


# BESA Research 7.1 - Update History

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## BESA Research 7.1 - Update History

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## BESA Research Release Notes

### Version 7.1 September 2024

#### Bugfixes

- **General**
  - When electrode positions are defined on a sphere, there were some cases where the electrodes are not displayed correctly in the 3D window of the Montage Editor and Source Analysis (BR-3356)
- **Data review and pre-processing:**
  - Data export:
    - To EDF:

- When exporting data to EDF, a visible spike of one sample length appeared at some point in each channel of the exported data file (BR-3354)
- When exporting a concatenated or segmented file, the start dates and times of the concatenated segments were wrong in the exported file (BR-3347)
- A short epoch with flat data was sometimes added unnecessarily (BR-3391)
- Exporting a file containing bad channels in the original recording montage, and selecting the option for Current montage in the export dialog, caused a crash when opening the exported file again in BESA Research. Also, bad channel signals were set to zeros in the exported file. To prevent this from happening, the Current montage option was disabled in the Export dialog for this scenario (data in original recording montage). To make use of this option in the future, the user can generate a new montage in the Montage Editor based on the original montage, then set this montage and then export as Current montage. This will automatically exclude the bad channels. (BR-3423)
- Intracranial channel data amplitudes were modified if the channels contained very high amplitudes (BR-3398)
- When exporting XLTEK recordings consisting of more than one data file, i.e. long recordings, invalid EDF files could be produced (BR-3406)
- To BESA foc:
  - When resampling for export to BESA foc, and file length was between 20 seconds and 40 seconds, then some parts of the data were distorted during export (BR-3353)
- To simple binary format:
  - If the original file contained bad channels, then this was not considered correctly when exporting to the simple binary format (BR-3400)
- Data reading:
  - If an EDF file contained different sampling rates for different channels, the data for channels with lower sampling rate was not displayed correctly (BR-3365)
  - If an EDF file with non-symmetric values for physical minimum and maximum was opened, data were not correctly balanced around the zero line. Also high amplitudes could then be capped (BR-3414)
  - If an EDF file contained space characters within the channel labels, then waveforms were not shown correctly (BR-3387)
  - Combined MEG-EEG data previously exported from BESA in EDF format could cause problems when later re-opening them in BESA Research (BR-3397)
  - Reading channel information from .elp files: In case that polygraphic channel labels had only numbers but no letters, this information was mis-interpreted during reading in, resulting in wrong waveforms for these channels (BR-3390)
  - CTF data: It was not possible to read a CTF-275 data file that contained trigger labels longer than 40 characters (BR-3357)
  - Brain Vision: If the complete file path to the data file was longer than 128 characters, the file could not be read (BR-3351)

- ERP analysis:
  - In the Top Viewer 3D map, a crash could occur in rare cases if very high amplitudes were mapped (BR-3380)
- FFT analysis:
  - In case that several mean FFTs which had been computed by batch were averaged for a grand average mean FFT, the number of averages was wrongly computed, and the displayed grand average mean FFT was then incorrect (BR-3366)
- Data review:
  - When changing the screen position by intervals that were multiples of full seconds, the second markers on the screen shifted slightly with respect to the data (BR-3389)

### Residual anomalies

The following known problems could not be fixed for this release version, and remain in the software:

- **General:**
  - After re-installation of the installation setup, the Sentinel Runtime Environment shortcut gets lost from the Start menu. Workaround: Sentinel can be accessed by typing in the browser `localhost:1947`, or by starting the link in the installation sub-folder: `\Utilities\License\System\Sentinel Admin Control Center`. (BR-3301)
- **Data review and pre-processing:**
  - Data reading:
    - NicoletOne-Nervus reader: There are problems with overlap of triggers and data if different sampling rates are used for different channels. Workaround: Use a recording mode with the same sampling rate for all channels. (BR-1612)
    - BESA Research does not support unicode characters in file name. Workaround: Use files names with non-unicode names. (BR-2929)
  - *Besa.ini* file: [Pattern] section in *Besa.ini* file has no effect: Names for patterns that are defined by the user are not applied. (BR-3242)
  - Data review:
    - There is a limited size of the data buffer used for the displayed data. With very high sampling rates, a large number of channels, or long display times, the program may crash (BR-3367). Workaround: reduce the data interval displayed, or down-sample the data. For example, with 380 channels, and a sampling rate of 2000 Hz, 100 seconds of data can be displayed without problem.
    - For some standard source montages (e.g. 25s), switching on the montage option Left-to-Right has no effect (BR-3292). Workaround: Use another standard source montage, e.g. *Brain Regions*.
  - Batch processing:
    - In the batch command to export around triggers, using the option to export only accepted events does not work correctly (BR-3370). Workaround: Use the manual export around triggers and select the condition of choice after running the artifact scan.
- **Source analysis and source imaging:**

- Batch processing:
  - An error occurs if consecutive SAImageExport commands are triggered. (BR-1596).  
Workaround: Place a batch command between the export commands to re-display the 3D window, like:
 

```
SAImageExport(%basename%_300_700ms_9_12Hz.dat,Single,ASCII,-)
SADisplayMRI(On,SmallWindow,NoChange)
SAImageExport(%basename%_300_700ms_9_12Hz.vmp,Single,BrainVoyager,HiRes)
```
  - Batch exporting 3D images with all time points fails if the batch is executed for several data files. Workaround: Explicitly set fit interval using batch command `SAFitInterval`. (BR-1549)
- The option to save a CLARA, sSLOFO, Beamformer, or DICS image as "NIfTI file, 1 mm resolution in ACPC (.nii)" in the Export image dialog is not available if no interval is defined (i.e. if the image was computed for only the cursor time-point). Workaround: Mark a short interval with two samples, or use a batch command to export. (BR-3294)
- A wrong source image method name is displayed in the 3D window after computing a User-Defined Volume image, if the user starts with the defaults of another non-iterative method and then modifies them. (BR-3260)
- Automated source estimation methods: In the R-MUSIC method, the SVD subspace correlation may not always work as expected. (BR-2524)
- **Connectivity:**
  - When exporting data to BESA Connectivity from a segmented file, the program still starts if the selected epoch with padding is larger than the file segment, but only shows one epoch. Workaround: Instead of working with a segmented file, use the continuous data file to send the epochs to BESA Connectivity. (BR-3268)

## Previous Versions

### Version 7.1 January 2024

#### Improvements

- **General:**
  - The Windows 11 operating system is now supported. Please note that Windows 7 support was deprecated for this version.
  - The UDI information was added to the About box. Information about where to find Instructions for Use was updated.
- **Data review and pre-processing:**
  - Event histogram: A histogram of trigger event frequency can be plotted. To invoke this, use menu *View / Histogram* or type the key *H* on the keyboard. In case that tags were marked for spike events, first run the batch *'Epilepsy/F6\_Spike\_Convert\_Tags\_And\_Average'* to create triggers from the tags (or press *F6* after setting BESA Research to EEG Review mode using

*Options / Reset Settings*). One histogram plot is presented for each trigger that is selected. Trigger selection can be adjusted using the menu '*Edit / Trigger Values...*'. The histogram plot will also be shown in the printout.

- Pattern search: When searching with Query, the dialog to accept or reject matches now enables showing a topographic map of the current candidate event.
- Data readers: Additional file formats are now supported:
  - OPM data format: Cerca Magnetics (using a proprietary script *cMEG2fif.py* to transform data to fif). Note that this option requires the purchase of an additional module license. A signal subspace projection can be applied to reduce external noise. This is active by default and can be toggled on or off using the menu *Filter / Signal Subspace Projection On/Off*.
  - MED Dark Horse data format
- Data readers: Improvements were implemented for the following formats:
  - Micromed version 5 is now supported
  - XLTEK version 9.3 is now supported
  - g.Tec HDF5 data can now be read
  - Curry 9 data can now be read
- Data export:
  - When exporting to EDF format, the quality of the exported data was improved for files with very high voltages
  - When exporting epochs around triggers, the size of the epoch is now used to determine and exclude epochs that overlap with marked artifacts in the data
- Batch processing:
  - For user-defined batch variables, defaults can now be set
  - The batch function DisplayMRI has an additional option now to enable showing the cortex view
  - The batch function SetInterval can now automatically set an onset interval for spike localization
  - The batch command SaveBitmap now enables saving as *.bmp* or *.png* format
  - A new batch command allows to run a Schmitt trigger detection using a previously defined Schmitt trigger settings file. Syntax: *SchmittTrigger(filename.smt)*.
- MATLAB interface: New dlls for versions R2022a, R2022b, R2023a, R2023b were added
- ERP processing:
  - The maximum length of a boolean expression for a condition was enlarged to allow defining more complex conditions.
- *Besa.ini* file:
  - New parameters are available to control the following:
    - OPM data default scaling: Section [OPM] , key `OPMScale={value in fT}` ;  
Default: `OPMScale=5000`

- Usage of an OPM slot for the current computer (for network installations):  
Section [OPM] , key: `OPMVersion={1 | On | 0 | Off}` ; Default:  
`OPMVersion=1`
- Usage of signal sub-space projection for Cerca OPM data: Section [OPM] , key  
`CercaSpatialProjection={On | Off}` ; Default:  
`CercaSpatialProjection=0n`
- It is now possible to remove all filters from the *Besa.ini* file to enable switching off all filters by default
- Channel label display: Only the first letter of channel labels is now capitalized to improve readability.
- Surface points view: When selecting an electrode in the Surface Points window, the corresponding channel is highlighted in the review window only if the original recording montage is selected, in order to prevent mismatches.
- Screenshots of the 3D mapping window can now be saved as png files or bitmaps, with increased resolution (using keyboard shortcut *Shift-S* in the mapping window).
- **MEG version:**
  - FFT mapping for MEG now supports 3D mapping as well as the previous 2D maps
- **Source analysis and source imaging:**
  - SESAME:
    - Usage of spatial priors: The Bayesian source imaging method SESAME can now use spatial priors. Compute or load any source image in the Source Analysis window. Then press the button '*Weight by Image*' before you start SESAME computation. The usage of spatial priors is indicated in the 3D results display window.
    - Hyperpriors: The hyperpriors integration was improved. Default settings were changed to run SESAME for a fixed 50 iterations since this enables convergence in nearly all cases.
  - Export to an AC-PC NIFTI file: If a co-registration with individual anatomy exists, any source image can be exported in the native AC-PC coordinate system of the subject. This can be done in two ways:
    - Using the menu entry '*Image / Export Image As...*' in the Source Analysis window: In the dialog that appears, select the option '*Nifti Files, 1 mm resolution in ACPC*'
    - Using a batch command: The batch command `Export` in section *Source imaging* has the option to export to Image format Nifti 1 mm AC-PC space for the cursor position. Create a batch for this, and put it on a function key of your choice by adding the batch to a function key (press *Shift + Function* key to select the batch to be added).
  - Source solutions: For solutions saved in Talairach or AC-PC coordinate systems, the baseline information is stored now. This will ensure a correct re-computation of confidence ellipsoids after loading the solution back at a later stage.
  - In the 3D window, source labels can now be displayed beside the source symbols. Use the context menu to toggle the display (default: off).

- Screenshots of the source analysis and / or 3D window can now be saved as png files or bitmaps, with increased resolution.
- **Connectivity:**
  - The Source Coherence module now uses OpenGL acceleration by default.
  - In the Source Coherence module, for time-frequency computations floating point precision rather than double precision is used in order to allow for larger datasets to be stored in memory.
  - The Source Coherence window now stays visible after computing the time-frequency beamformer. This facilitates adjusting parameters before re-computing the beamformer solution.

## Bugfixes

- General
  - If the Nicolet One-Nervus reader was installed previously, and then an update for BESA Research was installed, the Nicolet One-Nervus reader installer popped up frequently asking to run an update. This issue was fixed (BR-1510)
  - If a menu was opened after program start, and the dialog checking for updates came up at the same time, interaction was frozen until the ESC key was pressed This issue was fixed (BR-1502)
- **Data review and pre-processing:**
  - Data reading:
    - When reading XLTEK files, the setting for reading triggers in the BESA.ini file was not taken into account. This issue was fixed (BR-1632)
    - Curry data format: If electrode coordinates were embedded in the file, the reader did not make use of this information. This issue was fixed (BR-2069)
    - If Brain Products files or XDF files had embedded electrode coordinates, the reader did not make use of this information. This issue was fixed (BR-1519)
    - XDF files generated by TMSi could not be read. This issue was fixed (BR-1625)
    - Reading Nihon Kohden files with incomplete auxiliary data (e.g. patient information file missing after anonymization) was not possible. This issue was fixed (BR-1571)
    - After reading in Nicolet-Nervus files, a crash could occur when closing the file, or when opening the Head Surface Points dialog. This issue was fixed (BR-1600)
    - Some EDF+ files could not be read correctly (flat lines were shown). This issue was fixed (BR-1565)
    - When reading generic file format data with a file size of more than 2 GB, paging to the end of the file was not possible. This issue was fixed (BR-1631)
  - Data export:
    - to EDF: If data were exported to a network drive, and the connection is temporarily lost, then it was possible that the resulting file was shorter, and event positions no longer were correct. This bug was fixed (BR-2230)
    - to EDF: The gender field was filled with a default value even though the gender is not known. This issue was fixed (BR-2080)

- For montage channels with more than 12 characters, during export using the current montage the channel labels were truncated in MATLAB export, simple binary matrix export, and ASCII multiplex/vectorized export, even though these structures support longer labels, e.g. for atlas brain region sources. This issue was fixed (BR-1504)
- Printing:
  - to pdf: BESA Research occasionally froze when an information window was open during printing. This issue was fixed (BR-2150)
  - with a correlation info window open: The correlation plot was incorrectly shifted in the printout. This issue was fixed (BR-2128)
- ERP processing:
  - When averaging conditions, there was no warning if no artifact scan was performed. This issue was fixed (BR-3161)
  - In the artifact scan, for very large numbers of trials, the horizontal scroll bar became unresponsive, and the trial numbers were not displayed correctly. This issue was fixed (BR-1620)
- Batch processing:
  - If the user un-checked the box "Don't try to open file here" in the batch dialog file list, and then selected files, the check box was checked again automatically, and files were opened. This issue was fixed (BR-1623)
  - A Cancel dialog sometimes showed during opening of the batch dialog, which should not be shown. This issue was fixed (BR-1611)
  - The OK button can become enabled in the file list dialog of the batch, even though no batch is selected to be run. This issue was fixed (BR-1542)
  - If a file list contained files with different sampling rates and channel count, these values were not correctly updated after moving the position of files in the file list. This issue was fixed (BR-1489)
- Artifact correction:
  - ECG artifact correction in MEGIN MEG data did not always work correctly if there was signal on the EXCI channels. This issue was fixed (BR-1547). Related to this, an issue that the ECG channel information was not updated in the artifact correction information after setting polygraphic channels to BAD was also fixed (BR-1532)
  - For MEGIN MEG data files, the artifact selection dialog could display wrong variance values for artifact topography percentages if the dialog was closed and opened again after defining artifact topographies. This issue was fixed (BR-1531)
  - When working with combined EEG-MEG files, the waveform displayed for the artifact channel was not updated when the channel type for artifact correction was switched by clicking a channel group selection button. This bug was fixed (BR-1516)
- Pattern search: Searching in the current segment did not always work correctly if the marked block was near a segment boundary. This issue was fixed (BR-2511)
- Disabling the check for dongle updates in the BESA.ini was not possible (by setting `DaysBetweenUpdateChecks=-1`). This issue was fixed (BR-1624)
- User montages:



- When a previously used montage file could not be found by BESA Research, an unclear error message was displayed, and BESA Research sometimes crashed. This bug was fixed (BR-1529)
- For combined EEG-MEG files, a user montage containing both EEG and MEG channels did not always show all waveforms if the user switched from user montage to a standard montage and back again. This bug was fixed (BR-1490)
- If a user montage contained source channels and scalp channels with the same names (e.g. Fp1 as scalp channel and also Fp1 as source channel), then a crash could occur. This issue was fixed (BR-1505)
- BESA Research could crash if one data file was open, the user then cleared the database entry in the Head Surface Points dialog, and then proceeded to selected a montage group in the empty review window. This bug was fixed (BR-1515)
- MRI co-registration: In combined EEG-MEG files, if a common EEG reference channel was present but had no 10-10 label (e.g. "REF"), this channel was excluded from the co-registration head surface point file. This issue was fixed (BR-1503)
- **Source analysis and source imaging:**
  - Source image import:
    - BrainVoyager images that were imported were wrongly positioned by up to 1 mm. This bug was fixed (BR-3180)
    - When importing a previously exported ASCII source image, it was possible that the number of maxima differed. This issue was fixed (BR-3159)
    - When working with artifact-corrected data, and importing a source image, a wrong dialog informing about data distortion was shown. This issue was fixed (BR-2221). Also, a text "SSP distorted" was shown in the 3D window. This issue was also fixed (BR-1622)
    - If the user had previously computed a source image for several time points, and then loaded a source image for a different time point, the previously computed image was not cleared for the other time points, making it difficult to assess which image method was used for which time point. Now, the previous buffer is cleared (BR-1610)
    - After exporting and re-importing source image results in ANALYZE format, left and right were flipped. This bug is now fixed (ANALYZE was discontinued and replaced by NIFTI since it was ambiguous towards slice left-right orientation.) (BR-1530)
  - Source image export:
    - When exporting a source image of a non-iterative method to ASCII, the header had wrong or incomplete information about regularization. This issue was fixed (BR-3132)
    - When exporting a multi-latency source image file, the last sample was missing in the exported file. This issue was fixed (BR-1817)
    - When a source image was smoothed and then exported, the resulting exported image file contained only zeroes. This issue was fixed (BR-1607)
  - Smoothing of a source image after importing was not possible. This issue was fixed (BR-3069)
  - Batch processing:

- The batch command *Regularization* to set a regularization constant had no effect for time-domain Beamformer computations and also did not fully work for time-frequency beamformer computations. This issue was fixed (BR-3139)
- Seeding a source from a maximum using the command *GotoMax* did not work for cortical methods (Cortical CLARA, Cortical LORETA, Minimum Norm). This issue was fixed (BR-1498)
- Loading solutions:
  - After loading a previously saved source solution, the fitting intervals used to create the solution were not all restored correctly. This issue was fixed (BR-2105)
  - If the same source colours were defined for all sources, a few of the colours were changed after loading. This issue was fixed (BR-1621)
- Saving source solutions in device coordinates did not work correctly if device coordinates were different from head coordinates. This issue was fixed (BR-2078)
- Cortical imaging:
  - In Cortical CLARA, when dragging the cursor with the mouse to a different time point, the dragging mode could not be stopped. This issue was fixed (BR-1594)
  - In cortical images, settings for brain transparency were not applied if a maximum was highlighted. This issue was fixed (BR-1524)
- 3D Voltage mapping: When toggling between individual and standard head display using the context menu, the voltage map was not updated automatically. This issue was fixed (BR-1829)
- When sending a previously defined data interval to Source Analysis using the context menu in the review window, the last sample was missing. This issue was fixed (BR-2267)
- When computing a source image over an interval, the text in the 3D window indicating the source imaging method was lost after removing the cursor. This bug was fixed (BR-3191)
- Combining conditions in the Source Analysis window did not always work even if the channel configuration was the same. This issue was fixed (BR-1563)
- In a condition that contained only MEG data, pressing the MEG button in the Source Analysis window showed a wrong error message. This issue was fixed (BR-1506)
- **Connectivity:**
  - Exporting scalp surface channel montage data to BESA Connectivity did not always work correctly. This issue was fixed (BR-2388)
  - Batch command export to BESA Connectivity did not save the data in the specified folder if the folder did not exist yet. This issue was fixed (BR-2268)
  - Setting the default path to the connectivity program in the BESA.ini file did not have any effect. This issue was fixed (BR-1641)
  - In segmented data files, exporting data to BESA Connectivity led to a crash if the exported epochs were larger than the segment width. This issue was fixed (BR-1521)

### Residual anomalies

The following known problems could not be fixed for this release version, and remain in the software:

- **General:**

- After re-installation of the installation setup, the Sentinel Runtime Environment shortcut gets lost from the Start menu. Workaround: Sentinel can be accessed by typing in the browser `localhost:1947`, or by starting the link in the installation sub-folder: `\Utilities\License\System\Sentinel Admin Control Center`. (BR-3301)
- **Data review and pre-processing:**
  - Data reading:
    - NicoletOne-Nervus reader: There are problems with overlap of triggers and data if different sampling rates are used for different channels. Workaround: Use a recording mode with the same sampling rate for all channels. (BR-1612)
    - BESA Research does not support unicode characters in file name. Workaround: Use files names with non-unicode names. (BR-2929)
  - *Besa.ini* file: `[Pattern]` section in *Besa.ini* file has no effect: Names for patterns that are defined by the user are not applied. (BR-3242)
- **Source analysis and source imaging:**
  - Batch processing:
    - An error occurs if consecutive SAImageExport commands are triggered. (BR-1596). Workaround: Place a batch command between the export commands to re-display the 3D window, like:

```
SAImageExport(%basename%_300_700ms_9_12Hz.dat,Single,ASCII,-)
SADisplayMRI(On,SmallWindow,NoChange)
SAImageExport(%basename%_300_700ms_9_12Hz.vmp,Single,BrainVoyager,HiRes)
```
    - Batch exporting 3D images with all time points fails if the batch is executed for several data files. Workaround: Explicitly set fit interval using batch command `SAFitInterval`. (BR-1549)
  - The option to save a CLARA, sSLOFO, Beamformer, or DICS image as "NIFTI file, 1 mm resolution in ACPC (.nii)" in the Export image dialog is not available if no interval is defined (i.e. if the image was computed for only the cursor time-point). Workaround: Mark a short interval with two samples, or use a batch command to export. (BR-3294)
  - A wrong source image method name is displayed in the 3D window after computing a User-Defined Volume image, if the user starts with the defaults of another non-iterative method and then modifies them. (BR-3260)
  - Automated source estimation methods: In the R-MUSIC method, the SVD subspace correlation may not always work as expected. (BR-2524)
- **Connectivity:**
  - When exporting data to BESA Connectivity from a segmented file, the program still starts if the selected epoch with padding is larger than the file segment, but only shows one epoch. Workaround: Instead of working with a segmented file, use the continuous data file to send the epochs to BESA Connectivity. (BR-3268)

## Version 7.1 November 2021 (patch version 7.1.2.1)

### Bugfixes

- **Data review and pre-processing:**
  - Printout: When markers are shown in the waveform display, it was possible that markers including blocks or cursors appeared in the wrong position relative to the waveforms in the printout. Typically, this happened when a wide filter band was used. This bug was fixed (#995).

### Residual anomalies

The following known problems could not be fixed for this release version, and remain in the software:

- **Data review and pre-processing:**
  - Nicolet-Nervus reader: When reading a data file that contains channels with varying sampling rates, this might lead to wrong interpretation of event times. (#318). Workaround: Use an acquisition mode with constant sampling rate across channels

## Version 7.1 November 2021

### Improvements

#### **Data review and pre-processing:**

- o File readers:
  - Alpha-trace: The 24-bit amplifier is now supported.
  - Neuromag:
    - Strings of digitization points are now supported.
    - Two digital trigger channels are now simultaneously supported.
- o ERP averaging:
  - Averaging of artifact-corrected data: The workflow in the case that artifact correction is available was improved. It is now possible to switch artifact correction off for averaging, but automatically load artifact coefficients and correct the data after averaging. This leads to less distortion of the data.
- o Time-frequency plot:
  - The time-frequency plot that is available via right-click in the review window can now show frequencies up to just below the Nyquist limit (50% of sampling rate), if the option for "Display / Use High Frequencies in Time-Frequency Plots" is set.
- o Batch processing and combining conditions:
  - Application responsiveness during loading of the file list was improved.
  - Now multiple files can be removed from the list at once, and removing/adding can be interrupted if needed.
- o Update check:
  - The check for program updates was moved to a secure shell protocol (https).
- o Data export:

- Previously, when performing ICA and then exporting the file corrected for the selected artifact components, the extension *\*.foc* was not added automatically if the user changed the file name. In the new version of the program, the extension *\*.foc* will automatically be appended.

o Trigger visualization:

- Previously, when the option “Display/Show Internal Trigger Names Instead of Codes” was selected and trigger name was empty, the trigger label was not visible (only the trigger symbol was shown). Now if the trigger label is missing, the trigger code is displayed.

o ICA and pattern search:

- ICA decomposition and pattern search are now possible even if less than 12 electrodes are available.

### **Source analysis:**

o 3D display and volume imaging:

- In 3D visualizations of brain anatomy, a glass brain display can now be toggled to be shown or hidden on top of the sliced MRI image, using a new toolbar button in the 3D window. The amount of transparency of the glass brain can be changed on the fly using *Shift + UP / DOWN* arrow keys. The glass brain view can also be adapted in the 3D window options dialog.

- When starting an iterative volume image (CLARA; sSLOFO) without a fit region or a cursor, the cursor is now set automatically at the latency of maximum variance.

o Source waveform display:

- The number of displayed source waveforms is now user-controlled. The maximum number of displayed source waveforms can be adjusted in the Display tab of the Preferences dialog (accessible via the “Options/Preferences” menu entry). If the solution contains more source waveforms than the defined value, a scrollbar is shown to scroll through the waveforms.

### **Bug fixes**

#### **Data review and pre-processing:**

o File readers:

- Micromed (from version 4 file format): It was possible that a wrong channel configuration was loaded from file resulting in duplicated channels and/or flat lines for intracranial EEG recordings. This bug was fixed (#894).

- MEG file formats: If a *\*.pos* file resided in the data folder together with an *\*.sfh* file and was used (the user selected *Yes* in the “Channel and digitized head surface point information” dialog) the MEG channels had wrong coordinates. The scenario could arise if a co-registration had been triggered, and subsequently the database entry for the file was deleted. In that case, the values in the “Channel and digitized head surface point information” dialog were reset. This issue was fixed (#924).

o Average buffers:

- An average buffer that was created in one data file can be displayed in another data file if electrodes match, which is useful for e.g. copying search templates from one file to another. However, no notification was provided to warn the user about the data origin. This is now fixed; also, it is not possible now to perform source analysis of average buffers which were copied over from different data files (#956).

o Review

- If several data files were open, with different marked blocks in them, then upon closing one of the data files it was possible that a block was marked in the wrong position in the remaining file(s). This issue was fixed (#889).

- BESA Research became unresponsive during processing of multiple files (#875) and during some long processing tasks (e.g. mean FFT computation) (#877). Both issues were fixed.

- If a trigger was deleted and then restored again using the “Clear Events” entry in the “Channel and digitized head surface point information” dialog, it was not updated in the Selected View dialog. This issue was fixed (#835).
- If pattern search was performed with a sub-group of channels, and the events were then exported to an .evt file, the wrong information about the search channel was exported. This issue was fixed (#896).
- The scaling of amplitudes in the review window was changed when the UP or DOWN arrow key was pressed in the DSA or Source Coherence window. This issue was fixed (#923).
- When the display interval was changed while a cursor and map was displayed, the cursor was removed but the map was left visible. This led to the issue that a subsequent printout showed a map for an unknown latency. Now the cursor is adjusted to the new display interval when possible; if the new interval does not contain the position, cursor and map are removed (#950).
- Changing electrode labels in section [Electrodes] in *BESA.ini* file had no effect. This issue was fixed (#925).
- o User-defined montages:
  - When defining a user montage containing both EEG and MEG channels, not all channels were displayed when switching between montages. This issue was fixed (#951).
  - When showing a sub-set of source montage channels and then changing orientation options, the application crashed. Now, changing the montage option for regional sources from "All traces" to another option or vice versa triggers display of all source channels (#191).
- o Filtering and artifact correction:
  - The polygraphic channel rectification was not working for unfiltered data. This issue was fixed (#670).
  - When polygraphic channels were rectified the amplitude value displayed in the status bar had the wrong signum (negative). This issue was fixed (#899).
  - When artifact topographies for one data set contained a mix of ICA-based and PCA-based artifact topographies, the PCA variance was not correctly reported (e.g. 99i instead of 99.34%). This issue was fixed (#904).
  - Surrogate Artifact parameters were not read from the *BESA.ini* file. Now they are read correctly (#890).
- o Batch processing and Combine Conditions:
  - In the previous program version, the default option was to leave data files open after the batch finished. This was unintended and was reverted to the default of closing data files after the batch (#874).
  - In certain scenarios it was possible to check “leave files in the file list open after running the batch” even when more than 50 files had been added to the file list. In BESA Research it is not possible to open more than 50 files at once, so some of the files were not opened in this situation. Now it is not possible to check this checkbox if there are more than 50 files in the file list (#871).
  - After averaging data by batch, the resulting average file was not correctly closed, causing problems if more data were to be appended to that file in the same session (#868).
  - Cortical Loreta settings were in some scenarios wrongly modified by the associated batch command. This issue was fixed (#174).
  - In the *Pause* batch command, if the text displayed contained a ‘%’, the subsequent text was replaced by the current file name. This issue was fixed (#851).
  - In the *GoTo* batch command, setting a cursor did not work if the “Relative” box was checked. This issue was fixed (#852).
  - The *Scale* batch command did not work correctly with MEG channels, and scaling values were not saved correctly after the batch ended. This issue was fixed (#855).
  - In the *Combine Conditions* script tab, *Load settings* and *Load previous settings* did not work. This issue was fixed (#893).
  - If several data files were open before starting the batch, then a different file became active in the Review window after closing the “Batch Processing” dialog. This issue was fixed (#916).

- o Head surface point view:

- When only a sub-set of channels was displayed in the review window, and an MEG channel was selected in the review window, then the wrong channel was highlighted in the head surface point view window. This issue was fixed (#326).

- When showing the sensor cloud (triggered by pressing the 'V' key in the Review window), an error "SceneLib Error Message" was sometimes shown. This issue was fixed (#917).

- o FFT:

- The settings in the dialog "Send to Matlab" were inconsistent with the settings in "File/Export FFT data". Also the state of the dialog was not correctly saved after changes. This issue was fixed (#876).

- o Mapping:

- In 2D maps the contour lines for negative voltage were black instead of blue. This issue was fixed (#898).

- o ERP:

- Using the ERP paradigm tabs could result in a change of filter settings in the review window. This issue was fixed (#939).

- o Top Viewer module:

- When concatenating several ASCII .avr files into .fsg files, and then starting the Top Viewer, the application could crash. This issue was fixed (#94).

### **Source analysis:**

- o SESAME:

- Computation of SESAME with MEG could lead to wrong results if the standard (spherical) MEG head model was used. This bug was fixed (#912).

- A too small voxel size (< 5 mm) set in the *Image settings* could lead to an error message or to a crash. Now, calculation of SESAME is prevented in this case (#942).

- o Realistic head models:

- When working with FEM or BEM models in combined MEG-EEG data sets, it could happen that the FEM or BEM table could no longer be loaded after switching to combined M/EEG and then back to EEG. This bug was fixed (#897).

- If two data sets with the same number of electrodes and the same electrode labels were used in source Analysis and both datasets were co-registered to the same MRI, but the data sets differed in electrode locations, the wrong FEM model could be applied. This issue was fixed (#906).

- o Volume imaging:

- The application could crash if the source sensitivity was computed after loading a source model. This issue was fixed (#909).

- In LORETA, LAURA, and sLORETA, a source image over the marked time interval did not show a simple mean source image, but the maximum value per voxel (MVV) in interval. This information is now provided directly in the image. Also, the user can now select either to display mean or MVV value in the *General* tab of *Image settings* (accessible by the *Image/Settings...* menu entry) (#708).

- Volume imaging with artifact-corrected data: The information that results can be distorted by the SSP projection was not provided clearly enough (only the text "ART" was displayed in the status bar). This was improved – a warning message is shown and a caption is visible in the image (#926).

- A wrong source image value was shown in a tooltip that appears when the mouse pointer was moved over the outside of head in the 3D window of the Source Analysis module. This issue was fixed (#935).

- The setting "Show crosshairs in 3D view" was not updated directly after pressing OK or Apply. It was updated after interaction with 3D window. Now it is updated immediately (#739).

- o Beamforming:

- When multiple conditions were used in Source Analysis and beamformer covariance matrices were available for more than one condition, wrong beamforming results could be shown after switching conditions. This issue was fixed (#953).
- When a new condition was defined in the ERP condition tab and used directly for beamformer computation, invalid time interval values could be used for its computation. This issue was fixed (#955).
- In the case that several conditions were defined, and the first condition had zero matches, this condition was not shown in the Average tab of the ERP paradigm dialog, which was intended. However, for the first valid condition that was shown, the beamformer could then not be computed. This issue was fixed (#907).
- After beamformer computation the BESA Research main window was put to the foreground instead of the Source Analysis window. This issue was fixed (#933).
- Computation of the time-domain beamformer could not be stopped when the “Averaging (calculating covariance matrices)” step was aborted by a user. This issue was fixed (#934).
- o DICS
- DICS computation using the current cross-hair position could be started even if the cross-hair was located outside of the head. This issue was fixed (#818).
- The application crashed after clicking the “Cancel” button in the DICS dialog and then adding a cursor. This issue was fixed (#941).
- o Other:
- A fit region was created after editing the condition label in the Channel Box of the Source Analysis window and then moving the mouse cursor. This behavior was not intended and was fixed (#928).

#### ***Connectivity and time-frequency module:***

- o Time-frequency computation:
- When a time-frequency decomposition was already computed for the Source Coherence module, and subsequently the artifact correction status of the data changed and the time-frequency display was re-opened, no re-computation was triggered – instead, the previous result was shown. This issue was fixed (#932).
- o Time-frequency beamformer and DICS:
- There was a possibility that wrong filter settings were applied during Beamformer/DICS calculation if the user changed filter settings while Time-Frequency calculation results were displayed, and then started the imaging from the time-frequency display without re-computing the time-frequency results. This issue was fixed (#940).

#### **Known issues**

The following known issue could not be fixed for this release, and remain in the software:

- o Nicolet-Nervus reader: When reading a data file that contains channels with varying sampling rates, this might lead to wrong interpretation of event times. (#318). Workaround: Use an acquisition mode with constant sampling rate across channels.

## **Version 7.1 March 2021**

### **Improvements**

#### ***Data review and pre-processing:***



- o Batch commands – The following new batch commands are available:
  - *FileClose*: close the currently open file.
  - *SaveBitmap*: this new batch command replaces *SAsaveBitmap*; allowing screenshots of the whole or specified sections, to be saved as *\*.bmp* files, of:
    - the main review window,
    - the map window,
    - the source analysis window and the 3D window of the source analysis window.
  - *SplineConstant*: set the spline constant used for mapping and channel interpolation.
  - *TriggerRecode*: recode a specified trigger number to another number.
  - *ViewSelected*: turn on or off Selected View.
  - *ViewChannelType*: emulates channel type pushbuttons; and allows to toggle between EEG and MEG.
  - *BatchWindowPosition*: determines location of Batch and Pause windows that are displayed during the batch runs.
- o Batch commands – The following batch commands were enhanced:
  - *GoTo*: added options 1) to draw a map at the selected cursor location; and 2) to go to a specified trigger.
  - *MarkBlock*: added an option to draw a map at a selected position relative to the marked block.
  - *Scale*: an option for auto-scaling was added. In addition, a multiplication factor for the auto-scaling can be applied.
  - *SearchAverageView*: an option was added to stop the search after a given number of matches was found.
  - *ViewAverageBuffer*: an option "Off" was added to turn off Average Buffer View.
  - *WindowPosition*: this command was extended to make positioning on the display more flexible and to allow for multiple displays. Also, Map defaults were added to the set of windows. Furthermore, a '-' can be entered to indicate unchanged coordinates in Custom mode.
- o Other batch improvements:
  - Enhancements to Batch List popup menu: increase and decrease indentation; and "Direct Edit" to edit the highlighted line.
  - The placeholder function in batches was extended by adding commands to set user-defined variables.
- o Data export:
  - When exporting data with the 'Current Montage' option to Besa binary or ASCII formats, the appendix '*\_avr*' or '*\_com*' was removed from channel labels for average reference or common reference montages. This facilitates reading the exported data files back into an EEG analysis software for further processing.
  - When exporting to the multiplexed data format (*\*.mul*), it is now possible to add compression steps. In this case, data are stored as integer, and the scaling factor is changed in the header.
  - When appending to an existing file: If the appended file has no defined start time, the start time is now defined as the time at the end of the previous file.
- o Source montages:
  - New source montages focused on specific brain regions were added. They are based on the 25r source montage with 25 regional sources covering the major cortical brain areas (cf. Scherg et al., Front. Neurol., 20 August 2019, <https://doi.org/10.3389/fneur.2019.00855>). The specific montages are in source montage sub-folder *25-regional*. They are:
    - 25F: frontal region
    - 25P: parietal region
    - 25T: temporal region
  - A new atlas-based source montage was added in the source montage sub-folder Atlas Montages:

- Desikan-Kiliany (two flavours: regional sources, and radially oriented dipoles)
- For all atlas-based source montages, regions in the cerebellum or other deep structures (e.g. amygdala, parahippocampus) were removed since signals from these regions are difficult to recover correctly in raw EEG data.
- o File opening: The filter for BESA file extensions was enhanced to show both \*.foc and \*.fsg files.
- o Adaptation of the positioning of info windows (e.g. Top Viewer window) is applied if a previously used screen arrangement is no longer available (e.g. moving from two-screen display to one-screen display).

### **Source analysis:**

- o The time-domain beamformer can now be used to compare two conditions. The target and control conditions can be selected in the dialog of the ERP module that initiates the beamformer calculation.
- o A single dipole fit can now be started directly using the Start Fit button, without having to place a dipole source first.
- o The Bayesian source imaging method SESAME is now available for all head models. Before, it was restricted to spherical models.
- o Beamformer and DICS can now be used with MEG finite element and boundary element models.
- o It is now possible to add noise sources to a solution, in order to generate source montages. They can be selected from several pre-defined source configurations, and only sources with a certain distance from existing sources will be added in order to describe brain activity that is unrelated to the activity of interest. The functionality is available from the *Solution* menu.
- o New batch command:
  - *LabelSource*: specify a label for a given source number.
- o Modified batch commands:
  - *AddSource*: a source configuration for adding noise sources can be specified.
  - *FitInterval*: if the fit interval defines only one point, set the cursor instead of a fit interval.
  - *SaveSolution*: enable saving a solution in MNI coordinates.
- o When exporting leadfields to MATLAB, the normalization factors for the source locations can now also be exported.
- o The fit region and cursor can now be moved using the mouse wheel even when the mouse pointer wheel is not located over the interval / cursor.
- o In cortical imaging methods, the number of nodes in the reduced mesh that is used for calculations can now be adjusted by the user. The default number can be modified in the Image Settings, in the *General* tab.

### **Bug fixes**

#### ***Data review and pre-processing:***

- o The program sometimes crashed during Search-Average-View or Search-Average-Write operations for pattern search. These issues were fixed (#776, #754, #734).
- o If a source montage was generated from oriented regional sources, the user could get the impression that the fitted orientations were used when in fact they were not (default orientations are used). This issue is fixed: The actual fitted orientations are indeed used (#802).
- o When marking a pattern using the cursor position, the pattern was sometimes not marked at the correct position. This issue was fixed (#771).

- o When data sampled with high sampling rate were displayed in a bipolar montage and no lowpass filter was set, it could happen that spikes were shown on the screen at random positions. This issue was fixed (#866).
- o Data reading:
  - Some CTF MEG files could not be opened in BESA Research. This issue was fixed (#602, #813).
  - Some XLTEK files only showed flat lines after reading. This issue was fixed (#793).
- o Data export:
  - When exporting data around trigger events, the program could hang if more than one trigger was defined at the same latency. This issue was fixed (#444).
  - When the user marked a part of an averaged segment, but not the whole segment, and exported this data block, the user expected the zero marker in the exported file to be that of the block, not that of the averaged segment in which the block was marked. The export behaviour was updated to reflect this (#761).
- o For MEG planar gradiometers (Neuromag Vectorview or MEGIN Triux), no 2D maps were displayed when defining an artifact topography. This issue was fixed (#861).
- o Atlas-based source montages for the Talairach atlas had some wrong coordinates and source labels.
- o Spectral analysis: When computing a mean FFT with artifact rejection, the artifact rejection interval was not accurate. This issue was fixed (#354).
- o ERP: If the artifact rejection interval defined in the Paradigm tab was very long (> 20 seconds), a crash could occur. This issue was fixed (#568).
- o Batch processing:
  - The *FileOpen* command could result in a crash if the file did not exist. This issue was fixed (#757).
  - Several issues with setting and clearing user-defined variables were fixed (#731, #752).
  - Concatenating several EEG files by batch could result in a program crash. This issue was fixed (#863).
  - The Cancel button did not work as expected in the dialog shown during batch processing. This issue was fixed (#780).
  - When the command *DefineArtifactTopography* was used twice during the same batch, the second topography was not defined correctly. This issue was fixed (#775).
- o Artifact correction:
  - When running a batch to define an artifact topography, and if that batch used an average buffer that was itself created using an already artifact-corrected data set, not the average buffer but the underlying raw data was erroneously used. This issue was fixed (#794)
  - When two or more different types of topography were used for artifact correction (e.g. eye blink and ECG), the virtual channels at the bottom of the display did not show the correct signal. This issue was fixed (#869).
- o Marking the whole average buffer block could mark one sample of the underlying raw data at the edge of the block. This issue was fixed (#810).
- o Starting BESA Research from another application (e.g. an EEG database) opened a new instance of BESA Research for each new data file, instead of opening the data file in the existing window of BESA Research. This issue was fixed (#714).
- o Paging through data with triple buffering on could lead to a crash if the displayed interval was larger than 60 seconds. This issue was fixed (#825).
- o The 64bit MATLAB interface could stay open after BESA Research was closed, using up CPU power. This issue was fixed (#833).

### **Source analysis:**

- o When working with individual head models of two different subjects simultaneously in the Source Analysis module, errors in localization could occur: If individual head models were calculated for at least two

patients; and a source analysis was done on the first patient with individual head model; then the Source Analysis module was **not** closed before the second patient was opened in the BESA Research software, data for the second patient was then loaded into the Source Analysis module, and the individual head model was selected for the second patient; then, the head model of the first patient was used for source localization, not that of the second patient. This issue was fixed (#824).

- o When an individual head model was computed in BESA MRI 3.0 by placing 10-10 electrodes, not using the \*.sfh file saved by BESA Research, but creating it independently in BESA MRI 3.0, and then computing the head model tables with this file, then using this head model could cause BESA Research to crash. Reason: 85 electrodes were used in the head model, but a different number of electrodes was recorded in the data file. This issue was fixed: the number of electrodes in the head model table and the data file needs to match in order to use the head model (#864).
- o When switching from a condition of a non-coregistered subject to another condition of a co-registered subject, wrong PCA components could be displayed. This issue was fixed (#839).
- o The program could crash when SESAME was computed using MEG data. This issue was fixed (#765).
- o Wrong confidence ellipsoid shown: When showing dipole fitting results in the individual anatomy with several sources, and then switching off one of the sources while the anatomy display was open, the confidence ellipsoids were then shown for the wrong sources. This issue was fixed (#805).

### **Connectivity:**

- o Orientations of beamformer virtual sources exported to BESA Connectivity were wrong. This issue was fixed (#803).
- o When starting BESA Connectivity with the original data recording montage, the exported electrode coordinates were wrongly defined. This issue was fixed (#850).
- o Time-frequency results in the Source Coherence module were not automatically re-computed if the montage was changed to a different montage with exactly the same channel labels. This issue was fixed (#720).
- o Source Coherence display: Source montage channels with labels containing underscore characters ('\_') were not always automatically sorted to the expected positions in the 2D TFC display. This issue was fixed (#721).

### **Known issues**

The following known issues could not be fixed for this release, and remain in the software:

- o During batch processing, files that were opened for writing are not always closed properly after the write process finishes, which means that they cannot be replaced by other data in the same session (#868).  
Workaround: Close and re-open BESA Research to complete file closing.
- o Data review of MEG data: When only showing a sub-set of channels using the channel sub-set dialog at the right side of the review window, and using the *Head Surface Points View* option for a 3D view of channels, if a user selects a channel label on the left, a wrong channel is highlighted in the 3D view. (#326).  
Workaround: Show all channels before opening the *Head Surface Points* view.
- o Nicolet-Nervus reader: When reading a data file that contains channels with varying sampling rates, this might lead to wrong interpretation of event times. (#318). Workaround: Use an acquisition mode with constant sampling rate across channels.
- o Coherence reader: Reading a Coherence data file that contains only intracranial channels may lead to a crash (#50).

- o Source imaging: Batch exporting source imaging data for all time points will only write all time points for the first data file; for subsequent data files, not all time points are written (#83). Workaround: Close Source Analysis module using the appropriate batch command after the export.
- o Export of FFT data: In the exported FFT file, a wrong data interval that was used for the FFT may be shown in the ASCII header (#176).
- o After concatenating BESA ASCII files to a common \*.fsg file, and subsequently starting the Top Viewer with that new file, BESA Research may crash (#94). Workaround: Work with the individual files.
- o When using an ICA montage and exporting this with option “*Epochs around triggers*” and “*Current montage*” to a multiplexed data file, in some scenarios BESA Research may crash (#537).
- o In the Movie dialog of the Source Analysis module, the video frame will not capture the correct frame if the Windows display scaling is not at 100% (#429). Workaround: Set windows scaling to 100% before video capture.
- o Rectifying a polygraphic channel does not work if data are unfiltered, unless the user selects the check box “*Unfiltered*” in the respective dialog box (menu *Filter / Polygraphic channels*). (#670). Workaround: Select the abovementioned check box.
- o Export to EDF format: If the ‘Current montage’ option is selected and no high pass filter and also no baseline correction is set, then the exported file can occasionally display jumps in channel amplitude (#755). Workaround: apply high pass filter before export.

Version 7.1 September 2020

## **New features**

### ***Data review and pre-processing:***

o Atlas-based source montages: Pre-computed atlas-based source montages are now available from the menu entry “*Montage / Source / Atlas montages*” as well as under the “Src” button in the control ribbon. The following atlases are supported for this feature:

- AAL (Automated Anatomical Labeling)
- AAL\_2015 (Automated Anatomical Labeling revision 2015)
- Brainnetome
- Brodmann
- Talairach

### ***Source analysis:***

o Boundary element model (BEM) integration: Boundary element head models for individual subjects computed in BESA MRI version 3.0 or higher are automatically loaded in the Source Analysis module, for EEG and / or MEG. They can be selected from the model selection dropdown. Finite element models (FEMs) and boundary element models for a subject can be loaded at the same time, so that it is possible to toggle between FEM and BEM model type and compare results.

o Combined MEG-EEG source modelling: Combining MEG and EEG for source imaging is now possible. Discrete source fitting as well as all distributed source imaging methods can use the combined model. Simply use the EEG / MEG / MEEG toggle button in the Source Analysis window to switch between the modalities. In case of MEG data with combined magnetometers and gradiometers, the user can also toggle whether one or both MEG channel types are combined with the EEG.

- Note that if individual head models are used, the same model type (BEM or FEM) needs to be selected for both EEG and MEG.

- Also note that the baseline interval needs to be well defined since MEG and EEG signals are noise-normalized for combining the modalities. The baseline interval can be adjusted by clicking on the baseline indicator bar at the top left of the Source Analysis window.

o MRI display in multi-slice view: The subject's MRI with overlay of source images, dipole solutions, atlases, can now be shown in multi-slice view. To invoke this view, use the multiple-view-toggle toolbar icon in the 3D window. A highly interactive control set allows to adjust settings on the fly for optimum viewing – available from the settings (cogwheel) icon in the same toolbar.

o Use of noise covariance data from individual trials: The full noise covariance matrix from individual trials can now be used in computation of minimum norm estimates. To invoke this, first run a time-domain beamformer solution in order to load the covariance matrix into the Source Analysis module. Then, the setting “*Use full baseline covariance matrix*” in the Image Settings dialog is available and allows to toggle between using the full covariance matrix, and using the channel-wise approach on averaged data.

## Improvements

### **Data review and pre-processing:**

o View inverted data: Data can now be viewed with inverted polarity. The menu entry “*View / Show Negativity Up*” toggles which polarity is plotted upwards. The default setting is to plot negativity up. The setting is remembered by the program.

o Parallel computing is now used for several tasks, e.g.:

- Remontaging and artifact correction

- fMRI artifact correction

- ICA

- SESAME

By default, it is active. It can be switched off by adding an entry to the *besa.ini* file in section [Defaults]:  
ParallelComputing=Off

o New data readers are now available for the following file formats:

- XDF

- Neuroscan CURRY 8

o Marker events can now be converted to trigger events. This is especially useful when data are read in file formats that do not support triggers. The new functionality is available from “*ERP / Edit Triggers*”. The associated dialog has a new section for converting markers or other event types to triggers.

o A new batch processing command is now available:

- *ExportToBesaConnectivity*: Allows exporting data in the format required by BESA Connectivity. Exported data can then be loaded directly into BESA Connectivity.

o Keyboard shortcuts: It is now even easier to mark artifact epochs or other epochs during data review. Outside the average buffer view, the numeric keys 6, 7 and 8 have the following meaning:

- 6: Add a comment event at the current cursor position

- 7: If a block is marked, mark the whole block as an artifact. If a cursor is set, mark the beginning or the end of an artifact epoch

- 8: If a block is marked, mark the whole block as an epoch. If a cursor is set, mark the beginning or the end of an epoch

o Drawing of waveforms: Double buffering is now used by default for a smoother display of waveforms and channels during data review. By default, it is switched on. It can be switched off by adding an entry to the *besa.ini* file in section [Mapping]: UseDoubleBuffering=Off

- o Top Viewer: A color scheme with white background is now available, useful e.g. for publications. To load it, in the Top Viewer, select "Options / Preferences / Load Preferences" and browse to the folder <Users>/Public/Documents/BESA/Research\_7\_1/Scripts/ColorSchemes/.

### **Source analysis:**

- o Confidence limit calculation and display: For dipole solutions and oriented regional sources, confidence limits are now calculated, displayed, and stored. The last fit interval used for a source is relevant for computing the confidence limit. This interval is also stored with the solution. In case of multi-dipole solutions or solutions which include spatial components, the full source model is taken into account for computation. Confidence limits are written to solution files if the coordinate system for export is set to Talairach. For these solutions, an import and display of the solution in BESA MRI is possible (BESA MRI 3.0 or higher). The limit that is computed corresponds to the 95% confidence limit.

- Note: Confidence limit display in the MRI window is only active if an individual MRI was co-registered.

- Also note that the confidence limit computed requires a baseline interval that is well defined. The baseline interval can be adjusted by clicking on the baseline indicator bar at the top left of the Source Analysis window.

- Confidence limits depend on many factors including the number of active sources, the signal-to-noise ratio, and the fit interval. In particular, the confidence limit does not account for other errors, e.g. head model errors, co-registration errors, or influence of artifacts on the solution. They should be regarded as a guideline and serve as a lower limit to the confidence of the solution, not as an upper limit.

- o Warning in case of potential baseline interval problems: In case that the baseline interferes with the fit region, or that the global field power exceeds 50% of the maximum already in the baseline interval, the baseline interval bar is plotted in red, and a warning message appears at the bottom.

- o For dipole and regional source solutions, the last fit interval used for each source is now indicated by default in the source waveform display box.

- o SESAME was improved to enhance robustness, as well as speed of computation and convergence. The use of hyper-priors achieves all of these, and is described in a publication pre-print (<https://arxiv.org/abs/2006.04141>). Also, parallel computing is used.

- o Calculation of beamformer virtual sensor montages based on atlas regions: In order to compute a beamformer virtual sensor montage based on atlas regions, first calculate a beamformer image on your data. Then select "File / Open Solution" and browse to the program installation folder, and into the sub-folder "Montages / Source Montages". Select the required solution file with a "\_BF" suffix in the name. This will create a virtual sensor solution, which can be saved as a source montage using the menu entry "File / Save Source montage as...".

- o 3D window: The toolbar icon set was enhanced in order to introduce:

- multi-slice view (using the existing multiple view toggle icon)

- show or hide confidence regions (the new icon is a three-state toggle between full region view, edge view, and no view)

- easy access to settings (cogwheel icon)

- o 3D window: The mouse wheel can now be used to slice through the 2D MRI slices.

- o Two new brain atlases were added: Yeo7 and Yeo17

- o The current solution can be saved for BESA MRI. If an MRI data set is co-registered, selecting "File / Save solution for BESA MRI" will save the current solution to the BESA MRI project folder of this subject. Solutions can then be opened directly in BESA MRI (version 3.0 or higher).

- o Montreal Neurological Institute (MNI) coordinates can now be used in the Source Analysis window. The MNI-Talairach coordinate transform proposed by Lancaster et al. 2007 (Human Brain Mapping 28:1194–1205) is used. They can be shown:

- in the source coordinates box at the top right

- in atlas coordinate plots in the 3D window (toggle between Talairach and MNI using the atlas settings dialog of the 3D window)
- and in solution export
  - o Pre-defined color configurations are now available, e.g. for creating publication figures. They can be loaded using the menu "Options / Colors / Open color set" and then browsing to the folder <Users>/Public/Documents/BESA/Research\_7\_1/Scripts/ColorSchemes/.
  - o The default source imaging method is now CLARA. If no cursor or fit region is set, CLARA will automatically be computed for the time point with the highest global field power.
  - o New or updated batch processing commands:
    - *BeamformerTimeDomain*: allows computing the time-domain beamformer.
    - *Regularization*: now allows adjusting regularization options for the time-domain beamformer, too
    - *DisplayMRI*: was enhanced to enable slice viewing of MRI
    - *SESAME*: usage of hyper-priors and setting fixed number of iterations was added
    - *ChannelTypeForFit*: was enhanced to enable selecting several fit types together (simultaneous EEG-MEG fitting)
    - *SaveSolution*: now enables saving the solution in the folder of the currently co-registered MRI, for viewing the solution in BESA MRI. Also, the MNI coordinate system was added.

## Bugfixes

### General:

- o In batch processing, the *%basename%* placeholder did not work correctly if it was not at the beginning of the string to be created (#717).
- o In batch processing, the *%label%* variable which enabled storing segment names in result files automatically, did not work as expected (#679).
- o If the batch command Export contained commas in the path of the file name, trying to edit the command in the batch editor lead to a crash (#492).

### Data review and pre-processing:

- o Waveform display could lead to aliasing if no low pass filter was active, suggesting wrong frequency content in the data (#689). Now, any hidden frequency content is indicated by showing the maximum and minimum amplitude for each pixel in that case.
- o The setting in *besa.ini* file "*TriggerScan=Off*" that is available for some file formats had no effect – data were still scanned (#716)
- o In the time-frequency plot, the maximum frequency of the data block transformation was less than 50 Hz (#709).
- o ICA computation: If the Extended InfoMax ICA transformation was computed on a screen with more than 32000 samples (e.g. 40 seconds on the screen at 1000 Hz sampling rate), the program sometimes stopped responding (#620).
- o In data sets with digitized electrodes, the electrode thickness supplied by the user (distance of digitizer point from head surface) was not considered for computing the head radius (#722).
- o Setting the spline smoothing constant for mapping to a different value had no effect (#680).
- o If an artifact topography file was created for a data set, and then the data set including the settings file "*\*.fst*" but not including the topography file "*\*.atf*" was copied to a different location, then the program crashed when loading the file from the new location (#491).



- o When sending continuous data to MATLAB, in addition to the actual data, an additional data block was sent that contained only the last 20 seconds of the data (#697).

### **Source Analysis:**

- o The amplitudes of mean CLARA and mean sSLOFO images over time intervals were not displayed correctly (#691, #702).
- o Setting dipole orientation to "Fixed" had no effect if the regional source scan option was On (#713).
- o In the 3D window, the tooltip text for toolbar scaling icons had wrong information (#711).
- o After maximizing the 3D window, it could sometimes not be reverted to its standard position (#690).
- o The list of head models that was shown upon right-click on the channel type button was sometimes incorrect (#631).
- o Checking the option "Automatically reopen 3D window at new session" could lead to a crash when reopening the Source Analysis window (#712).
- o Loading individual MRI scalp segmentation data that contained holes due to insufficient surface reconstruction could lead to a crash (#98).
- o Sending leadfield data to MATLAB did not work (#683).

### **Connectivity:**

- o When exporting data with source montage channels to BESA Connectivity, the channel labels could sometimes not be read in BESA Connectivity (#681).
- o If Source Coherence was started with the option for a control condition, but no control condition was supplied, Source Coherence did not open (#490).

### **Known issues**

The following known issues could not be fixed for this release, and remain in the software:

- o Data review of MEG data: When only showing a sub-set of channels using the channel sub-set dialog at the right side of the review window, and using the *Head Surface Points View* option for a 3D view of channels, if the user selects a channel label on the left, a wrong channel is high-lighted in the 3D view. (#326).  
Workaround: Show all channels before opening the *Head Surface Points* view.
- o Spectral analysis: When computing a mean FFT with artifact rejection, the artifact rejection interval may not be accurate (#354). Workaround: Reject artifacts using the ERP artifact rejection tool.
- o Source Coherence display: If the time-frequency decomposition of the Source Coherence module was computed previously for a source montage, and the montage was then changed to a different source montage with the same channel names, only differing in regularization or head model usage, then pressing the "Start Time-Frequency Analysis" button does not trigger re-computation of the time-frequency spectrum (#720). Workaround: change something in the paradigm definition (e.g. in artifact scan) before pressing the button; this will trigger the re-computation.
- o Nicolet-Nervus reader: When reading a data file that contains channels with varying sampling rates, this might lead to wrong interpretation of event times. (#318). Workaround: Use an acquisition mode with constant sampling rate across channels.
- o Coherence reader: Reading a Coherence data file that contains only intracranial channels may lead to a crash (#50).

- o Source imaging: Batch exporting source imaging data for all time points will only write all time points for the first data file; for subsequent data files, not all time points are written (#83). Workaround: Close Source Analysis module using the appropriate batch command after the export.
- o Export of FFT data: In the exported FFT file, a wrong data interval that was used for the FFT may be shown in the ASCII header (#176).
- o After concatenating BESA ASCII files to a common “\*.fsg” file, and subsequently starting the Top Viewer with that new file, BESA Research may crash (#94). Workaround: Work with the individual files.
- o When using an ICA montage and exporting this with option “*Epochs around triggers*” and “*Current montage*” to a multiplexed data file, in some scenarios BESA Research may crash (#537).
- o In the Movie dialog of the Source Analysis module, the video frame will not capture the correct frame if the Windows display scaling is not at 100% (#429). Workaround: Set windows scaling to 100% before video capture.
- o ERP: If the artifact rejection interval defined in the Paradigm tab is very long (> 20 seconds), a crash may occur. (#568). Workaround: Shorten the artifact rejection interval.
- o Data reading: Some specific CTF MEG data files cannot be opened in BESA Research (#602).
- o Source Coherence display: Source montage channels with labels containing underscore characters (“\_”) may not be automatically sorted to the expected positions in the 2D TFC display (#721). Workaround: Manually sort the channels by dragging the upper left edge.
- o Rectifying a polygraphic channel does not work if data are unfiltered, unless the user selects the check box “*Unfiltered*” in the respective dialog box (menu *Filter / Polygraphic channels*). (#670). Workaround: Select the abovementioned check box.

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## Attachments

None.

[Template Change History](#)

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