

Version 2022.2.1 (July 2022)

NEW FEATURES AND ENHANCEMENTS

New imaging and data handling engines

MBF Bioscience software includes new image acquisition and image/data display technologies that maximize efficiency and speed throughout Stereo Investigator. Compile, save, load, display, and process your files *much* faster than before. These new imaging and data-handling engines employ intelligent image loading, concurrent usage of CPU cores, and multiple levels of data caching for efficient use of RAM and GPU resources. The speed and capabilities of Stereo Investigator software are now limited only by the resources of the computer on which it's installed.

You will see major improvements in overall function and performance; highlights include:

- Acquire much, much larger images than was previously possible—in the multiple terabyte range
- Load very large image and data files noticeably faster than before—no lagging, no crashing
- Handle millions of data points simultaneously—faster software response than ever before
- Combine multiple data files, each containing massive numbers of markers, traced structures and/or stereology probe runs
- Display image adjustments immediately in both the 2D and 3D windows—without clicking any buttons

Improved slide scanning workflow

The new imaging engine dramatically increases the size of images that can be acquired. The speed of image acquisition and assembly in the slide scanning workflow has also been improved. Benefits include:

- Create larger slide-scans—at higher magnification and/or from larger specimens than possible in previous releases
- Preview images before finalizing your large-image compilation settings
- Include optional XY stitching for better image-tile alignment and cleaner compiled images
- Mitigate uneven illumination artifacts in fluorescence imaging using (optional) intelligent, image-data based flatfield correction
- View the amount of disk space needed for the slide scan before starting the image acquisition
- Compile large images faster
- Compile partial scans in the event an acquisition fails partway through

Automated assistance with hardware alignment and calibration

Use the new *Auto-calibration* button to automatically:

- Calibrate each lens to determine pixels per micrometer—no need to perform this task manually
- Algorithmically fine-tune camera-stage alignment—autocalibration compensates for micro-misalignment of camera and stage



Software authorization and options

- Easier software authorization—Stereo Investigator has a new, easier to use, licensing mechanism. License can be updated for renewal, or trial without having to connect to MBF staff.
- Floating licenses are now available—share one Stereo Investigator license on more than one computer

More options for opening images

- Indicate how you want Stereo Investigator software to handle and display your images
- Open all images in container files such as Leica .lif and Zeiss .czi formats
- Choose to display in a grid, stack images, or display on top of each other without stacking
- Drag and drop to open files—the new Image Opener window makes it easier and more powerful

Probe-workflow improvements

- Optional second counting frame in the Optical Fractionator Workflow makes it easier to count two sets of
 objects in a single pass—ideal for structures that are very different in size and/or population density
- Significantly easier method to launch the Optical Fractionator Workflow using images that were acquired on other (non-MBF Bioscience) microscope systems, such as a confocal microscope

3D visualization window

The highly versatile 3D visualization environment includes a full suite of image optimization tools with state-of-the-art features that support your analysis and publication needs. Improvements include:

- A new subvolume function in the 3D window enables you to easily and systematically focus on portions of images/image stacks
- Color channel selection in the 3D window via a new Channel panel enables you to select one or more color channels to view and hide
- New tool that clips tracings to a partial projection view

Other improvements

- New Freehand Selection tools provide more options for selecting markers or contours
- Updates to the Image Montage tool that support automatic z-alignment and the option to consider image names in the 2D image-alignment process
- The default data-file format is now .xml
- Research Resource Identifier (RRID) is now recorded in every xml data file
- Simpler automatic exposure (in the camera settings) to achieve the target luminance for each image acquisition
- Updated the Illumination Correction tool
- Updated tool tips that display when hovering on buttons and tools throughout the software
- New hardware support for the following:
 - Zeiss Apotome 3
 - o Luminera CMOS camera
 - Basler cameras
- New support for the following image formats
 - Big tiff



- o Hdf5
- Custom Z offset is now available for use in Device command sequences

ISSUES RESOLVED

Numerous bug fixes throughout the software. These include:

- The Account for missing section in the Cavalieri Estimator is fixed
- When using SRS stack acquires for the Spaceballs probe, it is now easier to change to using a sphere or a hemisphere
- Fixed options for saving the current plane
- Export tracing as an image in monochrome is fixed

