THE UNIVERSITY OF QUEENSLAND
AUSTRALIA
CREATE CHANGE

NeuroDesk

Reproducibility anywhere at anytime - An interactive session introducing NeuroDesk

Steffen & Saskia Bollmann

The University of Queensland

Acknowledgement of **Country**

The University of Queensland (UQ) acknowledges the Traditional Owners and their custodianship of the lands on which we meet.

We pay our respects to their Ancestors and their descendants, who continue cultural and spiritual connections to Country.

We recognise their valuable contributions to Australian and global society.

Declaration of Financial Interests or Relationships

Speaker Name: Saskia and Steffen Bollmann

I have the following financial interest or relationship to disclose with regard to the subject matter of this presentation:

Company Name: Oracle Cloud

Type of Relationship: Cloud credits to support NeuroDesk container hosting and development platform. If you are interested in taking part in Cloud Credit Program: contact Research Advocate, Peter Winn (peter.winn@oracle.com)

Company Name: Siemens Healthineers

Type of Relationship: Previous Employment (Steffen, 2019) + joint grants (ARC Linkage + ITTC) + joint patents

How we organize the talk

A researcher using NeuroDesk

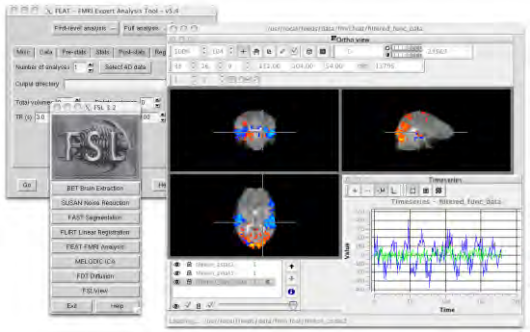
One of the NeuroDesk developers

Motivation

Large ecosystem of scientific software …

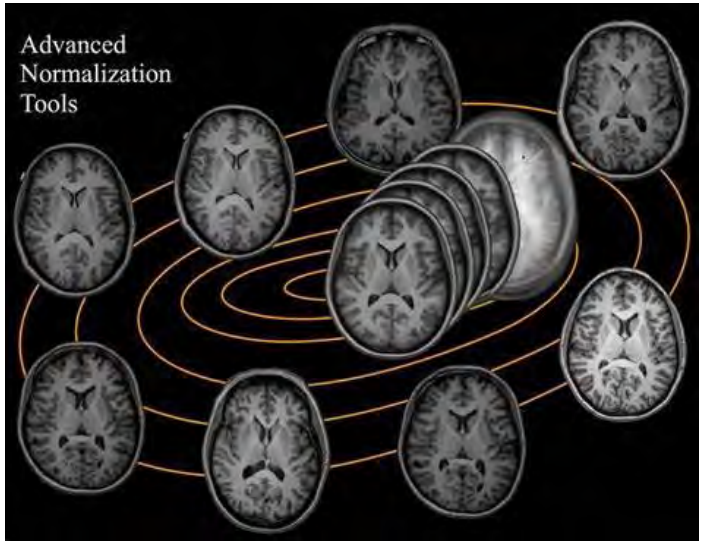
FreeSurfer

itk-SNAP

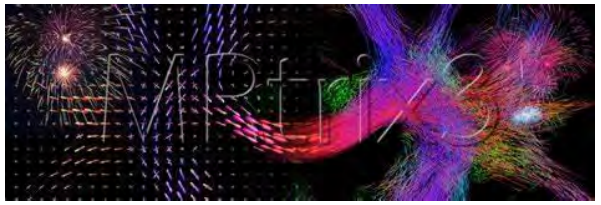


python™

Advanced Normalization Tools



julia



ANTs

Dependencies for specialised tools

Developement has been first inspired from the VMTK toolbox, but as of today the script has and is currently beiing actively revamped. It is currently used on Linux and MACOS. The dependences are:

- ITK >= 4.9, < 5.0 (do not forget to set ITK_DIR)
- python 2.7 (not tested with 3.5 and higher) with numpy, dipy, scikit-image (non exhaustive list)
- ANTs (https://github.com/ANTsX/ANTs). ITK 5.0 will be installed during ANTs compilation; ignore this version
- cmake + cmake-gui
- MACOS: realpath

```
RUN apt-get update -qq \
    && apt-get install -y -q --no-install-recommends apt-utils bzip2 \
        ca-certificates curl wget locales unzip cmake g++ gcc git cmake \
        cmake-curses-gui make pigz zlib1g-dev libboost-all-dev \
    && apt-get clean \
    && rm -rf /var/lib/apt/lists/* /tmp/* /var/tmp/* \
    && sed -i -e 's/# en_US.UTF-8 UTF-8/en_US.UTF-8 UTF-8/' /etc/locale.gen \
    && dpkg-reconfigure --frontend=noninteractive locales \
    && update-locale LANG="en_US.UTF-8" \
    && chmod 777 /opt && chmod a+s /opt
```

```
bash /src/install_scripts/install_itk.sh > log_00_itk
bash /src/install_scripts/install_boost.sh > log_01_boost
bash /src/install_scripts/install_braincharter.sh > log_02_braincharter
bash /src/install_scripts/install_afni_fsl.sh > log_03_afni_fsl
```

Trying out new versions and keeping things consistent

Advantages of cortical surface reconstruction using submillimeter 7 T MEMPRAGE

Natalia Zaretskaya [a,b,c,d,*], Bruce Fischl [d,e,f], Martin Reuter [d,e,f,g], Ville Renvall [h], Jonathan R. Polimeni [d,e,i]

Recon with native submillimeter resolution

See also HighFieldRecon

This page describes how to run the FreeSurfer recon-all for data with voxel sizes less than 1mm3 at native resolution. Several FreeSurfer binaries have been fixed to enable this feature. The pipeline is still under development, so please use with caution.

Required FreeSurfer version

dev version built after August 2015 or FreeSurfer 6

Note on the voxel size

The method works well for voxel sizes 0.75 mm3. It should work with voxel between 1mm3 and 0.75mm3. Inputs with 0.5 mm3 voxels or below will have a brainmask failure (we are working on it!), but if you fix the brainmask manually, the rest of recon-all should work well. We haven't tested the stream for inputs with anisotropic voxels.

Freesurfer 6 release downloads and setup: here.

Important Note: *When processing a group of subjects for your study, it is essential to process all your subjects with the same version of FreeSurfer, on the same OS platform and vendor, and for safety, even the same version of the OS. While we continue to work to ensure that results match across platforms, there are none-the-less system-level libraries that are OS dependent. An exception to this rule is that you may view and edit files across any platform or version, and run some post-processing tools (outside the recon-all stream) if you check with us first (for instance you may run the longitudinal processing with newer versions).*

GLIBC 2.5 vs 2.18

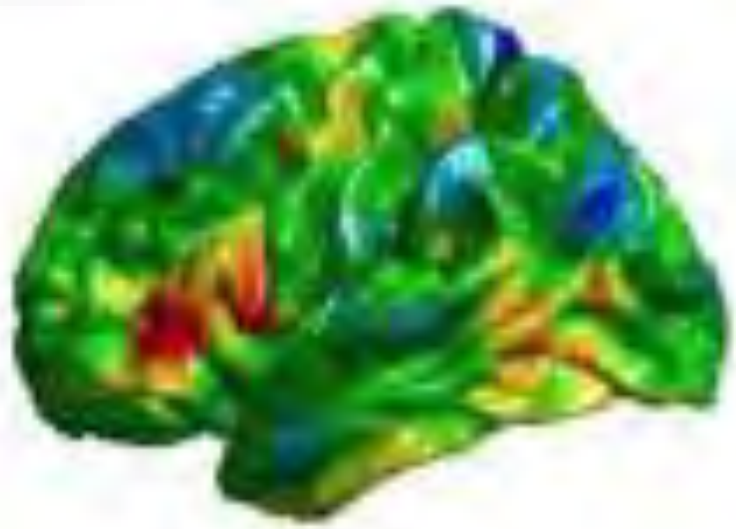
Reproducibility of neuroimaging analyses across operating systems

Tristan Glatard[1,2], Lindsay B. Lewis[1], Rafael Ferreira da Silva[3], Reza Adalat[1], Natacha Beck[1], Claude Lepage[1], Pierre Rioux[1], Marc-Etienne Rousseau[1], Tarek Sherif[1], Ewa Deelman[3], Najmeh Khalili-Mahani[1] and Alan C. Evans[1]

```
expf(1.54051852226257324218750000000)
      =4.667009353637695312500000

expf(1.54051852226257324218750000000)
      =4.667009830474853515625000
```

- glibc 2.5 vs 2.18 deliver different floating-point results
- leads to significant differences in long pipelines



… creating problems for researchers:

Most tools require Linux

… creating problems for researchers:

- Most tools require Linux
- Tools are not available in standard package systems

```
(base) uqsbollm@uqsbollm-7952:~$ sudo apt install freesurfer
[sudo] password for uqsbollm:
Reading package lists... Done
Building dependency tree
Reading state information... Done
Package freesurfer is not available, but is referred to by another package.
This may mean that the package is missing, has been obsoleted, or
is only available from another source

E: Package 'freesurfer' has no installation candidate
```

… creating problems for researchers:

- Most tools require Linux
- Tools are not available in standard package systems
- Compiling from source often a nightmare

Then run ccmake .. and set CMAKE_INSTALL_PREFIX to be the desired directory as the above cmake command is ignoring the setting.

make -j 4

This will fail configuring beast.
Edit /home/564/sb1053/minc-toolkit-v2/minc-toolkit-v2/BEaST/CMakeLists.txt
and commend out FIND_PACKAGE(NETCDF) (in two places).

run make -j 4 again.

This will fail to compile /home/564/sb1053/minc-toolkit-v2/minc-toolkit-v2/minctools/progs/mincdump/mincdump.h
Edit this file and replace enum with #define:

… creating problems for researchers:

- Most tools require Linux
- Tools are not available in standard package systems
- Compiling from source often a nightmare
- Conflicting dependencies

```
freeview.bin: error while loading shared libraries:
 libpng12.so.0: cannot open shared object file: No
such file or directory
```

… creating problems for researchers:

- Most tools require Linux
- Tools are not available in standard package systems
- Compiling from source often a nightmare
- Conflicting dependencies
- Reinstalling tools on different platforms takes time

… creating problems for researchers:

- Most tools require Linux
- Tools are not available in standard package systems
- Compiling from source often a nightmare
- Conflicting dependencies
- Reinstalling tools on different platforms takes time
- Differing results between software versions

The organic solution …

Use this one when you do the ‘normal’analysis

This has the ‘high-resolution’ version installed

This one is for the study running since 1999
DO NOT TOUCH

This is the only one where we managed to get minc compiled

NeuroDesk Architecture

Acknowledgements

Australian Research Container Orchestration Service (ARCOS)

nectar

National Imaging Facility

Martin Grignard

Australian Research Data Commons

OHBM 2020
A Virtual Experience for Engaging Minds & Empowering Brain Science

Peter Winn

ORACLE Cloud

Jakub Kaczmarzyk

Google Summer of Code

Niruhan Viswarupan

Dao Thanh Thuy

Aswin Narayanan

Yorguin Jose Mantilla

Will Woods

Steffen Bollmann

Tom Johnstone

Angela Renton

David White

Thomas Shaw

Oren Civier

Megan Campbell

Paris Lyons

Ryan Sullivan

What exists already and how can we combine efforts?

CVL | Characterisation Virtual Laboratory

Funded by ARDC Australian Research Data Commons

Design principles for NeuroDesk

Linux, Mac, Windows	• Docker
Scale to HPC	• Singularity
Interactive	• Full Linux desktop interface
Lightweight	• Tools are installed on demand
Re-use existing tech	• NeuroDebian, conda, NeuroDocker

Neurodesk makes imaging analyses …

F
- Findable

A
- Accessible

I
- Interoperable

R
- Reusable

Neurodesk Architecture

Neurodesktop

Neurocommand

Transparent-Singularity

Neurocontainers

Neurodocker

Advanced users directly using Docker/Singularity

Neurocontainers – Automated Container building

Advanced Users on HPC/Linux

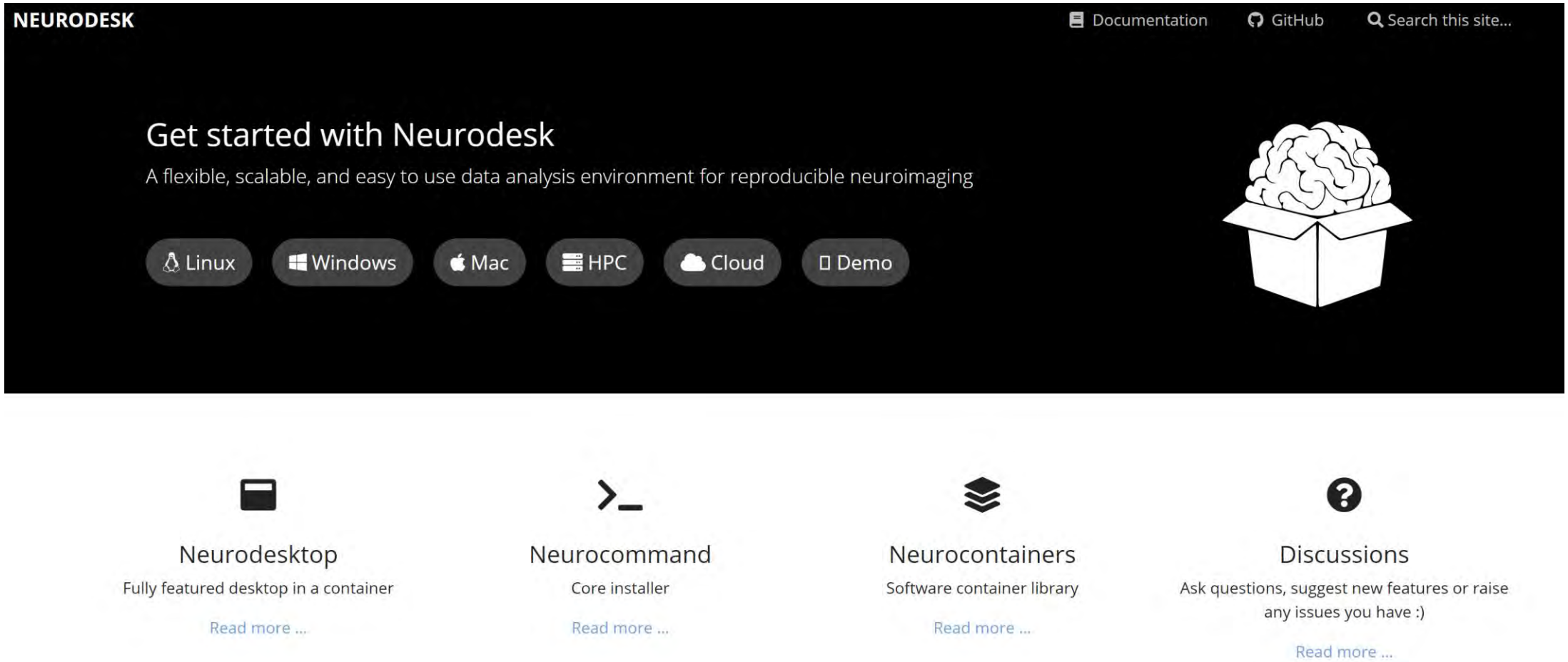
Neurocommand – Integrating our containers on any Linux OS

Researchers on Windows, Mac, Linux

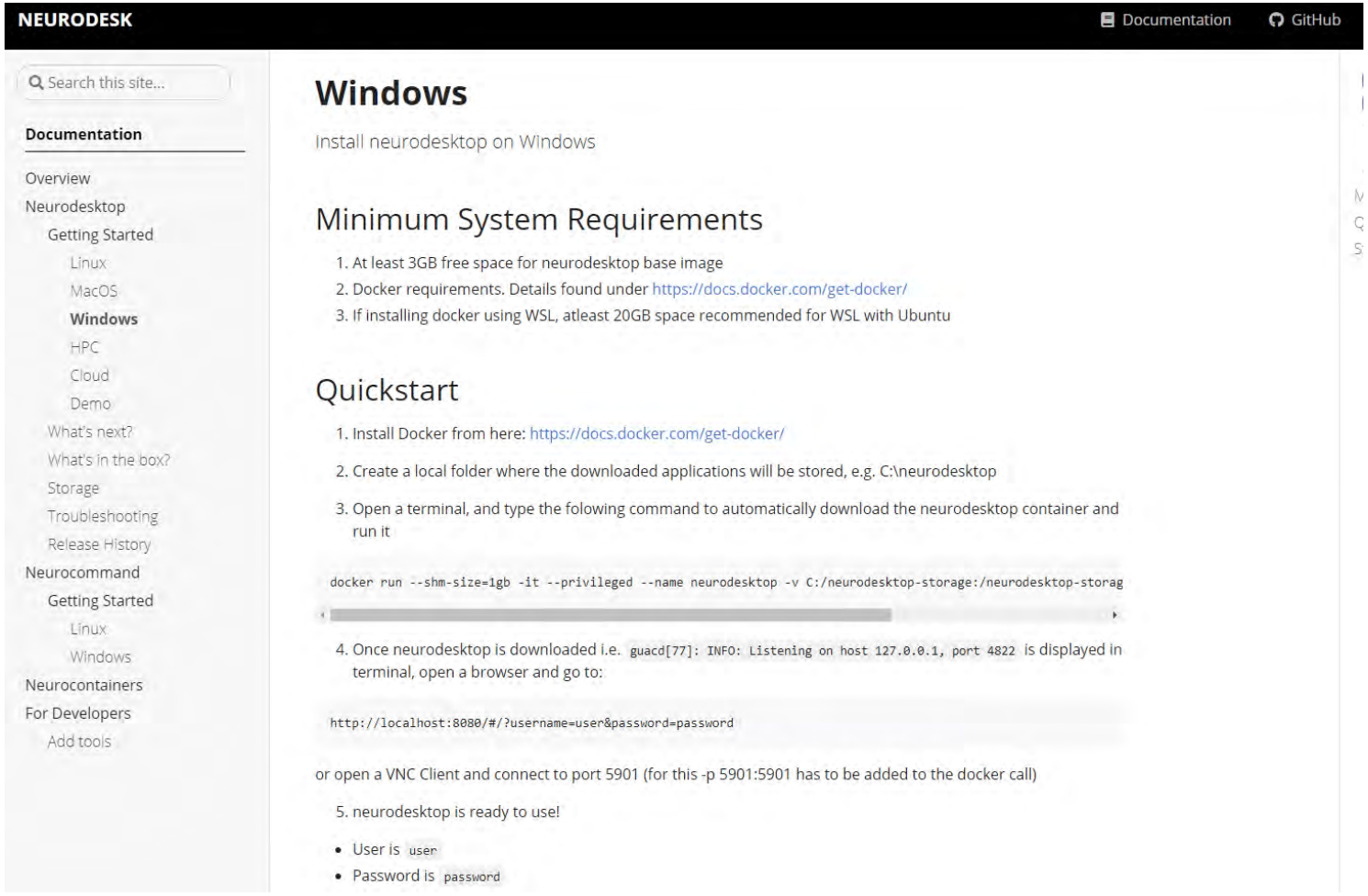
Neurodesktop – Lightweight Linux Desktop with everything installed

NeuroDesktop on Windows

http://neurodesk.github.io/



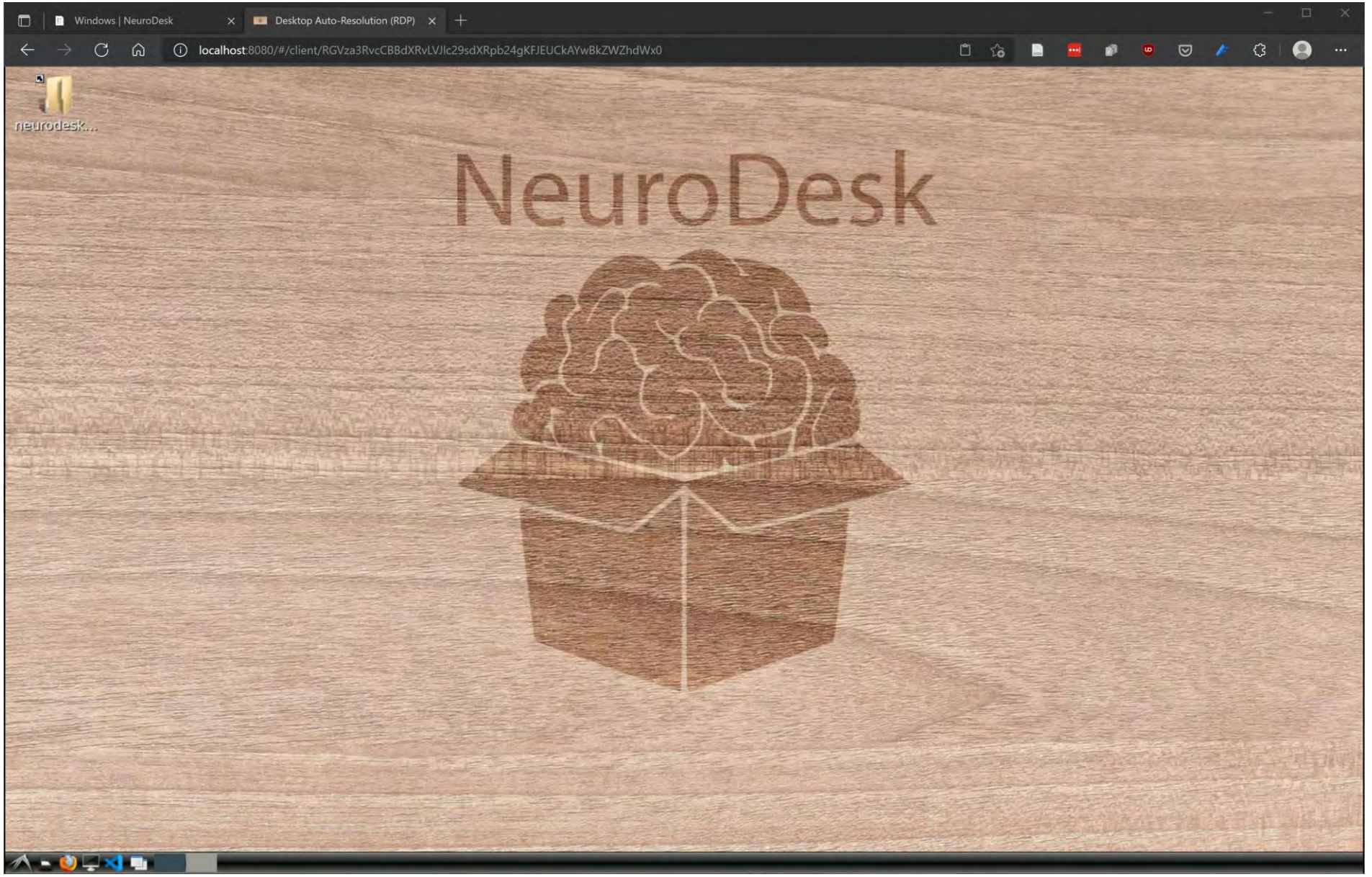
Start NeuroDesktop



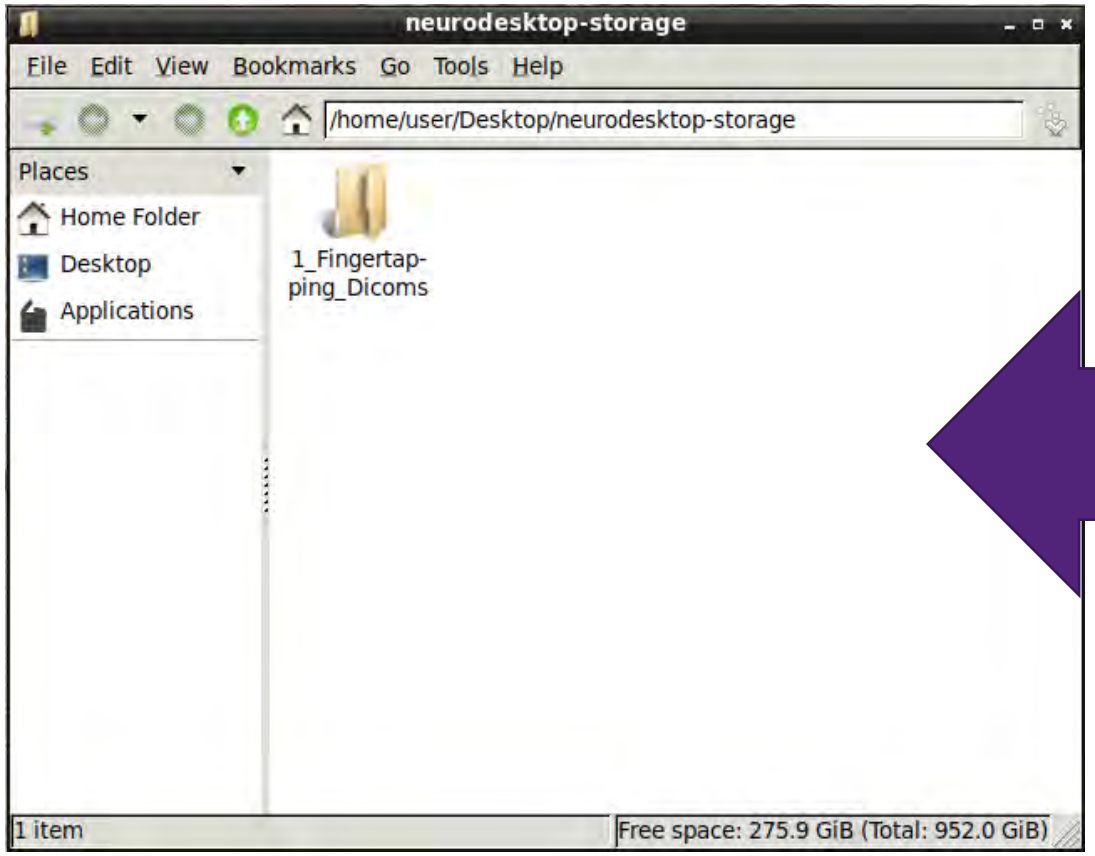
```
Using CATALINA_TMPDIR: /usr/local/tomcat/temp
Using JRE_HOME:        /usr
Using CLASSPATH:       /usr/local/tomcat/bin/bootstrap.jar:/usr/local/tomcat/bin/tomcat-juli.jar
Using CATALINA_OPTS:
Tomcat started.
================================================================
Starting Guacamole Daemon
----------------------------------------------------------------
    Use this link for direct Neurodesktop:
!!! http://localhost:8080/#/?username=user&password=password !!!
    Once connected to the session, your user info is:
    Username: "user"
    Password: "password"
----------------------------------------------------------------
guacd[657]: INFO:       Guacamole proxy daemon (guacd) version 1.3.0 started
guacd[657]: DEBUG:      Successfully bound socket to host 127.0.0.1, port 4822
guacd[657]: INFO:       Listening on host 127.0.0.1, port 4822
```

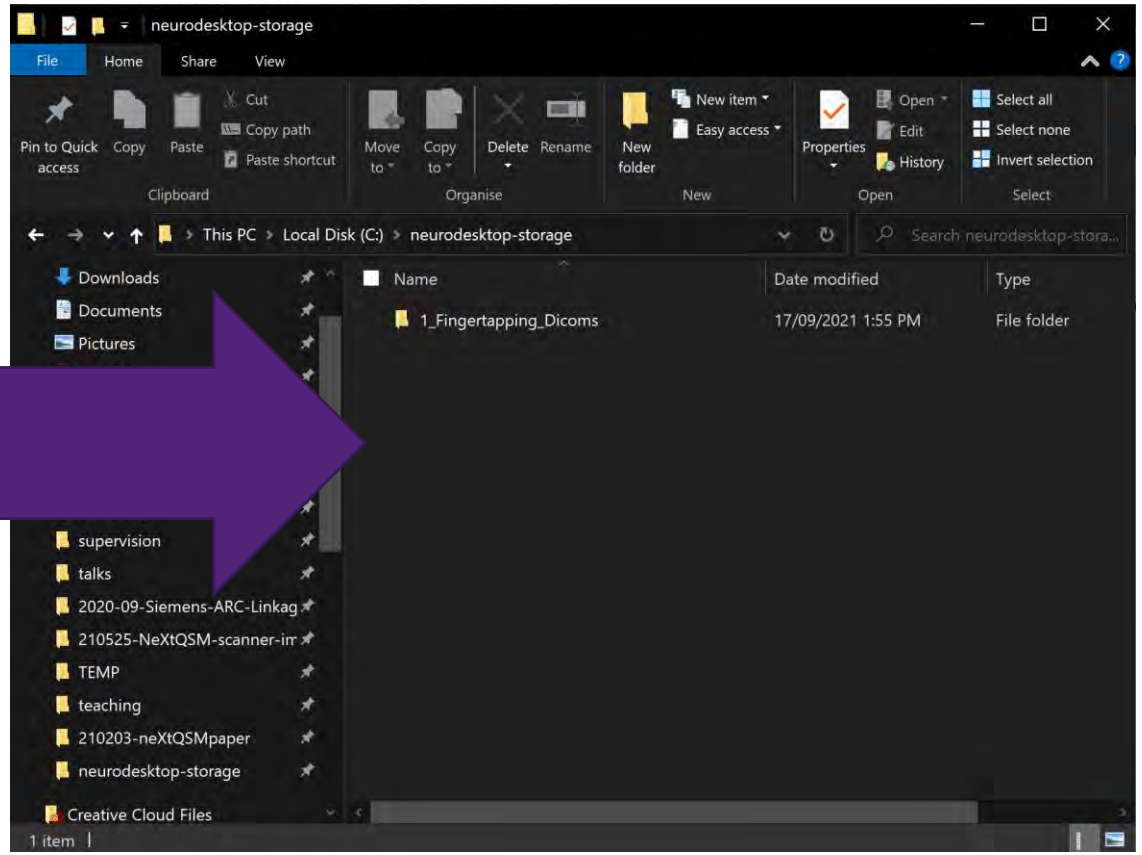
ALL CONNECTIONS

- Command Line (SSH)
- Desktop Auto-Resolution (RDP)
- Desktop Fixed-Resolution (VNC)

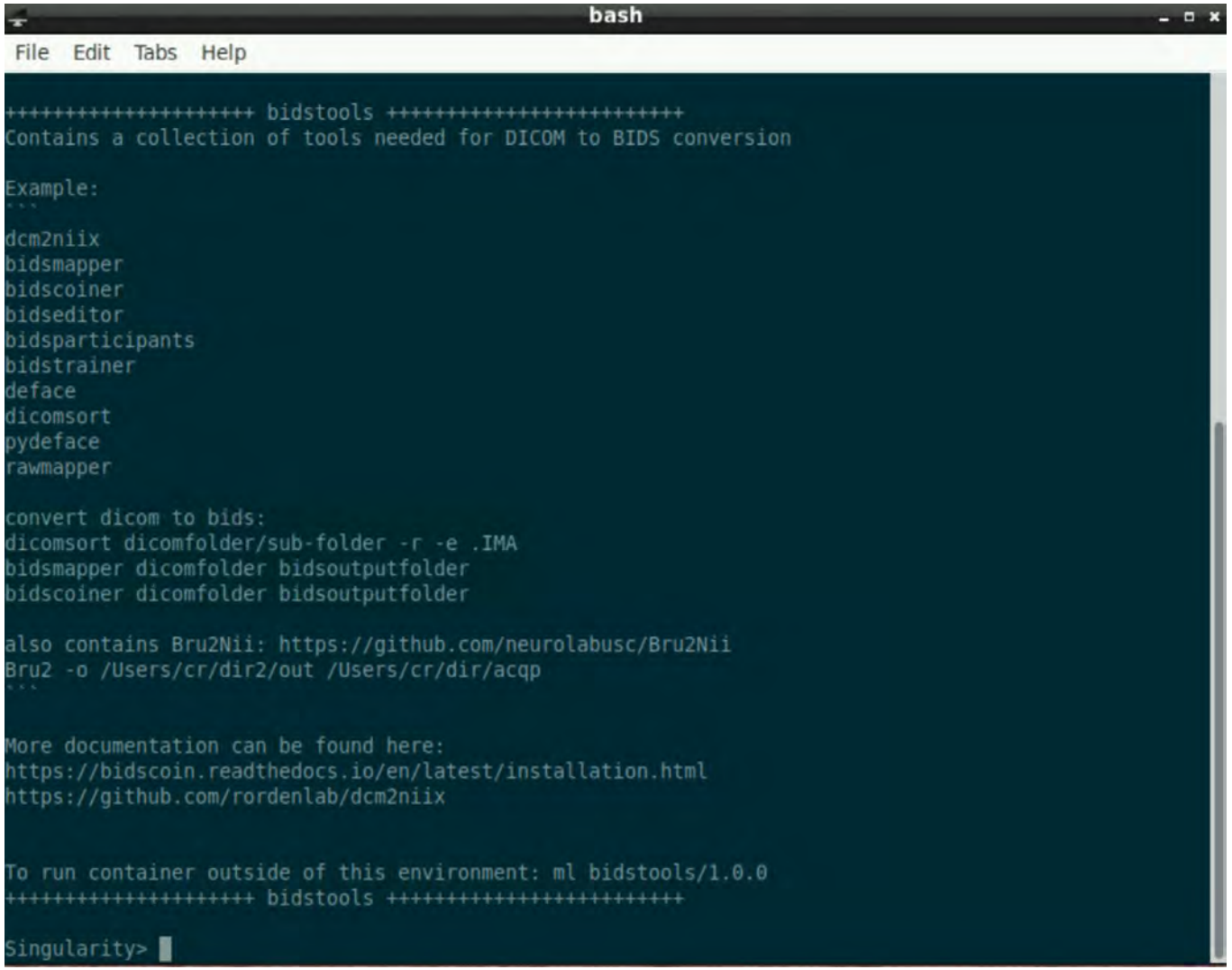

Windows | NeuroDesk
Desktop Auto-Resolution (RDP)
localhost:8080/#/client/RGVza3RvcCBBdXRvLVJlc29sdXRpb24gKFJEUCkAYwBkZWZhdWx0
neurodesk...
NeuroDesk

Getting access to my data:





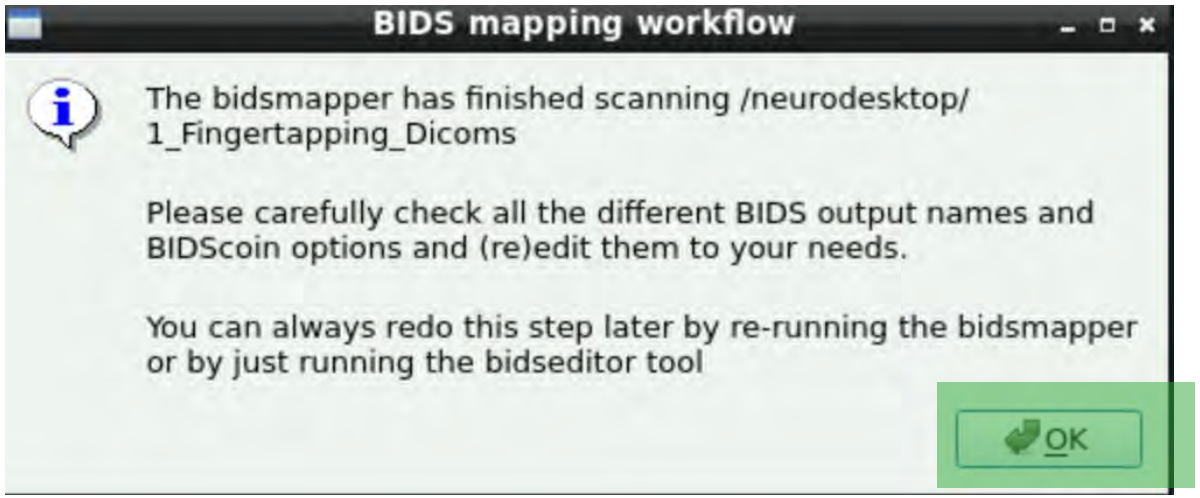
Accessories
Graphics
Internet
Neurodesk
Programming
System Tools
Preferences
Run
All Applications
Data Organisation
Diffusion Imaging
Functional Imaging
Image Reconstruction
Image Registration
Image Segmentation
Programming
Quantitative Imaging
Spectroscopy
Structural Imaging
bidstools
datalad
bidstools 1.0.0


bash
File Edit Tabs Help
++++++++++++++++++++ bidstools ++++++++++++++++++++++++
Contains a collection of tools needed for DICOM to BIDS conversion
Example:
```
dcm2niix
bidsmapper
bidscoiner
bidseditor
bidsparticipants
bidstrainer
deface
dicomsort
pydeface
rawmapper
convert dicom to bids:
dicomsort dicomfolder/sub-folder -r -e .IMA
bidsmapper dicomfolder bidsoutputfolder
bidscoiner dicomfolder bidsoutputfolder
also contains Bru2Nii: https://github.com/neurolabusc/Bru2Nii
Bru2 -o /Users/cr/dir2/out /Users/cr/dir/acqp
```
More documentation can be found here:
https://bidscoin.readthedocs.io/en/latest/installation.html
https://github.com/rordenlab/dcm2niix
To run container outside of this environment: ml bidstools/1.0.0
++++++++++++++++++++ bidstools ++++++++++++++++++++++++
Singularity>

```
user@f0db12773d42:~$ cd /neurodesktop-storage/
user@f0db12773d42:/neurodesktop-storage$ ll
total 4
drwxrwxrwx 1 root root 4096 Sep 17 06:44 .
drwxr-xr-x 1 root root 4096 Sep 17 06:41 ..
drwxrwxr-x 1 root root 4096 Sep 17 06:44 1_Fingertapping_Dicoms
user@f0db12773d42:/neurodesktop-storage$
```

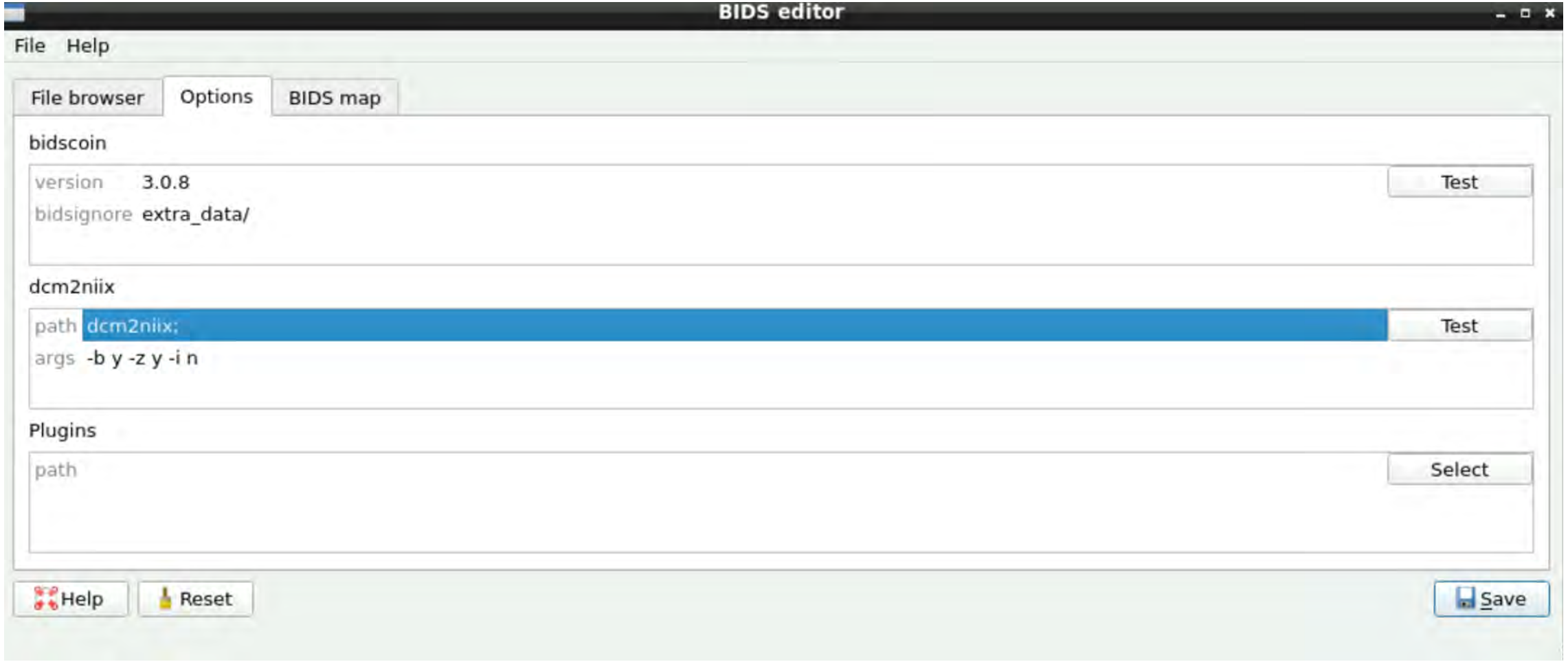
```
Singularity> dicomsort 1_Fingertapping_Dicoms/sub-01/ -r -e .IMA
2021-09-17 00:21:51 - bidscoin -      >> Sorting: 1_Fingertapping_Dicoms/sub-01 (469 files)
2021-09-17 00:21:51 - bidscoin -         Creating:  1_Fingertapping_Dicoms/sub-01/006-mp2rage_highRes_0p5iso_slab_UNI-DEN
2021-09-17 00:22:01 - bidscoin -         Creating:  1_Fingertapping_Dicoms/sub-01/020-fingertapping_run1_SBRef
2021-09-17 00:22:01 - bidscoin -         Creating:  1_Fingertapping_Dicoms/sub-01/021-fingertapping_run1
Singularity>
```

```
Singularity> mkdir bids
Singularity> bidsmapper 1_Fingertapping_Dicoms/ bids/
2021-09-17 00:23:28 - bidscoin -
2021-09-17 00:23:28 - bidscoin -        -------------- START BIDSmapper ------------
2021-09-17 00:23:28 - bidscoin -        >>> bidsmapper sourcefolder=/neurodesktop/1_Fingertapping_Dicoms bidsfolder=/neurodesktop/bids bidsmap=bidsmap.yaml  template=bidsmap_template.yaml subprefix=sub-
 sesprefix=ses- store=False interactive=1
2021-09-17 00:23:28 - bidscoin -        No existing bidsmap file found: /opt/miniconda-latest/lib/python3.6/site-packages/heuristics/bidsmap.yaml
2021-09-17 00:23:28 - bidscoin -        Reading: /opt/miniconda-latest/lib/python3.6/site-packages/heuristics/bidsmap_template.yaml
QStandardPaths: XDG_RUNTIME_DIR not set, defaulting to '/tmp/runtime-user'
2021-09-17 00:23:33 - bidscoin -        Parsing: /neurodesktop/1_Fingertapping_Dicoms/sub-01 (subject 1/1)
2021-09-17 00:23:37 - bidscoin -        Found 'extra_data' DICOM sample: /neurodesktop/1_Fingertapping_Dicoms/sub-01/006-mp2rage_highRes_0p5iso_slab_UNI-DEN/S16_SB_006_mp2rage_highRes_0p5iso_slab_UNI-DE
N_00001_00001.IMA
2021-09-17 00:23:41 - bidscoin -        Found 'extra_data' DICOM sample: /neurodesktop/1_Fingertapping_Dicoms/sub-01/020-fingertapping_run1_SBRef/SB_020_fingertapping_run1_SBRef_00001_00001.IMA
2021-09-17 00:23:45 - bidscoin -        Found 'extra_data' DICOM sample: /neurodesktop/1_Fingertapping_Dicoms/sub-01/021-fingertapping_run1/SB_021_fingertapping_run1_00001_00001.IMA
2021-09-17 00:23:45 - bidscoin -        Writing bidsmap to: /neurodesktop/bids/code/bidscoin/bidsmap.yaml
```

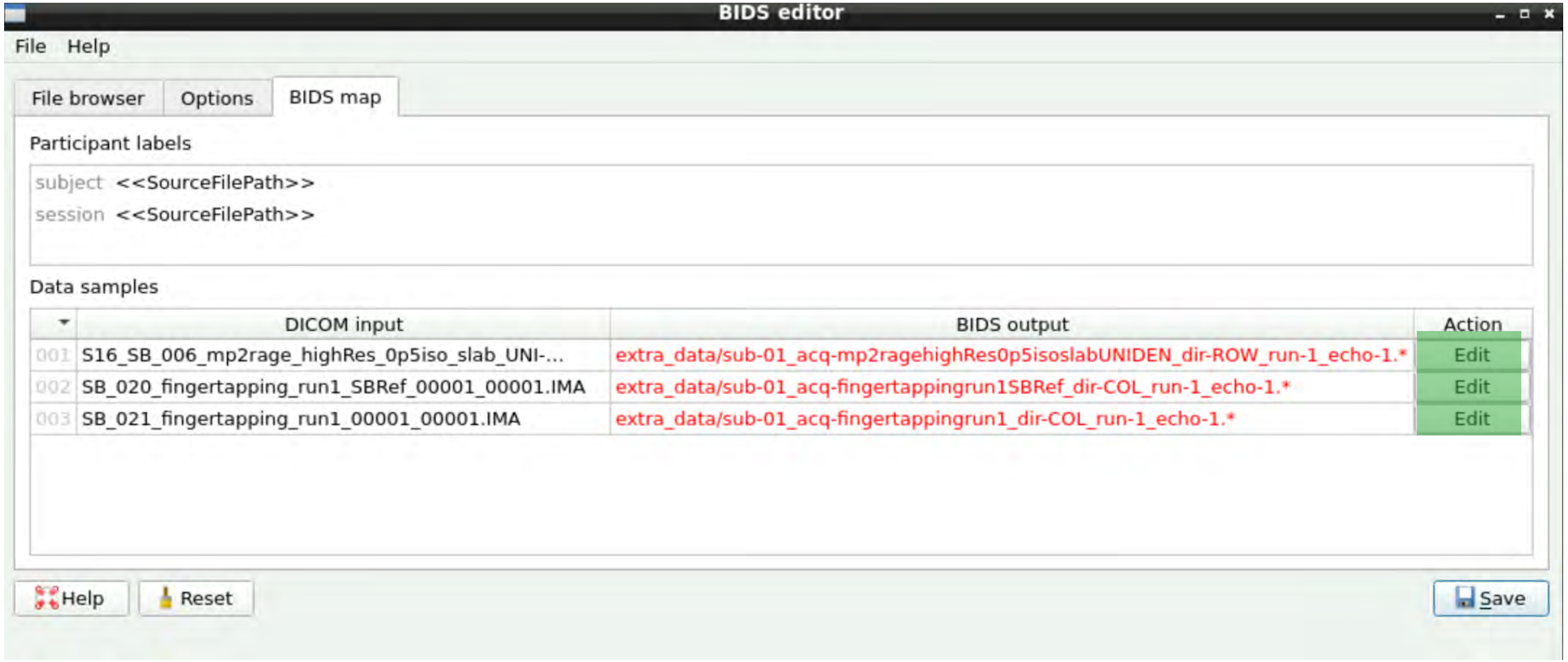


BIDS editor
File Help
File browser
Options
BIDS map
Participant labels
subject <<SourceFilePath>>
session <<SourceFilePath>>
Data samples
DICOM input
BIDS output
Action
001 S16_SB_006_mp2rage_highRes_0p5iso_slab_UNI-...
extra_data/sub-01_acq-mp2ragehighRes0p5isoslabUNIDEN_dir-ROW_run-1_echo-1.*
Edit
002 SB_020_fingertapping_run1_SBRef_00001_00001.IMA
extra_data/sub-01_acq-fingertappingrun1SBRef_dir-COL_run-1_echo-1.*
Edit
003 SB_021_fingertapping_run1_00001_00001.IMA
extra_data/sub-01_acq-fingertappingrun1_dir-COL_run-1_echo-1.*
Edit
Help
Reset
Save

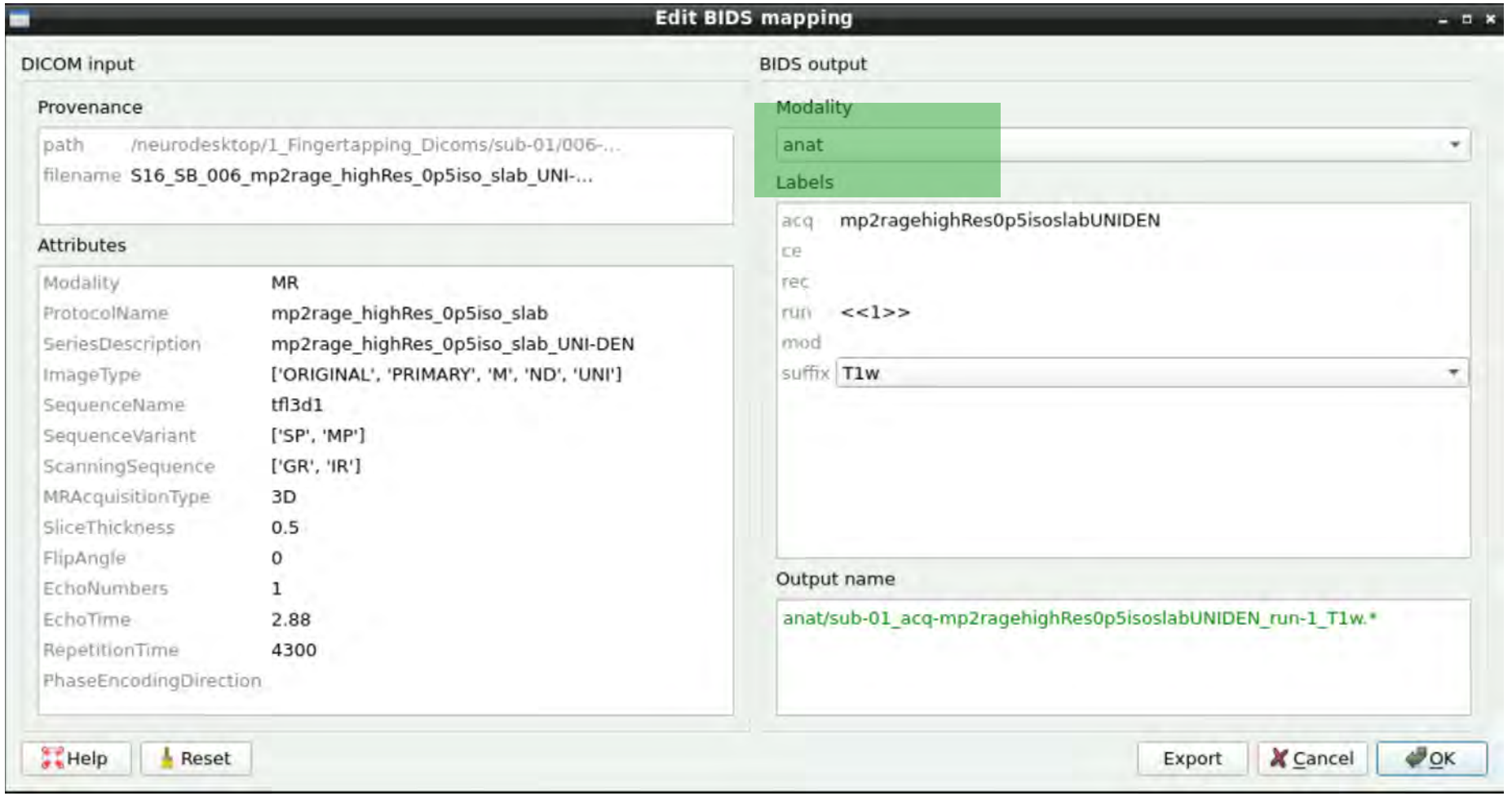
Change path to dcm2niix



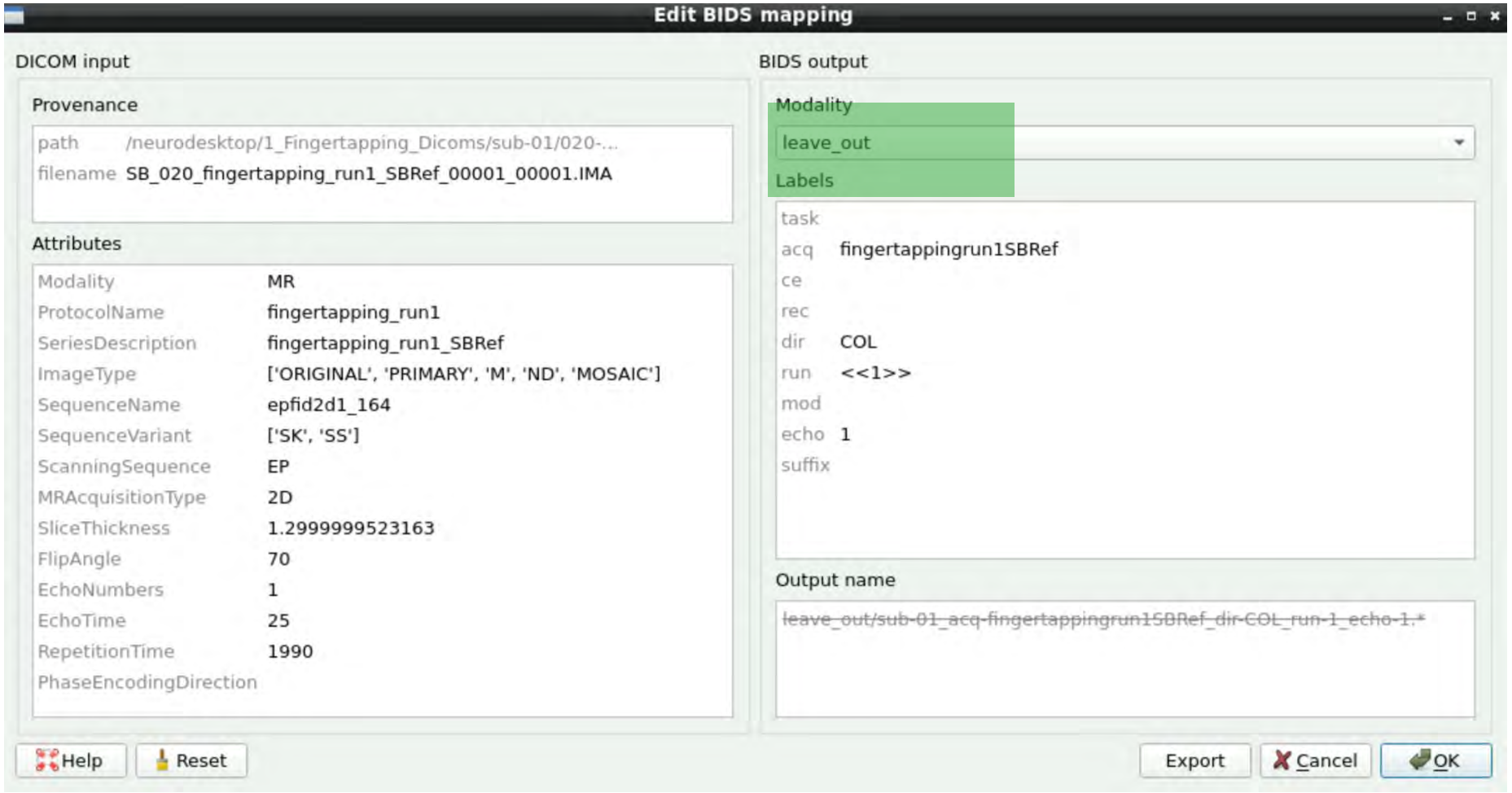
Edit the runs and assign what they are



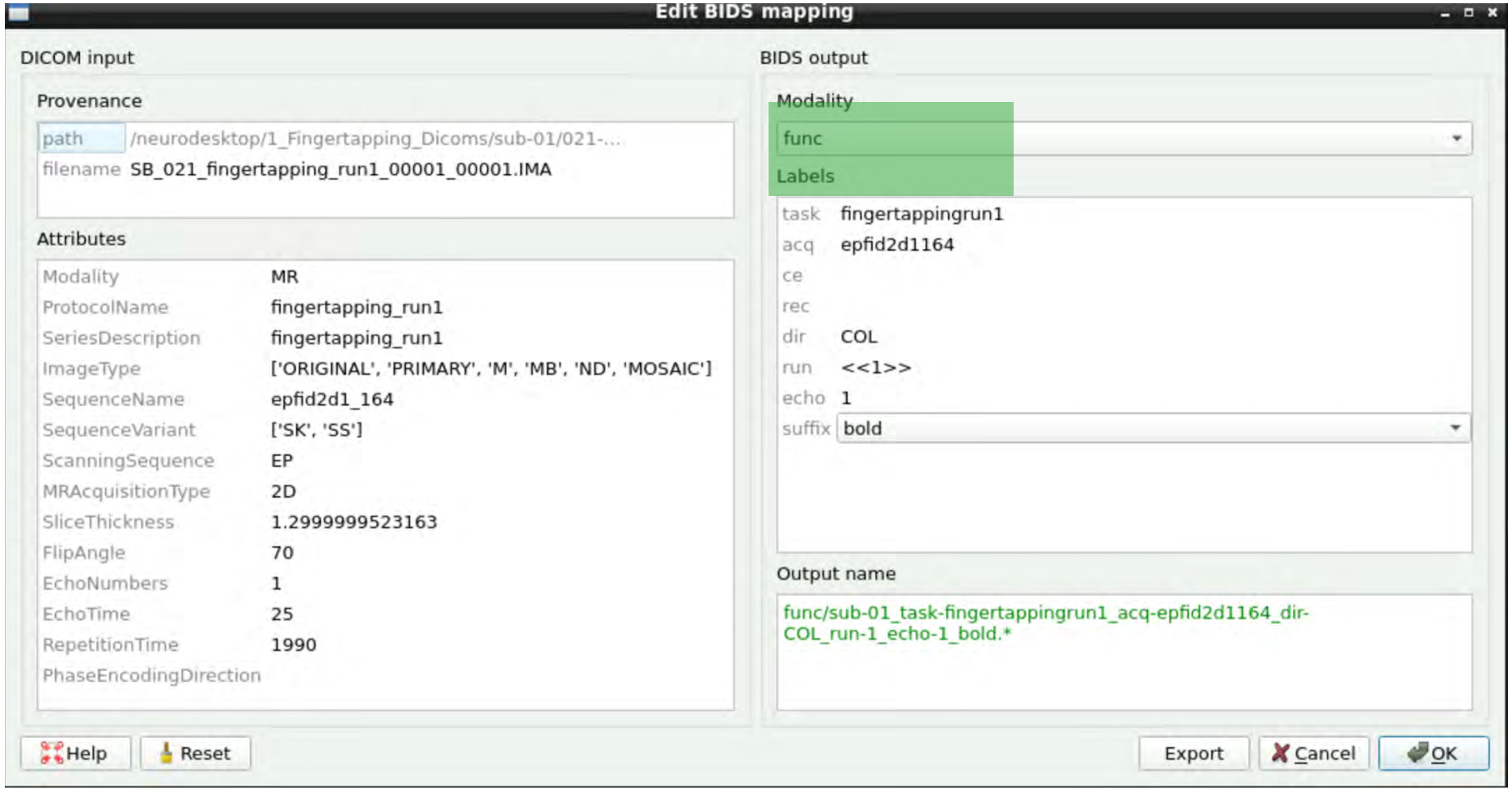
First one is anatomy



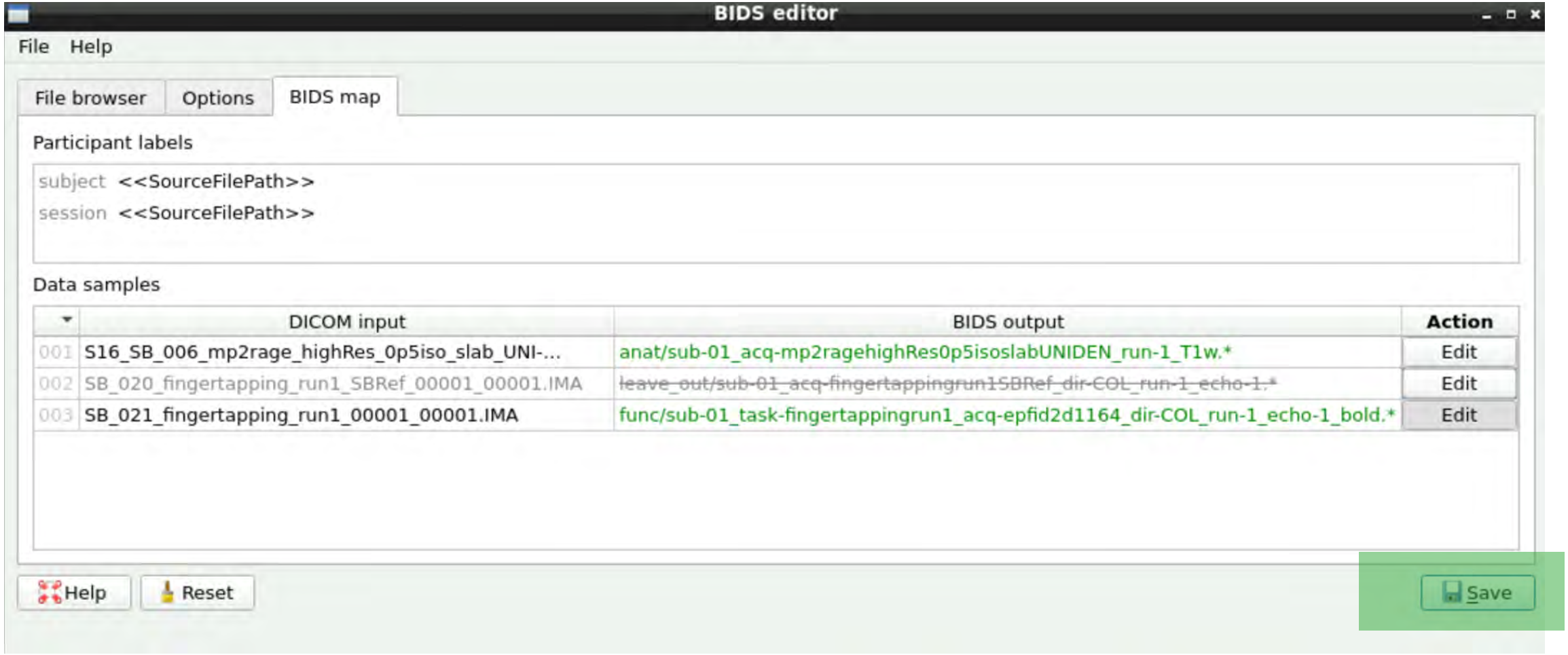
Second is reference scan – not needed



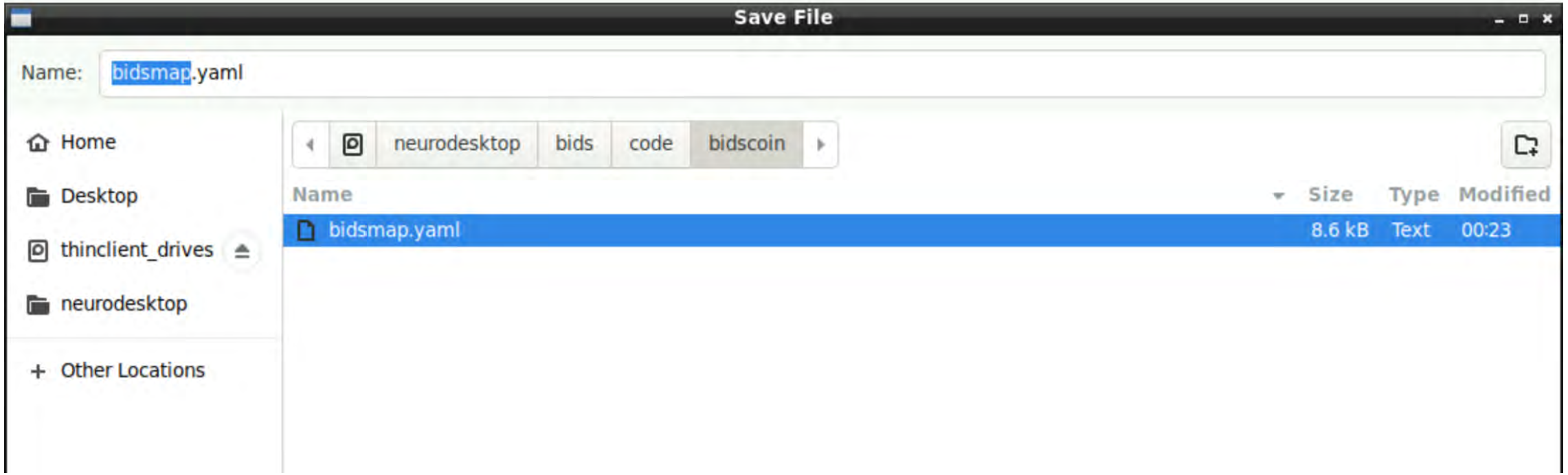
Change to “func” Modality



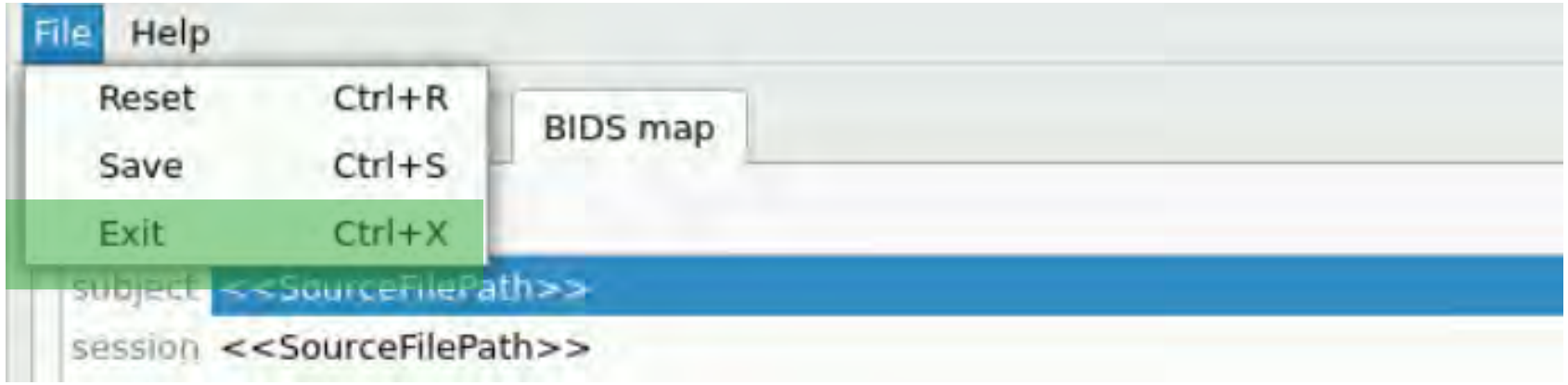
Hit Ok and Save



Save bidsmap.yaml in the suggested location



Exit BIDS editor

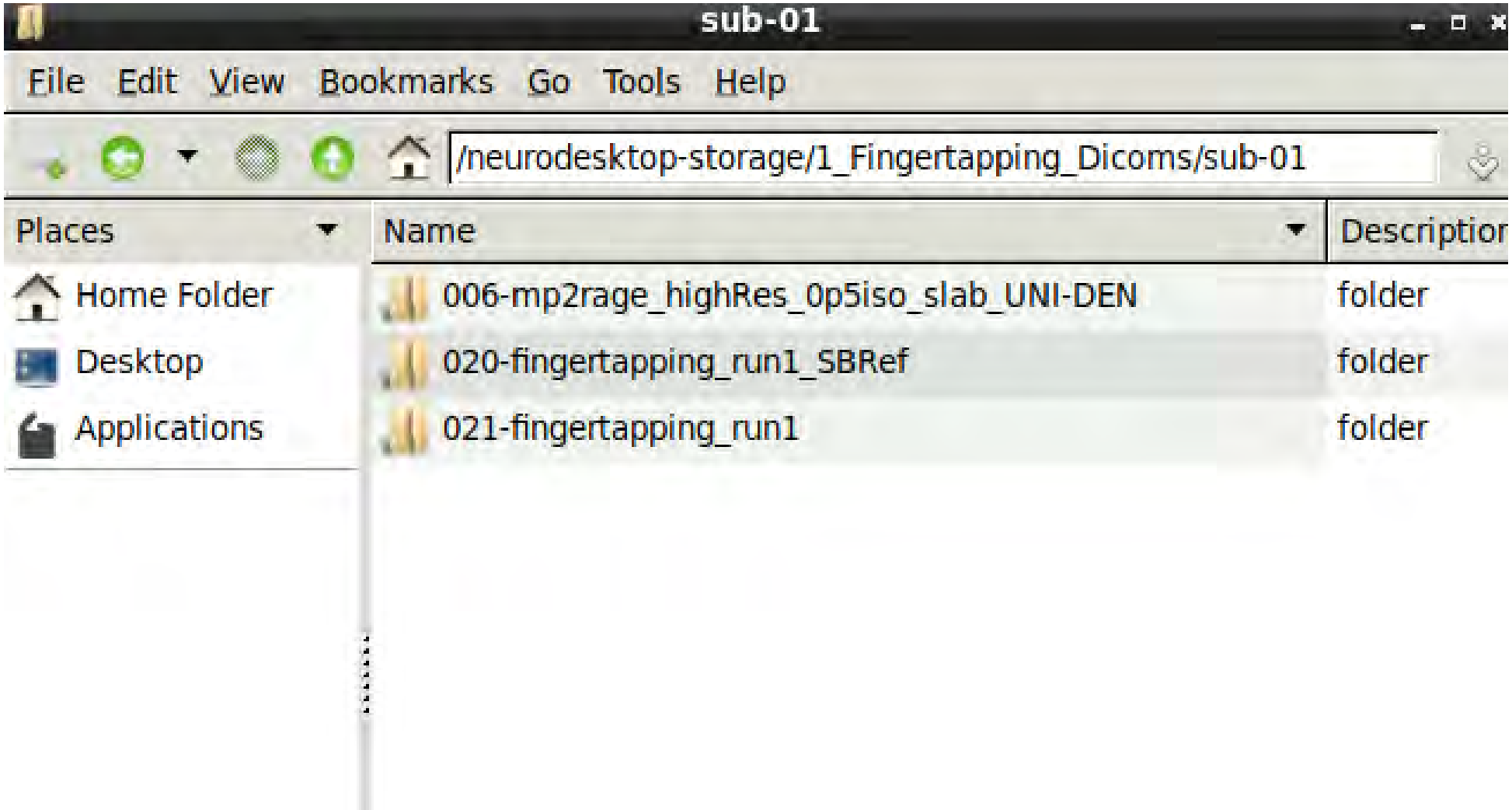


Start the conversion to bids ☺

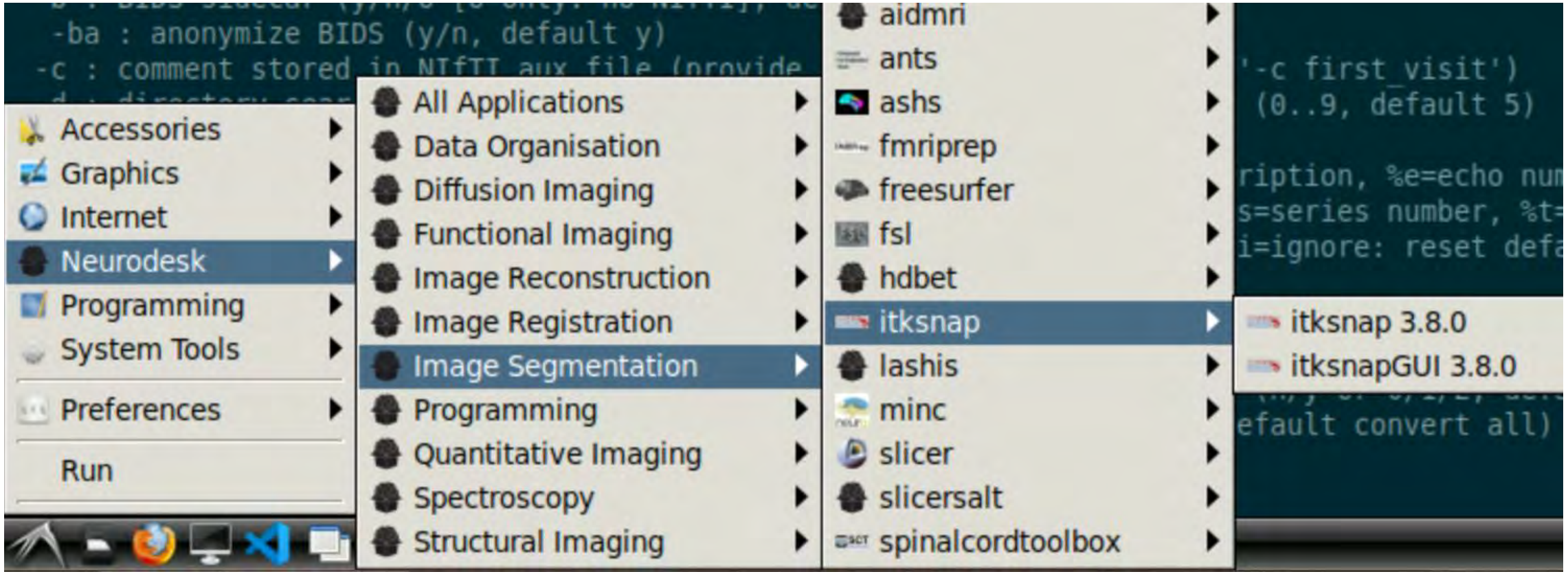
```
bidscoiner 1_Fingertapping_Dicoms/ bids/
```

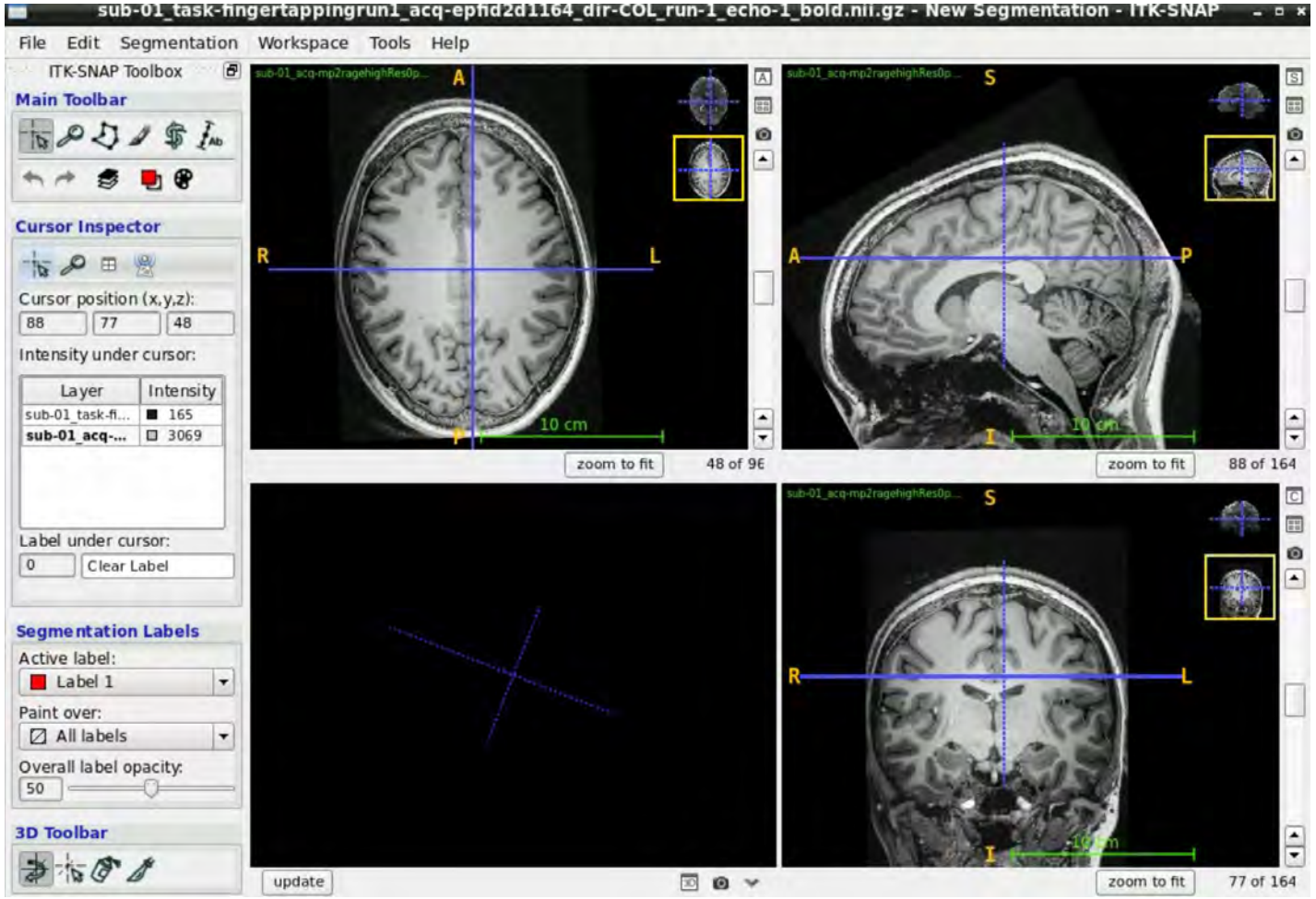
```
Singularity> bidscoiner 1_Fingertapping_Dicoms/ bids/
2021-09-17 00:33:03 - bidscoin -
2021-09-17 00:33:03 - bidscoin -        ------------- START BIDScoiner 3.0.8: BIDS 1.2.2 ------------
2021-09-17 00:33:03 - bidscoin -        >>> bidscoiner sourcefolder=/neurodesktop/1_Fingertapping_Dicoms bidsfolder=/neurodesktop/bids subjects=None force=False participants=False bidsmap=bidsmap.yaml s
ubprefix=sub- sesprefix=ses-
2021-09-17 00:33:03 - bidscoin -        Creating dataset description file: /neurodesktop/bids/dataset_description.json
2021-09-17 00:33:03 - bidscoin -        Creating README file: /neurodesktop/bids/README
2021-09-17 00:33:03 - bidscoin -        Reading: /neurodesktop/bids/code/bidscoin/bidsmap.yaml
2021-09-17 00:33:03 - bidscoin -        Writing ['extra_data/'] entries to /neurodesktop/bids.bidsignore
2021-09-17 00:33:03 - bidscoin -        ------------------- Subject 1/1 -------------------
2021-09-17 00:33:03 - bidscoin -        Coining session: /neurodesktop/1_Fingertapping_Dicoms/sub-01
2021-09-17 00:33:03 - bidscoin -        Processing: /neurodesktop/1_Fingertapping_Dicoms/sub-01/006-mp2rage_highRes_0p5iso_slab_UNI-DEN
2021-09-17 00:33:03 - bidscoin -        Running: dcm2niix;dcm2niix -b y -z y -i n -f "sub-01_acq-mp2ragehighRes0p5isoslabUNIDEN_run-1_T1w" -o "/neurodesktop/bids/sub-01/anat" "/neurodesktop/1_Fingertapp
ing_Dicoms/sub-01/006-mp2rage_highRes_0p5iso_slab_UNI-DEN"
2021-09-17 00:33:10 - bidscoin -        Output:
Chris Rorden's dcm2niiX version v1.0.20201102  GCC9.3.0 x86-64 (64-bit Linux)
usage: dcm2niix [options] <in_folder>
 Options :
  -1..-9 : gz compression level (1=fastest..9=smallest, default 6)
  -a : adjacent DICOMs (images from same series always in same folder) for faster conversion (n/y, default n)
  -b : BIDS sidecar (y/n/o [o=only: no NIfTI], default y)
   -ba : anonymize BIDS (y/n, default y)
  -c : comment stored in NIfTI aux_file (provide up to 24 characters e.g. '-c first_visit')
  -d : directory search depth. Convert DICOMs in sub-folders of in_folder? (0..9, default 5)
  -e : export as NRRD instead of NIfTI (y/n, default n)
  -f : filename (%a=antenna (coil) name, %b=basename, %c=comments, %d=description, %e=echo number, %f=folder name, %i=ID of patient, %j=seriesInstanceUID, %k=studyInstanceUID, %m=manufacturer, %n=name
 of patient, %o=mediaObjectInstanceUID, %p=protocol, %r=instance number, %s=series number, %t=time, %u=acquisition number, %v=vendor, %x=study ID; %z=sequence name; default '%f_%p_%t_%s')
  -g : generate defaults file (y/n/o/i [o=only: reset and write defaults; i=ignore: reset defaults], default n)
  -h : show help
  -i : ignore derived, localizer and 2D images (y/n, default n)
  -l : losslessly scale 16-bit integers to use dynamic range (y/n/o [yes=scale, no=no, but uint16->int16, o=original], default n)
  -m : merge 2D slices from same series regardless of echo, exposure, etc. (n/y or 0/1/2, default 2) [no, yes, auto]
  -n : only convert this series CRC number - can be used up to 16 times (default convert all)
  -o : output directory (omit to save to input folder)
  -p : Philips precise float (not display) scaling (y/n, default y)
```

Look at the output files created

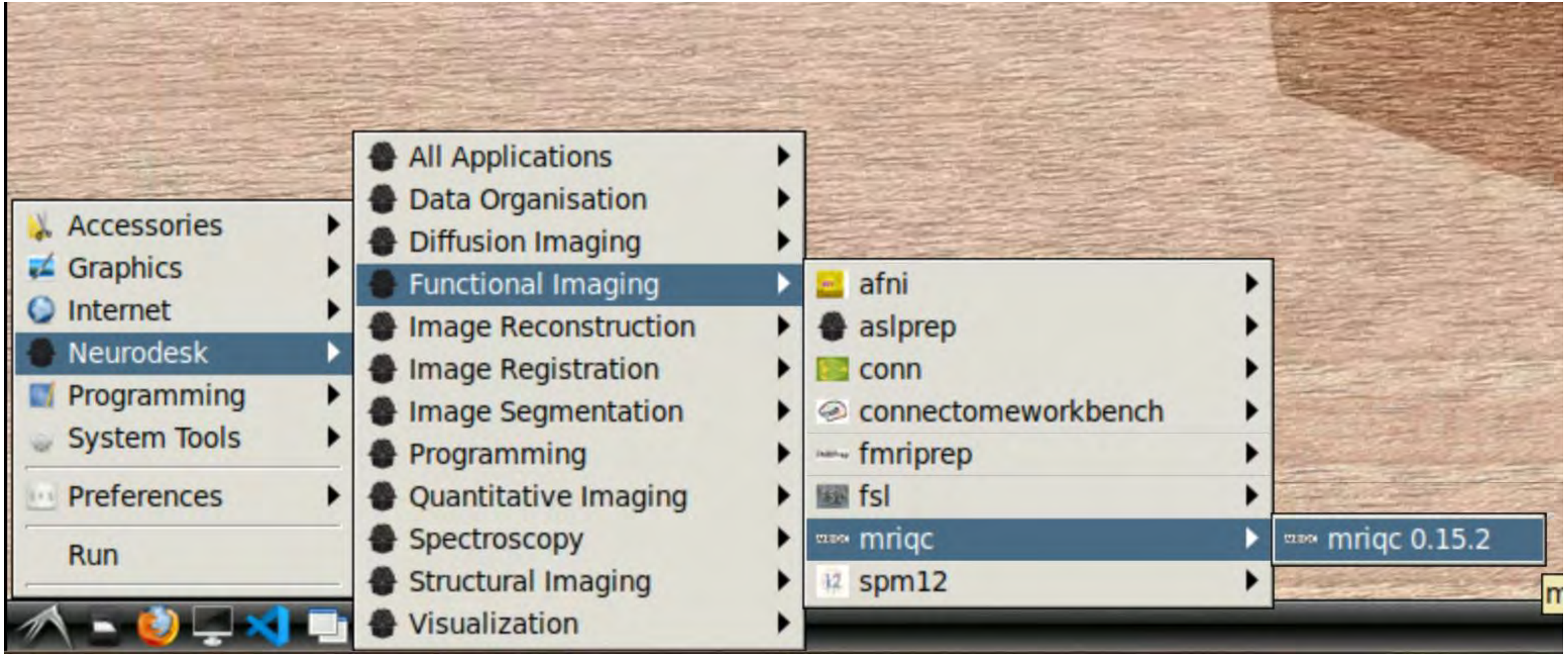


Look at data in ITKsnap

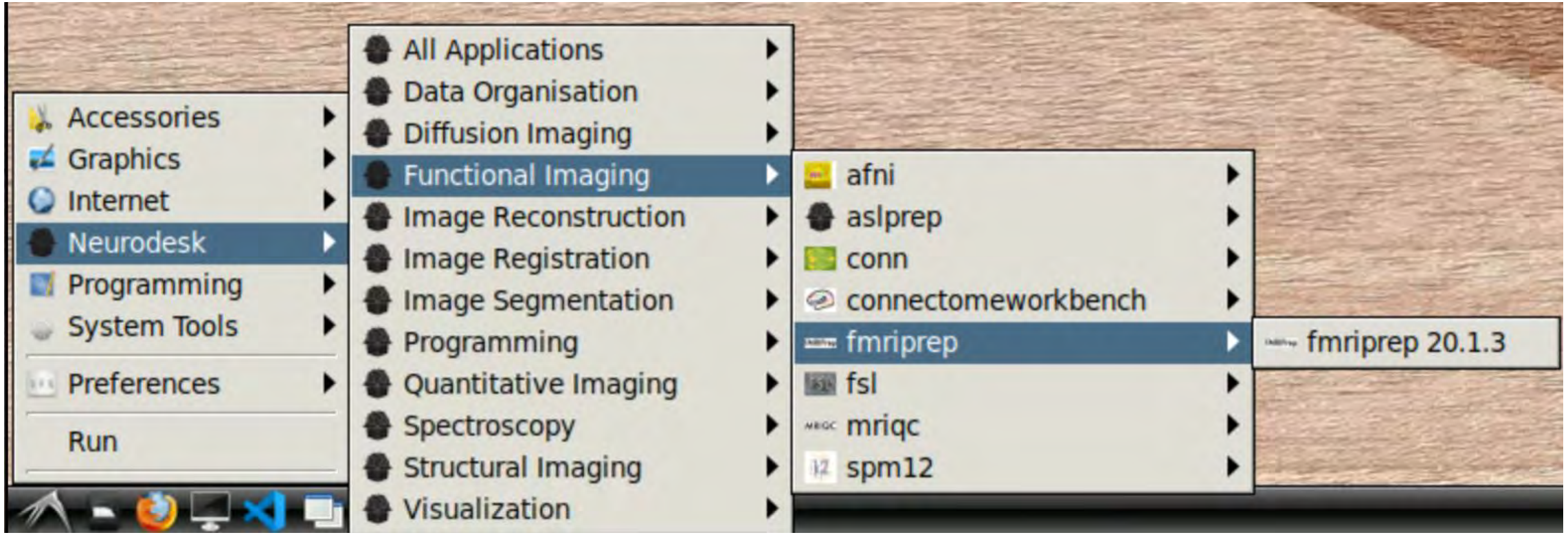



sub-01_task-fingertappingrun1_acq-epfid2d1164_dir-COL_run-1_echo-1_bold.nii.gz - New Segmentation - ITK-SNAP
File
Edit
Segmentation
Workspace
Tools
Help
ITK-SNAP Toolbox
Main Toolbar
Cursor Inspector
Cursor position (x,y,z):
88
77
48
Intensity under cursor:
Layer
Intensity
sub-01_task-fi...
165
sub-01_acq-...
3069
Label under cursor:
0
Clear Label
Segmentation Labels
Active label:
Label 1
Paint over:
All labels
Overall label opacity:
50
3D Toolbar
A
P
R
L
S
I
10 cm
zoom to fit
48 of 96
88 of 164
77 of 164
update

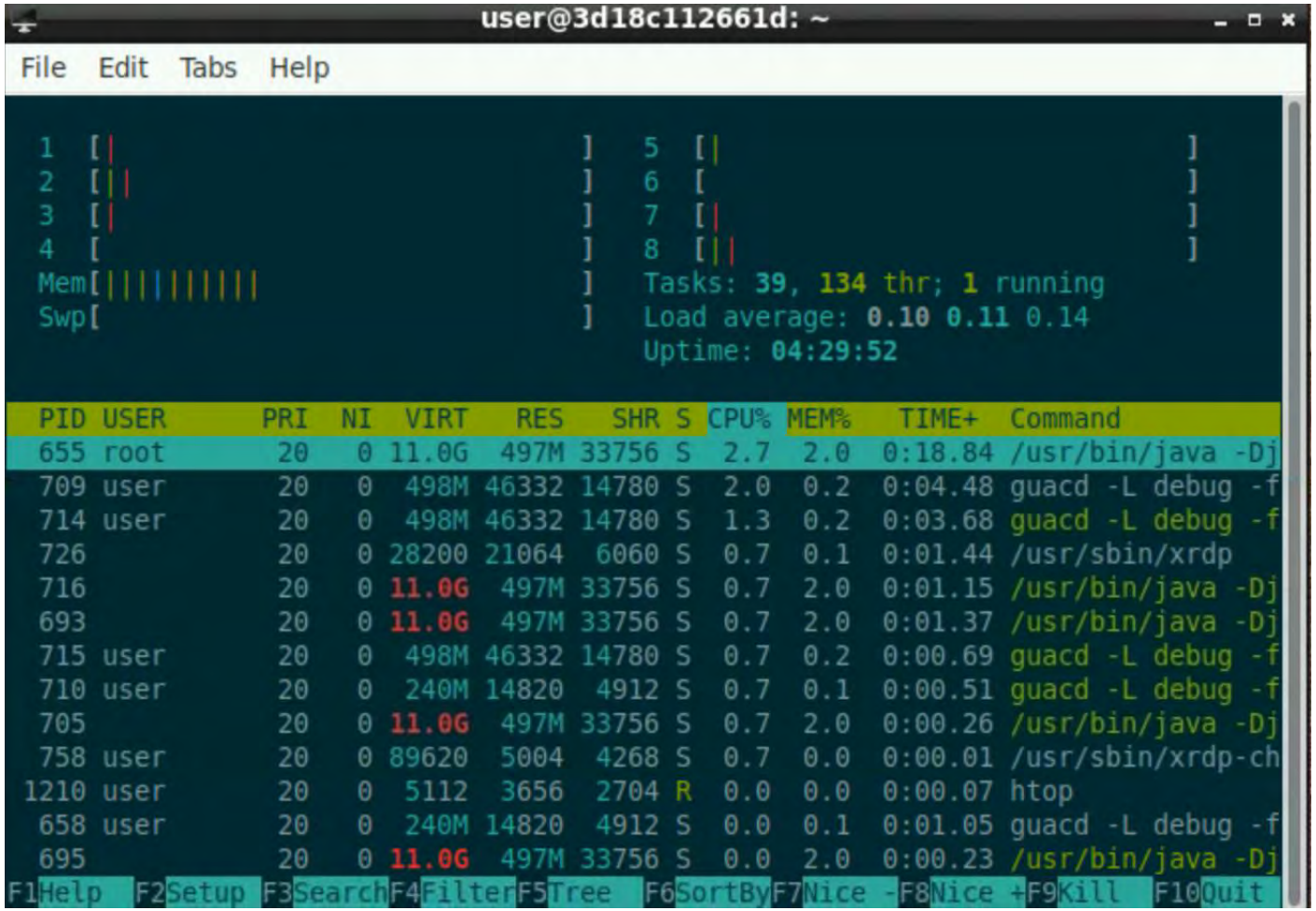
now we could use MRIqc



or fMRIprep

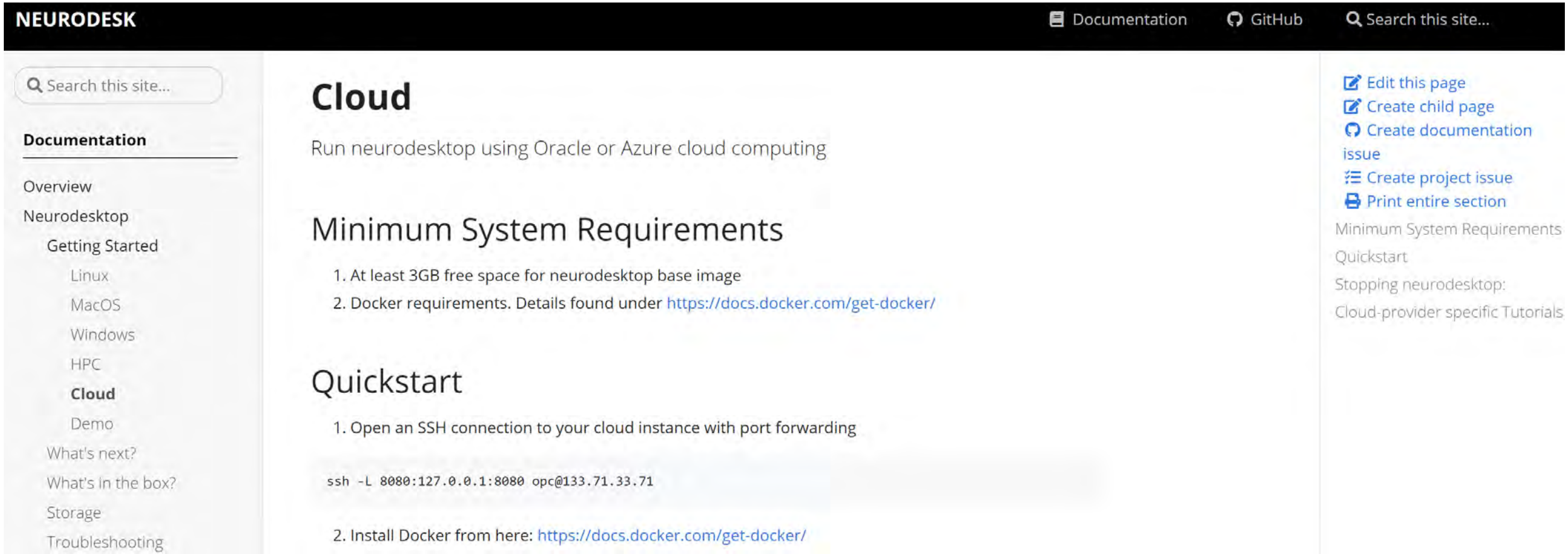

Accessories
Graphics
Internet
Neurodesk
Programming
System Tools
Preferences
Run
All Applications
Data Organisation
Diffusion Imaging
Functional Imaging
Image Reconstruction
Image Registration
Image Segmentation
Programming
Quantitative Imaging
Spectroscopy
Structural Imaging
Visualization
afni
aslprep
conn
connectomeworkbench
fmriprep
fsl
mriqc
spm12
fmriprep 20.1.3

BUT: computer too slow



NeuroDesktop in the Cloud

Cloud setup – connect to cloud instance with tunnel




```
ssh -L 8080:127.0.0.1:8080 opc@152.67.98.39
```

Start Neurodesktop in the cloud

```
[opc@neurodesk ~]$ sudo docker run --shm-size=1gb -it --privileged --name neurodesktop -v ~/neurodesktop:/neurodesktop -e HOST_UID="$(id -u)" -e HOST_GID="$(id -g)" -p 8080:8080 vnmd/neur
odesktop:20210917
Unable to find image 'vnmd/neurodesktop:20210917' locally
Trying to pull repository docker.io/vnmd/neurodesktop ...
20210917: Pulling from docker.io/vnmd/neurodesktop
35807b77a593: Already exists
c437049e42e2: Pull complete
4f2c86384465: Pull complete
a48fd7885107: Pull complete
2f6bfd9717ed: Pull complete
a214dad4d0d5: Pull complete
76e8846454c6: Pull complete
ea49baeab7f7: Pull complete
fa07df76b394: Pull complete
d2dbf549b363: Pull complete
0e3b6f679c40: Pull complete
7f33d04c8695: Pull complete
f1f13f2d6905: Pull complete
13c01807ec10: Pull complete
6d12a01dfa41: Extracting [==================================================>]  1.559kB/1.559kB
e3ceb6309db5: Download complete
f46a4d16b597: Download complete
4c9c971bf06c: Download complete
80f27ec6015f: Download complete
7e34cf62418f: Download complete
1388325df2f9: Download complete
537491dc8667: Download complete
732a930002ee: Download complete
aa36700b2e1e: Download complete
63ee34713a09: Download complete
3fb276372cc1: Download complete
82052eeb7161: Download complete
df71ea59471d: Download complete
fb5f580fbca3: Download complete
050f481e3aa2: Download complete
48595544fb94: Download complete
```

```
================================================================
Starting Guacamole Daemon
----------------------------------------------------------------
    Use this link for direct Neurodesktop:
!!! http://localhost:8080/#/?username=user&password=password !!!
    Once connected to the session, your user info is:
    Username: "user"
    Password: "password"
----------------------------------------------------------------
guacd[656]: INFO:       Guacamole proxy daemon (guacd) version 1.3.0 started
guacd[656]: DEBUG:      Successfully bound socket to host 127.0.0.1, port 4822
guacd[656]: INFO:       Listening on host 127.0.0.1, port 4822
```

Connect to cloud storage

Storage

Add storage to Neurodesktop

Cloud-storage

The easiest way to get your data into Neurodesktop is to use a cloud storage provider like CloudStor, Dropbox, OneDrive and their sync tools like OwnCloud, Nextcloud or very flexible tools like rclone or davfs2. Another good option could be to utilize Globus for large amounts of data.

Nextcloud and Owncloud desktop clients

Under the menu item “Accessories” you can find “Nextcloud” and “ownCloud” desktop sync clients that you can configure with your cloud service accounts.

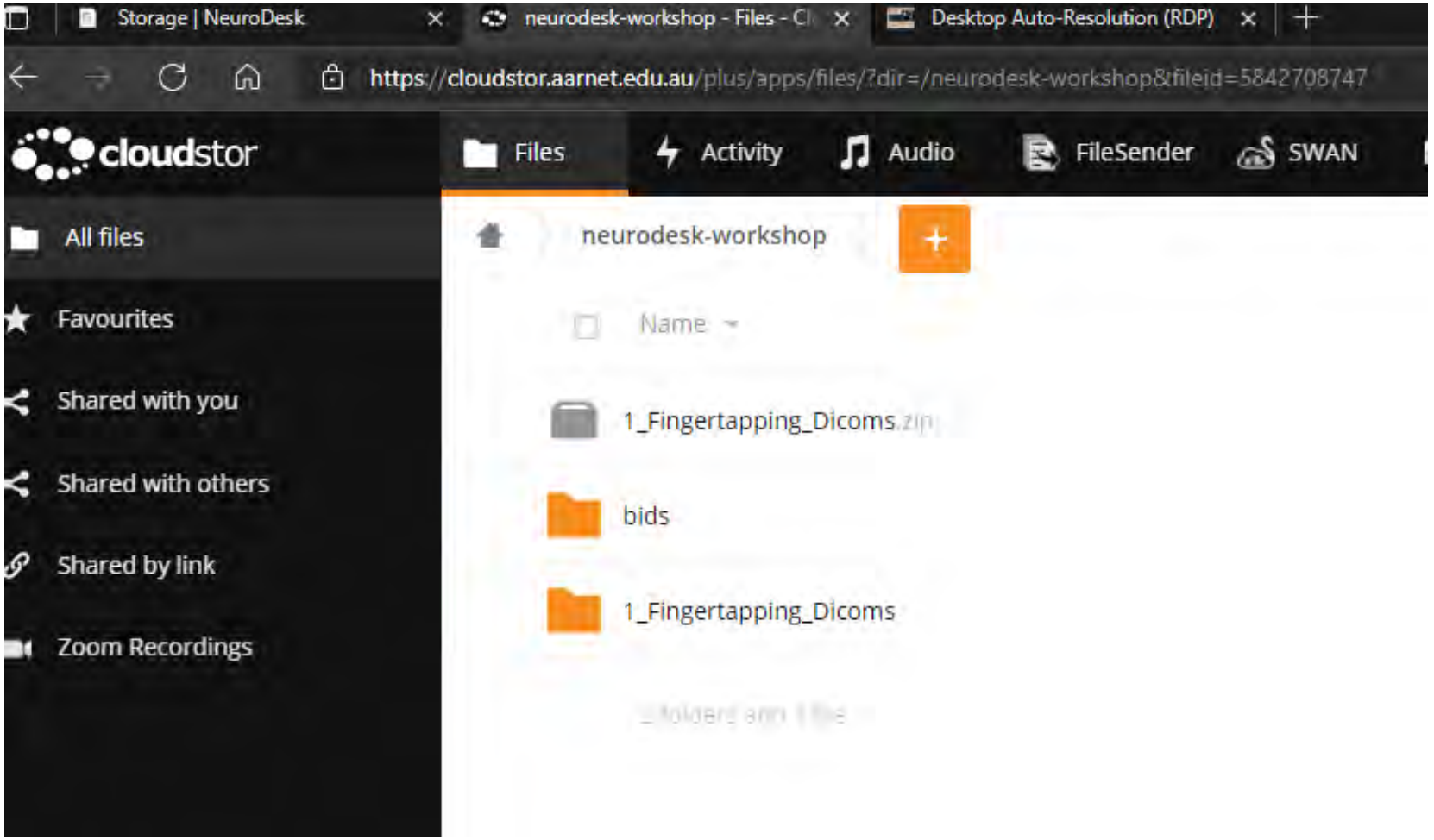
Mounting webdav storage using davfs2

Another option is to directly mount webdav storage. Here is an example how to mount CloudStor into Neurodesktop:

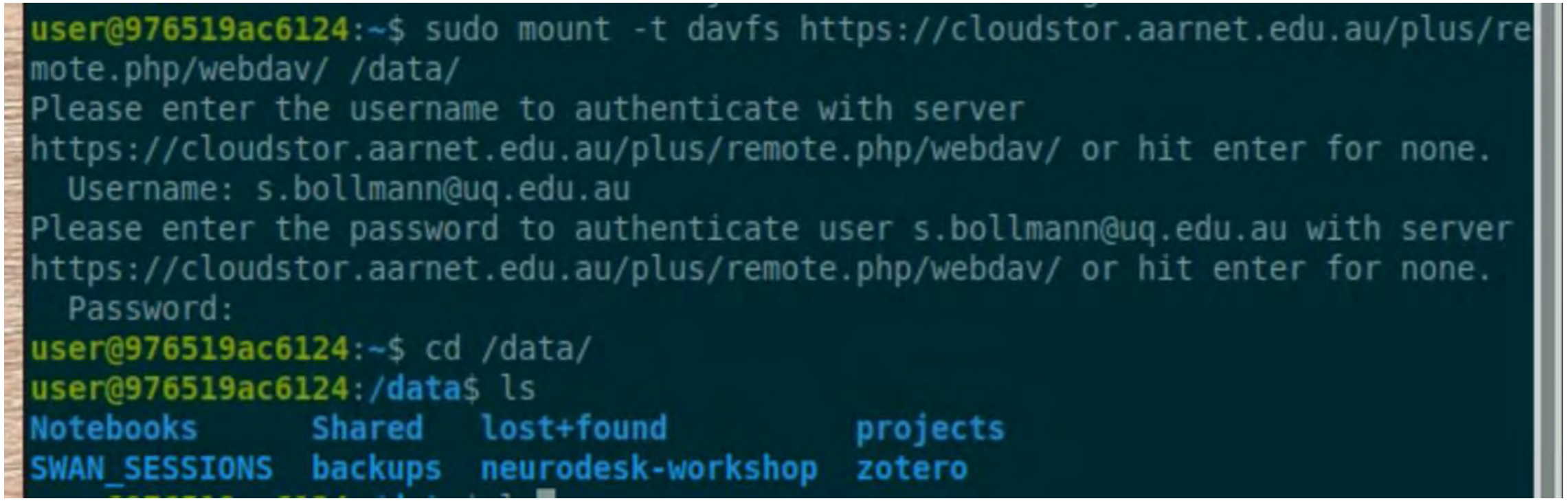
```
sudo mount -t davfs https://cloudstor.aarnet.edu.au/plus/remote.php/webdav/ /data/
```

It then asks you for a username and password, which you can generate here:
https://cloudstor.aarnet.edu.au/plus/settings/personal?sectionid=security

https://cloudstor.aarnet.edu.au/plus/apps/files



CloudStor storage mounted ☺



Start MRIQC in cloud

bash

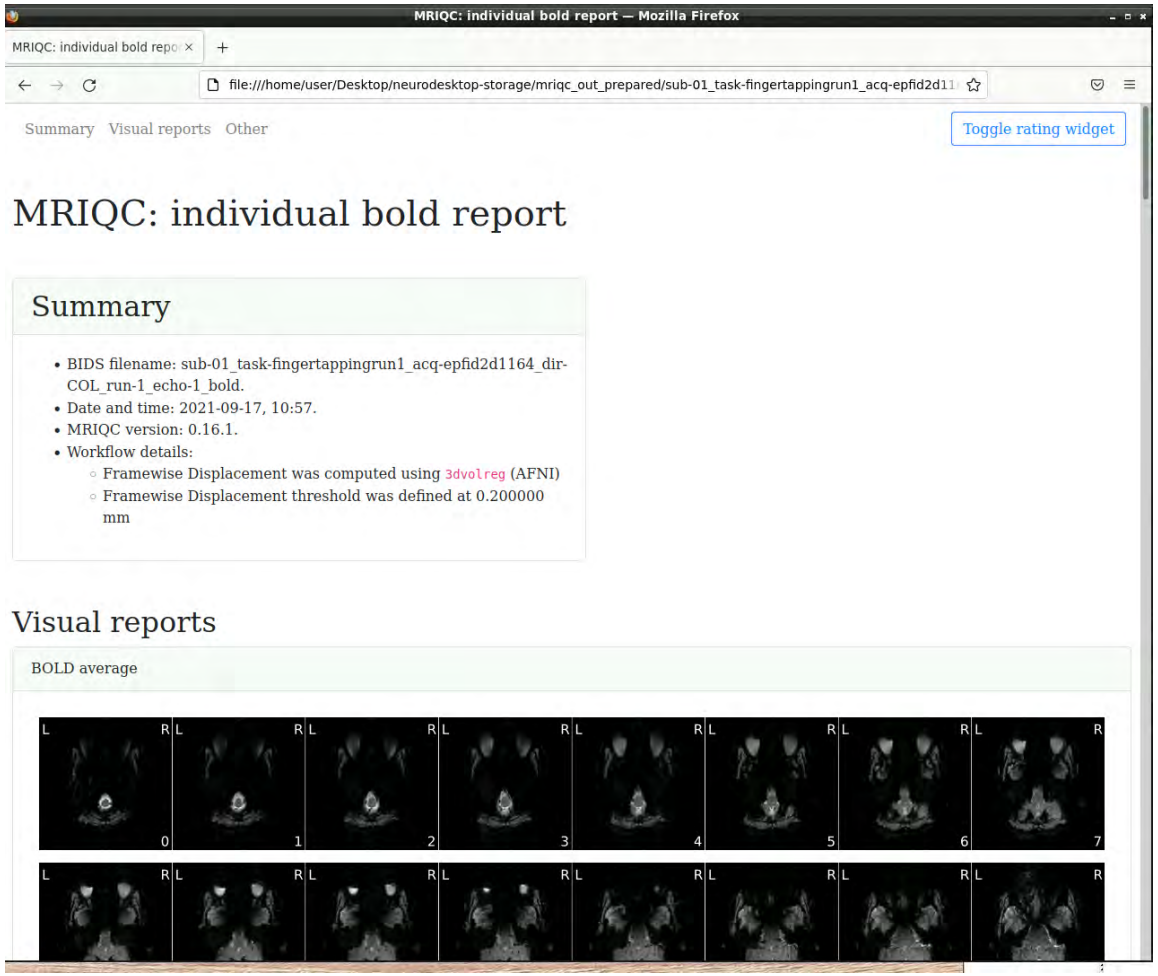
File Edit Tabs Help

```
usage: mriqc [-h] [--version]
             [--participant_label [PARTICIPANT_LABEL [PARTICIPANT_LABEL ...]]]
             [--session-id [SESSION_ID [SESSION_ID ...]]]
             [--run-id [RUN_ID [RUN_ID ...]]]
             [--task-id [TASK_ID [TASK_ID ...]]]
             [-m [MODALITIES [MODALITIES ...]]] [--dsname DSNAME]
             [-w WORK_DIR] [--verbose-reports] [--write-graph] [--dry-run]
             [--profile] [--use-plugin USE_PLUGIN] [--no-sub] [--email EMAIL]
             [-v] [--webapi-url WEBAPI_URL] [--webapi-port WEBAPI_PORT]
             [--upload-strict] [--n_procs N_PROCS] [--mem_gb MEM_GB]
             [--testing] [-f] [--ica] [--hmc-afni] [--hmc-fsl]
             [--fft-spikes-detector] [--fd_thres FD_THRES]
             [--ants-nthreads ANTS_NTHREADS] [--ants-float]
             [--ants-settings ANTS_SETTINGS] [--deoblique] [--despike]
             [--start-idx START_IDX] [--stop-idx STOP_IDX]
             [--correct-slice-timing]
            bids_dir output_dir {participant,group} [{participant,group} ...]
```

More documentation can be found here: https://mriqc.readthedocs.io/en/stable/running.html

```
Singularity> mriqc /data/bids/ /data/qc_output participant
```

Open Firefox and inspect MRIQC outputs



Neurocommand on CVL

https://desktop.cvl.org.au/strudel-web/#/system-selector

Search this site...

Documentation

Overview
Neurodesktop
Getting Started
Linux
MacOS
Windows
HPC
Cloud
Demo
What's next?
What's in the box?
Storage
Troubleshooting
Release History
Neurocommand
Getting Started
Linux
Windows
Neurocontainers
For Developers
Add tools

Linux

Install neurocommand on Linux

Requirements:

Required

- python 3.6+ https://docs.conda.io/en/latest/miniconda.html#linux-installers
- singularity https://sylabs.io/guides/3.5/user-guide/quick_start.html
- git

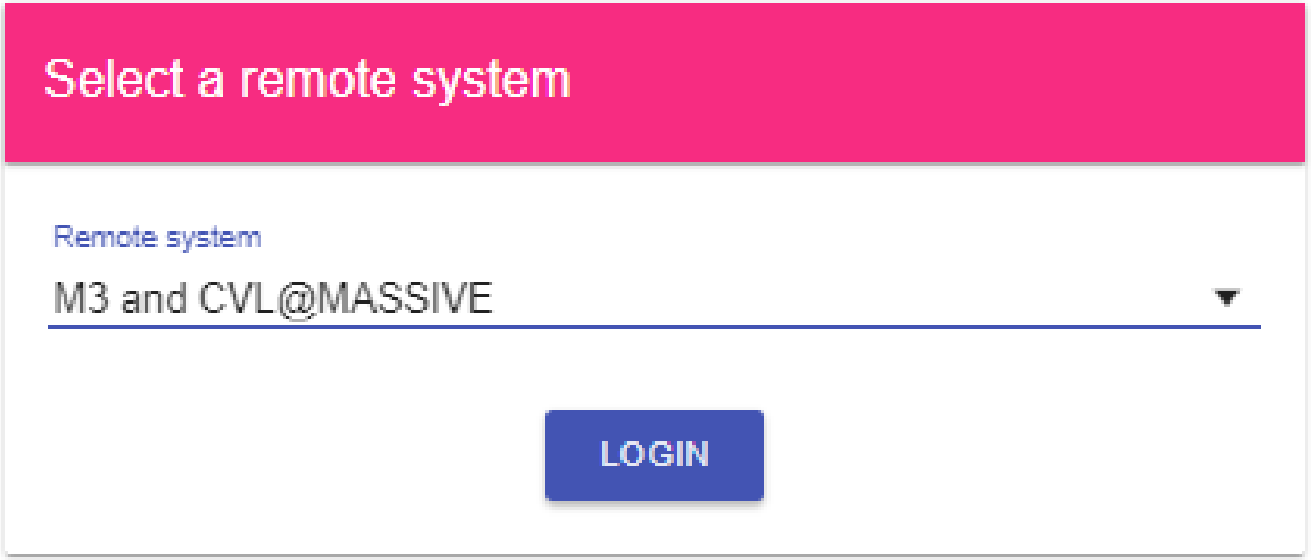
Optional

- lmod https://lmod.readthedocs.io/en/latest/

command line mode - For non-desktop experience (e.g. running on an HPC)

If running on cli only ...

- Load singularity and for best performance it should be 3.x e.g. `module load singularity/3.5.0`
- Load or install aria2 to optimize the download performance of our containers e.g. `module load aria2c`
- make sure the current directory is not a symlink (singularity bug): `pwd -P` and then cd there
- Run `git clone https://github.com/NeuroDesk/neurocommand.git` to clone the repository - make sure to clone this to a directory with enough storage, write permissions and NOT a symbolic link (to be sure run cd `pwd -P`)!
- Run `cd neurocommand` to change into the directory
- Run `pip3 install -r neurodesk/requirements.txt --user` to install pre-requisite python packages
- Run `bash build.sh --cli` to install in cli mode
- Run `bash containers.sh` for installing indiviual containers or `bash containers.sh --all` for installing all containers
- Run `module use $PWD/local/containers/modules/` to add the containers to your module search path. Add this to your .bashrc if working.
- Run `ml avail` to see the installed containers at the top of the list (neurodesk containers will take preference over system modules with the same name). If a container is not yet there run `ml --ignore_cache avail`


Select a remote system
Remote system
M3 and CVL@MASSIVE
LOGIN

fMRIPrep

- Automatically pre-process fMRI data
- Reads in BIDS and outputs BIDSderivative

nature methods

ARTICLES

https://doi.org/10.1038/s41592-018-0235-4

fMRIPrep: a robust preprocessing pipeline for functional MRI

Oscar Esteban[1*], Christopher J. Markiewicz[1], Ross W. Blair[1], Craig A. Moodie[1], A. Ilkay Isik[2], Asier Erramuzpe[3], James D. Kent[4], Mathias Goncalves[5], Elizabeth DuPre[6], Madeleine Snyder[7], Hiroyuki Oya[8], Satrajit S. Ghosh[5,9], Jessey Wright[1], Joke Durnez[1], Russell A. Poldrack[1,10] and Krzysztof J. Gorgolewski[1,10*]

```
[uqsbollm@m3p008 neurocommand]$ module use local/containers/modules/
[uqsbollm@m3p008 neurocommand]$ module avail fmriprep

---------------------------- local/containers/modules/ -----------------------------
fmriprep/20.1.3
```

Outlook

The organic solution …

Use this one when you do the ‘normal’analysis

This has the ‘high-resolution’ version installed

This one is for the study running since 1999
DO NOT TOUCH

This is the only one where we managed to get minc compiled

The neurodesk solution …

Use this one when you do the ‘normal’analysis

This has the ‘high-resolution’ version installed

This one is for the study running since 1999
DO NOT TOUCH

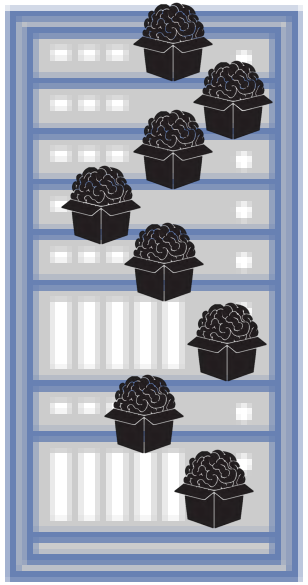
This is the only one where we managed to get minc compiled

… reproducibility anywhere at anytime

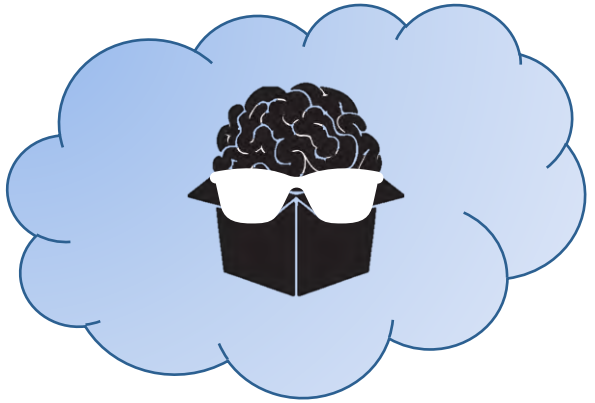
… on your notebook

… on your lab workstation

… on the university's high performance cluster

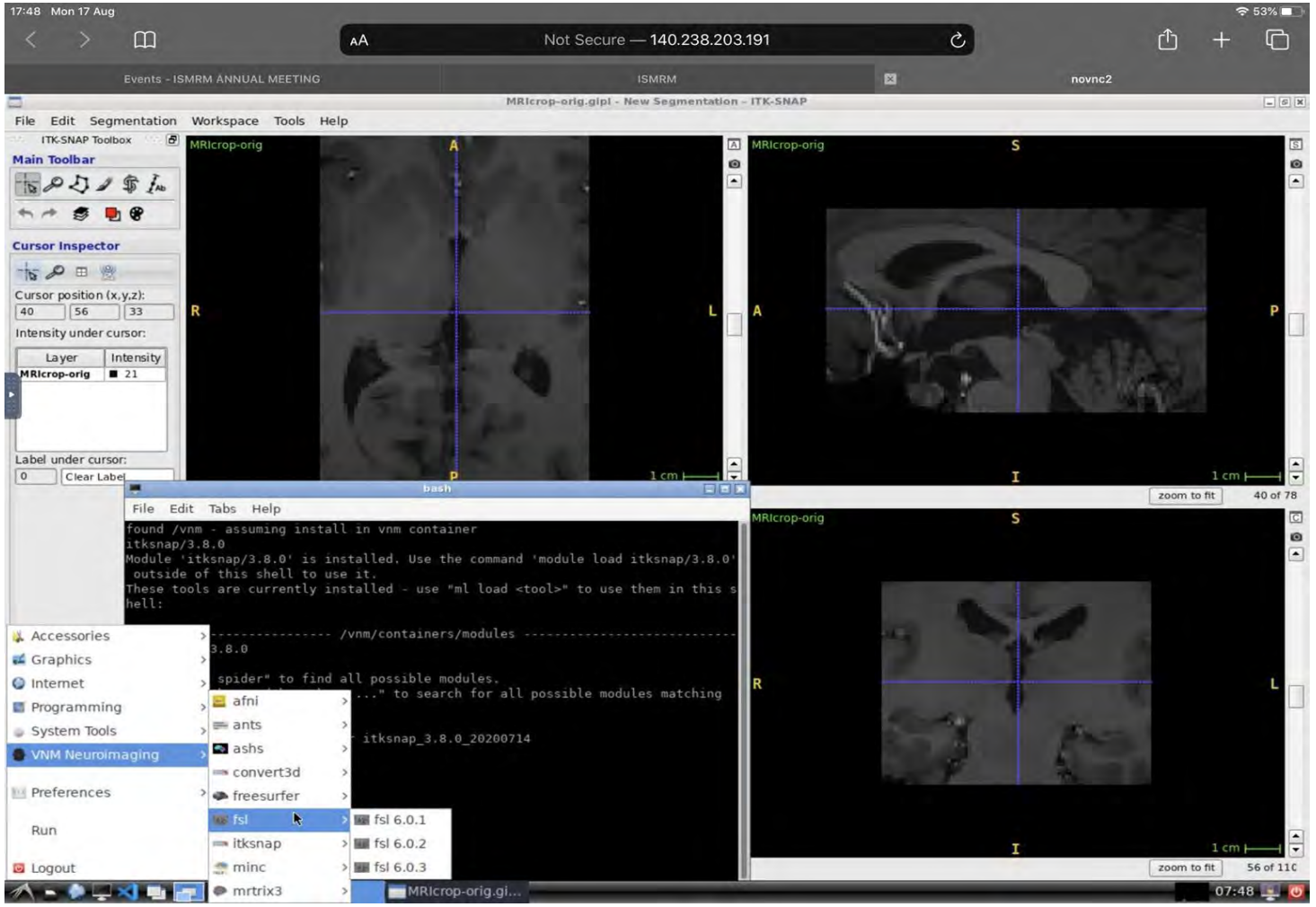


… on any cloud provider – the sky is the limit



Outlook - github.com/NeuroDesk

- Make start even easier (currently requires command lines -> develop GUI)
- Integrate GPUs for DL applications
- Integrate more applications



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nectar

National Imaging Facility

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Australian Research Data Commons

OHBM 2020
A Virtual Experience for Engaging Minds & Empowering Brain Science

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ORACLE Cloud

Jakub Kaczmarzyk

Google Summer of Code

Niruhan Viswarupan

Dao Thanh Thuy

Aswin Narayanan

Yorguin Jose Mantilla

Will Woods

Steffen Bollmann

Tom Johnstone

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