USNA GPU Project Details

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FLEXCONN

The FLEXCONN software v1.1 from (**???**) is located at https://www.nitrc.org/projects/flexconn. The `README.txt` indicates to install the necessary requirements:

```
pip install -r requirements.txt
```

which includes `tensorflow_gpu`, which indicates GPU units are required.

Image Processing in R

The `extrantsr` and `smri.process` packages perform a lot of the image processing required to get the raw data into a form for FLEXCONN. These packages rely on `ANTsR`, a large C++-based library that has been wrapped in R. It takes a long time to compile.

To install these packages in R, you must: 1) Install R from https://cran.r-project.org/. 2) Install the `remotes` package by:

```r
install.packages("remotes")
```

3) Install the packages using:

```r
remotes::install_github("muschellij2/smri.process")
```

There may be an easier way to install these using Neuroconductor (Muschelli et al. 2018) by the following command:

```r
source("https://neuroconductor.org/neurocLite.R")

# From the Latest Release on NeuroC
neuro_install('smri.process', release = "stable", release_repo = latest_neuroc_release(release = "stabl
```

4) Download the data The `msmri` package has download functions to download data from http://johnmuschelli.com/open_ms_data/. Install this package using:

```r
remotes::install_github("muschellij2/msmri")
```

Third Party software

The above tools also rely on FSL (Jenkinson et al. 2012), which is a neuroimaging software suite. It can be downloaded at https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/FslInstallation and installed using the `python` installer script. Be aware aware the defaults are for a global installation, therefore requiring `root` privileges.

Details of Image Processing

Namely, the 5 steps required are: 1) Inhomogeneity correction using N4 (Tustison et al. 2010).
2) Skull Stripping. The `extrantsr::malf` function will perform this, which is wrapped in `smri.process::smri_prenormalize`

3) Image registration: aligning the T1-weighted, FLAIR and other imaging sequences in the same space. 4) Inhomogeneity correction on the brain-only image.

5) Resampling the data to a 1x1x1 grid or registering it to a template.

The `raw` data from the open MS data needs these steps performed, but the `coregistered` data do not, as these have are "Spatially co-registered and bias corrected T1, T2, FLAIR images)" according to http: //lit.fe.uni-lj.si/tools.php?lang=eng. Therefore, we will use the `coregistered` data, but may re-run these processing steps on the raw data in the future.

Downloading One Subject

To download subject 1, we can use the following code

```
library(msmri)
dl = download_ms_patient(1, cohort = "cross_sectional", data = "coregistered")
names(dl) = neurobase::nii.stub(dl, bn = TRUE)
dl
```

```
##                                                                    brainmask
##    "/var/folders/1s/wrtqcpxn685_zk570bnx9_rr0000gr/T//RtmpoksaVV/file122413e4c3e9a/brainmask.nii.gz"
##                                                                  consensus_gt
## "/var/folders/1s/wrtqcpxn685_zk570bnx9_rr0000gr/T//RtmpoksaVV/file122413e4c3e9a/consensus_gt.nii.gz"
##                                                                         FLAIR
##        "/var/folders/1s/wrtqcpxn685_zk570bnx9_rr0000gr/T//RtmpoksaVV/file122413e4c3e9a/FLAIR.nii.gz"
##                                                                           T1W
##          "/var/folders/1s/wrtqcpxn685_zk570bnx9_rr0000gr/T//RtmpoksaVV/file122413e4c3e9a/T1W.nii.gz"
##                                                                         T1WKS
##        "/var/folders/1s/wrtqcpxn685_zk570bnx9_rr0000gr/T//RtmpoksaVV/file122413e4c3e9a/T1WKS.nii.gz"
##                                                                           T2W
##          "/var/folders/1s/wrtqcpxn685_zk570bnx9_rr0000gr/T//RtmpoksaVV/file122413e4c3e9a/T2W.nii.gz"
```

The data includes a brain mask (`brainmask.nii.gz`), "ground truth" (`consensus_gt.nii.gz`), FLAIR (`FLAIR.nii.gz`), T1-weighted image (`T1W.nii.gz`), T1-weighted image post injection (`T1WKS.nii.gz`), and T2-weighted image (`T2W.nii.gz`) images. The FLEXCONN model used only FLAIR and T1-weighted images to predict the ground truth.

Here we see (by default) the data is downloaded into a temporary directory. To change the output directly, one must pass in a directory path using the `outdir` argument. For example:

```
outdir = "/path/to/where/you/want/data"
dl = download_ms_patient(1, cohort = "cross_sectional", data = "coregistered", outdir = outdir)
names(dl) = neurobase::nii.stub(dl, bn = TRUE)
```

Resampling Images

All the processing steps have been completed on the data except for the resampling and applying the brain mask to the data.

```
library(neurobase)
imgs = check_nifti(dl)
imgs = lapply(imgs, mask_img, mask = imgs$brain_mask)
```

For this, we can use the `resample_image` function for the brain images:

```
library(extrantsr)
out_img = resample_image(imgs$FLAIR, parameters = c(1,1,1), interpolator = "linear")
```

which we can use different interpolators. We must write out the image back to disk if we want to use it with `FLEXCONN`:

```r
library(neurobase)
fname = file.path(dirname(dl["FLAIR"]), "FLAIR_1x1x1.nii.gz")
write_nifti(out_img, filename = fname)
```

or in whatever `outdir` you want.

We use a `nearestneighbor` interpolator for the binary images of the ground truth and the brain mask, similarly to the code here:

```r
out_img = resample_image(dl["consensus_gt"], parameters = c(1,1,1), interpolator = "nearestneighbor")
```

Jenkinson, Mark, Christian F. Beckmann, Timothy E. J. Behrens, Mark W. Woolrich, and Stephen M. Smith. 2012. "FSL." *NeuroImage* 62 (2):782–90. https://doi.org/10.1016/j.neuroimage.2011.09.015.

Muschelli, John, Adrian Gherman, Jean-Philippe Fortin, Brian Avants, Brandon Whitcher, Jonathan D Clayden, Brian S Caffo, and Ciprian M Crainiceanu. 2018. "Neuroconductor: An R Platform for Medical Imaging Analysis." *Biostatistics.*

Tustison, Nicholas J., Brian B. Avants, Philip A. Cook, Yuanjie Zheng, Alexander Egan, Paul A. Yushkevich, and James C. Gee. 2010. "N4ITK: Improved N3 Bias Correction." *IEEE Transactions on Medical Imaging* 29 (6):1310–20. https://doi.org/10.1109/TMI.2010.2046908.