additional **Grain Selection Filters** have been added, see [Table 2](#).

Table 2 New **Grain Selection Filters** of the **Inspection Tab**

Control	Function
	Surface Grains selects all grains touching the sample surface.
	Non-Surface Grains selects all grains not touching the sample surface.
 	ROI gives the user the option to define a Region of Interest and select grains relative to this by Intersection : <ul style="list-style-type: none"> • Centroid Inside selects all grains with centroids inside the ROI • Completely Inside selects all grains completely inside the ROI • Partially Inside selects all grains that are either fully or partially inside the ROI

User Interface Changes

Additional Meta Data The **DCT Data** and **Absorption Data** section of the **Project Status** now show additional information about the input data if the project file was created with this version.

Preference Plot Settings A few more options to the **Plot Settings** in the **Preference** section have been added as described in [Table 3](#). It is now possible to show the original Zeiss sample positions and other meta data in the DCP, see [Figure 4](#).

Table 3 New Plot Settings Preferences

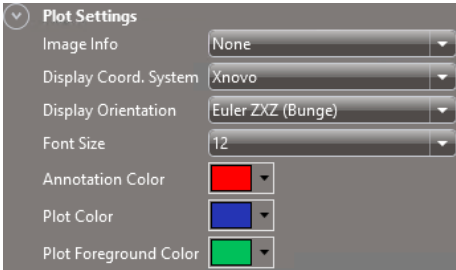
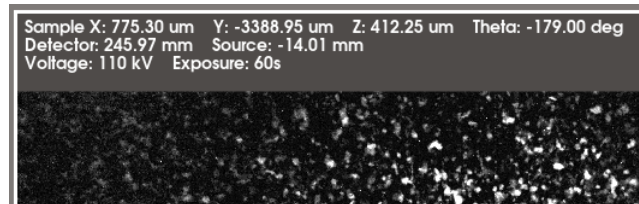
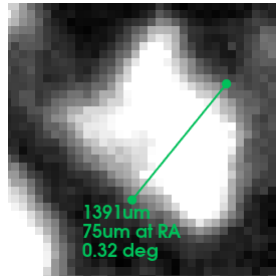
Control	Function
	<p>Choose Image Info to show additional information attached to DCPs in the DCT data views, either:</p> <ul style="list-style-type: none"> • None • Compact (Sample X, Sample Y, Sample Z, and Sample Theta), or • Detailed (Compact plus Source and Detector distances, Voltage and Exposure) <p>Choose Display Coordinate System to be shown for Image Info and MPVs, either Xnovo or Zeiss.</p> <p>Choose Display Orientation to change the parameterization of the crystallographic orientation displayed in the MPVs of the Grain or Inspection tab, either:</p> <ul style="list-style-type: none"> • Rodrigues vectors, • Euler ZXZ (Bunge), Euler angles (ϕ_1, Φ, ϕ_2), • Euler ZYZ (Matthies), Euler angles (α, β, γ), or • Quaternion

Figure 4 Detailed Image Info

Line Profile The line profile now shows for DCPs in addition to the distance on the detector, the distance at the rotation axis (RA) and the solid angle between the vectors spanned by the center at the RA and the start and end points on the detector, respectively.

Figure 5 Additional Line Profile Measurements



Export HDF The **Open File** option for **Export HDF** on the **Export Tab** (Table 4) previously used HDF Viewer (if this was installed). Now the default is to open the result file in GrainMapper3D Viewer.

Table 4 New **Open File** Behaviour of the **Export Tab**

Control	Function
	<p>Export HDF generates a result file which can be read in by supplemental analysis software.</p> <ul style="list-style-type: none"> • If Open File is checked when pressing Export, the *.h5 result file will be opened in GrainMapper3D Viewer.

DCT Acquisition Wizard



The DCT Acquisition Wizard is only to be installed on the primary workstation by ZEISS Service.


New Features and Product Enhancements


Number of Projections

DCT Acquisition Wizard 3.2 now allows to collect up to 25,000 projections, as opposed to the previous hard limit of 10,000 projections, on account of the enhanced memory handling of GrainMapper3D 3.2. However, the recommendation is still to keep below 2-3000 projections per scan if possible.

Importing Absorption Scan Recipes from Scout-and-Scan

DCT Acquisition Wizard 3.2 allows the user to import and run absorption recipes from Scout-and-Scan. Hence, the entire DCT experiment, from the acquisition of both the DCT and Absorption data to the automatic reconstruction of the latter, can be performed at once from within the DCT Acquisition Wizard. The only requirement is that the Absorption recipe with all relevant choices is set up inside Scout-and-Scan, since none of these parameters can be changed in the DCT Acquisition Wizard.

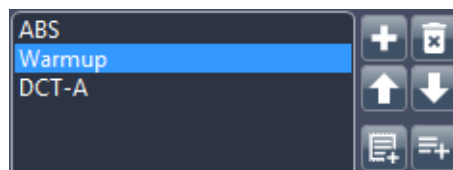
Press  in the Recipe Section, [Figure 6](#), to import *recipe points* from an existing *.dctrp or *.rcp file. A file dialogue opens, locate the file and press **Open**. The imported recipe points will be appended to the list of recipe points.

Press  to import the *recipe points* currently open in Scout-and-Scan.



Please note that for CrystalCT it is not possible to import Scout-and-Scan recipes (*.rcp).

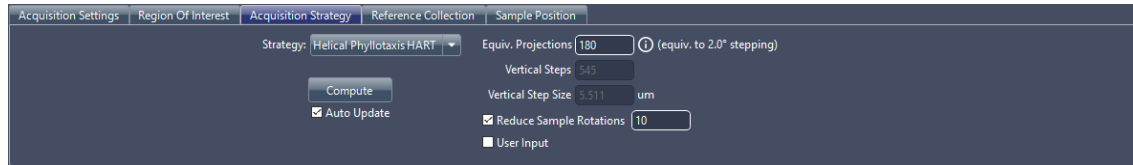
Figure 6 Import Recipes in the Recipe Section



Reduce Sample Rotations

Remove the check mark from **Reduce Sample Rotations** in the **Acquisition Strategy** tab, [Figure 7](#), to use the original Helical Phyllotaxis scanning scheme.

Figure 7 Typical **Acquisition Strategy** in the **DCT Acquisition Wizard**



For the original Helical Phyllotaxis scanning scheme the **Sample Y** translations between adjacent projections are always of the same magnitude and sign, while **Sample Theta** does large increments and frequent rewinds to achieve a $\sim 137.5^\circ$ rotation for every vertical sample translation, see [Figure 8a](#).

With **Reduce Sample Rotations** the sample stage only rewinds the given number of times over the number Equivalent Projections within the height of the aperture FOV, while the **Sample Y** movements between adjacent projections vary a lot in both magnitude and sign, see [Figure 8b](#).

Figure 8 Scan List from **Show Scheme** in **Recipe Section**

(a) Scan List for Helical Phyllotaxis HART

	Sample X	Sample Y	Sample Z	Sample Theta
1	-265.03	-20137.46	-950.29	90.00
2	-265.03	-20137.46	-66.46	90.00
3	-265.03	-20137.46	817.38	90.00
4	207.28	-20142.98	449.12	-132.49
5	-265.03	-20142.98	-66.46	-132.49
6	-737.34	-20142.98	-582.03	-132.49
7	-265.03	-20148.50	-66.46	5.02
8	180.59	-20154.02	-408.10	142.52
9	-265.03	-20154.02	-66.46	142.52
10	-710.64	-20154.02	275.19	142.52
11	-418.41	-20159.55	800.65	-79.97
12	-265.03	-20159.55	-66.46	-79.97
13	-111.65	-20159.55	-933.56	-79.97
14	-694.41	-20165.07	-741.46	57.54
15	-265.03	-20165.07	-66.46	57.54
16	164.35	-20165.07	608.55	57.54
17	-129.34	-20170.59	-29.98	-164.95
18	-400.72	-20170.59	-102.93	-164.95
19	-611.61	-20176.11	113.55	-27.45
20	81.56	-20176.11	-246.46	-27.45

(b) Scan List using Reduce Sample Rotations 10

	Sample X	Sample Y	Sample Z	Sample Theta
1	-129.34	-20170.59	-29.98	-164.95
2	-400.72	-20170.59	-102.93	-164.95
3	-693.68	-20214.75	-367.82	-144.89
4	-265.03	-20214.75	-66.46	-144.89
5	163.63	-20214.75	234.91	-144.89
6	207.28	-20142.98	449.12	-132.49
7	-265.03	-20142.98	-66.46	-132.49
8	-737.34	-20142.98	-582.03	-132.49
9	-593.68	-20187.15	-862.63	-112.43
10	-265.03	-20187.15	-66.46	-112.43
11	63.62	-20187.15	729.72	-112.43
12	-228.56	-20231.32	815.38	-92.37
13	-265.03	-20231.32	-66.46	-92.37
14	-301.49	-20231.32	-948.29	-92.37
15	-111.65	-20159.55	-933.56	-79.97
16	-265.03	-20159.55	-66.46	-79.97
17	-418.41	-20159.55	800.65	-79.97
18	-675.23	-20203.71	641.38	-59.91
19	-265.03	-20203.71	-66.46	-59.91
20	145.18	-20203.71	-774.29	-59.91

The two scanning schemes collect the exact same projections, the order is simply different. Notice for instance that projections 17 and 18 in [Figure 8a](#) correspond to projections 1 and 2 in [Figure 8b](#).

The default value of **Reduce Sample Rotations** is 10, which means that if a scan is aborted, the last 10th of the aperture FOV height will be poorly illuminated. An original Helical Phyllotaxis scan does not suffer from poor illumination at the edge of the FOV in case the scan is aborted. However, it is roughly 20% faster to collect data using Reduce Sample Rotations with the default value of 10.

Other Enhancements

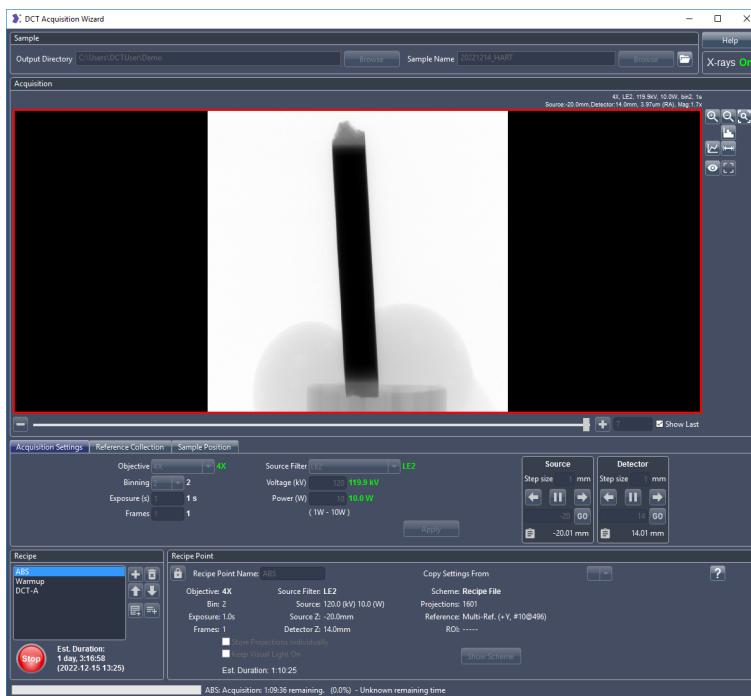
Additional Help Options Press **?** in the **Acquisition Strategy** tab, see [Figure 7](#), to open a summary of the recommended minimum number of projections as a function of detector working distance for the detector selected in the **Acquisition Settings**.

Click **?** in the **Recipe** section to open the **Quick Reference Guide**.

User Interface Changes

The layout of the DCT Acquisition Wizard interface has been optimized with a new aspect ratio and different text box design to make it look more like the Scout-and-Scan interface, see [Figure 9](#) for an example of the full layout while running an absorption recipe point.

Figure 9 DCT Acquisition Wizard Running Absorption Recipe Point



GrainMapper3D Viewer

GrainMapper3D Viewer 3.2 features a few updates in line with GrainMapper3D updates, namely:

New Features and Product Enhancements

Grain Selection Filters Additional **Grain Selection Filters** have been added as for GrainMapper3D, see [Table 2](#).

Additional Meta Data The **LabDCT Volume** and **Absorption Volume** section now show additional information about the input data if the project file was created with this version.

User Interface Changes

Preference Plot Settings Same as for GrainMapper3D, see [Table 3](#), except for the Image Info option, which is not applicable for the GrainMapper3D Viewer.

GrainMapper3D™

Release Notes

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