

Deconvolution

Deconvolution is an algorithm-based process that can be used to enhance the recorded data. The process tries to undo the distortion inherent to the microscope as well as reduce noise in the images. To obtain best results a high magnification objective should be used and the data should be oversampled. This means that the pixel size should be smaller than the 'optimal' given by the microscope. [Huygens offers a calculator app](#) that can be used to calculate the optimal sampling for deconvolution. Because the sampling needed for deconvolution is different from the normal sampling you need to decide whether or not you are going to deconvolve your data before you record it. It is also important to understand that while deconvolution tries to reconstruct structures and remove noise it does not guarantee that intensities within the image remain comparable.

It is important to understand that deconvolution does not benefit every sample nor can it be used to salvage bad data. If your signal is weak and your data is noisy you should try to optimize your sample and imaging protocols first. You can find more information from [here](#). We recommend you to discuss your options and aims with LMU staff if you have not worked with deconvolution software before.

Software available at LMU

<https://www.microvolution.com/> Microvolution is installed on the HELMI 3D virtual computer

<https://biii.eu/huygens> Huygens is installed on 3D Workstation on LMU premises

<https://biii.eu/autoquant> Autoquant is installed on 3D Workstation on LMU premises

Tested

<https://biii.eu/bigstitcher>

<https://biii.eu/multiview-reconstruction>

RESULTS FROM BISE

https://biii.eu/all-content?type=software&field_has_function_target_id%5B%5D=4081&field_type_target_id=All