

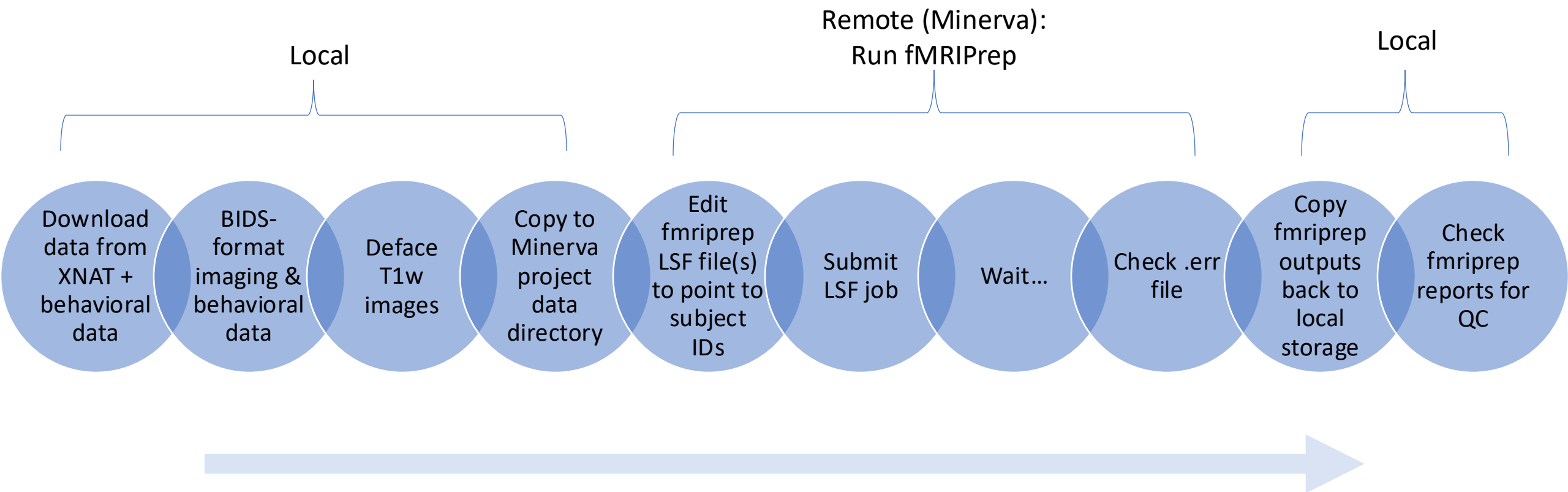
# Using Minerva (HPC) for preprocessing data using fMRIPrep

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# Minerva

- HPC scientific computing resource at Mount Sinai
- The supercomputer Minerva was upgraded in 2020, and utilizes 14,304 Intel Gold 8168 24C, 2.7 GHz compute cores (48 cores per node with two sockets in each node), 286 nodes with 192 GB of memory per node, 65.7 terabytes of total memory, 350 terabytes of solid-state storage and nearly 30 petabytes of spinning storage accessed via IBM's Spectrum Scale/General Parallel File System (GPFS) for a total of 1.2 petaflops of compute power.
- See <https://labs.icahn.mssm.edu/minervalab/> for Minerva documentation and training dates/slides



# Workflow

# Minerva cluster @ Mount Sinai



## Chimera Partition:

- 3x **login nodes** - Intel 8168 24C, 2.7GHz - **384 GB** memory
- Compute nodes -
  - 275 **regular memory nodes** - Intel 8168 24C, 2.7GHz - 48 cores per node - **192 GB/node)**
  - 37 **high memory nodes** - Intel 8168/8268, 2.7/2.9GHz - **1.5 TB** mem
  - **GPU nodes:**
    - 12 -Intel 6142, 2.6GHz - 384 GB memory - 4x V100-**16 GB** GPU
    - 8 - Intel 8268, 2.9 GHz - 384 GB memory - 4x A100- **40 GB** GPU  
- **1.8 TB SSD per node**
    - 2 - Intel 8358, 2.6GHz - 2 TB memory - 4x A100- **80 GB** GPU  
- **7 TB SSD per node, NVlink**

## NIH FUNDED NODES

### BODE2 Partition:

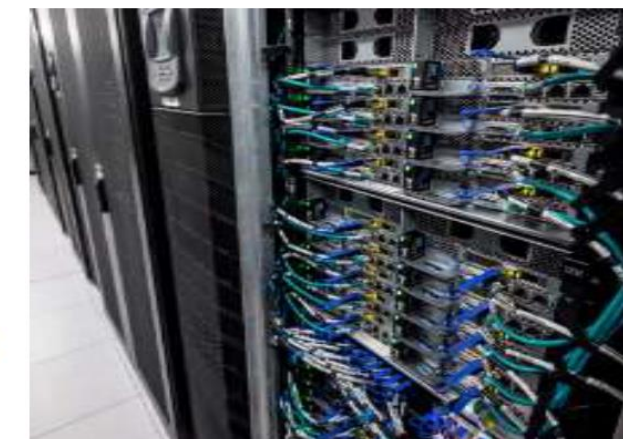
- \$2M S10 BODE2 awarded by NIH (Kovatch PI)
- 78 compute nodes - Intel 8268, 2.9 GHz -48 cores per node - **192 GB/node**

### CATS Partition:

- \$2M CATS awarded by NIH (Kovatch PI)
- 55 compute nodes - Intel 8358, 2.6 GHz- 64 cores per node -**1.5 TB** / node

**Storage:** 32PB of high-speed online storage as an IBM General Parallel File System (GPFS)

- **Path /sc/arion** : Use the system path environment variable in scripts **\$GPFS**



# Before you start...

- Request user account:  
<https://acctreq.hpc.mssm.edu/>
- Request project allocation (\$100/TB per year):  
<https://labs.ica hn.mssm.edu/minervalab/minerva-project-allocation/>
- Sign HIPAA agreement form

## HIPAA

- Minerva is HIPAA compliant as of October 1st, 2020, i.e., Protected Health Information (PHI) data is allowed to be stored and processed on Minerva.
- All users have to read the HIPAA policy and complete Minerva HIPAA Agreement Form **annually** (every Dec.) at <https://labs.ica hn.mssm.edu/minervalab/hipaa/>
- Users who have not signed the agreement will have their accounts locked until the agreement is signed.



# Logging in

## Minerva is a Linux machine with Centos 7.6

- Linux is command line based, not GUI
- Logging in requires **campus network**, **SSH client** installed on your machine, **username**, **memorized password**, and **one-time code** obtained from a Symantec VIP token

## Detailed procedures:

- Campus network (School VPN needed if off-campus)
- Apply for an account at <https://acctreq.hpc.mssm.edu/>
  - Apply account for external users following [here](#)
- Complete HIPAA form at <https://labs.ica hn.mssm.edu/minervalab/hipaa/> to activate your account
- Register your token at the Self Service Portal **school site** (<https://register4vip.mssm.edu/vipssp/>)
- SSH client: terminal (Mac), MobaXterm/Putty (Windows)
- Logging info at <https://labs.ica hn.mssm.edu/minervalab/logging-in/>

*Note: Minerva is school resource, so use your **school password and school portal** for register*

# Logging in - Linux / Mac

## Connect to Minerva via ssh

- Open a terminal window on your workstation
- `ssh your_userID@minerva.hpc.mssm.edu`
- To display graphics remotely on your screen, pass the “-X” or “-Y” flag:
  - `ssh -X your_userID@minerva.hpc.mssm.edu`
  - Mac: Install XQuartz on your mac first
  - Test by running the command: `xclock`
    - Should see a clock
- Landed on one of the login nodes, and at your home directory
  - Never run jobs on login nodes
  - For file management, coding, compilation, check/manage jobs etc., purposes only
  - Basic linux command: `cd`, `ls` and more

```
imac:~ gail01$ ssh -X gail01@minerva.hpc.mssm.edu
Please input your password and two factor token:
Password:
Last login: Mon Sep 13 16:24:06 2021 from 10.254.167.11
=====
====
Run "Minerva_help" for useful Minerva commands and websites

=== Upcoming Minerva Training Sessions ===
Session 1: 15 Sep 2021, 11:00AM-12:00PM – Introduction to Minerva
Session 2: 22 Sep 2021, 11:00AM-12:00PM – LSF Job Scheduler
Session 3: 29 Sep 2021, 11:00AM-12:00PM – Globus: Data Transfer
Zoom link for all sessions:
https://mssm.zoom.us/j/5420563013

=== Send ticket to hpchelp@hpc.mssm.edu ===
WE DO NOT BACKUP USER FILES
PLEASE ARCHIVE/BACKUP YOUR IMPORTANT FILES
=== Send ticket to hpchelp@hpc.mssm.edu ===
=====
gail01@li03c04: ~ $ pwd
/hpc/users/gail01
gail01@li03c04: ~ $ xclock
```

## **/hpc/users/seeles01/**

- land here when I log in
- store my .lsf files (scripts to run jobs)
- error and output log files written here

## **/sc/arion/scratch/seeles01**

- not a place to store anything you want to keep
- write fmriprep work directories here since they're huge (10TB limit)

## **/sc/arion/projects/psychres/WTC\_resilience\_imaging**

- project directory
- BIDS dataset and Singularity images live here
- fmriprep outputs written to subdirectory
- need to manually back up



# Singularity

- A container system for secure high performance computing
- Containerization is the packaging of software code with just the operating system (OS) libraries and dependencies required to run the code to create a single lightweight executable (a container) that runs consistently on any platform/cloud/machine.
  - Containerization is ideal for applications with a large number of dependencies, like fMRIPrep, which draws on modules from many software libraries (FreeSurfer, FSL, AFNI, etc.)
  - Reproducibility: preserves exact versions of software used.
  - “Singularity image” (used to be .simg, now .sif)

# User Software - Singularity Container Platform

**Singularity tool is supported, instead of docker (Security concern)**

- Docker gives superuser privilege, thus is better at applications on VM or cloud infrastructure
- It allows you to create and run containers that package up pieces of software in a way that is portable and reproducible. Your container is a single file and can be ran on different systems

**To load singularity module:** `$ module load singularity/3.6.4`

**To pull a singularity image:** `$ singularity pull --name hello.simg shub://vsoch/hello-world`

**To create a container within a writable directory (called a sandbox):**

`$ singularity build --sandbox lolcow/ shub://GodloveD/lolcow` (create container within a writable directory)

**To pull a **docker** image:** `$ singularity pull docker://ubuntu:latest`

**To shell into a singularity image:** `$ singularity shell hello.simg`

**To run a singularity image:** `$ singularity run hello.simg`

**To get a shell with a specified dir mounted in the image**

`$ singularity run -B /user/specified/dir hello.simg`

**Note:** /tmp, user home directory, and /sc/arion/is automatically mounted into the singularity image.

- fMRIPrep already published as a Docker image
- After logging into Minerva:

```
$ ml singularity
```

```
$ singularity pull docker://nipreps/fmriprep:latest
```

\*or specific version

- Make sure you have Templateflow templates installed:  
<https://www.nipreps.org/apps/singularity/#templateflow-and-singularity>
  - Issue for HPC: fmriprep tries to download templates from server but no internet access on Minerva

*Minerva  
resources  
requested*

*Templateflow =  
templates for spatial  
alignment/norm*

*binding directories to  
container (-B <dir>)*

*fmripreg usage  
arguments*

```
1  #!/bin/bash
2  #BSUB -J sub-015                #job name
3  #BSUB -P acc_federa03a          #project allocation number
4  #BSUB -q express                #queue to run on
5  #BSUB -n 1                      #1 job slot
6  #BSUB -R affinity[core(16)]     #with 16 cores
7  #BSUB -R rusage[mem=120000]     #with 120GB memory dynamically allocated across cores
8  #BSUB -a openmp                 #use openmp multithreading
9  #BSUB -W 12:00                 #wall time
10 #BSUB -o %J.out                 #output file to t.out
11 #BSUB -e %J.err                 #error file to t.err
12
13 module purge
14 module load singularity
15
16 export SINGULARITYENV_TEMPLATEFLOW_HOME=/hpc/users/seeles01/.cache/templateflow
17 export OMP_NUM_THREADS=2
18
19 singularity run --cleanenv \
20     -B /sc/arion/projects/psychres/WTC_resilience_imaging/data:/data \
21     -B /hpc/users/seeles01/.cache/templateflow:/opt/templateflow \
22     /sc/arion/projects/psychres/my_images/fmripreg-21.0.1.sif \
23     /data/BIDS_data /data/BIDS_data/derivatives/fmripreg \
24     --work /sc/arion/scratch/seeles01 \
25     participant --participant-label 015 \
26     --fs-license-file /hpc/users/seeles01/minerva/license.txt \
27     --skip_bids_validation \
28     --n_cpus 16 --omp-nthreads 2 --mem-mb 120000 \
29     -vv --notrack
```

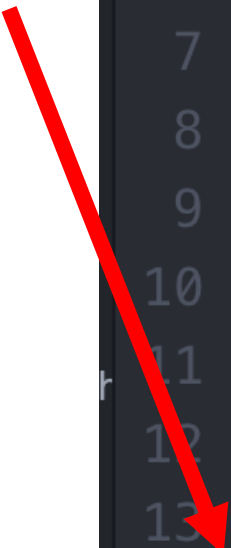


```

collect_fmripreg_WTC.py      tedana_singularity.lsf      batch_process_tedana.sh
40 # mask=compute_epi_mask(sub+'_task-'+task+'_dir-AP_run-0'+run+'_echo-1_space-native_desc-partialPre
41 # mask.to_filename(sub+'_task-'+task+'_dir-AP_run-0'+run+'_echo-1_space-native_desc-mask.nii.gz');"
42
43
44 #process partially preproc (fmriprep) data using tedana ME-ICA:
45 #(no_gscontrol, low kdaw, and removal of a few initial volumes should help wih occasional convergence iss
46 tedana -d \
47 $sub"_task-"$task"_dir-AP_run-0"$r"_echo-1_space-native_desc-partialPreproc_bold.nii.gz" \
48 $sub"_task-"$task"_dir-AP_run-0"$r"_echo-2_space-native_desc-partialPreproc_bold.nii.gz" \
49 $sub"_task-"$task"_dir-AP_run-0"$r"_echo-3_space-native_desc-partialPreproc_bold.nii.gz" \
50 $sub"_task-"$task"_dir-AP_run-0"$r"_echo-4_space-native_desc-partialPreproc_bold.nii.gz" \
51 -e 11.0 29.7 48.4 67.1 --tedpca "kundu-stabilize" \
52 --mask epi1_mask.nii.gz \
53 --out-dir $sub_outdir --png \
54 --debug
55
56 #rename relevant output files so they're not overwritten:
57 #log file
58 mv $sub_outdir/"report.txt $sub_outdir/"$sub"_task-"$task"_run-0"$r"_report.txt"
59 #denoised optimally combined time series (for future analysis)
60 mv $sub_outdir/"dn_ts_OC.nii $sub_outdir/"$sub"_task-"$task"_run-0"$r"_space-native_desc-tedanaDenoised
61 mv $sub_outdir/"$sub"_task-"$task"_run-0"$r"_space-native_desc-tedanaDenoised.nii"

```

Can also call your  
own scripts to run  
other processes



o\_WTC.py

tedana\_singularity.lsf

```

Cresil_tedana #job name
cc_federa03a #project allocation
kpress #queue to run on
#1 job slot:
affinity[core(16)] #with 16 cores
7 #BSUB -R rusage[mem=120000] #with 120GB m
8 #BSUB -W 06:00 #wall time
9 #BSUB -o %J.out #output file
10 #BSUB -e %J.err #error file
11
12 module load python/3.7.3
13
14 bash batch_process_tedana.sh sub-051
15

```

# TemplateFlow issue fix:

From <https://github.com/nipreps/fmriprep/issues/2717#issuecomment-1047238017>

1. Log into Minerva
2. Run the following:

```
$ wget  
https://raw.githubusercontent.com/nipreps/fmriprep/master/scripts/fetch\_templates.py
```

```
$ python fetch_templates.py -h (to see script usage instructions)
```

```
$ python fetch_templates.py (to pull the templates)
```

*Then make sure the lines circled in green are in your LSF file:*

1. changes the definition of the environment variable SINGULARITYENV\_TEMPLATEFLOW\_HOME to the path where you downloaded the templates

2. binds that location in your fMRIPrep container (so fMRIPrep can access it)

```
1  #!/bin/bash
2  #BSUB -J sub-015                #job name
3  #BSUB -P acc_federa03a          #project allocation number
4  #BSUB -q express                #queue to run on
5  #BSUB -n 1                      #1 job slot
6  #BSUB -R affinity[core(16)]    #with 16 cores
7  #BSUB -R rusage[mem=120000]    #with 120GB memory dynamically allocated across cores
8  #BSUB -a openmp                 #use openmp multithreading
9  #BSUB -W 12:00                  #wall time
10 #BSUB -o %J.out                 #output file to t.out
11 #BSUB -e %J.err                 #error file to t.err
12
13 module purge
14 1. module load singularity
15
16 export SINGULARITYENV_TEMPLATEFLOW_HOME=/hpc/users/seeles01/.cache/templateflow
17 export OMP_NUM_THREADS=2
18
19 singularity run --cleanenv \
20   2. -B /sc/arion/projects/psychres/WTC_resilience_imaging/data:/data \
21   -B /hpc/users/seeles01/.cache/templateflow:/opt/templateflow \
22   /sc/arion/projects/psychres/my_images/fmriprep-21.0.1.S11 \
23   /data/BIDS_data /data/BIDS_data/derivatives/fmriprep \
24   --work /sc/arion/scratch/seeles01 \
25   participant --participant-label 015 \
26   --fs-license-file /hpc/users/seeles01/minerva/license.txt \
27   --skip_bids_validation \
28   --n_cpus 16 --omp-nthreads 2 --mem-mb 120000 \
29   -vv --notrack
```

- Submit a job:

**\$ bsub < run\_fmriprep\_21.0.1\_048.lsf**

- *NB: There is a better way to submit multiple jobs as a batch, but I haven't spent time to figure that out yet, see <https://labs.ica hn.mssm.edu/minervalab/resources/the-minerva-user-group-and-training-classes/>*

- Get list of jobs you have running for a specific project account:

**\$ bjobs -P acc\_federa03a**

- Kill a job you started:

**\$ bkill <jobid>**



# LSF: Queue structure (bqueues)

Queue structure in Minerva		
Queue	Wall time limit	available resources
<b>interactive</b> (Dedicated to interactive jobs)	12 hours	4 nodes+2 V100 GPU nodes
<b>premium</b>	6 days	275 nodes + 37 himem nodes+BODE2+CATS
<b>express</b>	12 hours	275 nodes + 4 dedicated nodes (may change)+BODE2+CATS
<b>long</b>	2 weeks	6 dedicated (288 cores) + 12 BODE2
<b>gpu</b>	6 days	40 V100 32 A100 8 A100-80GB
<b>private</b>	unlimited	private nodes

**\*default memory : 3,000MB / per core**

# Transferring data to/from HPC

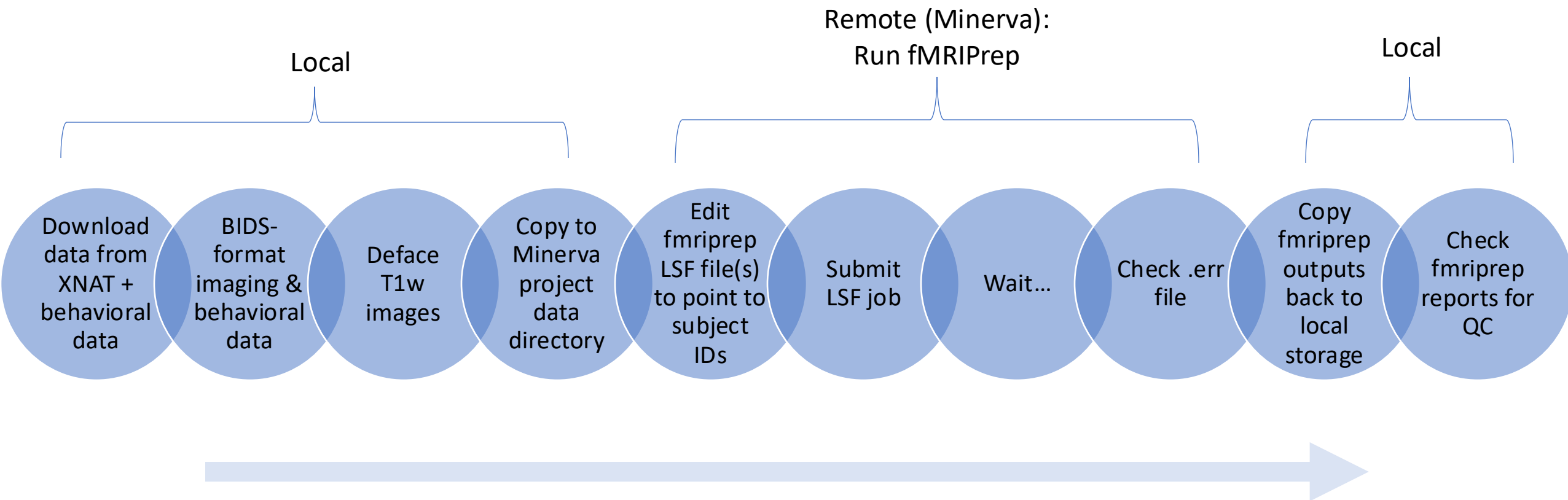
- Globus recommended:

<https://labs.icaohn.mssm.edu/minervalab/documentation/services/globus-high-assurance-hipaa-file-manager/>

- rsync also works (defaced images):

```
$ rsync -rv --<args> <from> <to>
```

```
rsync -rv --ignore-existing  
seeles01+vkrb@chimera.hpc.mssm.edu:/sc/arion/projects/psychres/WTC_resilience_imaging/data  
/BIDS_data/derivatives/fmriprep/  
/Volumes/External/WTC_resilience_imaging/data/BIDS_data/derivatives/fmriprep
```



*Next steps:*

- *Finish report QC & flag subs/runs to drop*
- *TEDANA denoising (vs. regressors?)*
- *Fix subjects w/fmripred errors & re-run*

Keeping track of fMRIPrep reports QC after inspecting them – example:

[illegible]



```
[seeles01@li03c04 minerval]$ cat 60451070.err
Traceback (most recent call last):
  File "/opt/conda/lib/python3.8/site-packages/fmriprep/cli/run.py", line 114, in main
    fmriprep_wf.run(**config.nipype.get_plugin())
  File "/opt/conda/lib/python3.8/site-packages/nipype/pipeline/engine/workflows.py", line 638, in run
    runner.run(execgraph, updatehash=updatehash, config=self.config)
  File "/opt/conda/lib/python3.8/site-packages/nipype/pipeline/plugins/base.py", line 192, in run
    report_nodes_not_run(notrun)
  File "/opt/conda/lib/python3.8/site-packages/nipype/pipeline/plugins/tools.py", line 96, in report_nodes_not_run
    raise RuntimeError(
RuntimeError: Workflow did not execute cleanly. Check log for details
```

During handling of the above exception, another exception occurred:

```
Traceback (most recent call last):
  File "/opt/conda/bin/fmriprep", line 8, in <module>
    sys.exit(main())
  File "/opt/conda/lib/python3.8/site-packages/fmriprep/cli/run.py", line 175, in main
    failed_reports = generate_reports(
  File "/opt/conda/lib/python3.8/site-packages/fmriprep/reports/core.py", line 105, in generate_reports
    report_errors = [
  File "/opt/conda/lib/python3.8/site-packages/fmriprep/reports/core.py", line 106, in <listcomp>
    run_reports(
  File "/opt/conda/lib/python3.8/site-packages/fmriprep/reports/core.py", line 88, in run_reports
    return Report(
  File "/opt/conda/lib/python3.8/site-packages/niworkflows/reports/core.py", line 291, in __init__
    self._load_config(Path(config or pkgrf("niworkflows", "reports/default.yml")))
  File "/opt/conda/lib/python3.8/site-packages/fmriprep/reports/core.py", line 47, in _load_config
    self.index(settings["sections"])
  File "/opt/conda/lib/python3.8/site-packages/niworkflows/reports/core.py", line 378, in index
    self.errors = [read_crashfile(str(f)) for f in error_dir.glob("crash*.")]
  File "/opt/conda/lib/python3.8/site-packages/niworkflows/reports/core.py", line 378, in <listcomp>
    self.errors = [read_crashfile(str(f)) for f in error_dir.glob("crash*.")]
  File "/opt/conda/lib/python3.8/site-packages/niworkflows/utils/misc.py", line 138, in read_crashfile
    return _read_txt(path)
  File "/opt/conda/lib/python3.8/site-packages/niworkflows/utils/misc.py", line 195, in _read_txt
    cur_key, cur_val = tuple(line.split(" = ", 1))
ValueError: not enough values to unpack (expected 2, got 1)
[seeles01@li03c04 minerval]$
```

## ← Example of .err file contents

### Troubleshooting tips:

- Try googling “fmriprep <error message, e.g. *not enough values to unpack*>”
- Search posts on Neurostars forum (neurostars.com) and fMRIprep Github issues forum
- Look at the last line, but also see if you can find exactly where fMRIprep crashed (scroll up, look earlier in log)