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GDPR compliant TVB image processing container workflows with HPC on EBRAINS



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TVB Image Processing Pipeline





magnetic resonance imaging

brain network model



Schirner et al., 2018

Pipeline input









T1-weighted MRI

Diffusion- T2-weighted MRI functional MRI weighted MRI

Pipeline output



Structural connectivity



Region-wise fMRI

Functional
connectivity







Projection matrices

Surface triangulations

Brain maps



TVB-on-EBRAINS cloud infrastructure



Brain modeling requires personal data subject to GDPR



Access control, encryption and sandboxing protect personal data



EBRAINS provides core services



Services are connected via RESTful API



TVB services can be used through a variety of deployments and interfaces









Core services

HPC

Data privacy

- Petabytes of valuable brain imaging data are generated every year.
- Openly sharing/processing human data on our shared infrastructures can compromise the privacy of the personal data of research participants.

BIG DATA













We have "fingerprints" all over our bodies



Rich personal data like MRI or connectomes cannot be easily pseudonymized and therefore require thorough protection.

MRI contains highly personal information

A positive-negative mode of population covariation links brain connectivity, demographics and behavior

Stephen M Smith¹, Thomas E Nichols², Diego Vidaurre³, Anderson M Winkler¹, Timothy E J Behrens¹, Matthew F Glasser⁴, Kamil Ugurbil⁵, Deanna M Barch⁴, David C Van Essen⁴ & Karla L Miller¹

We investigated the relationship between individual subjects' functional connectomes and 280 behavioral and demographic measures in a single holistic multivariate analysis relating imaging to non-imaging data from 461 subjects in the Human Connectome Project. We identified one strong mode of population co-variation: subjects were predominantly spread along a single 'positive-negative' axis linking lifestyle, demographic and psychometric measures to each other and to a specific pattern of brain connectivity.



picture vocabulary test fluid intelligence (number of correct responses) delay discounting (area under the curve for discounting of \$200)

> life satisfaction list sorting working memory test oral reading recognition test

sustained attention continuous performance test (specificity) delay discounting (area under the curve for discounting of \$40000) picture sequence memory test

peg-board dexterity test (time taken) visual acuity (ratio) no history of psychiatric or neurologic disorders - father pattern comparison processing speed 2-minute walking endurance test

Included in CCA

Variance explained: 2% **17%** thought problems score (self-report) still smoking perceived stress score regional taste intensity score rule breaking behavior score (self-report) anger-physical aggression score times used any tobacco today Pittsburgh sleep quality index (higher is worse) drug or alcohol problems - father total weekdays with any tobacco in last week

positive test for THC (cannabis)



NEURO

SCIENCE

in

High-accuracy individual identification using a "thin slice" of the functional connectome

Lisa Byrge and Daniel P. Kennedy

Department of Psychological and Brain Sciences, Indiana University, Bloomington, IN, USA

Keywords: Functional connectivity MRI, Individual differences, Single-subject fMRI, Resting state, Within-subject reliability

ABSTRACT

nature communications

ARTICLE

https://doi.org/10.1038/s41467-019-10933-3 OPEN

Estimating the success of re-identifications in incomplete datasets using generative models

Luc Rocher () ^{1,2,3}, Julien M. Hendrickx¹ & Yves-Alexandre de M

Science

Identifying Personal Genomes by Surname Inference

Melissa Gymrek^{1,2,3,4}, Amy L. McGuire⁵, David Golan⁶, Eran Halporis^{7,8,9}

+ See all authors and affiliations

It's often possible to re-identify us based on very little information. At the same time more and more records of us are accessible through open infrastructures ("clouds").



European Union General Data Protection Regulation (GDPR)

https://blog.eid.as/



Art. 4 GDPR **Definitions**





Data subject gives consent that data is processed for scientific purposes Controller determines alone or jointly with others the purposes and means of processing

Processor processes personal data **on behalf** of the data controller.

Art. 24 GDPR Responsibility of the controller

"...shall implement appropriate technical and organisational measures to ensure and...demonstrate that processing is performed in accordance with this Regulation"

Controller determines **alone or jointly with others** the purposes and means of processing Responsible for protecting the personal data!

8

- Art. 25 (Data protection by design and by default)
 - "by default personal data are not made accessible without the individual's intervention to an indefinite number of natural persons."
- Art. 32 (Security of processing):
 - Controller and processor shall implement T+O measures to mitigate risks
 - Pseudonymisation, encryption, resilience of systems, restore availability, regular testing
 - Adherence to code of conduct and certification may used to demonstrate compliance
 - Prevent unlawful processing by people (staff, etc.) who have access to the data



Information about race, ethnic origin, sexual orientation, political views, religious beliefs, genes, biometrics, health, etc. are <u>sensitive personal data</u> processing of which is <u>generally prohibited</u>.



Art. 9 GDPR Processing of special categories of personal data

- Processing of personal data revealing racial or ethnic origin, political opinions, religious or philosophical beliefs, or trade union membership, and the processing of genetic data, biometric data for the purpose of uniquely identifying a natural person, data concerning health or data concerning a natural person's sex life or sexual orientation shall be prohibited.
- 2. Paragraph 1 shall not apply if one of the following applies:
 - (a) the data subject has given explicit consent to the processing of those personal data for one or more specified purposes, except where Union or Member State law provide that the prohibition referred to in paragraph 1 may not be lifted by the data subject;



Art. 9 GDPR Processing of special categories of personal data

(j) processing is necessary for archiving purposes in the public interest, scientific or historical research purposes or statistical purposes in accordance with Article 89(1) based on Union or Member State law which shall be proportionate to the aim pursued, respect the essence of the right to data protection and provide for suitable and specific measures to safeguard the fundamental rights and the interests of the data subject.

"Processing for...scientific...research...shall be subject to appropriate safeguards...technical and organisational measures...ensure respect for the principle of **data minimisation**."

TVB Image Processing Pipeline: container workflows







bids/mrtrix3_connectome

nipreps/fmriprep

thevirtualbrain/tvbpipeline-converter



Configure processing with GUI

Download results



Orchestrator runs containers on supercomputer, stores provenance information with DataLad

Data privacy risks



Intercept during transit



Break-in on device



User impersonation

Data protection



encryption

access control



sandboxing



automation

Protecting cloud workflows: Encryption



2BpfrRRC%2FtkuF01V%2F35n mKB%2F7UmTrKuWaR9%2Fu9 84jcWvPUPy%2B2V%2B6%2B NaJ%2Fl0%2Fl0TKvwLyi3TtP36 a7i4ogdm%2Fd1iv84T%2F529f zzyUozbf%2BYE5NcJR9Lvv%

- Sensitive data is always encrypted by default and only decrypted for the actual processing
- In shared environments unencrypted data is sandboxed during processing

Protecting workflows in shared environments: Encryption



- Personal data is encrypted before it leaves the computer of the data controller
- Results are encrypted before being returned to the data controller
- The keys for decryption are created ad-hoc shortly before the processing and stay always in a safe location at the destination site of the data
- All (intermediate) processing results are only written inside sandboxed file systems and securely deleted before termination.

Protecting cloud workflows: Access control

🗧 🔶 🖸 👔 🖬 🖬 🖉 🖓 😧 👘 😨 🚓 🚱 🔅 😨 😓 🚱 🗧 😓 🚱 🗧 😓 🚱 😓 🚱 🗧 🚱 🚱 🖓 🗧



Log In

michael.schirner@charite.de						
Password						
•••••						
LogIn	Forgot Password?	Register				



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LEAD INSTITUTIONS

(Aix*Marseille universite

Baycrest

CHARITÉ

USER DETAILS

DISPLAY NAME	Michael Schirner		
USERNAME	michaels		
ROLE	administrator manage other users		
DATA	o.o KiB		
ACCOUNT	Account management console		

ABOUT THIS VERSION

*	You may use this version on your personal computer.		
*	You may also install it on a server and make it accessible to an unlimited number of users.		
	Please make sure that your server has appropriate hardware ressources like a decent multi-core CPU and at least 16 GB of RAM.		
*	You may also install it on a cluster (similar to a server installation but with parallelization support).		
	Please note that for cluster installations, OAR is expected to be configured separately from TVB.		

User D F

🛔 Simul

Analysi

Stimulu

I Connectivity





Large Scale Connectivity View Connectivity Regions. Perform Connectivity Instance



Allen Connectome Builder Download data from Allen dataset and create a mouse connectome



Local Connectivity Create or view existent Local Connectivity entities.

Image Preprocessing Pipeline Launch Image Preprocessing pipeline

Image Preprocessing Pipeline

D Project

	nectivity: 7			
Pipeline Job1				
Select MRI data for upload	Choose file No file chosen			
Participant Label 👔	sub-Con03			
Number of cpus 🕐	1			
Estimated runtime (hours) 👔	1			
Configure pipeline steps				
Run step 1: MRtrix3				
	Select Output Verbosity	0 1 0 2 0 3 0 4		
	Select Analysis Level	Preproc Participant Group t1w preproc		
Run step 2: fmriprep				
	Skip Bids Validation	1.		
	Anat Only	•		
	No Reconall			
	6 DoF			
	MNI normalization			
Run step 3: freesurfer				
Run step 4: tvb-pipeline-converter				
🛔 User 🗈 Project	🛔 Simulator	Analysis	♀ Stimulus	I Connectivity

Protecting cloud workflows: Sandboxing



- Provide only a controlled set of resources (storage, network, memory, CPU, devices) to a process.
- Often used to isolate potentially malicious software from the system to avoid harm.

 In shared environments unencrypted personal data and secrets may only be written into a temporary filesystem namespace that is entirely invisible from the host and which is fully and securely cleaned up when the last process exits.

Automation: cryptography & sandboxing workflow



Reproducibility crisis

- "Returning to work...later...we had a question: which were the final versions, the ones which should go in the article?...It is possible...that we...put the wrong version of some figures in the final copy"
- "When he went back to the old software library to try and do it, he couldn't remember how the software worked...he abandoned the project"
- "Unfortunately, from the paper itself he couldn't figure out what ...
 [parameters] ... were being used. He spoke the author of the paper, who replied: "...we forgot which parameters gave the nice picture you see in the published article...and thought it best to leave things vague""

From Buckheit & Donoho, 1995

Reproducibility crisis

- "Data available upon reasonable request"
- "When I run it on my machine it gives me the following error: …"
- "What is the difference between data_version8_final_edit.csv and data_version8_new_final.csv?
- "Which value did you set when it asks for input at step 9?"
- "But the code worked when I ran it last month!"
- "Where did this file come from?"
"An article about computational *science in a scientific* publication is not the scholarship itself, it is merely advertising of the scholarship. The actual scholarship is the *complete software development* environment and the complete set of instructions which generated the figures."

"When we publish articles containing figures which were generated by computer, we also publish the complete software environment which generates the figures."

From Buckheit & Donoho, 1995

Reproducible workflows

- version control datasets
- data provenance: history of digital objects
- nest datasets in hierarchy of modular units
- organize data with widely-used standards (e.g. BIDS)
- annotate and describe data with metadata and documentation
- automatically update products using continuous integration pipelines
- make the data accessible via web interfaces
- make code and computational environment reproducible with software containers (Docker, Singularity) and virtual environments

Research data management

- to create, use, publish, share, archive, re-use, destroy
- digital objects
 - code / software
 - raw data
 - processed data
 - results
 - figures, manuscripts
- in a way that makes these digital assets
 - findable
 - accessible
 - interoperable
 - re-usable

С	github.com/BIDS-Apps/MRtrix3_connectome/blob/master/Dockerfile	←	\rightarrow G	github.com/BIDS-Apps/MRtrix3_connectome/blob/master/Dockerfile
			137	SUBJECTS_DIR=/opt/treesurter/subjects \
168	lines (155 sloc) 8.52 KB		138	FSLDIR=/opt/fsl \
			139	FSLOUTPUTTYPE=NIFTI \
	FROM ubuntu:18.04		140	FSLMULTIFILEQUIT=TRUE \
2	MAINTAINER Robert E. Smith <robert.smith@florey.edu.au></robert.smith@florey.edu.au>		141	FSLTCLSH=/opt/fsl/bin/fsltclsh \
3			142	FSLWISH=/opt/fsl/bin/fslwish \
	<pre># Core system capabilities required</pre>		143	LD_LIBRARY_PATH=/opt/fsl/lib:\$LD_LIBRARY_PATH \
5	RUN apt-get update && DEBIAN_FRONTEND=noninteractive apt-get		144	PATH=/opt/mrtrix3/bin:/usr/lib/ants:/opt/freesurfer/bin:/opt/freesurfer/m
6	bc \		145	PYTHONPATH=/opt/mrtrix3/lib:\$PYTHONPATH
	build-essential \		146	
8	curl \		147	# MRtrix3 setup
9	dc \		148	<pre># Commitish is 3.0.2 plus relevant hotfix</pre>
10	git \		149	RUN git clone https://github.com/MRtrix3/mrtrix3.git /opt/mrtrix3 && \
11	libegl1-mesa-dev \		150	cd /opt/mrtrix3 && \
12	libopenblas-dev \		151	git checkout 4ab54489f40997f7da1e1915c2adde3373cf6039 && \
13	nano \		152	python3 configure -nogui && \
14	perl-modules-5.26 \		153	python3 build -persistent -nopaginate && \
15	python2.7 \		154	git describetags > /mrtrix3_version && \
16	python3 \		155	rm -rf .git/ cmd/ core/ src/ testing/ tmp/ && $\$
17	tar \		156	cd /
18	tcsh \		157	
19	tzdata \		158	# Acquire extra MRtrix3 data
20	unzip \		159	RUN wget -q "https://osf.io/v8n5g/download" -0 /opt/mrtrix3/share/mrtrix3/lab
21	wget		160	wget -q "https://osf.io/ug2ef/download" -0 /opt/mrtrix3/share/mrtrix3/lab
22			161	
23	# PPA for newer version of nodejs, which is required for bids	s	162	# Acquire script to be executed
24	RUN curl -sL https://deb.nodesource.com/setup_12.x -o nodesou	l	163	COPY mrtrix3_connectome.py /mrtrix3_connectome.py
25	bash nodesource_setup.sh && \		164	RUN chmod 775 /mrtrix3_connectome.py
26	rm -f nodesource_setup.sh && \		165	
27	apt-get install -y nodejs		166	COPY version /version
28			167	
29	# NeuroDebian setup		168	<pre>ENTRYPOINT ["/mrtrix3_connectome.py"]</pre>



- "Git for data"
- based on Git and git-annex
- command-line tool for Linux, OS X, Windows
- version control arbitrarily large files
- provenance tracking
- share and obtain data
- reproducible workflows
- domain-agnostic



- DataLad datasets
 - are directories managed by DataLad
 - are Git repositories
 - can be nested: linked subdirectories
 - can be created or installed
 - can branch and merge





datalad create

datalad save

Create empty dataset

datalad download-url datalad status record state of dataset to history incl. commit message obtain web content and record origin

report tracking state



Record where you got it from, where it is now, and what you did to it



link input, code, output, and software with datalad containers-run

save all modifications of the dataset

Containerization captures software and environment as provenance





```
$ datalad run -m "analyze iris data with classification analysis" \
  --input "input/iris.csv" \ retrieved on demand
                                            only specified output
  --output "prediction report.csv" \
                                             files get unlocked
  --output "pairwise relationships.png"
 "python3 code/script.py"
[INFO ] Making sure inputs are available (this may take some time)
get(ok): input/iris.csv (file) [from web...]
[INFO ] == Command start (output follows) =====
[INFO ] == Command exit (modification check follows) =====
add(ok): pairwise relationships.png (file)
add(ok): prediction report.csv (file)
save(ok): . (dataset)
                                      Execute the analysis script
action summary:
  add (ok: 2)
                                         in a computationally
  get (notneeded: 2, ok: 1)
                                         reproducible manner
```

```
$ datalad containers-run -n neuroimaging-container \
 --input 'mri/* bold.nii --output 'sub-*/LC timeseries run-*.csv' \
 "bash -c 'for sub in sub-*; do for run in run-1 ... run-8;
    do python3 code/extract lc timeseries.py \$sub \$run; done; done'"
-- Git commit -- Michael Hanke < ... @gmail.com>; Fri Jul 6 11:02:28 2019
    [DATALAD RUNCMD] singularity exec --bind {pwd} .datalad/e...
   === Do not change lines below ===
    "cmd": "singularity exec --bind {pwd} .datalad/environments/nilearn.simg bash..",
    "dsid": "92ealfaa-632a-11e8-af29-a0369f7c647e",
    "inputs": [
     "mri/*.bold.nii.gz",
     ".datalad/environments/nilearn.simg"
    "outputs": ["sub-*/LC timeseries run-*.csv"],
                                                  Track computations
   ^^^ Do not change lines above ^^^
                                             performed with containers
sub-01/LC_timeseries run-1.csv | 1 +
```

```
$ git log
commit df2dae9b5af184a0c463708acf8356b877c511a8 (HEAD -> master)
Author: Adina Wagner adina.wagner@t-online.de
Date: Tue Dec 1 11:58:18 2020 +0100
```

[DATALAD RUNCMD] analyze iris data with classification analysis

```
=== Do not change lines below ===
 "chain": [],
 "cmd": "python3 code/script.py",
 "dsid": "9ffdbfcd-f4af-429a-b64a-0c81b48b7f62",
 "exit": 0,
 "extra inputs": [],
 "inputs": [
 "input/iris.csv"
],
 "outputs": [
 "prediction report.csv",
  "pairwise relationships.png"
 "pwd": "."
   Do not change lines above ^^^
```

datalad (containers) - run
 produces a machine-readable
 provenance record, identified by a
 Git commit hash



- the dataset logs everything that was done, by whom & when
- reset dataset to historic state
- add, remove or revisit individual steps

```
$ datalad rerun df2dae9b5af1
datalad rerun df2dae9b5af18
[INFO ] run commit df2dae9; (analyze iris data...)
[INFO ] Making sure inputs are available (this may take some time)
unlock(ok): pairwise relationships.png (file)
unlock(ok): prediction report.csv (file)
[INFO ] == Command start (output follows) =====
[INFO ] == Command exit (modification check follows) =====
add(ok): pairwise relationships.png (file)
add(ok): prediction report.csv (file)
action summary:
```

- add (ok: 2) get (notneeded: 3) save (notneeded: 2) unlock (ok: 2)
- rerun recorded computations via commit hash
- helps to reproduce and verify a result (via content) • hash)
- granularity can be freely decided
- recompute: not everything needs to be stored or ۲ transported

Create an input dataset

If your data is not yet a DataLad dataset, you can transform it into one with the following commands.

```
# create a dataset in an existing directory
$ datalad create -f .
# save its contents
$ datalad save . -m "Import all data"
```

For large datasets (e.g. HCP, UK Biobank), we create subdataset for each subject

Create a new DataLad dataset

First we create a new empty dataset and then add existing containers to it.

\$ datalad create pipeline
\$ cd pipeline

Add container(s)

Add a software-container to the dataset using *datalad containers-add* from the datalad-container extension. The *--url* parameter can be a local path to your container image, or a URL to a container hub such as Dockerhub or Singularity Hub.

\$ datalad containers-add cat --url<path/or/url/to/image> \
--call-fmt "singularity run -B {{pwd}} --cleanenv {img} {cmd}"

Re-usable container pipeline dataset

Create empty dataset and then clone and add the container as subdataset

Here we create an empty dataset and then clone and register our needed container(s) as a subdataset (documentation). Arguments like --*bind* that are intended for singularity rather than the underlying command should be specified with --*call-fmt* when calling *containers-add*. It's also fine to edit the cmdexec value in .*datalad/config* after the fact.

Create a source dataset for all analysis components
source_ds="pipeline"
datalad create \$source_ds
cd \$source_ds

clone the container-dataset as a subdataset. containername='tvbpipe-fmriprep' containerstore="/scratch/snx3000/bp000225/tvbpipe-fmriprep" datalad clone -d . \${containerstore} code/pipeline

Register the container in the top-level dataset.

- # If necessary, configure your own container call in the
- # --call-fmt argument. If your container does not need a
- # custom call format, remove the --call-fmt flag and its
- # options below.

datalad containers-add 🔪

--call-fmt 'singularity run -B {{pwd}} --cleanenv {img} {cmd}' \

-i /scratch/snx3000/bp000225/\${source_ds}/code/pipeline/.datalad/environments/\${container
\$containername

amend the previous commit with a nicer commit message
git commit --amend -m 'Register pipeline dataset'

Analysis superdataset to specify all dependencies of an analysis

Further reading https://arxiv.org/abs/2102.05888

[Submitted on 11 Feb 2021 (v1), last revised 29 Mar 2021 (this version, v2)]

Brain Modelling as a Service: The Virtual Brain on EBRAINS

Michael Schirner, Lia Domide, Dionysios Perdikis, Paul Triebkorn, Leon Stefanovski, Roopa Pai, Paula Popa, Bogdan Valean, Jessica Palmer, Chloê Langford, André Blickensdörfer, Michiel van der Vlag, Sandra Diaz-Pier, Alexander Peyser, Wouter Klijn, Dirk Pleiter, Anne Nahm, Oliver Schmid, Marmaduke Woodman, Lyuba Zehl, Jan Fousek, Spase Petkoski, Lionel Kusch, Meysam Hashemi, Daniele Marinazzo, Jean-François Mangin, Agnes Flöel, Simisola Akintoye, Bernd Carsten Stahl, Michael Cepic, Emily Johnson, Gustavo Deco, Anthony R. McIntosh, Claus C. Hilgetag, Marc Morgan, Bernd Schuller, Alex Upton, Colin McMurtrie, Timo Dickscheid, Jan G. Bjaalie, Katrin Amunts, Jochen Mersmann, Viktor Jirsa, Petra Ritter

The Virtual Brain (TVB) is now available as open-source cloud ecosystem on EBRAINS, a shared digital research platform for brain science. It offers services for constructing, simulating and analysing brain network models (BNMs) including the TVB network simulator; magnetic resonance imaging (MRI) processing pipelines to extract structural and functional connectomes; multiscale co-simulation of spiking and large-scale networks; a domain specific language for automatic high-performance code generation from user-specified models; simulation-ready BNMs of patients and healthy volunteers; Bayesian inference of epilepsy spread; data and code for mouse brain simulation; and extensive educational material. TVB cloud services facilitate reproducible online collaboration and discovery of data assets, models, and software embedded in scalable and secure workflows, a precondition for research on large cohort data sets, better generalizability and clinical translation.

Summary

- TVB uses access control, encryption, sandboxing and automation to protect
 personal data in shared environments
- The pipeline can be configured via a web-GUI
- Containers capture all software and environment
- DataLad captures all inputs, the containers, and how the containers were executed to return fully reproducible datasets

Thank you for listening.



Import custom code

Here we can copy custom code into the dataset. For example, FreeSurfer (part of fmriprep, MRtrix3_connectome) needs a license file (free but must be individually obtained), which is now copied from the home folder into the data set.

committing changes after copying license file
cp ~/license.txt code/license.txt
datalad save -m "Add Freesurfer license file"

Quickly test-run the container on the login node

Before we create SLURM batch scripts we will give the container a test run to make sure we set up everything correctly so far.

```
# load Singularity module again in case there was an
# environment change
module load singularity
# the subject we test
subid="sub-CON03"
# create workdir for fmriprep inside the dataset to
# simplify singularity call PWD will be available in the
# container
mkdir -p .git/tmp/wdir
# Replace the command with an fmriprep parametrization
# that fits your analysis
datalad containers-run \
 -m "Compute ${subid}" \
 -n tvbpipe-fmriprep 🔪
```

```
--explicit \
```

```
-o fmriprep/${subid} \
```

```
-i inputs/data/${subid}/ses-postop/ \
```

```
-i code/license.txt \
```

```
"inputs/data/${subid} . participant --participant-label $subid \
    --anat-only -w .git/tmp/wdir --fs-no-reconall --skip-bids-validation \
```

```
--fs-license-file code/license.txt"
```

Setting up a reproducible, version-controlled, provenance-tracked workflow

Install DataLad

With Miniconda DataLad can be installed with just three commands

ssh daint # or the supercomputer you are working on module load daint-mc # supercomputer-specific module module load cray-python/3.8.5.0 # load Python environment

```
# The easiest way to install DataLad with all
# dependencies on a supercomputer without root
# permissions is by using conda
wget https://repo.anaconda.com/miniconda/Miniconda3-latest-Linux-x86_64.sh
bash Miniconda3-latest-Linux-x86_64.sh
# acknowledge license, initialize Miniconda3, close and
# re-open shell
conda install -c conda-forge datalad
```

Install DataLad extensions



pip install datalad-neuroimaging datalad-container

Configure DataLad

Setup your git identity. Specify your git username and email, which will be used to track changes in your DataLad data set: changes you make are associated with your name and email address.

```
cd ~
git config --global --add user.name "MichaelSchirner"
git config --global --add user.email m.schirner@fu-berlin.de
```

Limitations

- not every feature of DataLad may work "out of the box"
- sometimes customization is required

Find-out-more: Fine-tuning: Enable re-running

If you want to make sure that your dataset is set up in a way that you have the ability to rerun a computation quickly, the following fMRIprep-specific consideration is important: If fMRIprep finds preexisting results, it will fail to run. Therefore, all outputs of a job need to be removed before the job is started[3]. We can simply add an attempt to do this in the script (it wouldn't do any harm if there is nothing to be removed):

(cd fmriprep && rm -rf logs "\$subid" "\$subid.html" dataset_descriptic (cd freesurfer && rm -rf fsaverage "\$subid")

pybids (inside fmriprep) gets angry when it sees dangling symlir # of .json files -- wipe them out, spare only those that belong to # the participant we want to process in this job find sourcedata -mindepth 2 -name '*.json' -a ! -wholename "\$1"'*'

meanwhile fixed in PyBIDS thanks to community interaction https://github.com/bidsstandard/pybids/issues/6 31

