BESA Research 7.1 - Update History

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.

- 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.

- 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.

- 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.

- File opening: The filter for BESA file extensions was enhanced to show both *.foc and *.fsg files.

- 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:

- 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.

- A single dipole fit can now be started directly using the Start Fit button, without having to place a dipole source first.

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- 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).

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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.

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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

- 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.

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- 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).

- 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)

- 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).

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.

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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.