

BESA Research 7.0 Update History

Version 7.0 June 2018

Improvements

- **Data review and pre-processing:**
 - The coordinate labeling system of choice can now be set during the installation: electrode labels either follow the 10-10 system, or the 10-5 system (which includes the 10-10 system as a sub-set). The former is recommended for clinical users, whereas the latter will be of interest for researchers with high-density electrode caps or nets. The choice can be changed at a later stage by an administrator, using the batch **DefaultECD.bat** in the program installation folder.
 - New or enhanced batch processing commands are now available:
 - *MarkBlock*: Now enables copying a marked block to an average buffer.
 - *MarkChannels*: This command enables marking one or more channels.
 - *SearchAverageView*: This command starts the Search-Average-View analysis path.
 - *TriggerTagDelete*: This command enables deleting triggers, tags, or markers.
 - *ViewAverageBuffer*: This command enables viewing a particular average buffer.
 - *GoTo*: Was enhanced to allow moving relative to the current display center.
 - *MaxInInterval*: This command enables finding the maximum absolute amplitude value in a specified channel within the marked block. A cursor, tag, or trigger can be set at that position.
 - *PolygraphicFilters*: This command allows for special filtering of polygraphic or additional channels.
 - *Scale*: This command changes the scaling of amplitudes and/or the displayed time interval.
 - *BatchError command*: A loop can now be left if an error occurs.
 - The Search-Average-View dialog was enhanced to include a signal-to-noise criterion, and to allow zeroing the baseline of the search template, or to use zero mean.
 - The default scaling of source montage channels can now be pre-set in the *besa.ini* file. In section [Defaults], a variable `SrcScale` can be specified.
 - A default source montage of choice can now be pre-set in the *besa.ini* file. For this purpose, the section [Montage] can be used. For details, see *Help / Special Topics*.
 - A new standard source montage 25s with 25 dipolar sources distributed over relevant brain regions facilitates the review of clinical data.
 - In the review of data with source montages containing regional sources, the automated orientation of sources to show the most prominent activity was improved.

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- In the pre-defined user montage AV25, the order of displayed channels was updated to be consistent with other pre-defined user montages (CA25 and the new source montage 25s).
- When invoking Selected View, the first trigger code is automatically selected in the dialog. Pressing the 'S' key on the keyboard will launch Selected View for this selection.
- When exporting data, patient identifiable information can now be anonymized using an additional check box in the Export dialog.
- Automated creation of paradigm files for data in the formats BrainVision and EGI was improved to enable trigger naming in cases where names contain blanks.
- **Source analysis:**
 - New batch processing command:
 - *SetElectrodeConfiguration*: This command allows switching between actual channel configuration and standard (interpolated) electrode configuration in the Source Analysis module.

Bugfixes

Data review and pre-processing:

- Exporting data with current filters on, or using the ICA decomposition, using BESA Research 7.0 March 2018, resulted in erroneous data.
- MEG source montages showed wrong waveforms in BESA Research 7.0 March 2018. This problem affected only MEG, not EEG, and did not affect source analysis results. However, it did affect pattern search when MEG source montages were on, and time-frequency or FFT estimates that worked on MEG source montages.
- Exporting data around triggers: If two triggers were at the same latency, the program could get hung up during export.
- Exporting several data files to simple binary or EDF format via batch commands could result in a program crash.
- The default coordinates for four EEG channel with labels in the 11/12 row (lowest row) had accidentally changed slightly in BESA Research 7.0 March 2018, with a small effect on topography calculation in cases where these electrode labels were defined, and no digitized coordinates were available. These labels were: FT11, FT12, SP1, SP2.
- In some installations, the *Public Documents* folder containing examples, batches, paradigms, and user montages, was not copied to the correct location during the installation process.
- Averaging of FFT data that had been saved in different files was sometimes not possible even though the channel configurations were the same in the different files.
- Artifact coefficient files could not be loaded when *elp* and *sfp* files were used at the same time.
- Artifact correction could change the signal of polygraphic channels if a common reference electrode was specified.
- If file settings were not available in the data base (e.g. after manually copying data folders to a different location), then the previous settings for the file (filters, montage) were not read correctly.
- Evoking a 3D map in Selected View, and switching back to standard EEG view without switching off the map could result in a program crash.

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- In batch processing for correcting fMRI artifacts, a realignment file could not be loaded if a short (relative) path was supplied by the user.
- In the dialog for fMRI artifact correction, a movement threshold that was too small (resulting in rejection of all epochs) could lead to a program crash.
- Using a *default.trig* file for aiding the trigger import from EGI files did not work anymore. Details about the procedure are provided in a dedicated document in the */Help* sub-folder of the installation.
- Reading EGI MFF files that did not contain triggers could result in a program crash.
- The CTF data reader showed wrongly scaled amplitudes for EEG channels (not for MEG channels).
- Reading Neuromag / Elekta *fif* files in batch mode could lead to a crash of the software.
- Reading *.pos* files for Neuromag / Elekta MEG data caused problems if bad channels were defined.
- The Neuromag / Elekta *fif* file reader could cause a program crash when scanning for triggers.

Source Analysis:

- The default settings for the SESAME method were not correctly applied until the user explicitly enforced it (i.e. noise and amplitude scaling values of 1.0 instead of 1.5 were used).
- When exporting a *.vmp* file in of the current source image BrainVoyager format, the wrong transformation was used.
- Image import of an external image file (e.g. of *.vmp* files) did not work in BESA Research 7.0 March 2018.
- When changing the head model after computing a source image, the old image was still shown even though it was no longer valid.
- The batch function *ImageImportfMRI* data did not work correctly.

Connectivity:

- Exporting epoched data for connectivity analysis could overwrite existing data in case that the same data file, the same montage, and the same condition was used as in a previous case.
- When exporting two conditions for connectivity analysis, and subsequently loading them in BESA Connectivity, automatic condition naming inserted the name of the 2nd condition as that of the 1st condition.
- Exporting source montage data to BESA Connectivity that contained regional sources, with the “All Traces” option on, wrote a wrong channel file, thus not showing the channels correctly in BESA Connectivity.

Known issues

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

- 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

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- channel is high-lighted in the 3D view. (#326). Workaround: Show all channels before opening the Head surface points view.
- Co-registration: If a digitized head surface points file exists, and a co-registration is performed to create a „*.sfh“ file, then subsequently the file is re-opened and only the „*.sfh“ file is used, the spatial transformation of sensor locations may become faulty (#161). Workaround: Use both digitized head surface points and „*.sfh“ file as is the default.
 - 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.
 - 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.
 - Coherence reader: Reading a Coherence data file that contains only intracranial channels may lead to a crash (#50).
 - Exporting data using the batch command „Export“ with the „between markers“ option ignores this option – instead, export works on the whole data set (#86). Workaround: Use the export from the File menu.
 - Source imaging: Repeatedly sending EEG-MEG source imaging data to Matlab (#151) may lead to a crash if a realistic head model is used for one of the modalities but not the other. Workaround: Close and re-open the Source Analysis module between sends.
 - 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.
 - 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).
 - 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.
 - When loading an EDF file containing trigger event information (e.g. after previous export from BESA Research), different event codes are shown (#481). Workaround: Export events separately from BESA Research, and load event file again after importing the EDF file.

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New features

- **Data review and pre-processing:**
 - Simultaneous EEG-fMRI data review: Correction of fMRI artifacts is now possible directly in the BESA Research review window. One of three methods can be selected, and the effects on the correction matrix directly visualized.
 - A new layout of the control ribbon in the review window enables direct access to the most important features and methods.
 - New batch processing commands are available for several new features including fMRI artefact correction, Bayesian source imaging, and brain atlas overlay.
 - A new ICA method (SOBI) was introduced.
 - New readers for the following data formats are available:
 - EEG: Neuroscan Curry version 7
 - EEG: Neuralynx
 - MEG: RICOH
- **Source analysis:**
 - Semi-Analytic Monte-Carlo Estimation (SESAME) of sources is a new automated localization method using Bayesian statistics that finds the most likely solution and displays the likelihood distribution as a volume image.
 - Time-domain beamforming was introduced using either multiple or single sources, which can be applied as vector or scalar beamformer; various options for calculating spatial filters and weights are available. Source waveforms can be reconstructed, and virtual sensors can be derived from the results; virtual sensor montages can be applied to raw data in further analyses.
 - Brain atlases are available. Several state-of-the-art atlases can be selected, and displayed in user-defined overlay modes. It is possible to combine brain atlas images with other source imaging results.
- **Brain connectivity / source coherence:**
 - The new BESA Connectivity program can be started directly from the Coherence dialog, for enhanced methods in time-frequency decomposition and brain connectivity analysis.
 - Single events or any data block can now be plotted in a time-frequency plot.

Improvements

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

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- Data recorded with the 10-5 electrode naming convention can now be read correctly in BESA Research without additional coordinate files.
- Source montages can now be fully displayed even if the montage contains more channels than the original data file.
- After running a batch, the previous settings for channel scaling and sub-selection of channel display will be restored.
- It is now possible to show the internal trigger names instead of trigger codes. This is preferable for some data formats, e.g. EGI, BrainVision, where trigger events do not necessarily have a numerical code when they are recorded. Note that trigger handling in the readers of EGI and BrainVision data files was changed recently, such that for these file formats, in pseudo-randomized sequences, unique trigger codes will now be assigned which are consistent across data files, enabling using one paradigm file to describe the whole experiment.
- When selecting a channel, the waveform of that channel will now be shown in bold print for easier identification of the waveform.
- In batch command creation, two new variables have become available: For batches, %label% in a file save command inserts the condition label, if a previous *MarkBlock* command has marked a condition. Use %LABEL% to also include the no. of averages as part of the label. The variable %t% in the Log command will insert the time in seconds since the start of the batch for the current file. %T% will insert the current time and date.
- Combining conditions is no longer limited to 50 files; there is no upper limit now.
- **Source analysis:**
 - NIFTI fMRI data files can now be imported.
 - fMRI statistical thresholds can now be applied to compute maps for display in the Source Analysis 3D window.
 - In Source Imaging, the cerebellum can now be removed from the source space to avoid the creation of “ghost sources”. The option is available in the Image Settings / General tab.
 - Exporting source waveform data with mixed source types: When exporting non-oriented regional sources along with oriented or dipole sources, waveforms may have different types if the user does not choose the correct export type (e.g. power for non-oriented, amplitudes for oriented). The user is now explicitly warned about this.
 - For the age-appropriate template head models, the default was changed to be consistent with other pre-computed head models: The order is now from older age to younger age.
- **Brain connectivity / source coherence:**
 - When starting beamformer imaging, a warning message is now shown if too few time-frequency samples for a good covariance matrix estimation were selected.

Bugfixes

The following bugs were fixed for this release:

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

- Source montages created from MEG FEM: Signals from regional sources were not displayed correctly. Now, the strongest components for the strongest two orientations of each regional source are automatically shown, as for other MEG head models.
- In the “Create Triggers from EMG” dialog, channel labels in the “Trigger Channels” box could not be identified due to the small size of the box. This is now fixed.
- Various problems with defining artifact topographies in combined EEG-MEG files were fixed.
- Averaging of artifact-corrected data: Problems with data files that had a common reference electrode configuration without specifying the reference electrode, were fixed.
- Topography maps were not always correct if average buffers were overplotted over the raw data. This issue was fixed.
- Exporting several average buffers to one BESA ASCII file (extension “.avr”) did not work correctly. This is now fixed.
- Co-registration of data files with existing surface point file where bad channels sometimes issued an error message and could not be completed. This is now fixed.
- In batch processing, artifact topographies associated with data files were not always loaded. This is now fixed.
- When sending several data segments to Matlab, the data structure in Matlab contained the first data segment twice. This is now fixed.
- After exporting standard deviations and then changing to a data file without standard deviation information, it was possible that the setting for exporting standard deviation could not be switched off in the next export. This is now fixed.
- The “Check for updates” function could lead to a crash if no internet connection was available. This issue was fixed.

- **Source analysis**

- Some inconsistencies in the “Send to Matlab” dialog user interface were fixed.
- There was a problem with exporting Residual Variance and Global field power to Matlab using the Source Waveforms option, which is now fixed.
- An issue with exporting sSLOFO results using age-appropriate head models was fixed.
- When working with age-appropriate head models, it was not possible to add a source from a beamformer maximum at the surface of the brain. This is now fixed.
- Using a batch for sending cortical CLARA results to Matlab sometimes created an error message. This is now fixed.
- With certain Windows font sizes, not all graphical user interface elements were visible in the Settings dialog. This is now fixed.

- **Source coherence**

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- When computing a time-frequency beamformer, in the presence of polygraphic channels, the data waveforms displayed in the Source Analysis window were incorrect (which did not affect the actual beamformer image, which was already correct). This is now fixed.
- If bad channels were defined, the reference channel for DICS could not be selected. This is now fixed.
- Export of time-frequency data did not show enough precision to show the correct frequency range if the option with spacing of 0.25 Hz was selected. This is now fixed.

• **General**

- Saving bitmaps from results windows (Source Analysis, Mapping, Source Coherence) did not work correctly. This is now fixed.

Known issues

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- 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.
- Source imaging: When the user first calculates volume images, and subsequently changes the head model, the grid of valid points in the brain is not re-computed. Thus, some points may be regarded as valid brain locations even though they are not, or vice versa (#379). Workaround: Assign the head model prior to computing the volume image. When changing the head model after a volume image computation, close and re-open the Source Analysis module.
- Co-registration: If a digitized head surface points file exists, and a co-registration is performed to create a „*.sfh“ file, then subsequently the file is re-opened and only the „*.sfh“ file is used, the spatial transformation of sensor locations may become faulty (#161). Workaround: Use both digitized head surface points and „*.sfh“ file as is the default.
- 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.
- 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.
- Coherence reader: Reading a Coherence data file that contains only intracranial channels may lead to a crash (#125).
- When reading a Biosemi data file where previously an artifact correction was performed, and the artifact coefficient file was saved under a different file name, this file may be

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- ignored upon re-reading, thus not performing the artifact correction (#123). Workaround: Re-name the artifact coefficient file such that it has the same base file name.
- Exporting data using the batch command „Export“ with the „between markers“ option ignores this option – instead, export works on the whole data set (#86). Workaround: Use the export from the File menu.
 - Source imaging: Repeatedly sending EEG-MEG source imaging data to Matlab (#151) may lead to a crash if a realistic head model is used for one of the modalities but not the other. Workaround: Close and re-open the Source Analysis module between sends.
 - 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.
 - The batch function *ImageImportfMRI* data does not work correctly (#383). Workaround: Import fMRI data using the menu option in Source Analysis module.
 - If file settings are not available in the data base (#e.g. when manually copying data folders to a different location), then the previous settings for the file (filters, montage) are not read correctly (#384). Workaround: Work with the files at the original folder locations.
 - 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).
 - 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.