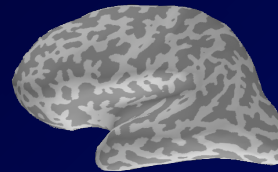


MNE software version 2.6

Matti Hämäläinen



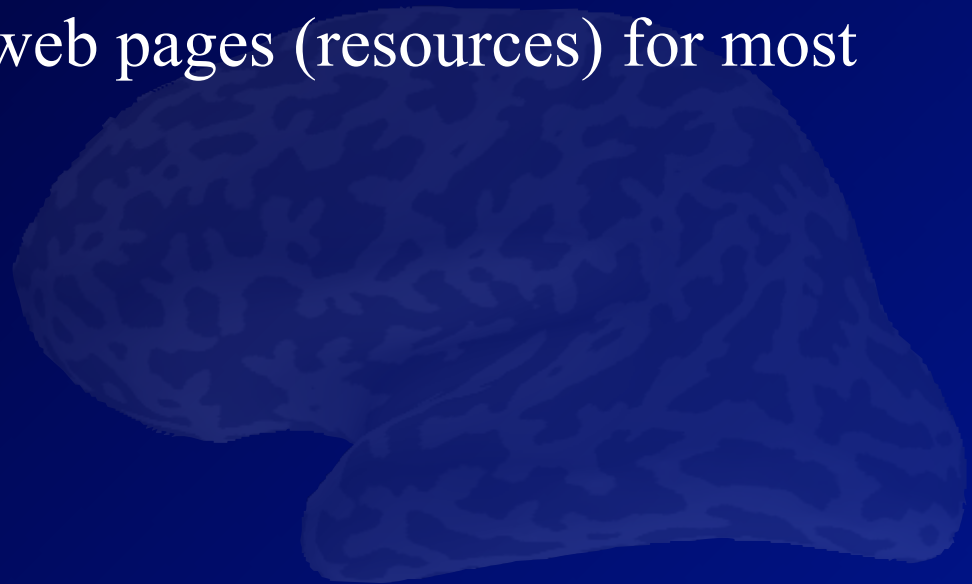
MGH/MIT/HMS Athinoula A. Martinos Center
for Biomedical Imaging

Charlestown, MA
USA



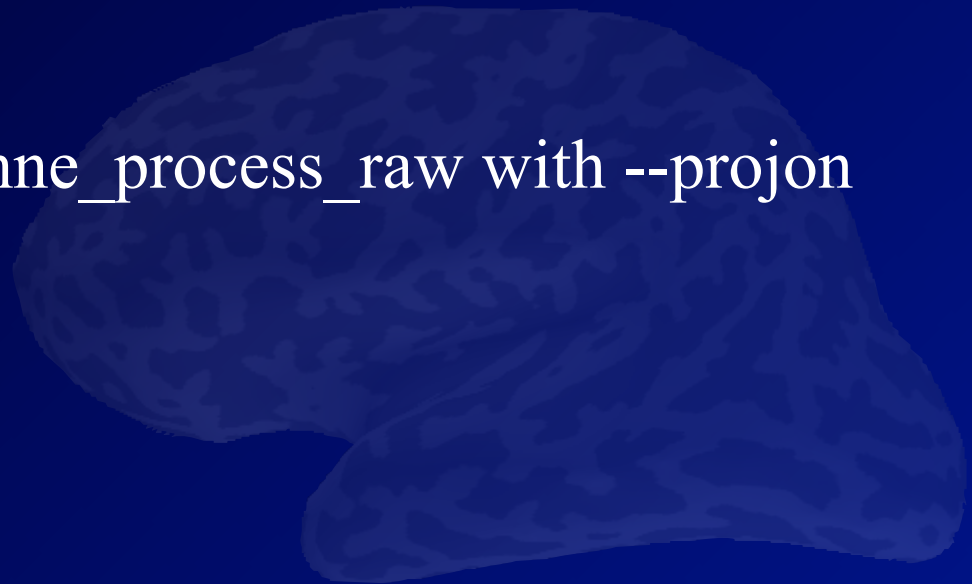
Overall changes

- Manual: description of the MEG/EEG and MRI coordinate systems (Chapter 5)
- Manual: (almost) all changes have been documented in appropriate sections, some reorganization of the manual
- Unrecognized command-line option result in an error: Check your scripts!
- Consult the MEG Core web pages (resources) for most up to date information



Removed obsolete utilities

- `mne_convert_dfs` (now in `mne_convert_surface`)
- `mne_surface2mat` (surfaces can be read directly using the Matlab toolbox)
- `mne_list_surface_nodes` (now in `mne_convert_surface`)
- `mne_dump_triggers` (use `mne_process_raw` with `--eventsout` option)
- `mne_mdip2stc`
- `mne_project_raw` (use `mne_process_raw` with `--projon` and `--save`)



New utilities

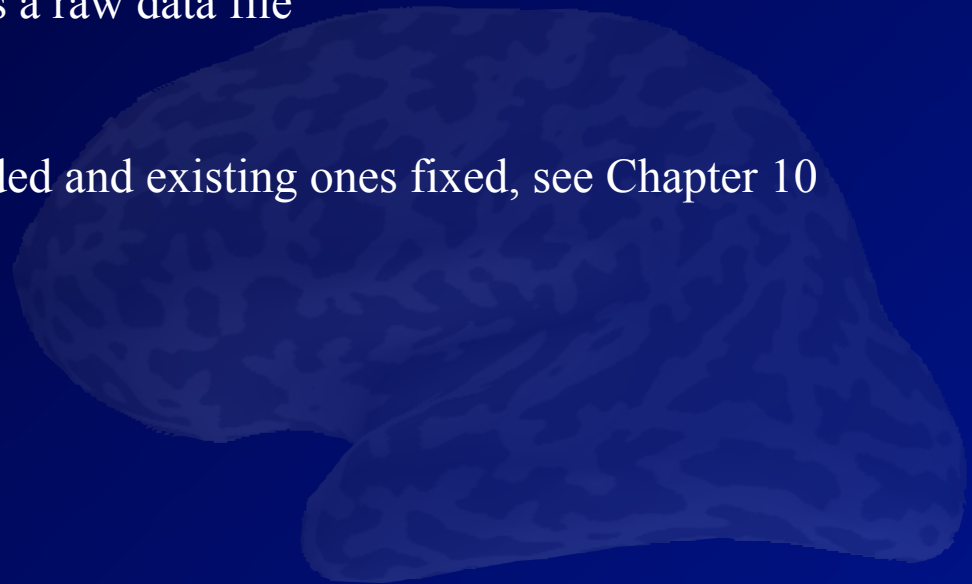
- `mne_convert_dig_data`
- EEG data converters:
 - `mne_edf2fiff`
 - `mne_brain_vision2fiff`
 - `mne_eximia2fiff`
- `mne_opengl_test`: Check the speed of your OpenGL rendering
- `mne_anonymize`: Remove subject information from data
- `mne_collect_transforms`: Put all coordinate transformations together
- `mne_volume_source_space`: volumetric and discrete
- `mne_volume_data2mri`: visualize volumetric data on MRI

Changes...

- `mne_add_patch_info`
 - Renamed options
 - Added `--labeldir`: produce labels for patches
- `mne_compute_raw_inverse`:
 - `--extra, --noextra`: Add desired additional channels to the output
 - `--split`: Split the output in pieces
 - `--labeldir, --out`: Compute one waveform per label
- `mne_convert_surface`: more surface file formats supported
- `mne_make_cor_set`:
 - If the input is `mgz`, MRI data are included in the `fif` file as well
 - Include Talairach transformation information in the output `fif` file
- `mne_make_source_space/mne_setup_source_space`:
 - `--spacing` option now works on the Mac platform as well

More changes...

- **mne_make_movie**
 - --pickrange: Produce a jpg, png, tif, or rgb file for each movie frame
- **mne_rename_channels**
 - Added the --revert option
- **mne_simu**
 - Added a scripting language for creating source waveforms
 - The output can be now saved as a raw data file
- **Matlab toolbox**
 - Several new functions were added and existing ones fixed, see Chapter 10



Changes in mne_browse_raw

- Stripchart display
 - The approximate wall-clock time is now shown on the status line
 - The mouse-wheel / trackball can be used to scroll in time and across selections
 - More keyboard shortcuts for browsing
- Events and annotations
 - The text event file format has changed slightly (read Section 4.10.5)
 - Events can be browsed from a list
 - User events can be annotated and are automatically saved
 - Real-time annotator is also available
 - In the batch mode, an event file per raw data file can be specified on the command line
- 2-GByte file size limit can be exceeded
 - Saved raw data files are automatically split in pieces if so desired

More changes in mne_browse_raw

- Derivations (linear combinations of channels)
 - Derivations can be now defined interactively
- Interactive definition of projections
 - ECG cancellation can be now defined easily
- Topographical displays
 - Additional items can be displayed (channel names, frames, zerolines, zerolevel)
 - Scale information included in the graphics output files
- Graphics output
 - Image file output improved (especially for Illustrator)
 - Annotations (time etc.) have been added
 - mne_browse_raw is now compatible with Neuromag cliplab software (drag and drop)
- Integration with mne_analyze
 - We will discuss this a little later...

Changes in mne_analyze

- Surface selection dialog was redesigned
 - Large number of subjects is not a problem any more
- Shortcut buttons were added to several file selection dialogs
- Image rotation with mouse wheel / trackball
- Integration with tkmedit
- Compatibility with cliplab
- FreeSurfer parcellation data can be loaded as labels
- Coordinates of a surface point can be displayed
- Single ECD fitting was added
- Dipole display in tkmedit or mrilab

Analysis pipeline

- `mne_browse_raw` and `mne_analyze` talk to each other
- Facilitates processing of clinical data:
 1. Identify interesting time from raw data (or use the annotated events)
 2. Corresponding current estimate and field/potential patterns are displayed in `mne_analyze`
 3. Current dipoles can be fitted in `mne_analyze`
 4. Display dipoles in `mnilab` or `tkmedit`

