BESA Research 7.1 - Getting Started

September 2020

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The MATLAB Interface of BESA Research

BESA Research 7.1 features a direct interface to MATLAB. During program installation, you will be asked which MATLAB version is installed on your computer, so that the interface gets configured correctly.
**Note:** For MATLAB versions 2009b and higher, you may need to modify your PATH environment variable on your computer. A detailed instruction is given in the BESA Research program help
(**Help / Help Topics / Chapter MATLAB Configuration**), or on the BESA Wiki page (call up
http://wiki.besa.de and search for "*How do I configure the Matlab interface*").

More information on the MATLAB interface and its features is provided by the following resources:
- **BESA Research program help** chapter MATLAB contains information on how the MATLAB interface works, how it can be configured, and what kind of data can be exchanged.
- The website **http://www.besa.de** provides sample MATLAB scripts and more information on toolboxes that can utilize the MATLAB interface of BESA Research.
- The BESA Wiki (**http://wiki.besa.de**) provides information about several aspects of the Matlab interface.

Program Modules and Feature Overview

BESA Research is distributed in several different module configurations. The figures below illustrate these for the configurations Basic, Standard, and Complete, with the optional MEG module.
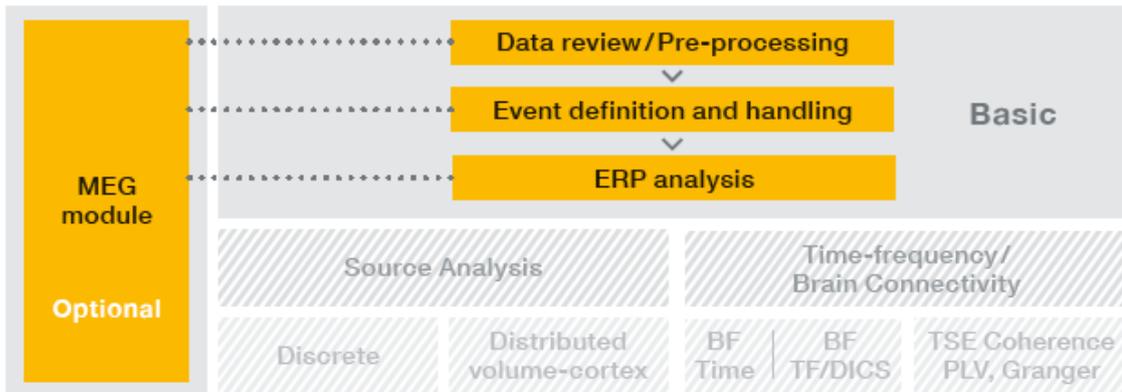
Basic: Includes tools for: Data review, Pre-processing, Mapping; Artifact/Event handling, Spectral analysis; ERP analysis
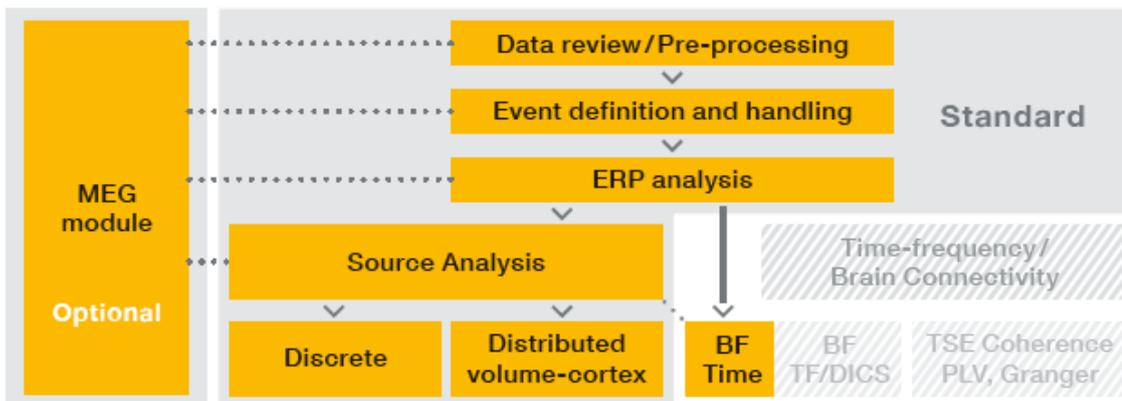
Standard: Additional tools for: Discrete source analysis (dipoles, regional sources); Distributed source imaging (volume and cortex), Beamformer (BF), Bayesian source imaging, EEG-fMRI, Brain Connectivity
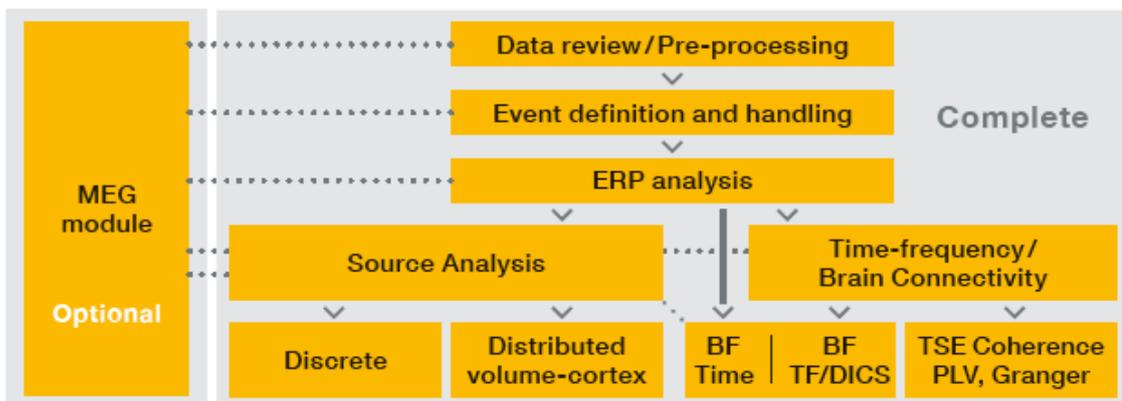
Complete: More tools for: Time-frequency analysis, TSE, ITPL; Coherence, PLV, Granger causality, PDC, DTF; Beamformer (BF), DICS

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The BESA Research Folder Structure

BESA Research generates the following default directories on your computer:

- The **installation folder** contains the executable programs of BESA Research. By default, the **BESA\Research_7_1** subfolder of your default **Program Files (x86)** folder is used for the installation.
- **Example data, montages, scripts and the BESA Research initialization file BESA.ini** are located in the **BESA\Research_7_1** subfolder of the **Public Documents** folder. The default location of the Public Documents folder is:

  C:\Users\Public\Public Documents

You can change the above default locations by modifying the initialization file **BESA.ini**. Please refer to the BESA Research Help chapter in the program help (**Help / Help Topics / Chapter Special Topics / The initialization file: BESA.ini**).

Configuring BESA For Your Own Needs

Review: BESA Research 7.1 is available in the standard review layout, or in a layout optimized for clinical use, where pattern search and event review options are optimized for clinicians. To switch between these, use the menu entry **Options Open "Reset Settings" Dialog** and then select **Set Options for EEG Review** at the bottom of the dialog box.

Data file readers: BESA Research 7.1 supports a large amount of data formats. For some of them, additional readers need to be installed. Please refer to **https://www.besa.de/downloads/besa-research /** and browse to the sub-section **User Documentation** for a list of available data readers.

Hot keys: Many functions can be achieved by using the keyboard. In the review window, these hot keys are fixed. In Source Analysis and the Montage Editor, you can define your own hot keys. A list of common hot keys is provided in the Quick Reference section below.

Batches: For most analysis steps, batch commands are available. Pre-defined batches for typical analysis tasks are also provided, and can be assigned to function keys. To do this, press the **Shift** key and the function key of choice; then select the batch that will be run when you press that function key.
Run any batch by pressing the **BAT** push button in the review window, or define a batch by **Shift-click** on that button. The pre-configured assignments are listed in the Quick Reference section below.

Tutorials and Help

For an introduction on how to use BESA Research 7.1, please refer to the following sources:

- **BESA Wiki:** The BESA Wiki offers help on many aspects of BESA usage, from typical FAQs to recipes on how to achieve complex goals with BESA. Simply visit **wiki.besa.de** and type your question, or browse through the content.
- **YouTube channel:** The BESA GmbH YouTube channel on **https://www.youtube.com/c/BesaGmbH** holds short tutorial videos, workshop talks, webinars, and other informative material on how to use the BESA Research software.
- **BESA Program Help:** All features of BESA Research are described in the program help. It can be started from the menu item **Help / Help Topics**.
- **BESA Research Tutorials:** These tutorials provide hands-on step-by-step examples on specific types of data analysis. The tutorials use the BESA Research example data that is installed with the software. In addition to the material provided in this package, please also refer to our website
- **BESA Homepage (www.besa.de)**: In the **Tutorials** section, tutorial material is available as **.pdf** download.
- **BESA Research Support:** If you have any program-related questions that are not answered by the material mentioned above, please send us an email through our web-interface here: **https://www.besa.de/contact/support/form.php**.

You can request additional documents related to the instructions for use in printed paper form at no additional cost.

Quick Reference

Frequently Used Hotkeys

Review window	
Paging and navigation	
A	Turn on automatic paging
B / N	Page a half page back / forward
<space>	Page to next screen
<backspace>	Page a whole page back
<tab>	Go to next tag
Shift-<tab>	Go to previous tag
File I/O	
Ctrl-L	Load coordinate files
W	Write data (export data)
Event handling and viewing	
T	Tag an event (if cursor set)

Ctrl-D, <del>	Delete the current event (if cursor set)
S	Show the selected view
E	Toggle artifact correction on / off
1-5	Define tag # (if cursor set)
6	Define marker (if cursor or epoch set)
7	Define an artifact epoch (if epoch set) or start / end of artifact epoch (if cursor set)
8	Define an epoch (if epoch set) or start / end of epoch (if cursor set)
Data analysis and viewing	
Ctrl-E	Toggle artifact correction on / off
F	Calculate FFT spectrum of the marked data block
R	Run a batch on the current file
Ctrl-R	Run last-used batch on the current file
Shift-R	Open the batch editor
V	View coordinates of sensors
Shift-V	View coordinates of sensors including MEG

Batches

Batches and montages can be assigned to function keys.
Function keys **F2 – F8** can be used to store batches. Function keys **F9 – F12** can be used to store montages that are frequently used. The assignment is user-specific.
To set a batch, press **Shift + <Function key>**. A selector box opens from which the batch of choice can be selected.
For clinical use, batches and montages can be auto-set by using the option **Options Open "Reset Settings" Dialog**, and selecting **"Set Options for EEG Review"** in the dialog. In that case, function keys are assigned as follows:

Key	Set montage to	Set filter	Default block around cursor
F2	**BiHL** – bipolar mixed	HP: 0.53 Hz fw / TC 0.3 s	-250 ms : +150 ms
F3	**Av33** – average ref. a10	HP: 2 Hz zp – LP: 35 Hz zp	-250 ms : +150 ms
F4	no change in montage	HP: 4 Hz zp – LP: 30 Hz zp	-150 ms : +90 ms
F5	no change in montage	HP: 5 Hz fw – LP: 40 Hz zp	-250 ms : +150 ms
F6	Action: Convert tags to triggers 41-45 and average		
F7	Action: Fit sources to 1st spike onset & peak (Sp1)		
F8	**TR –Temporal Region**	HP: 3 Hz fw – LP: 20 Hz zp	-500 ms : +500 ms (for seizure analysis)

Montage function keys are then assigned as follows:

Key	Set montage to	Modify association by
F9	**Av33** – average ref. a10	pressing Shift + F9 to associate key with current montage
F10	**BiHL** – bipolar mixed	pressing Shift + F10 to associate key with current montage
F11	**TR – temporal sources**	pressing Shift + F11 to associate key with current montage
F12	**FR – frontal sources**	pressing Shift + F12 to associate key with current montage

Interaction with Other BESA Programs

BESA Research integrates with the other BESA Research programs BESA MRI, BESA Connectivity, and BESA Statistics for MRI co-registration and FEM/BEM, brain connectivity analysis, and statistical analysis. To start **MRI co-registration**, use the menu **File / MRI Coregistration** in the BESA Research main program. After co-registration, the MRI images and – if applicable – the BEM and / or FEM will automatically be available in BESA Research.

For **BESA Statistics**, use batch commands to automatically export data in the right format, whether source waveforms, volume images, signal or time-frequency data. If you work with sensor data or discrete sources, add one file that details the channel configuration to the data export folder (either using **File / Save Solution in Source Analysis, or File / Head Surface Points … / Save All Files in Head Coordinates**).

Start **BESA Connectivity** directly from the Coherence dialog, or use a batch command to export data for later use in BESA Connectivity.