BESA Statistics 2.1 - Update History

Documents are subject to workflows, and content shall only be used if the content is approved (indicated by a green ring-symbol)

⊙ Approved, Changed on: January 31st 2025 at 1:51:20 PM (UTC)

Release Notes 🔗

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BESA Statistics 2.1 Release Notes 🔗

Version 2.1 January 2025 🔗

Improvements

- Data import
    - Data that was written by Brain Vision Analyzer using *Generic Export* can now also be read when written with recent versions of the Brain Vision Analyzer software (BS-37).

Bugfixes

- Data import
    - Connectivity data that was exported with BESA Connectivity 2.x could not be imported if it was based on a Multitaper time-frequency transfom. This was fixed (BS-49).
- Data export
    - When exporting connectivity clusters after averaging over time, the frequency ranges of the clusters were not exported. This was fixed (BS-46).
- Data display

- In the Top Viewer, the plotted channel waveforms got too small if channels were very close together. This was fixed (BS-64).

Residual anomalies

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

- Data import
  - When starting an ANOVA workflow, proceeding to the Load Data workstep, and moving back to the previous workstep, the selection of number of conditions cannot be changed (BS-15). Workaround: Start a new workflow, then the number of conditions can be modified again.
  - When starting an ANCOVA workflow between subjects with covariate of no interest, the data order in covariates can currently not be changed (BS-10). Workaround: Ensure that data order of covariates matches the subjects for this scenario before starting BESA Statistics.
- Data display
  - If a previous project was finalized and a new project started, then in the Preliminary View the mask for significant epochs is not correctly shown in the right detail window and Top View (BS-52). Workaround: Re-start the program to start the new workflow.
  - When viewing Connectivity data, the display of the channel-to-channel connectivity matrix is transposed with respect to the display in BESA Connectivity. This is relevant only in case of evaluating directional methods, e.g. Granger Causality. E.g. in row 1, the second column shows connectivity from channel 2 to channel 1, whereas in BESA Connectivity this matrix element shows connectivity from channel 1 to channel 2. The label displayed in the detail window of BESA Statistics then needs to be interpreted in the following way: label "Ch1-Ch2" means "From Ch2 to Ch1" (BS-1).
- Statistics calculation
  - When working with time-frequency data transformed via wavelet or multitaper algorithms, the frequency range cannot be adjusted for calculating statistics (BS-39). Workaround: Select the desired range already when computing the time-frequency transform, or switch to complex demodulation for time-frequency transformation.

Previous Versions 🔗

Version 2.1 December 2020 🔗

General 🔗

BESA Statistics was re-classified according to guidelines of the European Medical Device Directive (MDR).
BESA Statistics 2.1 is not a medical device and can be used for research purposes only.

New features 🔗

In all workflows, the data type Connectivity can now be used. This enables direct import of results obtained by BESA Connectivity for group statistics on connectivity results in sensor space or source space.

For Image data, a configurable slice view is available that displays sequences in one of three available orthogonal orientation.

Improvements 🔗

Themes and user interaction:
The colour theme can be adjusted between BESA White and the previous BESA Standard.
Several new colour maps are available:
o For diverging data types (e.g. two-tailed t-tests): Standard, and Blue to Red.
o For sequential data types (e.g. F-tests): Standard, Rainbow, Viridis, and White to Red.
High DPI displays are supported, and the overall look and feel was modernized.
The data values are displayed on mouse-over in the detail windows.

In 2D data displays (time-frequency), the cursor can now be set by clicking into the detail windows or into the Top Viewer widgets.

Data import:

Time-frequency data stored by BESA Connectivity with wavelet analysis can now be read with the correct (logarithmic) frequency spacing.

Single-trial time-frequency data can now be read in the t-test workflow (*.tfcs data format). Note that the information about time interval and frequency interval used needs to be supplied by the user if it deviates from BESA Connectivity's defaults.

There is no upper limit on the number of data files imported into the workflow.

Data export:

Cluster summary results now also include:

o Project settings information

o The cluster threshold values to reach significance

o t-, F-, or r-value for each cluster

o channel, latency, frequency or coordinate of the cluster maximum as applicable for the data type

A new image export format is available (svg).

Screenshots and cluster summary results can now be copied to the clipboard using the right mouse popup menu.

Calculation:

The random number generator was improved.

Bugfixes ∅

Data import:

When loading an ANOVA project, a program crash could occur. This is fixed (#365, 660).

An error message occurred when total size of files to load exceeded approximately 650 Mbyte. This is fixed (#348).

Specifying identical image data for two conditions lead to a program crash. This is fixed (#241).

Workflows:

If an ANOVA workflow did not find a statistically significant cluster, it was not possible to finish the project. This is now possible (#665).

Re-scaling of the topographic plot did not work if a different project had previously been active. This is now fixed (#254).

The head scheme was shown for polygraphic or intracranial channels, insinuating that coordinates for these channels were in use. This is fixed (#246).

Data export:

Exported times for cluster start and end could be wrong if the time range was restricted. This is fixed (#261, #640).

Image export in time-frequency mode did not work correctly if the Time-frequency map was shown (#272).

Known issues

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

When starting an ANOVA workflow, proceeding to the Load Data workstep, and moving back to the previous workstep, the selection of number of conditions cannot be changed. Workaround: Start a new workflow, then the number of conditions can be modified again (#271).

When starting an ANCOVA workflow between subjects with covariate of no interest, the data order in covariates can currently not be changed. Workaround: Ensure that data order of covariates matches the subjects for this scenario (#259).

Page ID ∅

904527936

Change History (valid revision number) 🔗

Version	Effective Date	Approvals	Version Notes
1	Fri, Jan 31, 2025, 13:51:20 PM	>> *Action: approve, MK, Approval: Approved (State: Approval, Fri, Jan 31, 2025, 13:49:48 PM)	None