BESA MRI 3.0 - Update History

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○ Approved , Changed on: May 15th 2024 at 10:36:27 AM (UTC)

BESA MRI 3.0 - Update History

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BESA MRI 3.0 Release Notes

Version 3.0 May 2024

Prolonged the life cycle of BESA MRI.

Improvements

Included latest runtime environment for the BESA License Key.

Bugfixes

A typo (Transvere) appeared in the Slice View Settings (#710, BM-61). This typo was corrected (Transverse).

Known issues

The following known issues were not fixed for this release, and remain in the software.

- Segmentation
    - Automatic finalization of all unfinished segmentation projects does not work (#993, BR-68) if there is more than one unfinished project.
        - Workaround: Use automatic finalization of the current project, then proceed with the next one.
    - The "Set Orientation of T1 Data" workflow step is missing when modifying a completed segmentation project that previously contained this missing workflow step (#1073, BM-72).
        - Woraround: Start a new segmentation project and re-load the data.
- Coregistration
    - Disabling surface points from fitting: Additional surface points can only be disabled for the fit if their label starts with the text "SfcExtra_" (#695). Note that this issue does not affect electrodes.
        - Workaround: Before opening the *.sfh file that was stored by BESA Research at the start of the co-registration, edit the file manually with a text editor and change the labels of affected additional surface points.
    - An error occurs when changing channel weights after a manual fit correction (#990, BM-74).
        - Workaround: Re-start the co-registration workflow, then change channel weights before running the surface point fit.
    - BESA MRI crashes after starting BEM leadfield computation without an error message if BEM surfaces overlap each other (#1072, BM-71).
        - Workaround: In the Segmentation workflow, workflow step Set Markers, set the line for the cutting plane inferior to the nasion and most inferior brain points.

Previous Versions

Version 3.0 May 2020

New features

- *General*

  - *Head models: Subject-specific boundary element models (BEMs) can now be calculated with BESA MRI. These models can be used for source analysis in BESA Research (from version 7.1). It is possible to create BEMs for EEG and MEG data. The algorithm is provided by the OpenMEEG libraries (cf. https://openmeeg.github.io/). The BESA MRI implementation uses a three-shell model (brain, skull, and skin). If you use the BESA MRI BEM in publications, please cite the following references:*

    - *Gramfort A., Papadopoulo T., Olivi E., Clerc M. OpenMEEG: opensource software for quasistatic bioelectromagnetics. BioMedical Engineering OnLine 45:9, 2010*

    - *Kybic J., Clerc M., Abboud T., Faugeras O., Keriven R., Papadopoulo T. A common formalism for the integral formulations of the forward EEG problem. IEEE Transactions on Medical Imaging, 24:12-28, 2005*

- *Segmentation*

  - *Brain atlases: Several brain atlases can be displayed as overlay on the structural MRI data (Talairach-transformed). These include Brainnetome, AAL, Brodmann, AAL2025, Talairach, Yeo7, and Yeo17. Atlas overlays can be shown using different options. Talairach coordinates of the current crosshair position are shown, as well as the corresponding atlas region.*

  - *Visualization of dipole models: Dipole models exported from BESA Research can now be visualized on the structural MRI data (AC-PC and Talairach-transformed). If dipole solutions saved with BESA Research 7.1 or higher are opened, confidence limits can also be displayed.*

  - *Multi-slice view: The MRI, with or without overlay of atlas data or dipole solutions including confidence limits, can be viewed in a multi-slice view, with configurable orientation, range, and spacing between slices.*

  - *MEG sphere model visualization: The spherical model used for MEG can be visualized as overlay on the structural MRI data (AC-PC-transformed).*

- *Coregistration*

  - *Electrodes with standard labels following the 10-10 convention can now be placed on the reconstructed skin surface, without the need for digitization. This can be done in two ways:*

    - *either using an exported surface point file from BESA Research that contains only the electrodes used for the EEG recording,*

    - *or generating a surface point file from scratch in BESA MRI containing all 10-10 electrode labels, which can be read into BESA Research for an EEG recording, automatically using only the matching electrode labels.*

Improvements

- *Segmentation*
    - *DICOM data stored with lossless compression can now be read directly into BESA MRI.*
    - *The handling of the DICOM folder option was improved: it is now sufficient to select just the folder in the File Open Dialog.*
    - *The mouse wheel can now be used to slice through the MRI. This is particularly useful in work steps for identifying brain landmarks, and for reviewing segmentation results with overlay of atlas or dipole data*
    - *The MRI can now be viewed without inhomogeneity correction. This can be useful if certain landmarks, malformations, or anatomical structures are hi-lighted in the structural MRI data. The feature can be enabled or disabled by default using an entry in the BESA MRI.cfg file. For details, please consult the appendix of the User Manual.*
    - *When opening a data file, the "All Files" selector did not allow for Analyze, NIfTI, or vmr files. This is now possible.*
    - *The automatic scalp segmentation threshold for NIfTI data format was too low. This was improved.*
- *Coregistration*
    - *Surface points can be excluded from the fit using the right mouse button to exclude bad digitization points.*
    - *After completing the surface point fit, the projected position of electrodes on the skin can be displayed.*
    - *The MEG sensor array can be shown in relation to the head surface after the surface point fit.*

Bugfixes

- *Segmentation*
    - *When switching between Segmentation workflow and Coregistration workflow many times, an error sometimes occurred (#224). This was fixed.*
    - *If a data set is loaded that contains orientation information (DICOM), the work step Set Orientation is not required. If, however, a DICOM data set is loaded, then the user goes back in the workflow and changes the data set to a NIfTI file, the work step Set Orientation is required but was not shown in this case (#672). This problem was fixed – the work step will now appear even in this scenario.*
    - *When special characters appeared in the patient name imported from DICOM (e.g. Japanese characters), the project could not be saved (#213). This problem was fixed.*
- *Coregistration*
    - *If a head surface point file (*.sfh) written by BESA Research had special characters in the filename, it could not be read by BESA MRI (#229, #347). This is now possible.*
    - *When opening a previously finalized MEG FEM project, then changing something in the Fit Surface Points work step, this did not issue a re-calculation of the MEG FEM leadfields (#677), This problem was fixed.*
    - *If the user opened an input file that did not have fiducial information yet, then went back and changed the file to a data set that did have fiducial information, this information was not shown (#505). This problem was fixed – now the fiducials will be shown even in this scenario.*

Known issues

The following known issues were not fixed for this release, and remain in the software.

- *Segmentation*
    - *At time of release, no known issues remain in the software.*
- *Coregistration*
    - *Disabling surface points from fitting: Additional surface points can only be disabled for the fit if their label starts with the text "SfcExtra_" (#695). Note that this issue does not affect electrodes.*
        - *Workaround: Before opening the *.sfh file that was stored by BESA Research at the start of the co-registration, edit the file manually with a text editor and change the labels of affected additional surface points.*

Version 2.0 January 2017

- *General*
    - *Inside the European Union and in countries that recognize the CE certification for medical devices, results obtained with BESA MRI 2.0 January 2017 can be used for limited diagnostic purposes when BESA MRI is combined with the application BESA Research for the analysis of epileptiform activity. Diagnostic use is restricted to applications detailed in the Intended Use documents of BESA MRI and BESA Research, and to a group of users detailed in the Intended User documents of the respective applications. These documents need to be consulted together with the other safety instructions before any such use.*
    - *The About box was changed to clarify the usage restrictions of BESA MRI.*
- *Co-registration*
    - *With the upcoming April patch release of BESA Research 6.1, BESA MRI will be capable to auto-select the correct subject for the co-registration workflow, provided that name, first name, and date of birth were entered at the stage of both MRI and EEG/MEG recording. This will further facilitate a smooth user workflow with a minimization of scope for errors.*

Known issues

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

- *If holes appear in the scalp segmentation, this may lead to a crash in the BESA Research software after co-registration with this data set (#98). Workaround: Change the cutting plane for segmentation such that it covers the recorded MRI data.*
- *When special characters appear in the patient name imported from DICOM, the project can not be saved (#213). Workaround: Edit the patient name after import of DICOM and replace special characters with alphanumeric characters.*
- *When special characters appear in the file name of the *.sfh file written by BESA Research, the file cannot be opened by BESA MRI (#229). Workaround: Change the file name to replace special characters with alphanumeric characters.*
- *When switching many times between segmentation and co-registration workflow, an error may occur (#224). Workaround: Re-start BESA MRI from time to time.*

Version 2.0 March 2016

- *Segmentation*
  - *The cortex segmentation was enhanced in order to include cortex inflation as an optional additional feature. If an MRI with cortex inflation is co-registered with a sensor cloud, the inflated cortex is automatically available in the BESA Research Source Analysis window for the visualization of cortical methods like Cortical CLARA, Cortical Loreta, or Minimum Norm estimate (BESA Research version 6.1 and higher).*
  - *Problems with loading T2-weighted data sets in Analyze/NIFTI format in a combined T1- and T2-project were solved.*
  - *The subject naming and anonymization workflow was improved for data sets with T1 and T2-weighted MRI scans.*
- *Co-registration*
  - *An issue when turning "Optimize Scales during fit" off in the Advanced Settings after it had been used in a previous fit was solved.*
  - *For MEG data, turning off "Optimize Scales during fit" in the Advanced Settings could result in erroneous lead field tables. This is now fixed.*

Version 2.0 August 2014

- *FEM*
  - *The FEM model can now be generated for MEG sensors of all commercially available systems.*
- *Co-registration*
  - *The handling of head surface point files was improved. Export of *.sfh files, and copying of BESA MRI projects to different folders is now possible without loss of any previous results.*
- *Reader*
  - *The DICOM reader was improved and can now handle the situation where DICOM files for one scan are spread over several sub-folders.*
  - *The import functionality for Analyze data formats was improved and now also handles files with 12 bits per pixel correctly.*

Version 2.0 November 2013

- *FEM*
  - *Source space calculation is now optimized so that sources are restricted to positions where the leadfield can be most accurately computed.*
  - *It is now possible to manually adjust conductivity values for scalp, skull, brain and CSF.*
  - *A new smoothing parameter was introduced for scalp segmentation to improve handling of MRI scanner artifacts.*

- *Reader*
  - *The DICOM reader was improved so that individual scans can be selected based on the scan's metadata (subject name, series description, etc.) instead of using the filename of a slice belonging to the scan.*
- *Other*
  - *The use of internal memory was improved for segmentation and leadfield calculation.*

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Change History (valid revision number)

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1	Wed, May 15, 2024, 10:36:27 AM	>> *Action: approve, MK, Approval: QM Approval (State: QM Approval, Wed, May 15, 2024, 10:36:27 AM)	None

Attachments

Attachment	Description
N/A	N/A

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