

# Seder Tools

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# GENERALLY USEFUL TOOLS

- `seeder_setup`
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- `seeder_new_meg_raw`
- `seeder_new_mri_raw`
- `seeder_new_dataform`
- `seeder_name_dataforms`

# seder\_setup

- **USAGE:**
  - `seder_setup`
- **DESCRIPTION:**
  - Adds the SEDER tools to your path. Must be run **FIRST** before anything else from seder.
  - This is just an alias to a source file (like `nmrenv`)
- **NOTE:**
  - This one command must be **INSTALLED** on your account before you can use Seder.

# seeder\_new\_study

- **USAGE:**
  - seeder\_new\_study <study>
- **EXAMPLE:**
  - seeder\_new\_study epilepsy
- **DESCRIPTION:**
  - Adds this study to the study meta tree.

# seeder\_new\_subject

- **USAGE:**
  - seeder\_new\_subject <study> <lastname> <firstname>
- **EXAMPLE:**
  - seeder\_new\_subject epilepsy Smith Mary
- **DESCRIPTION:**
  - New subject ID is generated.
  - Subject is added to the subject meta tree
  - Subject is added to that study in the study meta tree.
  - Name <-> ID is stored in the secret master names list.

# seeder\_add\_subject\_to\_study

- **USAGE:**
  - seeder\_add\_subject\_to\_study <ID> <study>
- **EXAMPLE:**
  - seeder\_add\_subject\_to\_study nmr00382 epilepsy
- **DESCRIPTION:**
  - Adds the named subject to the named study in the study meta tree.

# seder\_new\_meg\_raw

- USAGE:

- `seder_new_meg_raw <ID> <megID> <yyyy> <mm> <dd> <study> <megraid #>`

- EXAMPLE:

- `seder_new_meg_raw nmr00383 clin_4942171 2003 09 28 epilepsy 8`

- DESCRIPTION:

- Adds the needed links and files for existing raw MEG data.

# seeder\_new\_mri\_raw

- USAGE:

- seeder\_new\_mri\_raw <NMR ID> <mri ID> <yyyy> <mm> <dd> <study>

- EXAMPLE:

- seeder\_new\_mri\_raw nmr00383 clin\_4942171 2003 09 28 epilepsy

- DESCRIPTION:

- Adds the needed links and files for existing raw MRI data.

# seeder\_new\_dataform

- **USAGE:**
  - seeder\_new\_dataform <ID> <study> <dataform>
- **EXAMPLE:**
  - seeder\_new\_dataform nmr00021 epilepsy dspm
- **DESCRIPTION:**
  - Sets up links and files **BEFORE** a new analysis is done.  
(Can be done after the fact, but requires some moving of files into the created directories)
- **NOTE:**
  - For meg\_raw: use seeder\_new\_meg\_raw

# seeder\_name\_dataforms

- **USAGE:**
  - seeder\_new\_dataform
- **DESCRIPTION:**
  - Will simply make a list for you of all the known dataforms so far. This way you can remind yourself of what they are called and how they are spelled etc.

# SPECIALIZED TOOLS

- `seder_collect_all_dipoles`
- `seder_database_builder`
- `seder_meta_recovery`

# seder\_collect\_all\_dipoles

- USAGE:
  - `seder_collect_all_dipoles`
- DESCRIPTION:
  - All `.bdip` files available in the current directory will be read, and collected into a single file, called *all\_runs.bdip*. If a file called *all\_runs.bdip* is already present, it is not read for the new collection. Therefore one can run this command repeatedly by accident without a problem.

# seeder\_database\_builder

- USAGE:

- `seeder_database_builder <ID file> <database file> <fields file> <output file>`

- EXAMPLE:

- `seeder_database_builder id_list.txt sphere.txt results.txt`

- DESCRIPTION:

- ID file and fields file: text files with one item per line. ID has a list of subject IDs, and fields has a list of database fields.

- database file is one of these: *clinical\_info.txt*, *contact.txt*, *NMR\_findings.txt* or *sphere.txt*

# seeder\_meta\_recovery

- **USAGE:**
  - seeder\_meta\_recovery
- **DESCRIPTION:**
  - This command is **ONLY** for administrators.
  - If the subject meta tree and the study meta tree have been totally lost, using the file called "seeder\_drives\_file.txt", this program will attempt to reconstruct the entire set of folders and links.
  - If a subject is linked to multiple studies, only the original study link can be reconstructed.