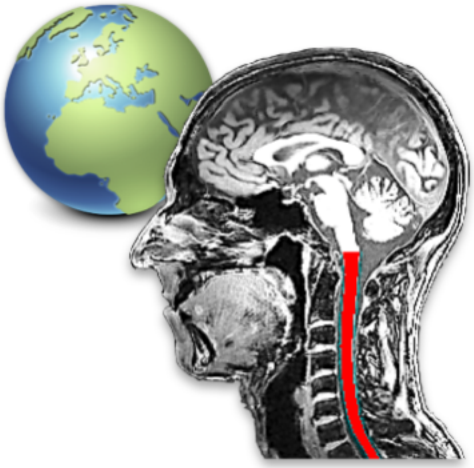
spine-generic Documentation

Julien Cohen-Adad

Dec 03, 2020

Table of contents



Quantitative spinal cord MRI is fraught with a number of challenges, among which is the lack of standardized imaging protocols. Here we present quantitative MRI protocols (which, collectively, we refer to as the “spine generic protocol”) for the three main MRI vendors (GE, Philips and Siemens), that provide valuable metrics for assessing spinal cord macrostructural and microstructural integrity: T1w and T2w imaging for SC cross-sectional area (CSA) computation, multi-echo gradient echo for gray matter CSA, as well as magnetization transfer and diffusion weighted imaging for assessing white matter microstructure. The spine generic protocol was used in a single-subject reproducibility study across 19+ centers (spanning all three vendors) and in multiple subjects across 42+ centers.

The protocols and datasets are open-access and the data analysis code is open-source. Full documentation, including a description of the processing pipeline with detailed text and video instructions can be found in this website.

CHAPTER 1

Data collection and organization

1.1 Imaging Protocol

The “Spine Generic” MRI acquisition protocol is available at this link. Each site was instructed to scan six healthy subjects (3 men, 3 women), aged between 20 and 40 y.o. Note: there was some flexibility in terms of number of participants and age range.

If your site is interested in contributing to the publicly-available database, please coordinate with Julien Cohen-Adad.

1.2 Multi-center data

In the context of this project, the following dataset have been acquired and are available as open-access:

- Multi-center, single-subject
- Multi-center, multi-subject

1.3 Data conversion: DICOM to BIDS

To facilitate the collection, sharing and processing of data, we use the BIDS standard. An example of the data structure for one center is shown below:

```
data-multi-subject
│
├── dataset_description.json
├── participants.json
├── participants.tsv
├── sub-ubc01
├── sub-ubc02
├── sub-ubc03
├── sub-ubc04
```

(continues on next page)

(continued from previous page)

```
├── sub-ubc05
├── sub-ubc06
│   │
│   ├── anat
│   │   ├── sub-ubc06_T1w.json
│   │   ├── sub-ubc06_T1w.nii.gz
│   │   ├── sub-ubc06_T2star.json
│   │   ├── sub-ubc06_T2star.nii.gz
│   │   ├── sub-ubc06_T2w.json
│   │   ├── sub-ubc06_T2w.nii.gz
│   │   ├── sub-ubc06_acq-MToff_MTS.json
│   │   ├── sub-ubc06_acq-MToff_MTS.nii.gz
│   │   ├── sub-ubc06_acq-MTon_MTS.json
│   │   ├── sub-ubc06_acq-MTon_MTS.nii.gz
│   │   ├── sub-ubc06_acq-T1w_MTS.json
│   │   └── sub-ubc06_acq-T1w_MTS.nii.gz
│   │
│   └── dwi
│       ├── sub-ubc06_dwi.bval
│       ├── sub-ubc06_dwi.bvec
│       ├── sub-ubc06_dwi.json
│       ├── sub-ubc06_dwi.nii.gz
│       ├── (sub-ubc06_acq-b0_dwi.json)
│       └── (sub-ubc06_acq-b0_dwi.nii.gz)
│
└── derivatives
    │
    └── labels
        └── sub-ubc06
            │
            ├── anat
            │   ├── sub-ubc06_T1w_RPI_r_seg-manual.nii.gz  <---------- manually-
↪corrected spinal cord segmentation
            │   ├── sub-ubc06_T1w_RPI_r_seg-manual.json  <------------ information␣
↪about origin of segmentation (see below)
            │   ├── sub-ubc06_T1w_RPI_r_labels-manual.nii.gz  <------- manual␣
↪vertebral labels
            │   ├── sub-ubc06_T1w_RPI_r_labels-manual.json
            │   ├── sub-ubc06_T2w_RPI_r_seg-manual.nii.gz  <---------- manually-
↪corrected spinal cord segmentation
            │   ├── sub-ubc06_T2w_RPI_r_seg-manual.json
            │   ├── sub-ubc06_acq-T1w_MTS_seg-manual.nii.gz  <-------- manually-
↪corrected spinal cord segmentation
            │   ├── sub-ubc06_acq-T1w_MTS_seg-manual.json
            │   ├── sub-ubc06_T2star_rms_gmseg-manual.nii.gz  <------- manually-
↪corrected gray matter segmentation
            │   └── sub-ubc06_T2star_rms_gmseg-manual.json
            │
            └── dwi
                ├── sub-ubc06_dwi_moco_dwi_mean_seg-manual.nii.gz  <-- manually-
↪corrected spinal cord segmentation
                └── sub-ubc06_dwi_moco_dwi_mean_seg-manual.json
```

To convert your DICOM data folder to the compatible BIDS structure, you need to install dcm2bids. Once installed, download this config file (click File>Save to save the file), then convert your Dicom folder using the following command (replace xx with your center and subject number):

```
dcm2bids -d PATH_TO_DICOM -p sub-ID_SITE -c config_spine.txt -o SITE_spineGeneric
```

For example:

```
dcm2bids -d /Users/julien/Desktop/DICOM_subj3 -p sub-milan03 -c ~/Desktop/config_
↪spine.txt -o milan_spineGeneric
```

A log file is generated under `tmp_dcm2bids/log/`. If you encounter any problem while running the script, please open an issue and upload the log file. We will offer support.

Once you have converted all subjects for the study, create the following files and add them to the data structure:

dataset_description.json (Pick the correct values depending on your system and environment)

```
{
    "Name": "Spinal Cord MRI Public Database",
    "BIDSVersion": "1.2.0",
    "InstitutionName": "Name of the institution",
    "Manufacturer": "YOUR_VENDOR",
    "ManufacturersModelName": "YOUR_MODEL",
    "ReceiveCoilName": "YOUR_COIL",
    "SoftwareVersion": "YOUR_SOFTWARE",
    "Researcher": "J. Doe, S. Wonder, J. Pass",
    "Notes": "Particular notes you might have. E.g.: We don't have the ZOOMit license,
↪ unf-prisma/sub-01 and unf-skyra/sub-03 is the same subject.
}
```

Example of possible values:

- **Manufacturer**: “Siemens”, “GE”, “Philips”
- **ManufacturersModelName**: “Prisma”, “Prisma-fit”, “Skyra”, “750w”, “Achieva”
- **ReceiveCoilName**: “64ch+spine”, “12ch+4ch neck”, “neurovascular”
- **SoftwareVersion**: “VE11C”, “DV26.0”, “R5.3”, . . .

participants.json (This file is generic, you don’t need to change anything there. Just create a new file with this content)

```
{
    "participant_id": {
        "LongName": "Participant ID",
        "Description": "Unique ID"
    },
    "sex": {
        "LongName": "Participant gender",
        "Description": "M or F"
    },
    "age": {
        "LongName": "Participant age",
        "Description": "yy"
    },
    "date_of_scan": {
        "LongName": "Date of scan",
        "Description": "yyyy-mm-dd"
    }
}
```

participants.tsv (Tab-separated values)

```
participant_id  sex age date_of_scan    institution_id  institution manufacturer   ␣
↪manufacturers_model_name    receive_coil_name    software_versions    researcher
sub-unf01   F   24  2018-12-07  unf Neuroimaging Functional Unit (UNF), CRIUGM,␣
↪Polytechnique Montreal  Siemens Prisma-fit  HeadNeck_64 syngo_MR_E11    J. Cohen-
↪Adad, A. Foias
sub-unf02   M   29  2018-12-07  unf Neuroimaging Functional Unit (UNF), CRIUGM,␣
↪Polytechnique Montreal  Siemens Prisma-fit  HeadNeck_64 syngo_MR_E11    J. Cohen-
↪Adad, A. Foias
sub-unf03   M   22  2018-12-07  unf Neuroimaging Functional Unit (UNF), CRIUGM,␣
↪Polytechnique Montreal  Siemens Prisma-fit  HeadNeck_64 syngo_MR_E11    J. Cohen-
↪Adad, A. Foias
sub-unf04   M   31  2018-12-07  unf Neuroimaging Functional Unit (UNF), CRIUGM,␣
↪Polytechnique Montreal  Siemens Prisma-fit  HeadNeck_64 syngo_MR_E11    J. Cohen-
↪Adad, A. Foias
sub-unf05   F   23  2019-01-11  unf Neuroimaging Functional Unit (UNF), CRIUGM,␣
↪Polytechnique Montreal  Siemens Prisma-fit  HeadNeck_64 syngo_MR_E11    J. Cohen-
↪Adad, A. Foias
sub-unf06   F   27  2019-01-11  unf Neuroimaging Functional Unit (UNF), CRIUGM,␣
↪Polytechnique Montreal  Siemens Prisma-fit  HeadNeck_64 syngo_MR_E11    J. Cohen-
↪Adad, A. Foias
```

Once you've created the BIDS dataset, remove any temp folders (e.g., `tmp_dcm2bids/`) and zip the entire folder. It is now ready for sharing! You could send it to Julien Cohen-Adad via any cloud-based method (Gdrive, Dropbox, etc.).

1.4 Checking acquisition parameters

To ensure the acquisition protocol was properly followed by each site, we implemented a parameter validator that verifies if the pulse sequence parameters match the required ones from the generic protocol (within a tolerance range). Basic parameters are checked, including: repetition time, echo time, flip angle. These parameters are read from the json sidecar file (generated by the DICOM to BIDS conversion). Note that BIDS file naming convention is also checked by the validator. If a parameter does not match, a warning message is triggered.

This validator is exposed in this command line interface (CLI) function: **sg_params_checker**. This function is run during continuous integration (CI), for each dataset, ensuring valid dataset throughout the life cycle of the project.

The json file containing the recommended acquisition parameters is located under */spinegeneric/cli/specs.json*.

Example usage and expected output:

```
sg_params_checker -path-in ~/data-single-subject/
WARNING: Incorrect FlipAngle: sub-douglas_T2w.nii.gz; FA=120 instead of 180
WARNING: Incorrect RepetitionTime: sub-mgh_T2w.nii.gz; TR=2 instead of 1.5
WARNING: Incorrect FlipAngle: sub-tokyoSigna1_T2star.nii.gz; FA=20 instead of 30
WARNING: Incorrect FlipAngle: sub-tokyoSigna2_T2star.nii.gz; FA=20 instead of 30
WARNING:sub-ucl_T2star.nii.gz Missing Manufacturer in json sidecar; Cannot check␣
↪parameters.
```

1.5 Ethics and anonymization

Each subject consented to be scanned and to have their anonymized data put in a publicly-available repository. To prove it, an email from each participant should be sent to the manager of the database (Julien Cohen-Adad). The email should state the following: "I am the subject who volunteered and I give you permission to release the scan freely to the public domain."

Anatomical scans where facial features are visible (T1w) could be "defaced" before being collected (at the discretion of the subject).

This can be done automatically using R or manually, in case the automatic defacing fails.

1.5.1 Automatic defacing with R

1. Install R, then open R (type "r" in the Terminal) and install the following dependencies:

```
install.packages("sessioninfo")
install.packages("remotes")
remotes::install_github("muschellij2/oro.nifti")  # answer "Yes" to "install from source?"
install.packages("fslr")
install.packages("argparser")
install.packages("devtools")
remotes::install_github("muschellij2/extrantsr")  # choose "1" when prompted
```

2. Download this repository and install Python's dependencies as instructed in *Getting started*.
3. Run:

```
sg_deface_using_r -i PATH_TO_BIDS_DATASET -o PATH_TO_DEFACED_BIDS_DATASET -f
sg_deface_using_r -i PATH_TO_BIDS_DATASET -o PATH_TO_DEFACED_BIDS_DATASET
```

4. To launch the QC report of the defacing across multiple subjects, run:

```
sg_qc_bids_deface
```

1.5.2 Manual Defacing

Automatic defacing might fail in some subjects, so this section explains how to deface manually. This procedure takes less than a minute per subject. Here we use FSLeyes but you can use any other NIfTI image editor.

Open FSLeyes and load the T1w scan. Go to **Tools > Edit mode**, Select the pencil with size 100, deface, then save.

Below is an example of a defaced subject:

1.6 Example of datasets

T1w - sub-vuiisAchieva02

T2w - sub-milan01

T2star - sub-brnoCeitec01

MTon_MTS - sub-barcelona04

MToff_MTS - sub-barcelona04

T1w_MTS - sub-barcelona04

DWI - sub-barcelona04

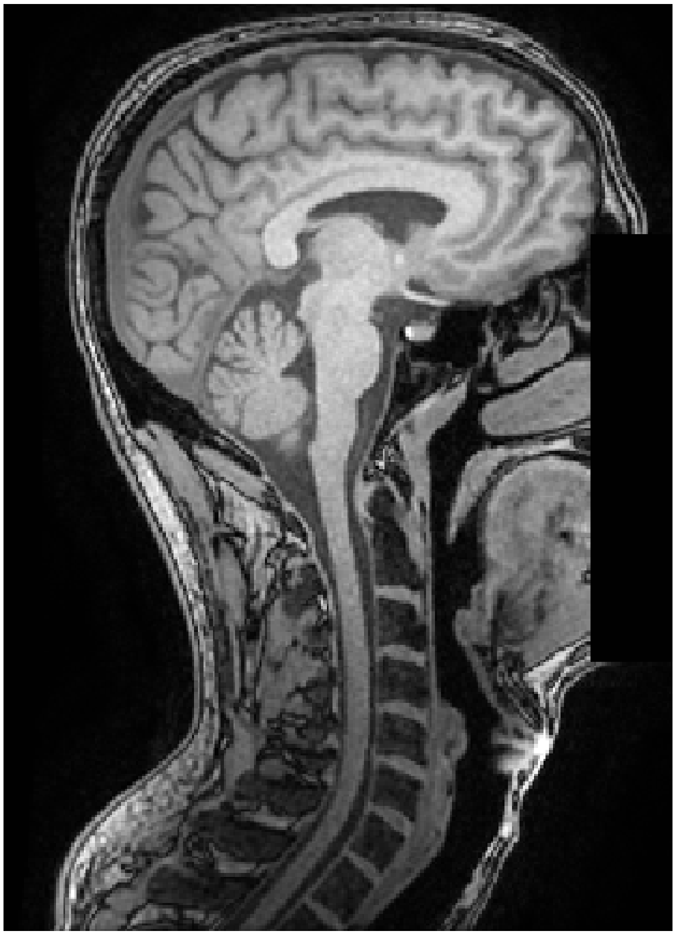


Fig. 1: Example of manual defacing.

CHAPTER 2

Analysis pipeline

This repository includes a collection of scripts to analyse BIDS-structured MRI data and output the following metrics for each contrast:

- **T1**: Spinal cord CSA averaged between C2 and C3.
- **T2**: Spinal cord CSA averaged between C2 and C3.
- **T2s**: Gray matter CSA averaged between C3 and C4.
- **DWI**: FA in WM averaged between C2 and C5.
- **MTS**: MTR in WM averaged between C2 and C5. Uses MTon_MTS and MToff_MTS.
- **MTS**: MTSat & T1 map in WM averaged between C2 and C5. Uses MTon_MTS, MToff_MTS and T1w_MTS.

2.1 Dependencies

MANDATORY:

- For processing: SCT 5.0.1.
- For generating figures: Python >= 3.7

OPTIONAL:

- FSLeyes for correcting segmentations.

2.2 Getting started

Download (or `git clone`) this repository:

```
git clone https://github.com/spine-generic/spine-generic.git
```

Install Python dependencies:

Note: If you prefer to preserve your default Python's libraries, you could first create a virtual environment, and then run the commands below.

```
cd spine-generic
pip install -e .
```

Create a folder where results will be generated (feel free to modify the destination).

```
mkdir ~/spineGeneric_results
```

Launch processing:

```
sct_run_batch -jobs -1 -path-data <PATH_DATA> -path-output ~/spineGeneric_results/␣
↪process_data.sh
```

Note: `<PATH_DATA>` points to a BIDS-compatible dataset. E.g., you could use one of the dataset listed in multi-center-data

2.3 Quality Control

After running the analysis, check your Quality Control (QC) report by opening the file `~/spineGeneric_results/qc/index.html`. Use the "Search" feature of the QC report to quickly jump to segmentations or labeling results.

2.3.1 Segmentation and vertebral labeling

If you spot segmentation or labeling issues, manually fix them using the procedure described below. Also see the video tutorial below.

- Create a .yml file that lists the data awating manual correction. You can create this file using any text editor (vim, nano, atom, etc.).
- In the QC report, enter the string "deepseg" to only display segmentation results or the string "vertebrae" to only display vertebral labeling.
- Review all spinal cord and gray matter segmentations and vertebral labeling. Use the keyboard shortcuts up/down arrow to switch between subjects and the left arrow to toggle overlay.
- If you spot *major* issues with the segmentation (e.g. noticeable leaking or under-segmentation that extends over several slices) or wrong labeling, add the image name into the yml file as in the example below:

```
FILES_SEG:
- sub-amu01_T1w_RPI_r.nii.gz
- sub-amu01_T2w_RPI_r.nii.gz
- sub-cardiff02_dwi_moco_dwi_mean.nii.gz
FILES_GMSEG:
- sub-amu01_T2star_rms.nii.gz
FILES_LABEL:
- sub-amu01_T1w_RPI_r.nii.gz
- sub-amu02_T1w_RPI_r.nii.gz
```

Some explanations about this yml file:

- `FILES_SEG`: Images associated with spinal cord segmentation
- `FILES_GMSEG`: Images associated with gray matter segmentation
- `FILES_LABEL`: Images associated with vertebral labeling

Hint: For the interest of time, you don't need to fix *all* slices of the segmentation but only the ones listed in the "Relevant levels" column of the table below.

Segmentation	Associated image	Relevant levels	Used for
sub-XX_T1w_RPI_r_seg.nii.gz	sub-XX_T1w_RPI_r.nii.gz	C2-C3	CSA
sub-XX_T2w_RPI_r_seg.nii.gz	sub-XX_T2w_RPI_r.nii.gz	C2-C3	CSA
sub-XX_T2star_rms_gmseg.nii.gz	sub-XX_T2star_rms.nii.gz	C3-C4	CSA
sub-XX_acq-T1w_MTS_seg.nii.gz	sub-XX_acq-T1w_MTS.nii.gz	C2-C5	Template registration
sub-XX_dwi_concat_crop_moco_dwi_mean_seg.nii.gz	sub-XX_dwi_concat_crop_moco_dwi_mean.nii.gz	C2-C5	Template registration

- After you finished the QC, run `sg_manual_correction` as in the example below:

```
sg_manual_correction -config files.yml -path-in ~/spineGeneric_results/results/data -
↪path-out <PATH_DATA>
```

This script will loop through all the files that need correction (as per the .yml file that you created earlier), and open an interactive window for you to either correct the segmentation, or perform manual labels. Each manually-corrected label is saved under the `derivatives/labels/` folder at the root of `<PATH_DATA>`, according to the BIDS convention. The manually-corrected label files have the suffix `-manual`.

Your name will be asked at the beginning, and will be recorded in the .json files that accompany the corrected labels.

2.3.2 Upload the manually-corrected files

A QC report of all the manual corrections will be created locally and archived as a zip file. To update the database with the manual corrections, follow this procedure:

- Commit and push the manually-corrected files, which should be placed in the appropriate folders under `derivatives/labels/`
- Create a pull request
- In the pull request body, briefly explain the purpose of these changes, and upload the zipped QC report so the admin team can easily review the proposed changes.
- If the team accepts the pull request, a new release of the dataset will be created and the zipped QC report will be uploaded as a release object.

Note: In case processing is ran on a remote cluster, it it convenient to generate a package of the files that need correction to be able to only copy these files locally, instead of copying the ~20GB of total processed files. If you are in this situation, use the script `package_for_correction`.

2.3.3 Re-run the analysis

After you have corrected all the necessary segmentations/labels, you can re-run the analysis (the `sct_run_batch` command above). If a manually-corrected file exists, it will be used instead of re-creating a new one automatically.

> **Warning:** If you re-run the analysis, make sure to output results in another folder (flag `-path-output`), otherwise the previous analysis will be overwritten.

2.4 Generate figures

Generate figures based on the output csv files using `sg_generate_figures.py` script. Run this script in `/results` folder (folder containing csv files) or specify this folder using `-path-results` flag. The flag `-exclude` points to a yml file containing the subjects to be excluded from the statistics. To generate html that contrains interactive figures, add the flag `-output-html` :

```
sg_generate_figures -path-results ~/spineGeneric_results/results -exclude subject_to_
↪exclude.yml
```

To generate a mosaic of images, run:

```
# Sagittal views of 3D T1w data
sg_create_mosaic -i *T1w_RPI_r_flatten.nii.gz -ifolder ~/project/results_multi_
↪20200907/data_processed/ -p sag -col 20 -row 13 -o fig_mosaic_T1w.png
# Axial views of GRE-T1w data
sg_create_mosaic -i *acq-T1w_MTS.nii.gz -ifolder ~/spineGeneric_results/data_
↪processed -s _seg -p ax -col 20 -row 13 -o fig_mosaic_GRE-T1w.png
```

2.5 Results

2.5.1 Cord CSA from T1w

2.5.2 Cord CSA from T2w

2.5.3 CSA agreement between T1w and T2w data

2.5.4 CSA agreement between T1w and T2w data per vendor

2.5.5 Gray matter CSA

2.5.6 Magnetization Transfer Ratio

2.5.7 Magnetization transfer saturation

2.5.8 T1

2.5.9 Fractional Anisotropy

2.5.10 Mean diffusivity

2.5.11 Radial diffusivity

CHAPTER 3

Contributors

A list of contributors for the analysis pipeline is available here. If you would like to contribute to this project, please see contribution guidelines.

CHAPTER 4

License