

BESA Research 7.1 - Update History

Version 7.1 September 2020

New features

Data review and pre-processing:

- 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:

- 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.
- 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.
- 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.
- 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

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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:

- 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.
- 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

- New data readers are now available for the following file formats:
 - XDF
 - Neuroscan CURRY 8
- 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.
- 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.
- 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
- 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
- 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:

- 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.
- 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.
- 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.
- 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.
- 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...”.
- 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)
- 3D window: The mouse wheel can now be used to slice through the 2D MRI slices.
- Two new brain atlases were added: Yeo7 and Yeo17
- 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).

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- 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
- 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/`.
- 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.
- 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:

- In batch processing, the `%basename%` placeholder did not work correctly if it was not at the beginning of the string to be created (#717).
- In batch processing, the `%label%` variable which enabled storing segment names in result files automatically, did not work as expected (#679).
- 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:

- 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.
- The setting in `besa.ini` file “`TriggerScan=Off`” that is available for some file formats had no effect – data were still scanned (#716)

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- In the time-frequency plot, the maximum frequency of the data block transformation was less than 50 Hz (#709).
- 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).
- 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).
- Setting the spline smoothing constant for mapping to a different value had no effect (#680).
- 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).
- 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:

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

Connectivity:

- When exporting data with source montage channels to BESA Connectivity, the channel labels could sometimes not be read in BESA Connectivity (#681).
- 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:

- 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

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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.

- 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.
- 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.
- 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).
- 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 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).
- 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.
- 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.
- Data reading: Some specific CTF MEG data files cannot be opened in BESA Research (#602).
- 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.
- 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.