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OF QUEENSLAND  
AUSTRALIA

CREATE CHANGE

# Neurodesk

An accessible, flexible, and portable data analysis environment for  
reproducible neuroimaging

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# 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 Potential Conflicts of Interest

## I receive research funding from:

1. Oracle for Research - partially fund Neurodesk project via cloud credits
2. Siemens Healthineers





Do we need an accessible, flexible, and portable environment for reproducible Neuroimaging?

# The Accessibility problem

Most of our neuroimaging tools require Linux, but are not available in standard package systems

```
[user@centos> sudo yum install minc
Loaded plugins: langpacks, ulninfo
No package minc available.
Error: Nothing to do
```

(Users on Debian/Ubuntu are often luckier thanks to Neurodebian)

Then run `cmake ..` 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 comment 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`:



# The Flexibility problem

Conflicting dependencies -> we often cannot install different versions of software and operating system updates can break our software installations

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

(for example specific versions of Freesurfer require specific operating system dependencies)

# The Portability problem

Reinstalling tools on different platforms is a mess and takes a lot of time ...



... on your notebook?



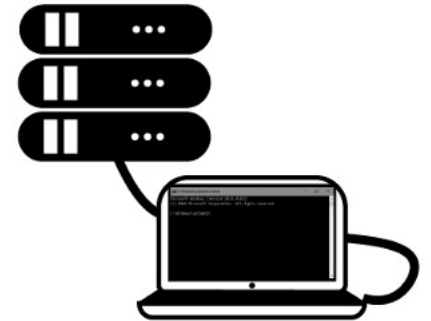
... on your lab workstation?



... on a cloud provider?



... on the university's high performance cluster?



# The Reproducibility problem

Differing results between software versions ☹️

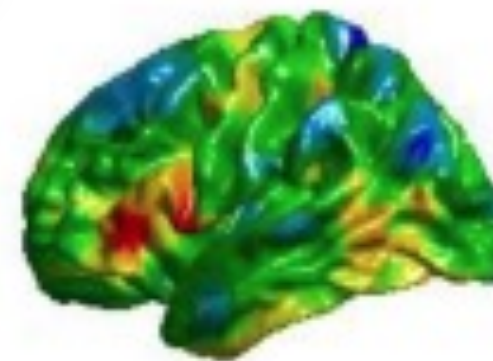
## Reproducibility of neuroimaging analyses across operating systems

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

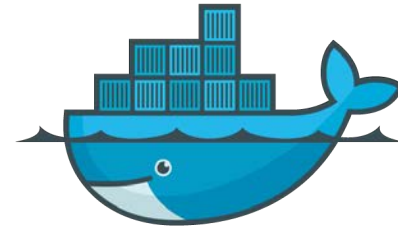
- glibc 2.5 vs 2.18 deliver different floating-point results
- leads to significant differences in long pipelines

```
expf(1.540518522262573242187500000000)  
=4.6670093536376953125000
```

```
expf(1.540518522262573242187500000000)  
=4.6670098304748535156250
```







docker

How could we build a data analysis platform that solves these problems by using existing technology and projects?



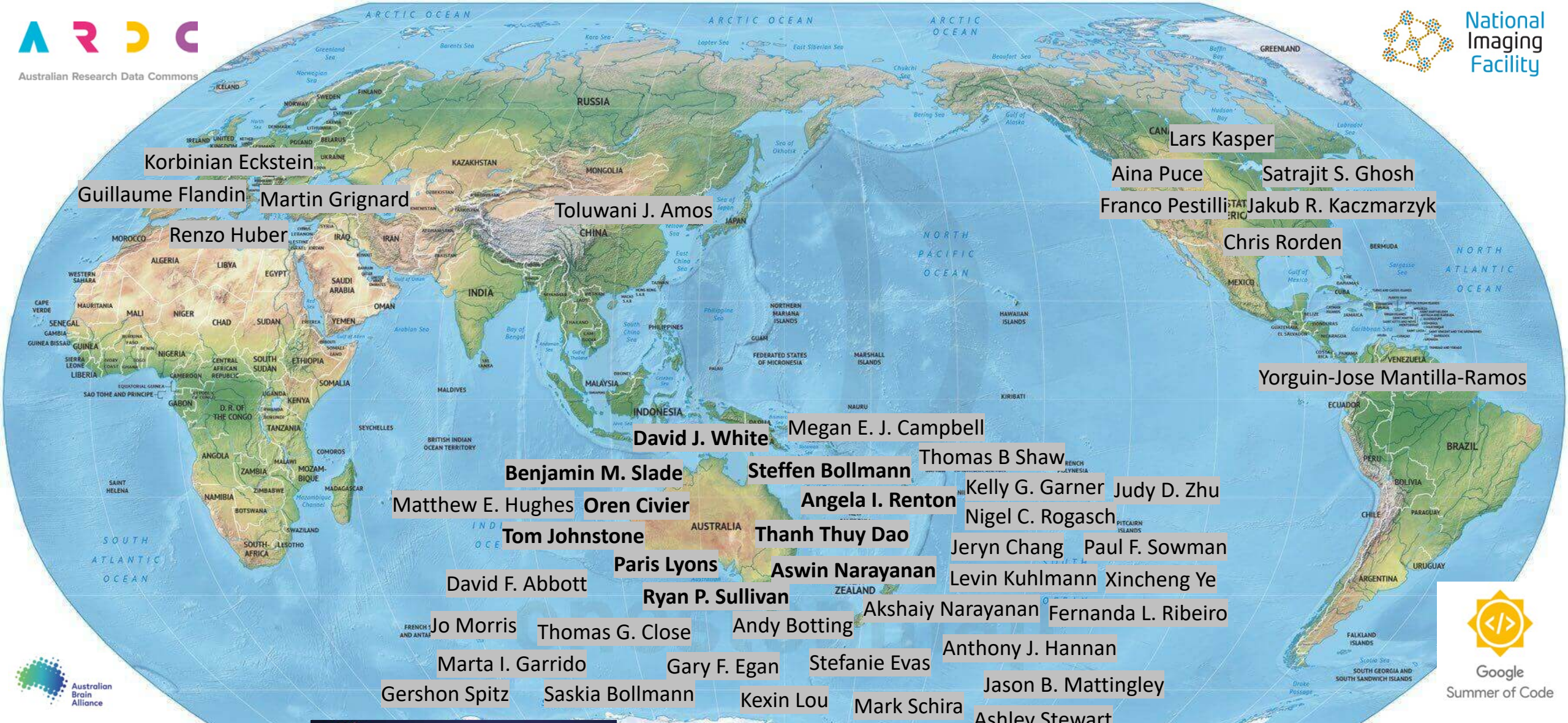
NeuroDebian



# Acknowledgements



Australian Research Data Commons



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Angela I. Renton

Nigel C. Rogasch

Tom Johnstone

Thanh Thuy Dao

Jeryn Chang Paul F. Sowman

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Paris Lyons

Aswin Narayanan

Levin Kuhlmann Xincheng Ye

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Kexin Lou

Mark Schira

Jason B. Mattingley

Ashley Stewart



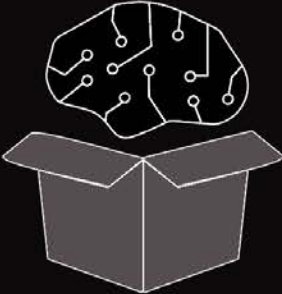
Google Summer of Code

**NEURODESK** Cite Documentation FAQ Applications Developers Tutorials GitHub News

## Quick start

A flexible and scalable data analysis environment for reproducible neuroimaging with Neurodesk.

[What is Neurodesk ?](#)
[▶ Play](#)
[Nectar](#)
[G Google Colab](#)
[Windows](#)
[Apple MacOS](#)
[Linux](#)



## Get started with Neurodesk

Select your setups and follow further instructions in the provided link.

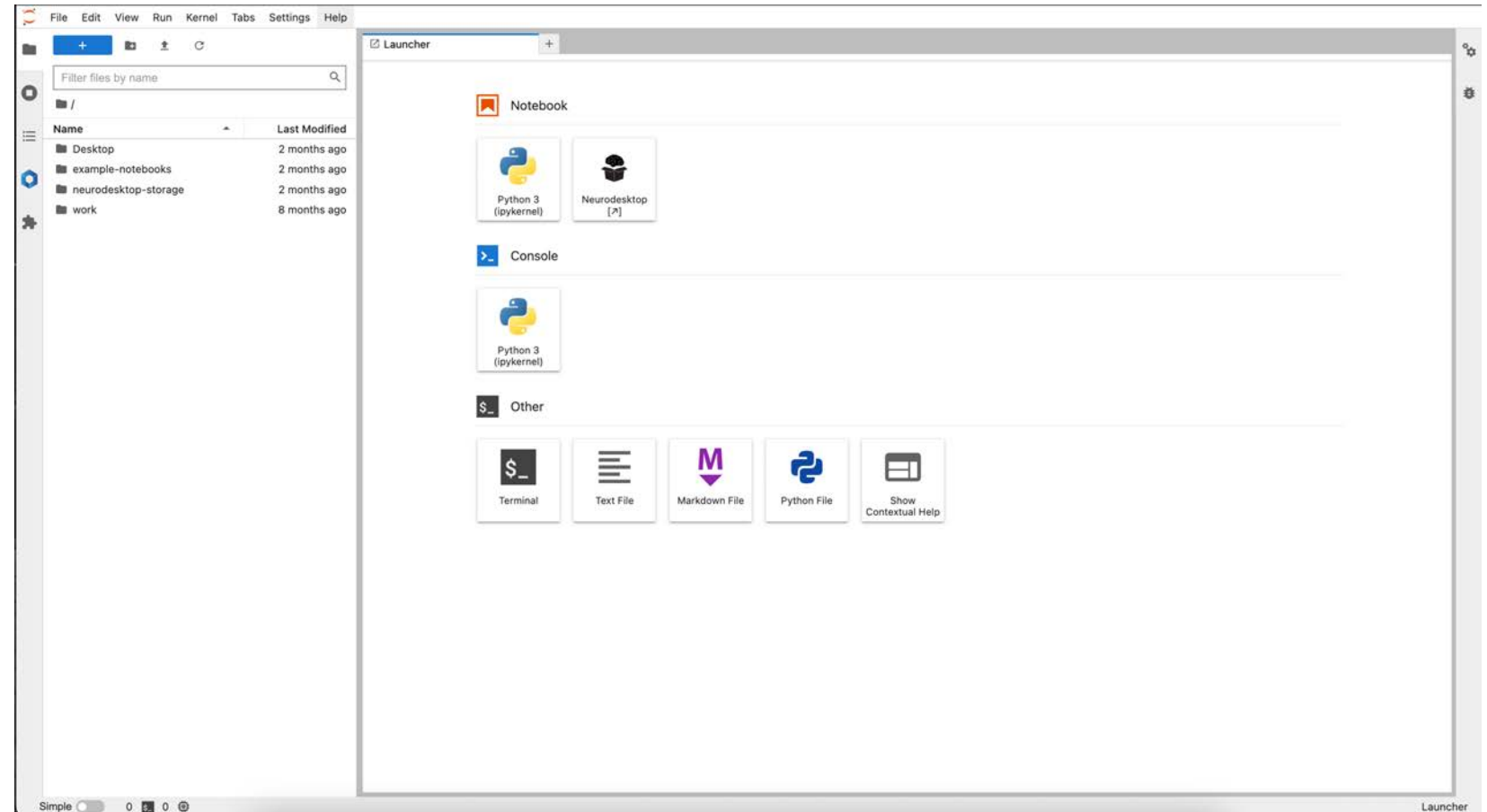
Compute Platform	Local PC	HPC	Cloud	Google Colab
Your OS	Linux	Mac	Windows	
Interface	Desktop	Command Line	Container	VSCode
Processor	x86	ARM	GPU	
Instructions:	<p>Follow the instruction at  <a href="https://www.neurodesk.org/docs/neurodesktop/getting-started/mac/">https://www.neurodesk.org/docs/neurodesktop/getting-started/mac/</a></p>			

# Interactive examples 😊

The next slides are backups

# Play – for teaching and quick tests

- jupyter notebook + full desktop
- no authentication required
- no data is saved across sessions



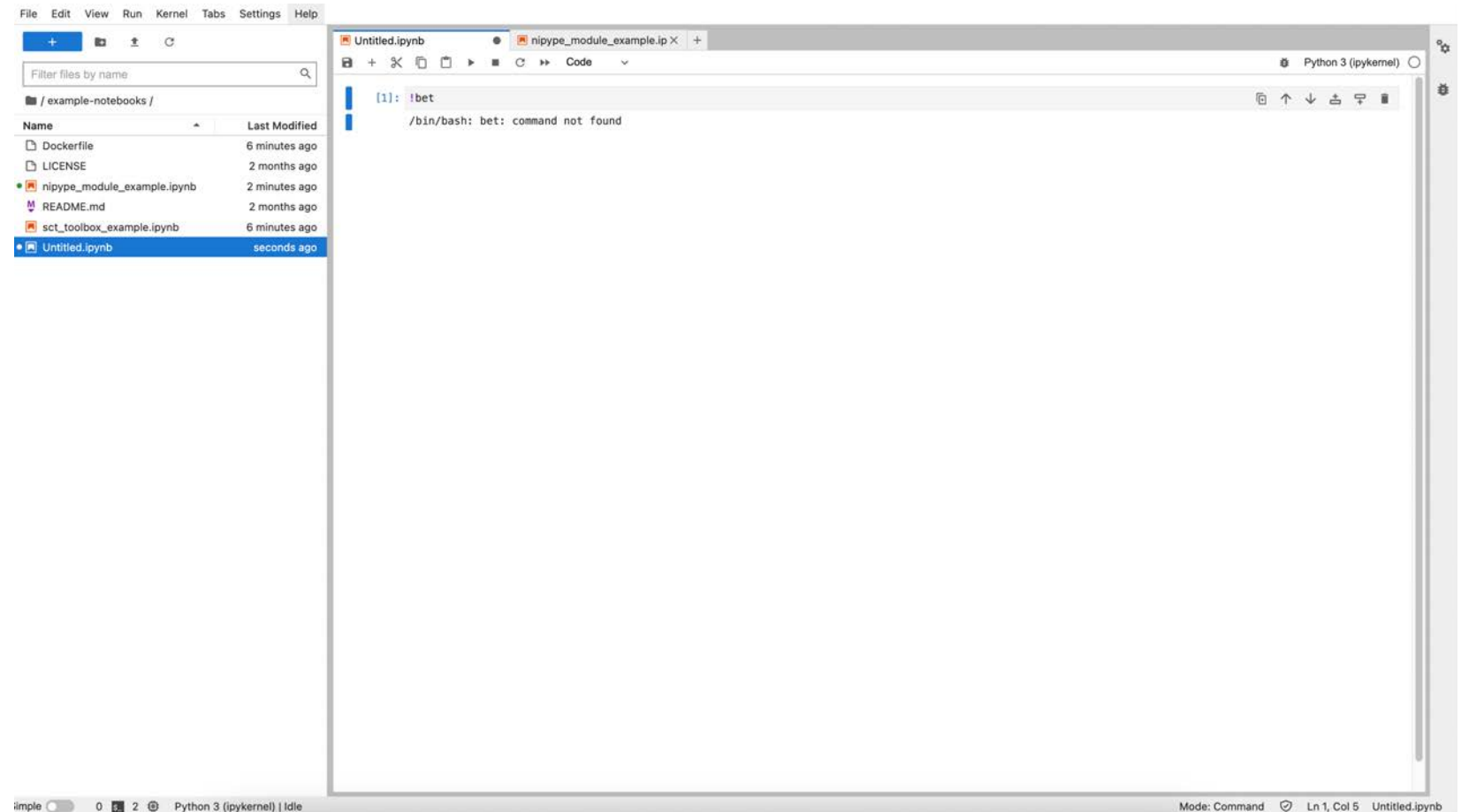
# Play – for teaching and quick tests

- full desktop and visual applications
- data can be uploaded with drag and drop
- show bet in desktop and module system there



# Play – for teaching and quick tests

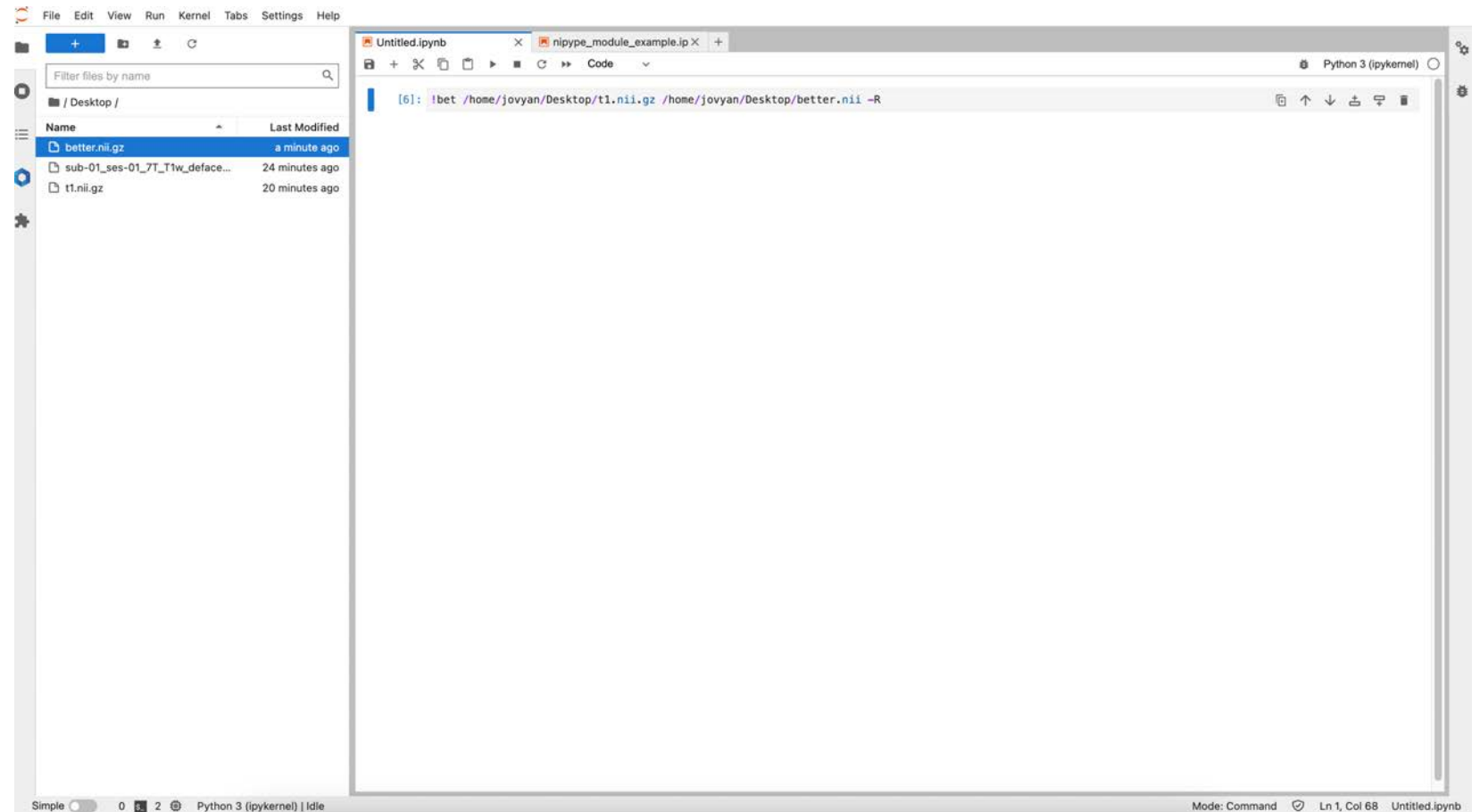
- jupyter notebook and desktop access the same data and tools!
- 1) show empty notebook without tools loaded



The screenshot displays the Jupyter Notebook interface. On the left, a file browser shows a directory structure with files like 'Dockerfile', 'LICENSE', 'nipype\_module\_example.ipynb', 'README.md', 'sct\_toolbox\_example.ipynb', and 'Untitled.ipynb'. The 'Untitled.ipynb' file is selected. The main area shows a code cell with the command `!bet` and the output `/bin/bash: bet: command not found`. The status bar at the bottom indicates the kernel is 'Python 3 (ipykernel)' and the mode is 'Command'.

# Play – for teaching and quick tests

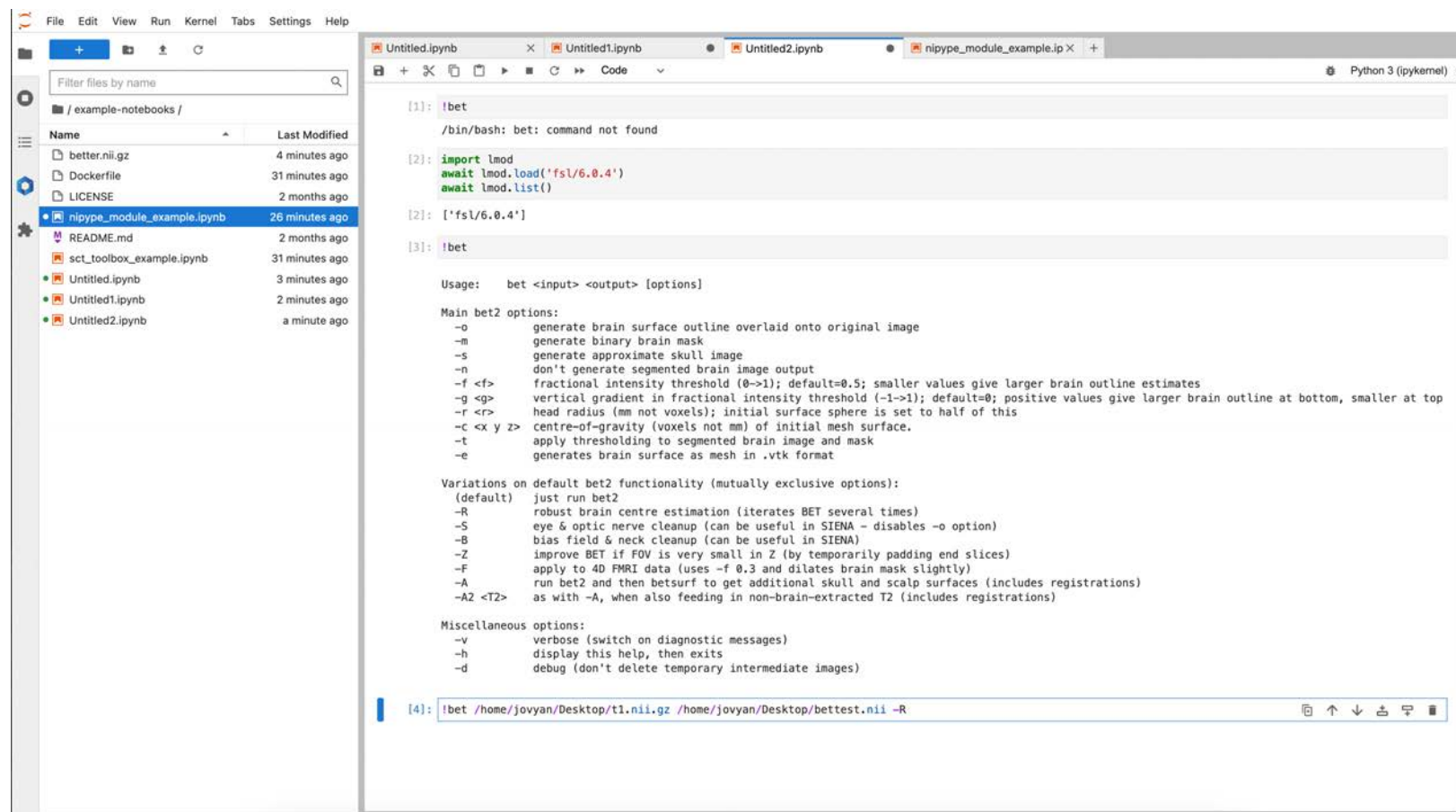
- show interactive loading of tool and running bet on same T1 data and download data





# Play – for teaching and quick tests

- now, this is not really reproducible, right?
- Let's unload bet and then specify which tool version we are using in code 😊



```
File Edit View Run Kernel Tabs Settings Help
+
Filter files by name
/example-notebooks /
Name Last Modified
better.nii.gz 4 minutes ago
Dockerfile 31 minutes ago
LICENSE 2 months ago
nipy_module_example.ipynb 26 minutes ago
README.md 2 months ago
sct_toolbox_example.ipynb 31 minutes ago
Untitled.ipynb 3 minutes ago
Untitled1.ipynb 2 minutes ago
Untitled2.ipynb a minute ago

Untitled.ipynb x Untitled1.ipynb x Untitled2.ipynb x nipy_module_example.ip x +
Python 3 (pykernel)

[1]: !bet
/bin/bash: bet: command not found

[2]: import lmod
await lmod.load('fsl/6.0.4')
await lmod.list()

[2]: ['fsl/6.0.4']

[3]: !bet

Usage: bet <input> <output> [options]

Main bet2 options:
-o generate brain surface outline overlaid onto original image
-m generate binary brain mask
-s generate approximate skull image
-n don't generate segmented brain image output
-f <f> fractional intensity threshold (0->1); default=0.5; smaller values give larger brain outline estimates
-g <g> vertical gradient in fractional intensity threshold (-1->1); default=0; positive values give larger brain outline at bottom, smaller at top
-r <r> head radius (mm not voxels); initial surface sphere is set to half of this
-c <x y z> centre-of-gravity (voxels not mm) of initial mesh surface.
-t apply thresholding to segmented brain image and mask
-e generates brain surface as mesh in .vtk format

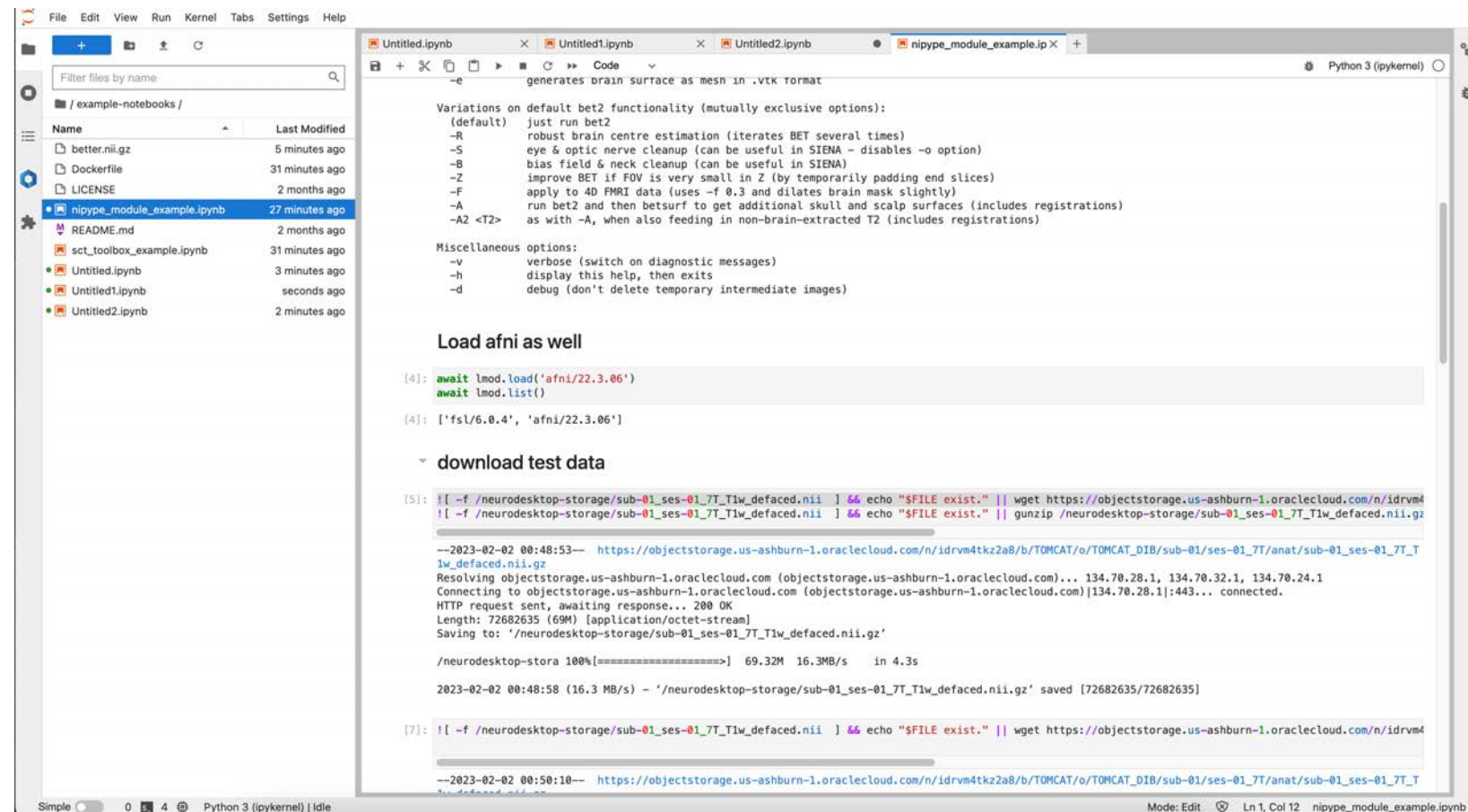
Variations on default bet2 functionality (mutually exclusive options):
(default) just run bet2
-R robust brain centre estimation (iterates BET several times)
-S eye & optic nerve cleanup (can be useful in SIENA - disables -o option)
-B bias field & neck cleanup (can be useful in SIENA)
-Z improve BET if FOV is very small in Z (by temporarily padding end slices)
-F apply to 4D FMRI data (uses -f 0.3 and dilates brain mask slightly)
-A run bet2 and then betsurf to get additional skull and scalp surfaces (includes registrations)
-AZ <T2> as with -A, when also feeding in non-brain-extracted T2 (includes registrations)

Miscellaneous options:
-v verbose (switch on diagnostic messages)
-h display this help, then exits
-d debug (don't delete temporary intermediate images)

[4]: !bet /home/jovyan/Desktop/t1.nii.gz /home/jovyan/Desktop/bettest.nii -R
```

# Play – for teaching and quick tests

- nipyne example
- cool thing is: these notebooks can now be shared and work identically on every neurodesk installation



The screenshot shows a JupyterLab interface with a file browser on the left and a code editor on the right. The file browser shows a directory named "/ example-notebooks /" with several files listed, including "nipyne\_module\_example.ipynb" which is highlighted. The code editor shows the following content:

```

generates brain surface as mesh in .vtk format

Variations on default bet2 functionality (mutually exclusive options):
(default) just run bet2
-R robust brain centre estimation (iterates BET several times)
-S eye & optic nerve cleanup (can be useful in SIENA - disables -o option)
-B bias field & neck cleanup (can be useful in SIENA)
-Z improve BET if FOV is very small in Z (by temporarily padding end slices)
-F apply to 4D FMRI data (uses -f 0.3 and dilates brain mask slightly)
-A run bet2 and then betsurf to get additional skull and scalp surfaces (includes registrations)
-A2 <T2> as with -A, when also feeding in non-brain-extracted T2 (includes registrations)

Miscellaneous options:
-v verbose (switch on diagnostic messages)
-h display this help, then exits
-d debug (don't delete temporary intermediate images)

Load afni as well

[4]: await lmod.load('afni/22.3.06')
      await lmod.list()

[4]: ['fs/6.0.4', 'afni/22.3.06']

download test data

[5]: ![-f /neurodesktop-storage/sub-01_ses-01_7T_T1w_defaced.nii ] && echo "FILE exist." || wget https://objectstorage.us-ashburn-1.oraclecloud.com/n/idrvm4
      ![-f /neurodesktop-storage/sub-01_ses-01_7T_T1w_defaced.nii ] && echo "FILE exist." || gunzip /neurodesktop-storage/sub-01_ses-01_7T_T1w_defaced.nii.gz

--2023-02-02 00:48:53-- https://objectstorage.us-ashburn-1.oraclecloud.com/n/idrvm4tkz2a8/b/TOMCAT/o/TOMCAT_DIB/sub-01/ses-01_7T/anat/sub-01_ses-01_7T_T1w_defaced.nii.gz
Resolving objectstorage.us-ashburn-1.oraclecloud.com (objectstorage.us-ashburn-1.oraclecloud.com)... 134.70.28.1, 134.70.32.1, 134.70.24.1
Connecting to objectstorage.us-ashburn-1.oraclecloud.com (objectstorage.us-ashburn-1.oraclecloud.com)|134.70.28.1|:443... connected.
HTTP request sent, awaiting response... 200 OK
Length: 72682635 (69M) [application/octet-stream]
Saving to: '/neurodesktop-storage/sub-01_ses-01_7T_T1w_defaced.nii.gz'

/neurodesktop-stora 100%[=====] 69.32M 16.3MB/s in 4.3s

2023-02-02 00:48:58 (16.3 MB/s) - '/neurodesktop-storage/sub-01_ses-01_7T_T1w_defaced.nii.gz' saved [72682635/72682635]

[7]: ![-f /neurodesktop-storage/sub-01_ses-01_7T_T1w_defaced.nii ] && echo "FILE exist." || wget https://objectstorage.us-ashburn-1.oraclecloud.com/n/idrvm4
      ![-f /neurodesktop-storage/sub-01_ses-01_7T_T1w_defaced.nii ] && echo "FILE exist." || gunzip /neurodesktop-storage/sub-01_ses-01_7T_T1w_defaced.nii.gz

--2023-02-02 00:50:10-- https://objectstorage.us-ashburn-1.oraclecloud.com/n/idrvm4tkz2a8/b/TOMCAT/o/TOMCAT_DIB/sub-01/ses-01_7T/anat/sub-01_ses-01_7T_T1w_defaced.nii.gz
Resolving objectstorage.us-ashburn-1.oraclecloud.com (objectstorage.us-ashburn-1.oraclecloud.com)... 134.70.28.1, 134.70.32.1, 134.70.24.1
Connecting to objectstorage.us-ashburn-1.oraclecloud.com (objectstorage.us-ashburn-1.oraclecloud.com)|134.70.28.1|:443... connected.
HTTP request sent, awaiting response... 200 OK
Length: 72682635 (69M) [application/octet-stream]
Saving to: '/neurodesktop-storage/sub-01_ses-01_7T_T1w_defaced.nii.gz'

/neurodesktop-stora 100%[=====] 69.32M 16.3MB/s in 4.3s

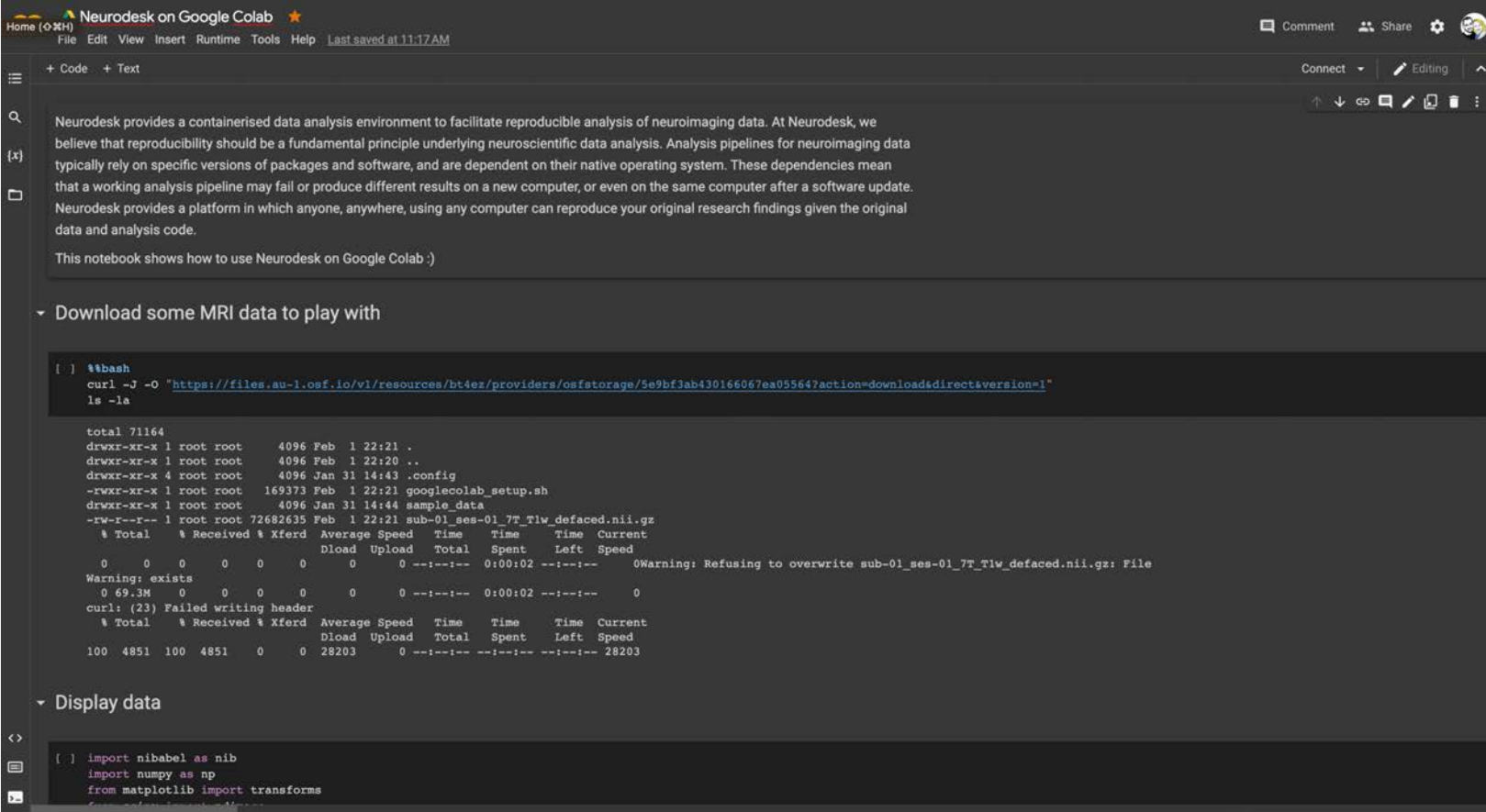
2023-02-02 00:50:15 (16.3 MB/s) - '/neurodesktop-storage/sub-01_ses-01_7T_T1w_defaced.nii.gz' saved [72682635/72682635]
  
```

# Lab – same thing, but data is saved across sessions

- requires github authentication

The image shows the JupyterHub logo, which consists of a stylized orange 'j' icon followed by the text 'jupyterhub' in a sans-serif font.The image shows a rectangular orange button with the text 'Sign in with GitHub' in white, centered on the button.

# This of course also works on google colab



Neurodesk provides a containerised data analysis environment to facilitate reproducible analysis of neuroimaging data. At Neurodesk, we believe that reproducibility should be a fundamental principle underlying neuroscientific data analysis. Analysis pipelines for neuroimaging data typically rely on specific versions of packages and software, and are dependent on their native operating system. These dependencies mean that a working analysis pipeline may fail or produce different results on a new computer, or even on the same computer after a software update. Neurodesk provides a platform in which anyone, anywhere, using any computer can reproduce your original research findings given the original data and analysis code.

This notebook shows how to use Neurodesk on Google Colab :)

### Download some MRI data to play with

```
[ ] %%bash
curl -NJ -O "https://files.au-1.osf.io/v1/resources/bt4ez/providers/osfstorage/5e9bf3ab430166067ea05564?action=download&direct&version=1"
ls -la
```

```
total 71164
drwxr-xr-x 1 root root 4096 Feb 1 22:21 .
drwxr-xr-x 1 root root 4096 Feb 1 22:20 ..
drwxr-xr-x 4 root root 4096 Jan 31 14:43 .config
-rwxr-xr-x 1 root root 169373 Feb 1 22:21 googlecolab_setup.sh
drwxr-xr-x 1 root root 4096 Jan 31 14:44 sample_data
-rw-r--r-- 1 root root 72682635 Feb 1 22:21 sub-01_ses-01_7T_T1w_defaced.nii.gz
  % Total    % Received % Xferd  Average Speed   Time    Time     Current
                                 Dload  Upload   Total   Spent    Left   Speed
  0     0     0     0     0     0      0      0  --:--:--  0:00:02  --:--:--    0Warning: Refusing to overwrite sub-01_ses-01_7T_T1w_defaced.nii.gz: File
exists
  0 69.3M     0     0     0     0      0      0  --:--:--  0:00:02  --:--:--    0
curl: (23) Failed writing header
  % Total    % Received % Xferd  Average Speed   Time    Time     Current
                                 Dload  Upload   Total   Spent    Left   Speed
100 4851 100 4851     0     0 28203     0  --:--:--  --:--:--  --:--:-- 28203
```

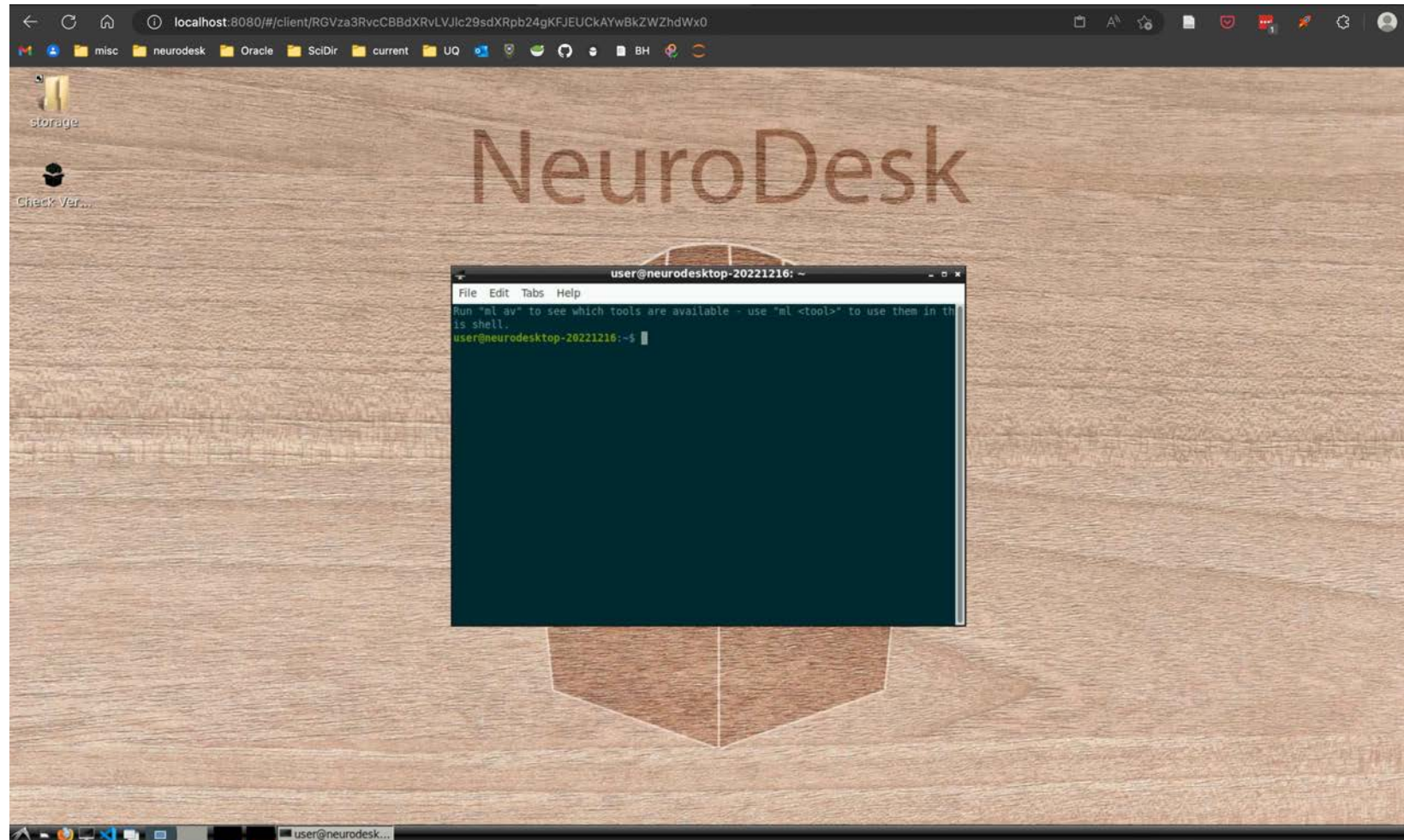
### Display data

```
[ ] import nibabel as nib
import numpy as np
from matplotlib import transforms
```

# Running Neurodesk on your own hardware

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

```
sudo docker run \  
  --shm-size=1gb -it --privileged --name neurodesktop \  
  -v ~/neurodesktop-storage:/neurodesktop-storage \  
  -e HOST_UID="$(id -u)" -e HOST_GID="$(id -g)" \  
  -p 8080:8080 \  
  -h neurodesktop-20221216 vnmd/neurodesktop:20221216
```



# Running Neurodesk on an HPC

```
ssh uqsbollm@bunya.rcc.uq.edu.au
```

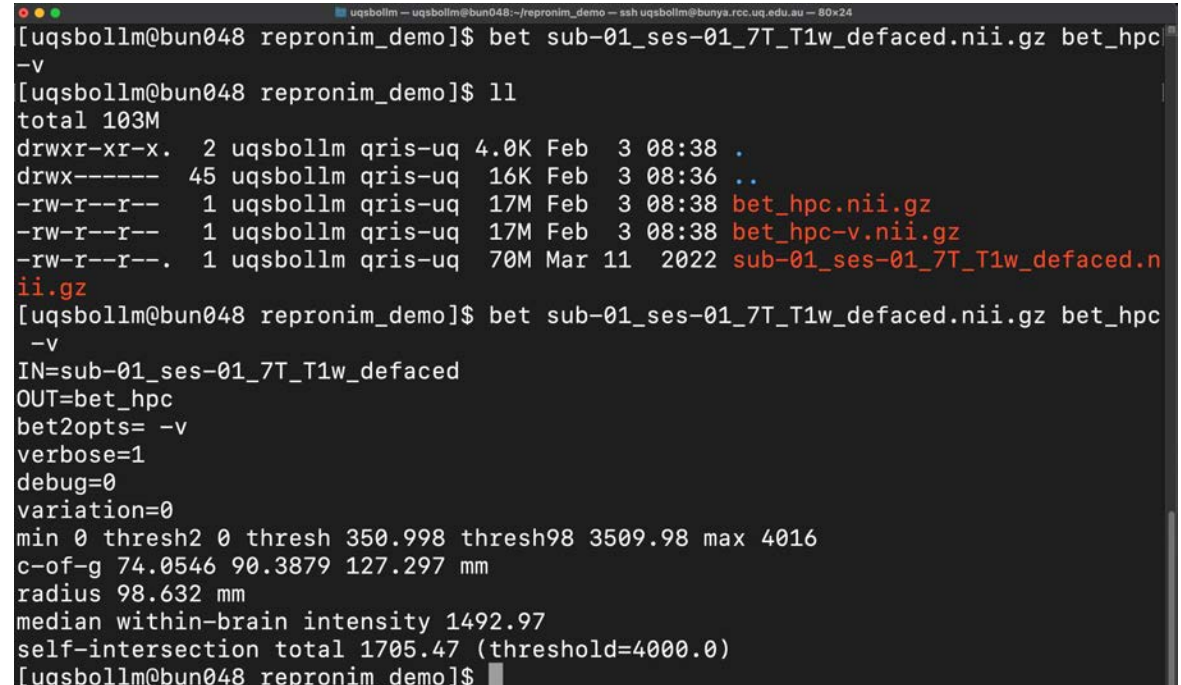
```
salloc --nodes=1 --ntasks-per-node=1 --cpus-per-task=1 --  
mem=50G --job-name=TEST --time=05:00:00 --partition=general -  
-account=a_barth srun --export=PATH,TERM,HOME,LANG --pty  
/bin/bash -l
```

```
module use  
/scratch/user/uqsbollm/neurocommand/local/containers/modules/
```

```
cd repronimdemo
```

```
ml fsl/6.0.4
```

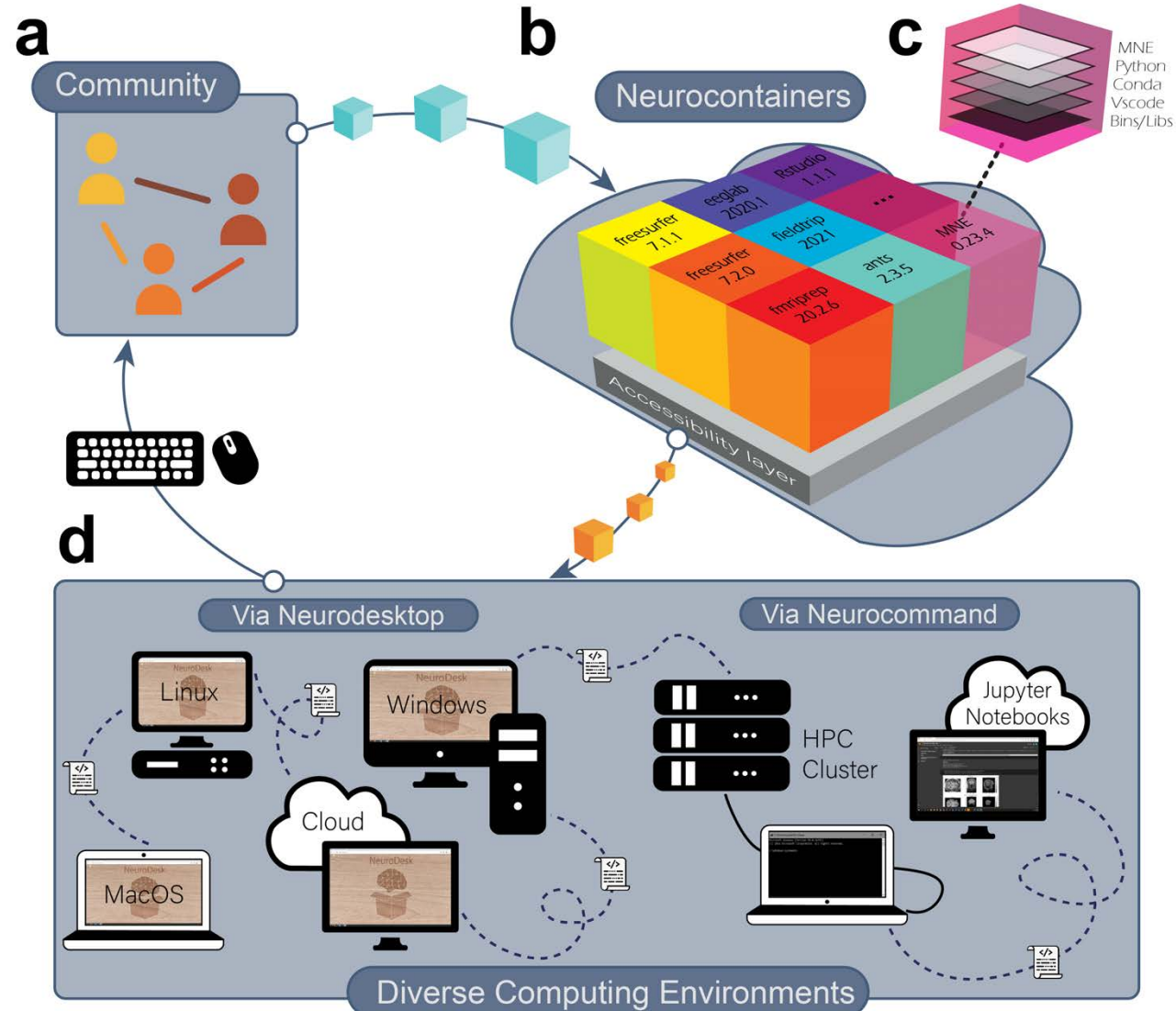
```
bet sub-01_ses-01_7T_T1w_defaced.nii.gz  
bet_hpc -v
```



```
uqsbollm@bun048 repronim_demo]$ bet sub-01_ses-01_7T_T1w_defaced.nii.gz bet_hpc  
-v  
[uqsbollm@bun048 repronim_demo]$ ll  
total 103M  
drwxr-xr-x.  2 uqsbollm qris-uq  4.0K Feb  3 08:38 .  
drwx----- 45 uqsbollm qris-uq  16K Feb  3 08:36 ..  
-rw-r--r--   1 uqsbollm qris-uq  17M Feb  3 08:38 bet_hpc.nii.gz  
-rw-r--r--   1 uqsbollm qris-uq  17M Feb  3 08:38 bet_hpc-v.nii.gz  
-rw-r--r--   1 uqsbollm qris-uq  70M Mar 11 2022 sub-01_ses-01_7T_T1w_defaced.n  
ii.gz  
[uqsbollm@bun048 repronim_demo]$ bet sub-01_ses-01_7T_T1w_defaced.nii.gz bet_hpc  
-v  
IN=sub-01_ses-01_7T_T1w_defaced  
OUT=bet_hpc  
bet2opts= -v  
verbose=1  
debug=0  
variation=0  
min 0 thresh2 0 thresh 350.998 thresh98 3509.98 max 4016  
c-of-g 74.0546 90.3879 127.297 mm  
radius 98.632 mm  
median within-brain intensity 1492.97  
self-intersection total 1705.47 (threshold=4000.0)  
[uqsbollm@bun048 repronim_demo]$
```

Interactive examples end 😊

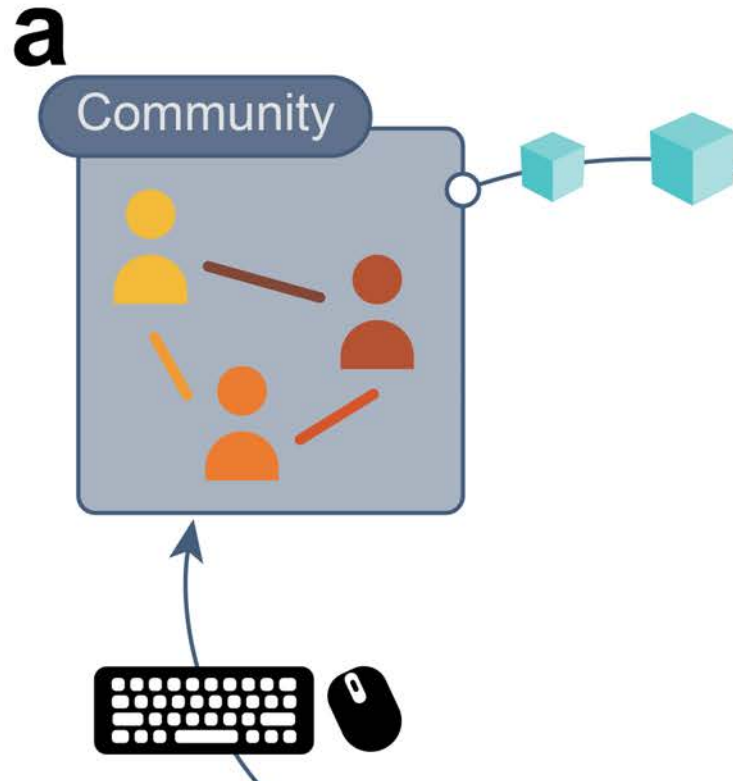
# The Neurodesk.org Open-Source Platform





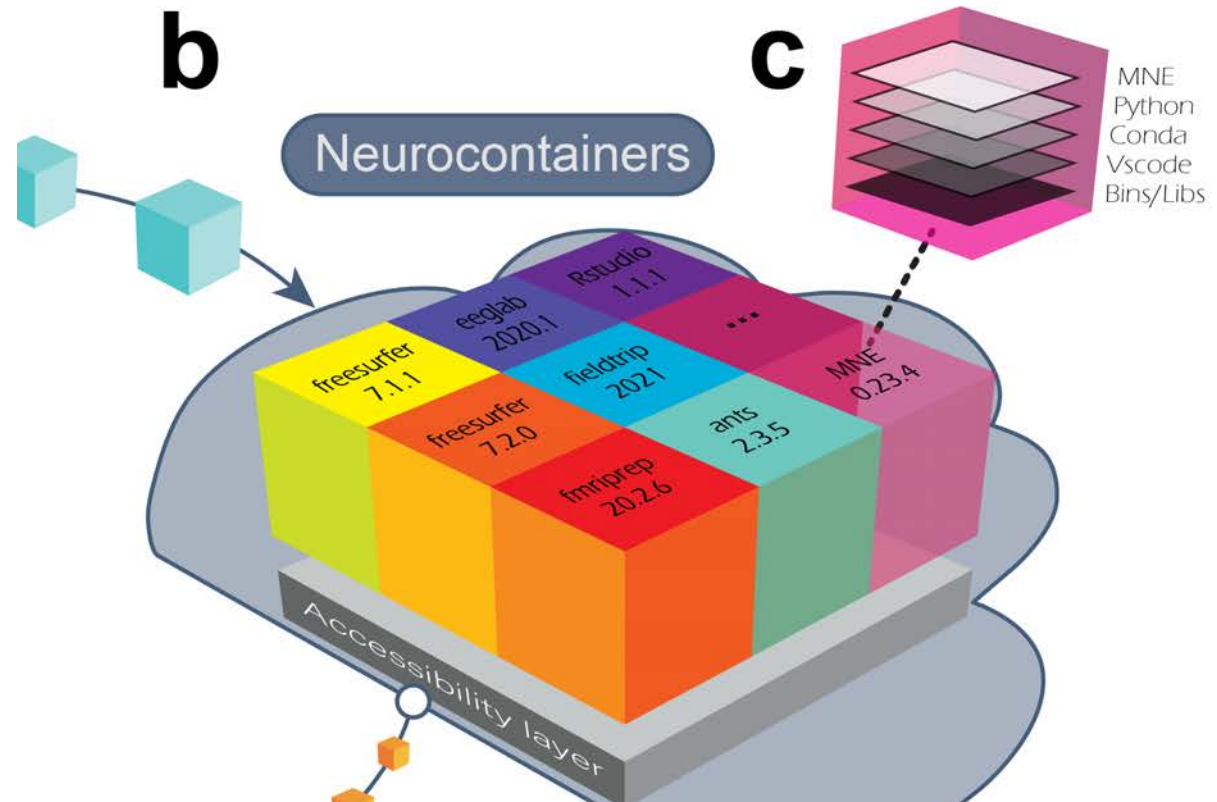
# The Neurodesk.org Open-Source Platform

Community builds and maintains software containers



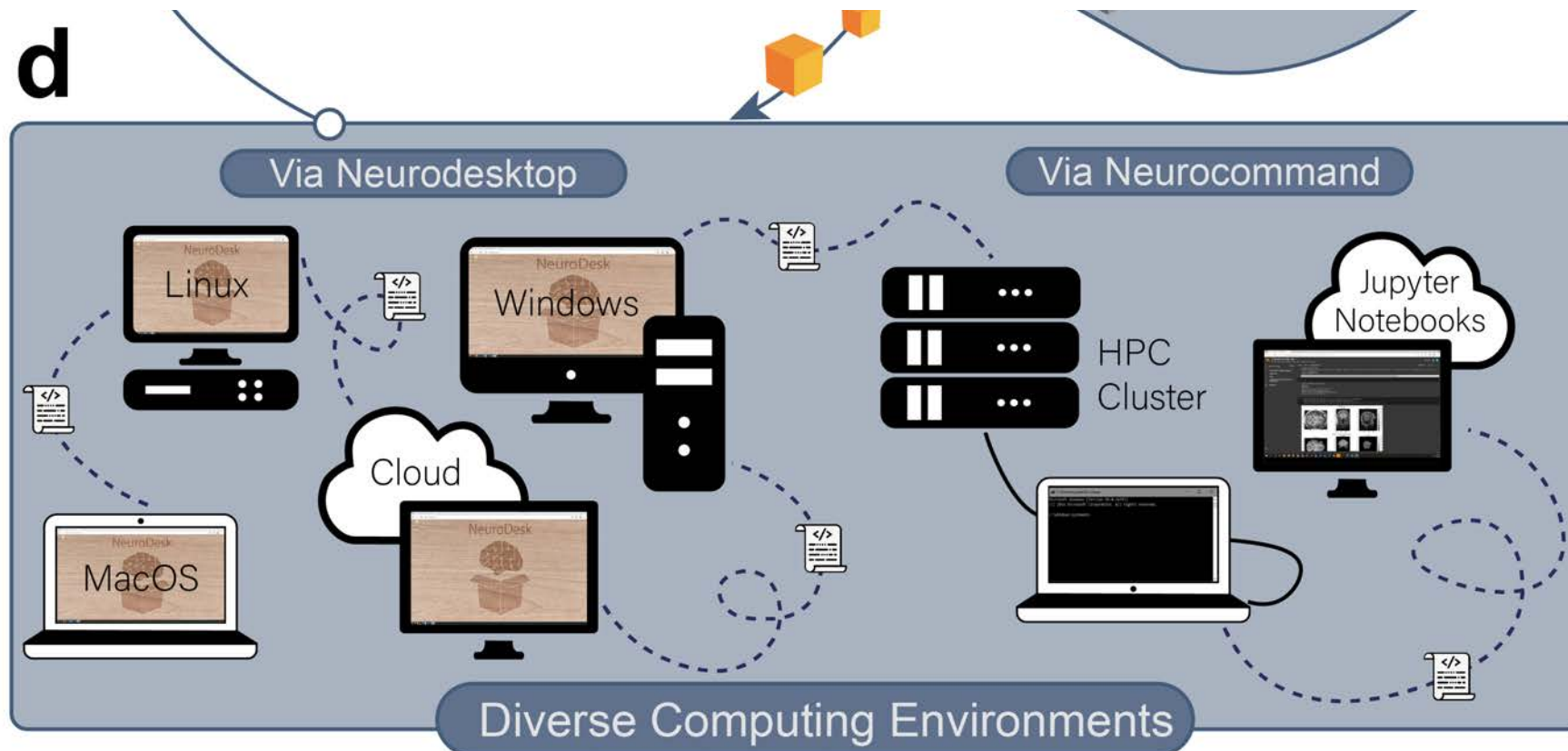
# The Neurodesk.org Open-Source Platform

Neurocontainers automatically builds and distributes a repository of software containers



# The Neurodesk.org Open-Source Platform

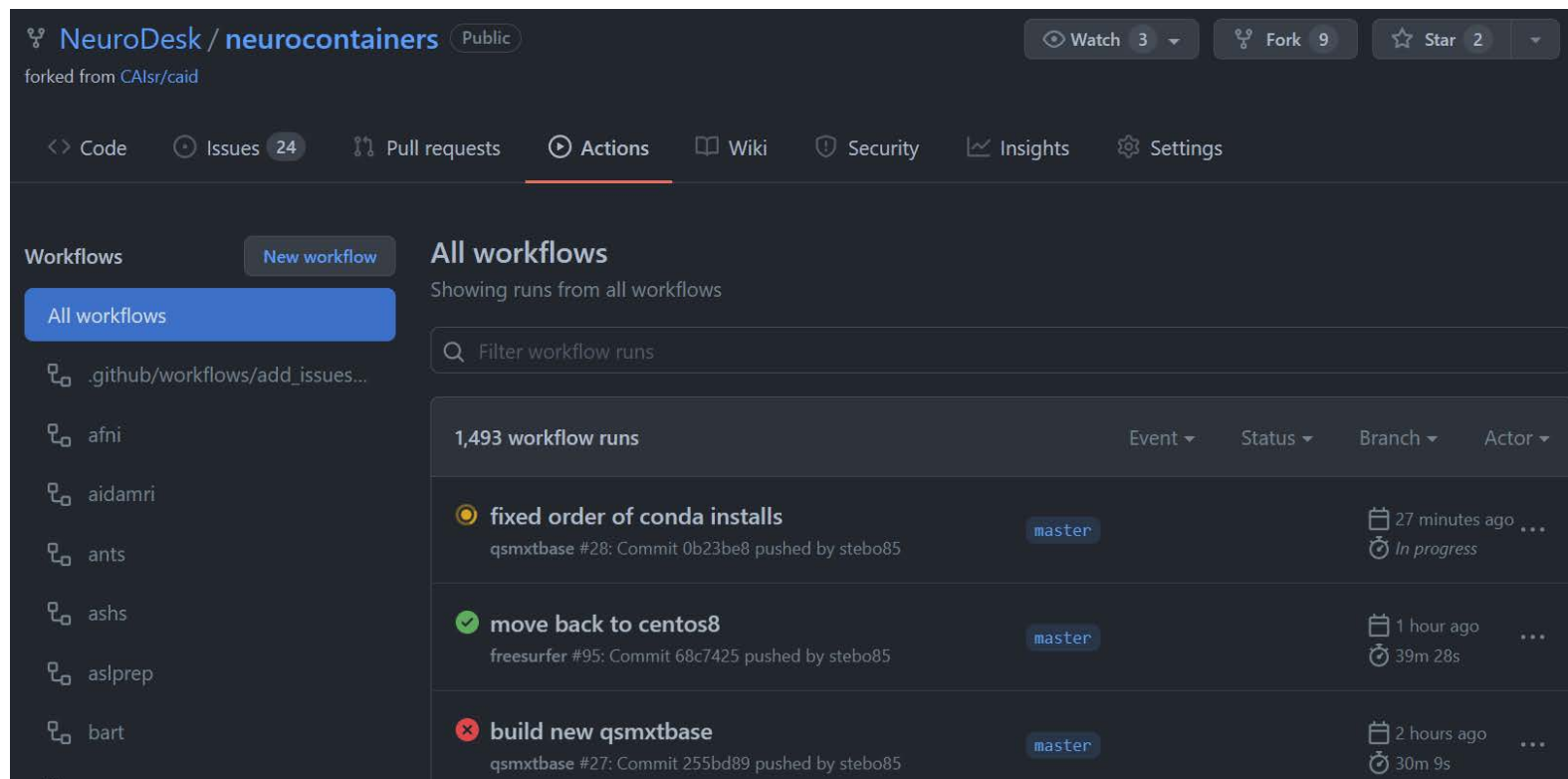
Software containers are available for all compute environments:



# Github actions build and upload the application containers

-- all automated

```
1 #!/usr/bin/env bash
2 set -e
3
4 export toolName='minc'
5 export toolVersion=1.9.17
6 # Don't forget to update version change in README.md!!!!
7
8 if [ "$1" != "" ]; then
9     echo "Entering Debug mode"
10    export debug=$1
11 fi
12
13 source ../main_setup.sh
14
15 neurodocker generate ${neurodocker_buildMode} \
16   --base-image ubuntu:18.04 \
17   --pkg-manager apt \
18   --run="mkdir ${mountPointList}" \
19   --copy README.md /README.md \
20   --${toolName} version=${toolVersion} \
21   --env DEPLOY_PATH=/opt/${toolName}-${toolVersion}/bin/:/opt
22 > ${imageName}.${neurodocker_buildExt}
23
24
25 if [ "$1" != "" ]; then
26     ../main_build.sh
27 fi
```



NeuroDesk / neurocontainers Public

forked from CAIsr/caid

Code Issues 24 Pull requests Actions Wiki Security Insights Settings




Workflows [New workflow](#)

All workflows

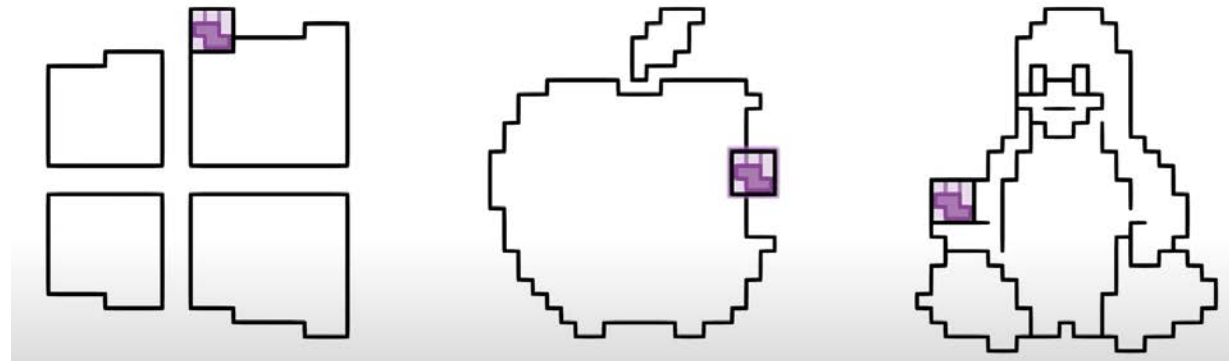
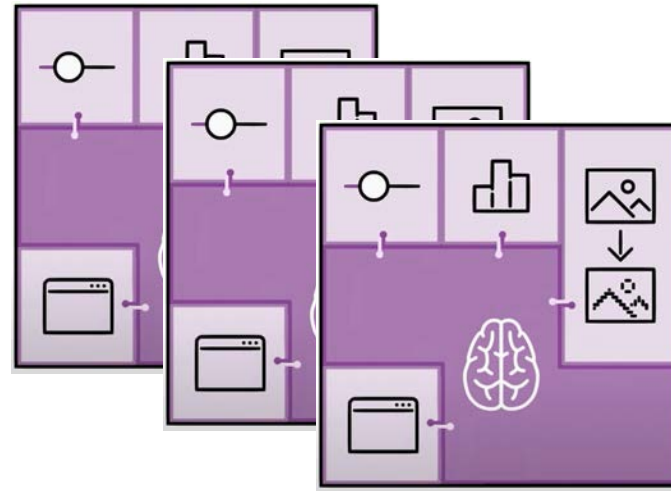
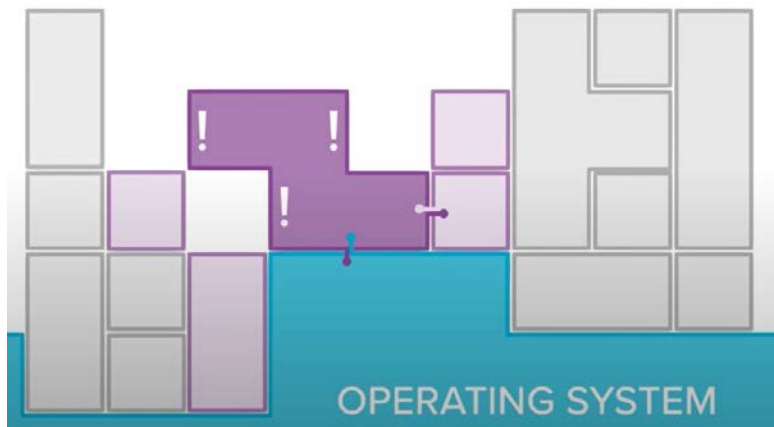
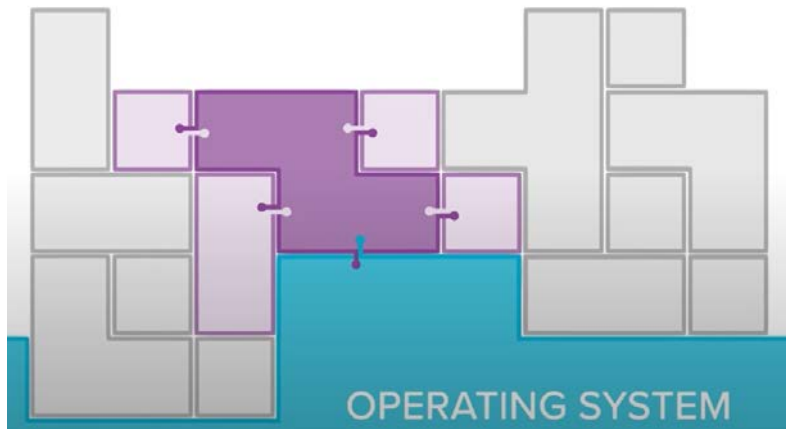
Showing runs from all workflows

Filter workflow runs

1,493 workflow runs

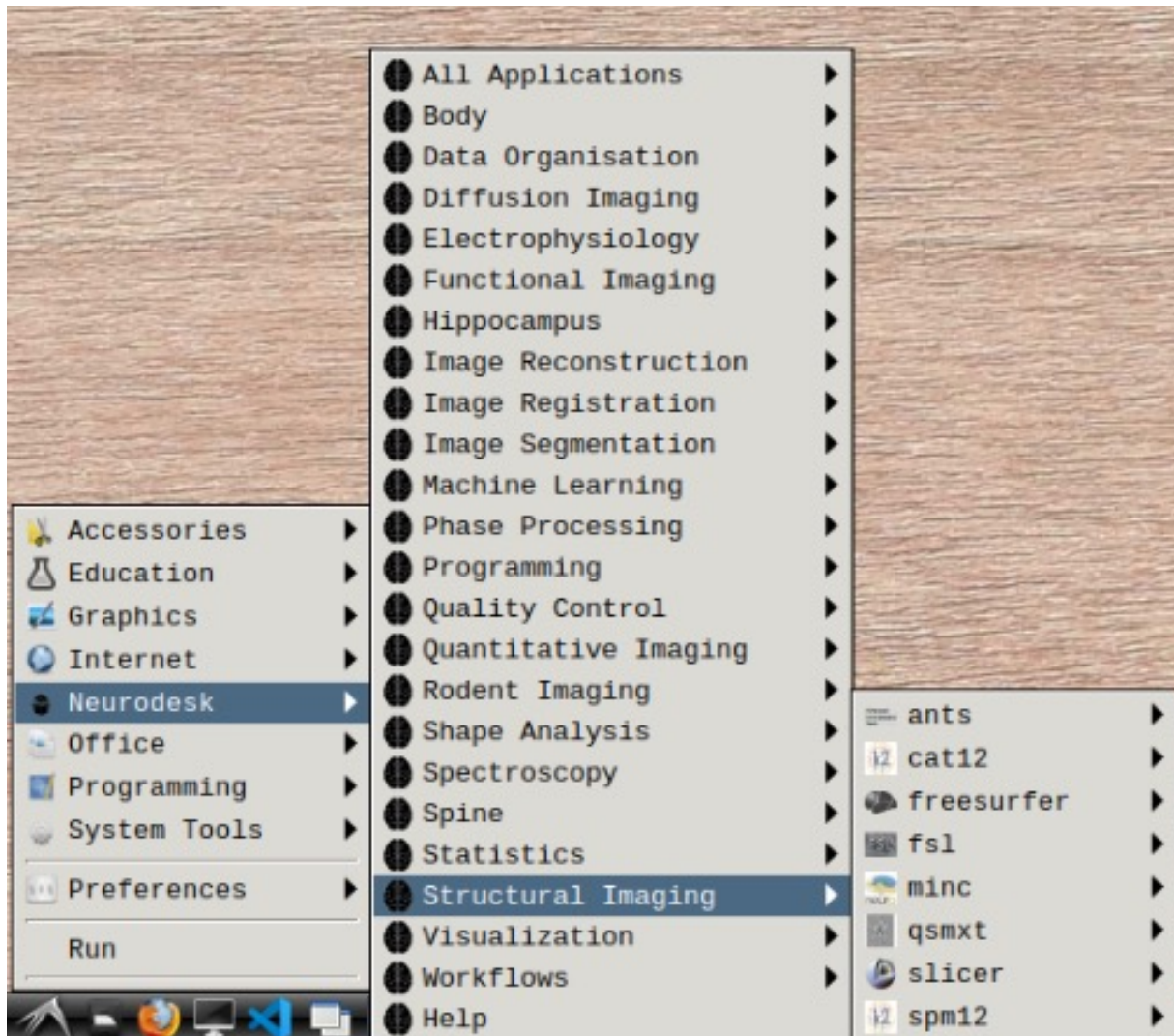
	Event	Status	Branch	Actor
 fixed order of conda installs	qsmxtbase #28: Commit 0b23be8 pushed by stebo85	master		27 minutes ago ... In progress
 move back to centos8	freesurfer #95: Commit 68c7425 pushed by stebo85	master		1 hour ago ... 39m 28s
 build new qsmxtbase	qsmxtbase #27: Commit 255bd89 pushed by stebo85	master		2 hours ago ... 30m 9s

# What is a software container, and how can it help?



-  Standardisation
-  Portability
-  Reliability
-  Reproducibility

# Neurodesktop – A Linux desktop accessible via the browser



The screenshot shows a Linux desktop environment with a menu open. The menu is organized into several categories:

- Neurodesk** (highlighted):
  - All Applications
  - Body
  - Data Organisation
  - Diffusion Imaging
  - Electrophysiology
  - Functional Imaging
  - Hippocampus
  - Image Reconstruction
  - Image Registration
  - Image Segmentation
  - Machine Learning
  - Phase Processing
  - Programming
  - Quality Control
  - Quantitative Imaging
  - Rodent Imaging
  - Shape Analysis
  - Spectroscopy
  - Spine
  - Statistics
  - Structural Imaging
  - Visualization
  - Workflows
  - Help
- Accessories**
- Education**
- Graphics**
- Internet**
- Office**
- Programming**
- System Tools**
- Preferences**
- Run**

Below the Neurodesk menu, a list of applications is visible:

- ants
- cat12
- freesurfer
- fsl
- minc
- qsmxt
- slicer
- spm12

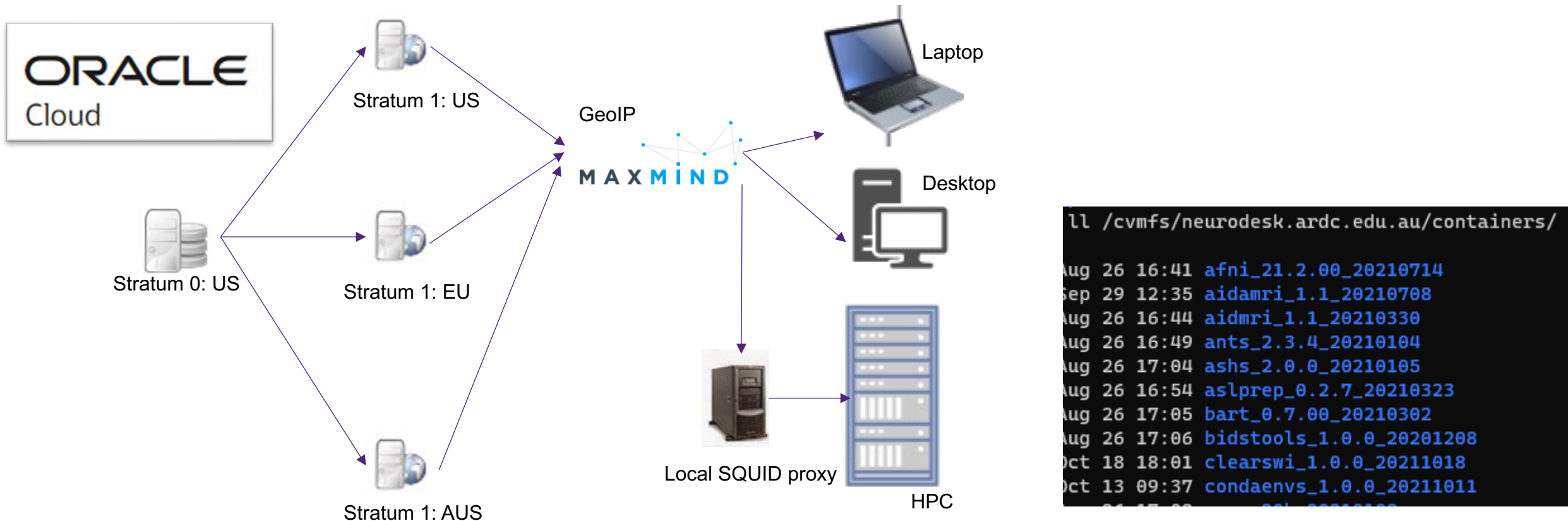
Containers solve dependency issues

Full GUI support

comes with a growing set of tools required for curating, processing, creating and using Neuroimaging Data

# High performance software distribution using CVMFS

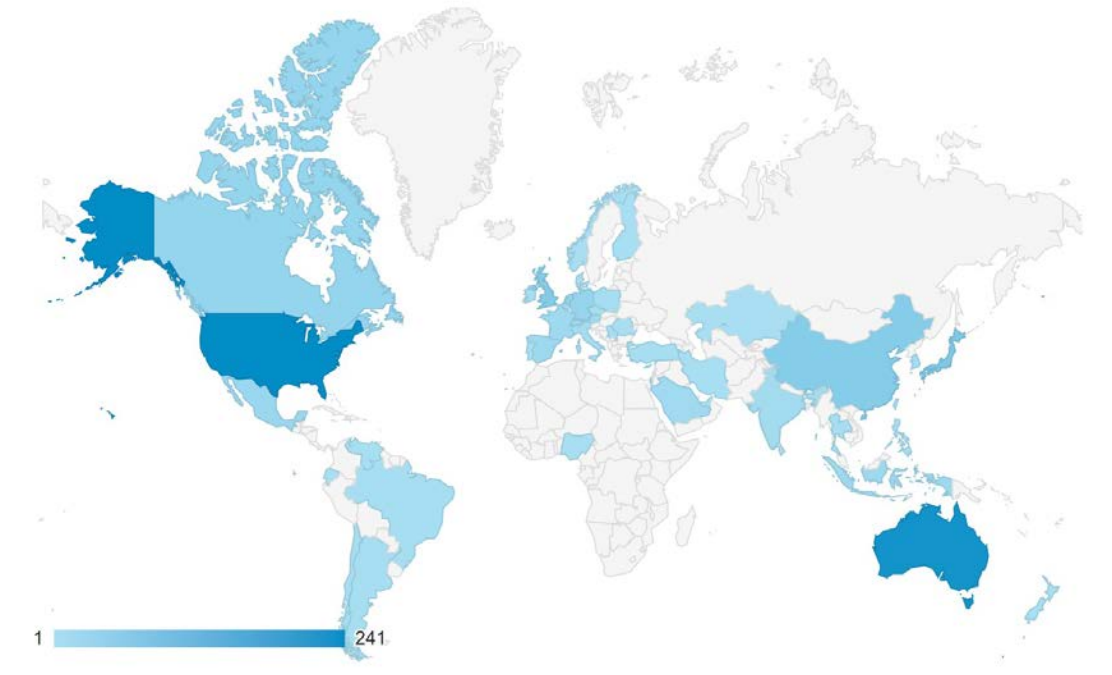
- download and unpack singularity/apptainer containers to CVMFS storage for distribution and on-demand access



```
ll /cvmfs/neurodesk.ardc.edu.au/containers/  
Aug 26 16:41 afni_21.2.00_20210714  
Sep 29 12:35 aidamri_1.1_20210708  
Aug 26 16:44 aidmri_1.1_20210330  
Aug 26 16:49 ants_2.3.4_20210104  
Aug 26 17:04 ashs_2.0.0_20210105  
Aug 26 16:54 aslprep_0.2.7_20210323  
Aug 26 17:05 bart_0.7.00_20210302  
Aug 26 17:06 bidstools_1.0.0_20201208  
Oct 18 18:01 clearswi_1.0.0_20211018  
Oct 13 09:37 condaenvs_1.0.0_20211011
```

# Uptake in the community

- **996 individual users** in the last 6 months from **47 countries**
- our repos on GitHub have **71 stars & 75 forks**
- development driven by hackathons (e.g. Brainhack Global)







# Reproducible Science

Are Neurodesk results reproducible?

How close are we to re-executable papers?

# Let's try to reproduce ...

## Reproducibility of neuroimaging analyses across operating systems

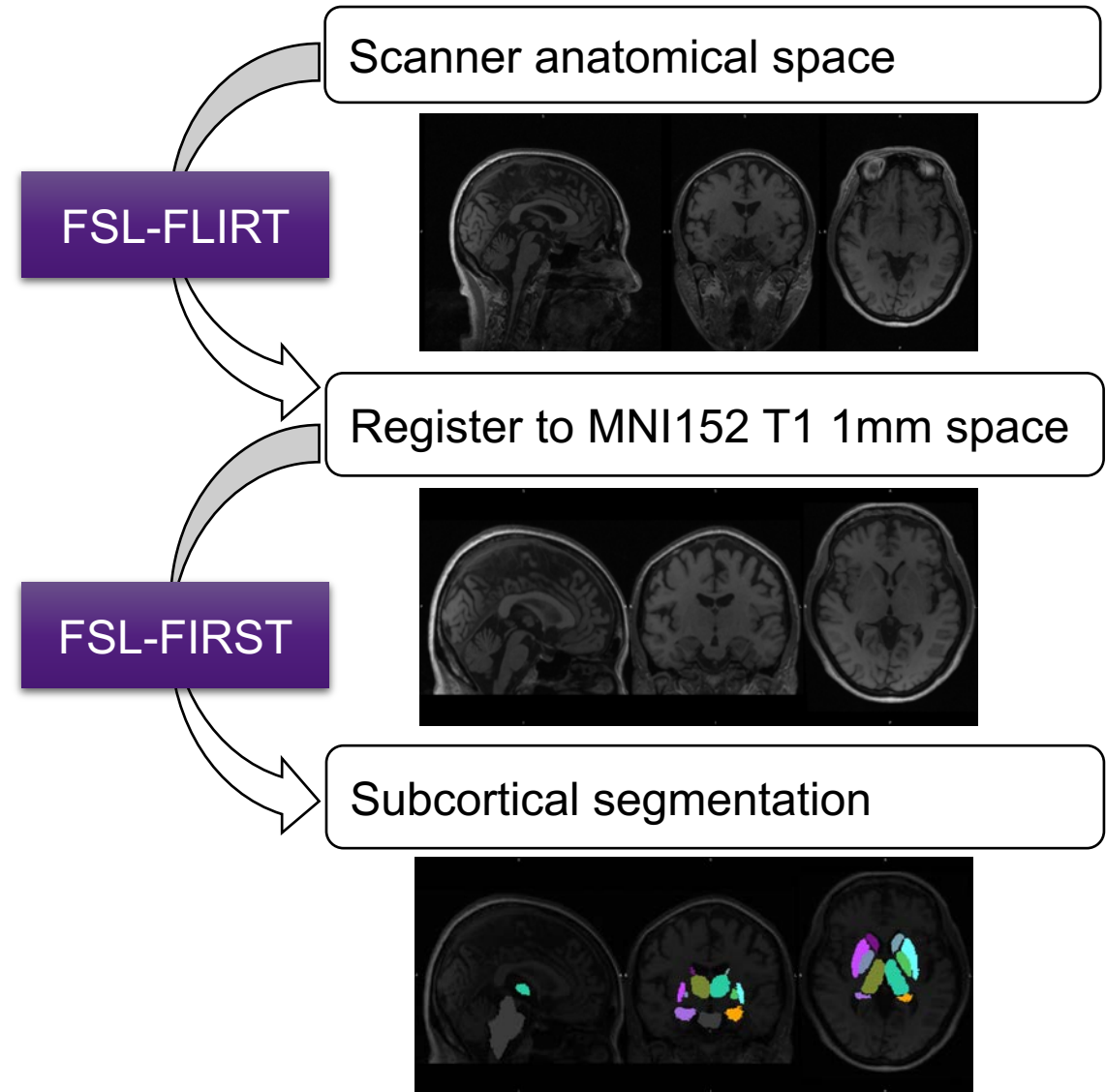
*Tristan Glatard<sup>1,2</sup>, Lindsay B. Lewis<sup>1</sup>, Rafael Ferreira da Silva<sup>3</sup>, Reza Adalat<sup>1</sup>, Natacha Beck<sup>1</sup>, Claude Lepage<sup>1</sup>, Pierre Rioux<sup>1</sup>, Marc-Etienne Rousseau<sup>1</sup>, Tarek Sherif<sup>1</sup>, Ewa Deelman<sup>3</sup>, Najmeh Khalili-Mahani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

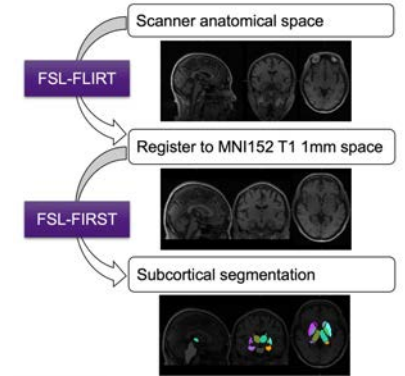
The following analyses were performed by **Thanh Thuy Dao** based on Glatard et al. approach using Neurodesk 😊



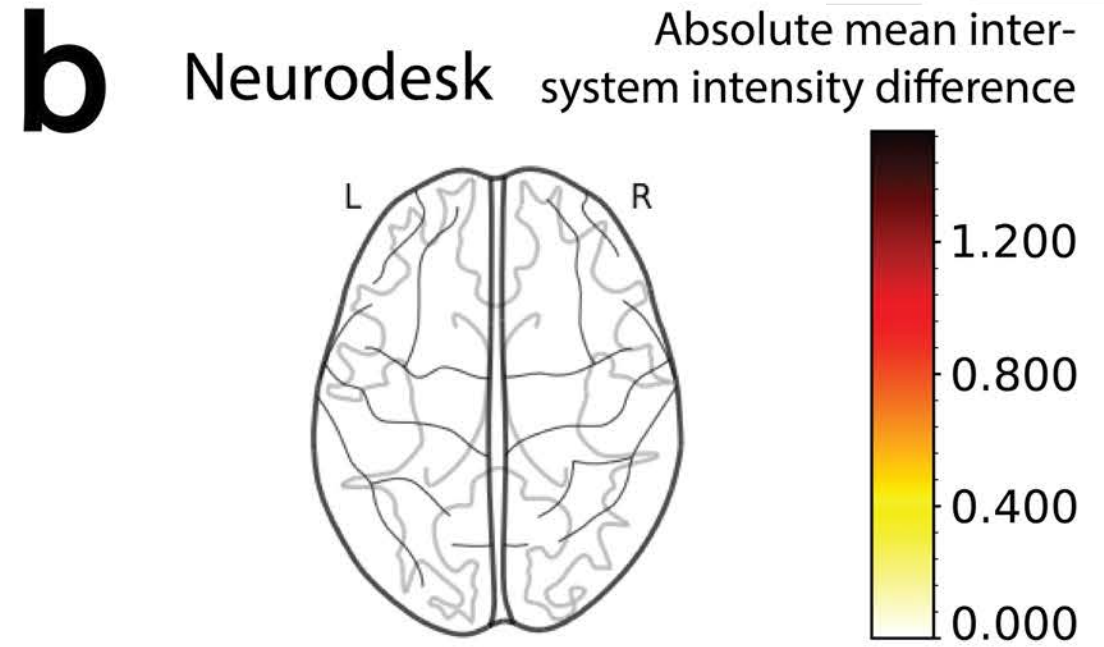
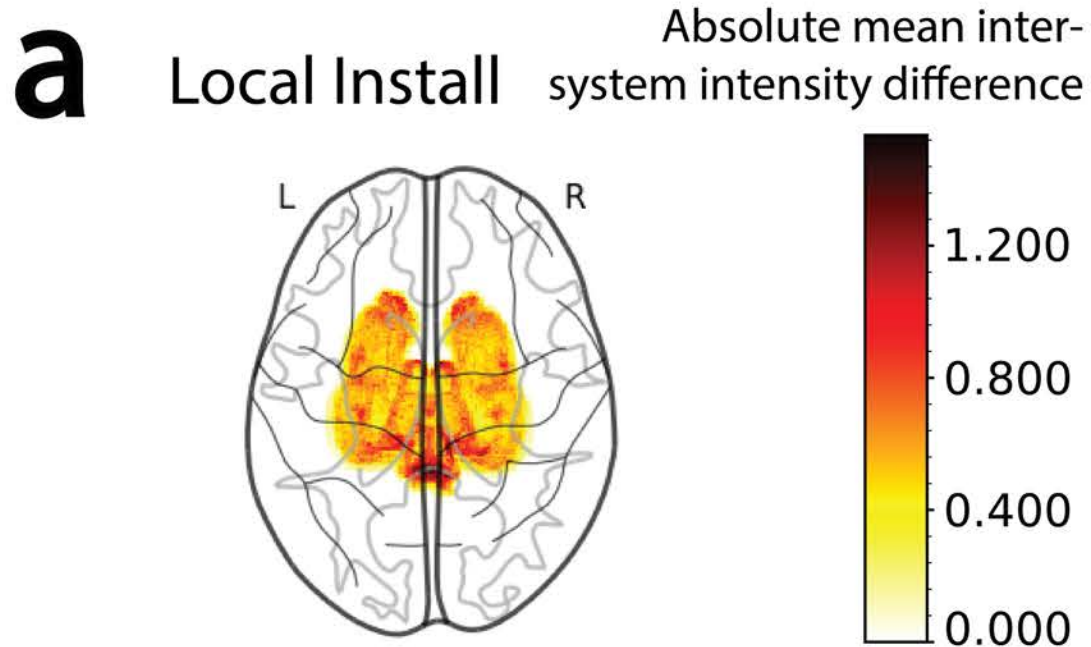
# The Analysis Setup

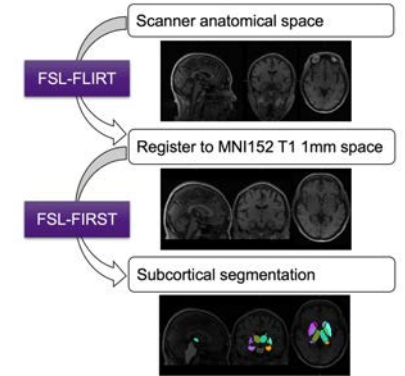
	System A		System B	
	Local	Neurodesk	Local	Neurodesk
Applications	FSL 6.0.5.1	FSL 6.0.5.1	FSL 6.0.5.1	FSL 6.0.5.1
Glibc version	2.31	2.23	2.28	2.23
OS	Ubuntu 20.04	Ubuntu 16.04.7	AlmaLinux 8.5	Ubuntu 16.04.7
Hardware	12th Gen Intel(R) Core(TM) i7-12700		AMD EPYC 7542 32-Core Processor	





# Image Intensity Differences (FSL FLIRT)

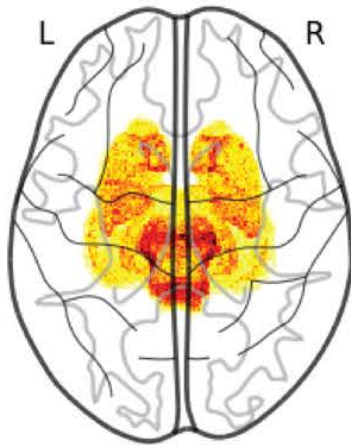




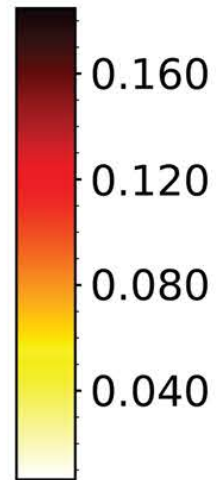
## Classification Differences (FSL FIRST)

**C**

Local Install

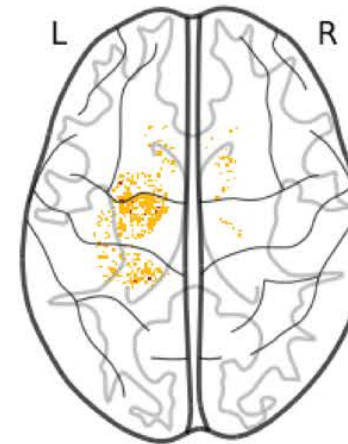


Mean inter-system  
disagreement in label

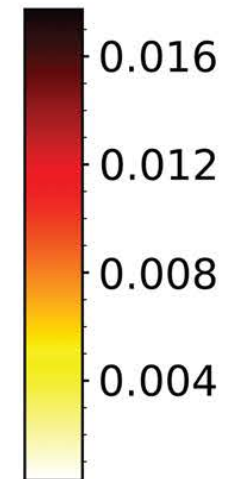


**d**

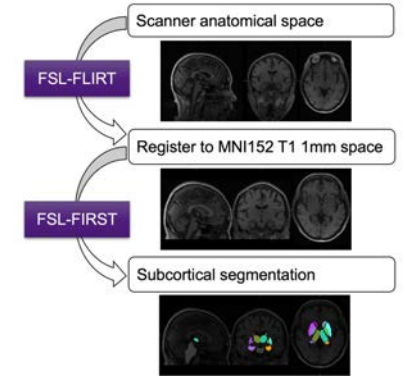
Neurodesk



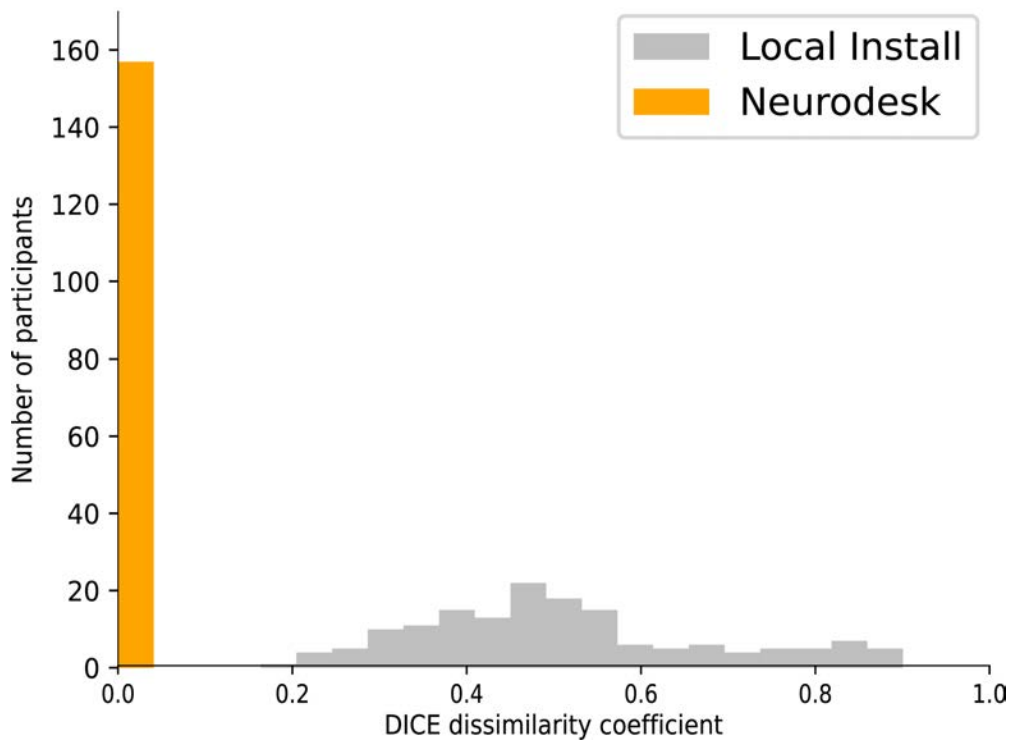
Mean inter-system  
disagreement in label



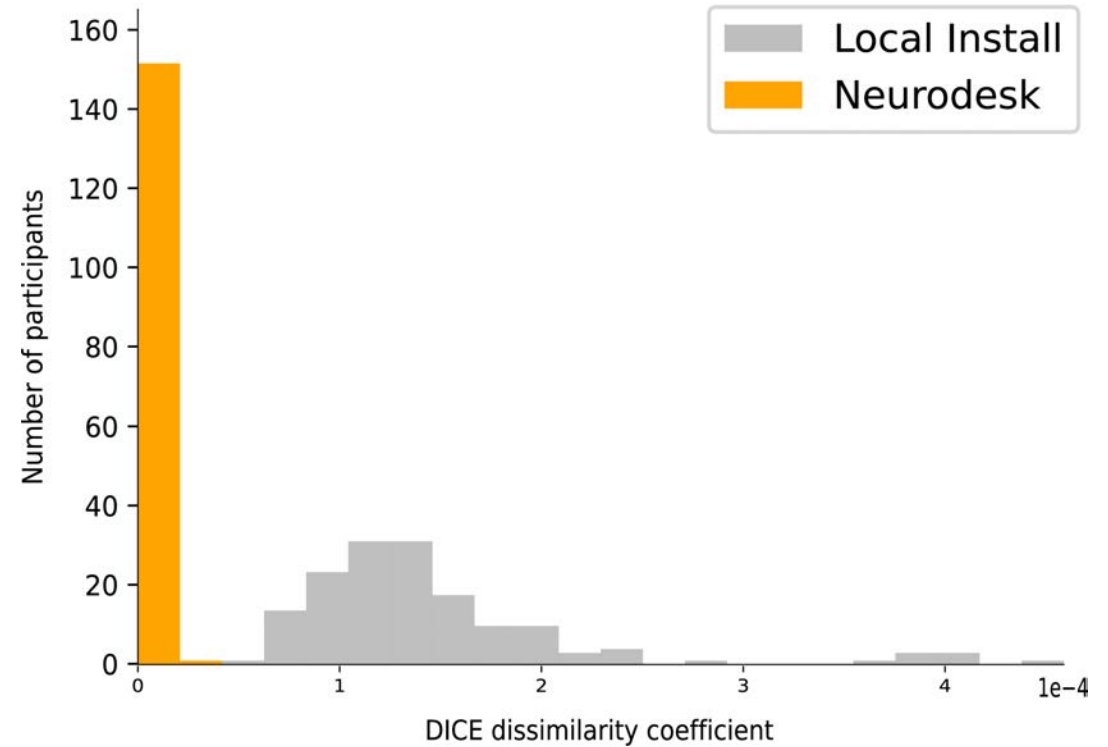
# DICE dissimilarity between System A and B

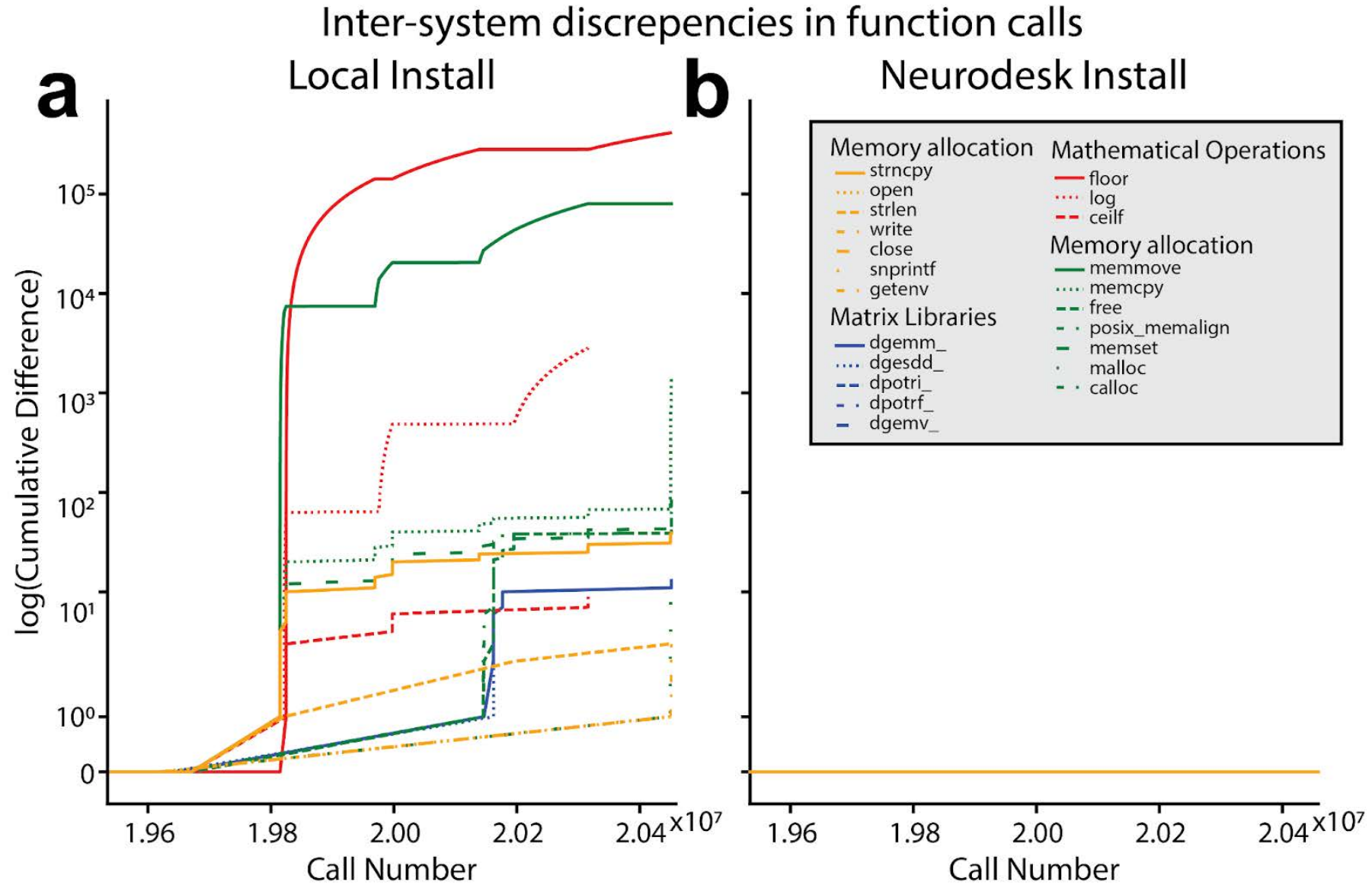


FSL-FLIRT



FSL-FIRST





# Interactive papers

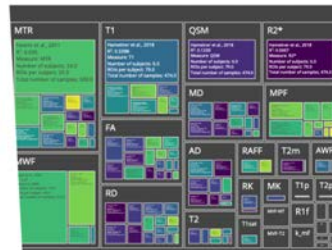


Supported by the **Canadian Open Neuroscience Platform (CONP)**.

## The quest for measuring myelin with MRI - An interactive meta-analysis

This study explores an important aspect of quantitative magnetic resonance imaging (qMRI): validation. Focusing specifically on myelin measures, we show the results of our meta-analysis comparing quantitative MRI with histology.

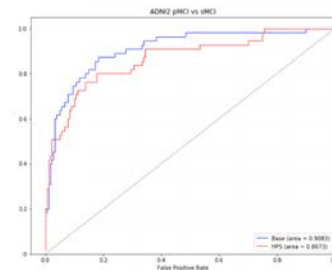
NeuroLibre Book GitHub Code



## A highly predictive signature (HPS) of Alzheimer's disease dementia from cognitive and structural brain features

A jupyter notebook containing analyses that give a highly predictive signature (HPS) of Alzheimer's disease dementia from cognitive and structural features using simulated data.

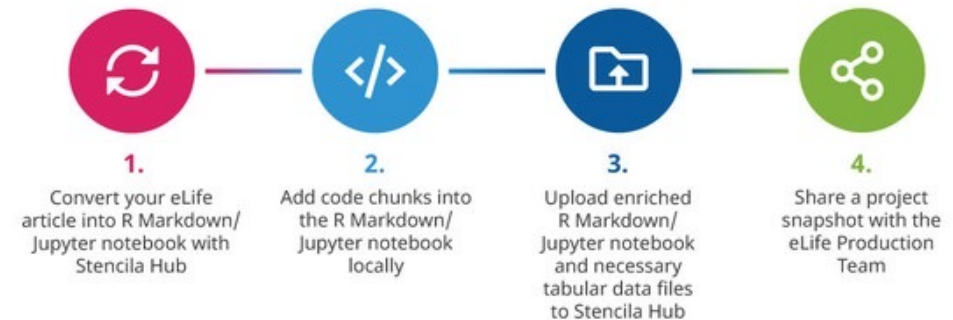
NeuroLibre Book GitHub Code



<https://www.neurolibre.com/>



## Steps to enrich your published article with code and data

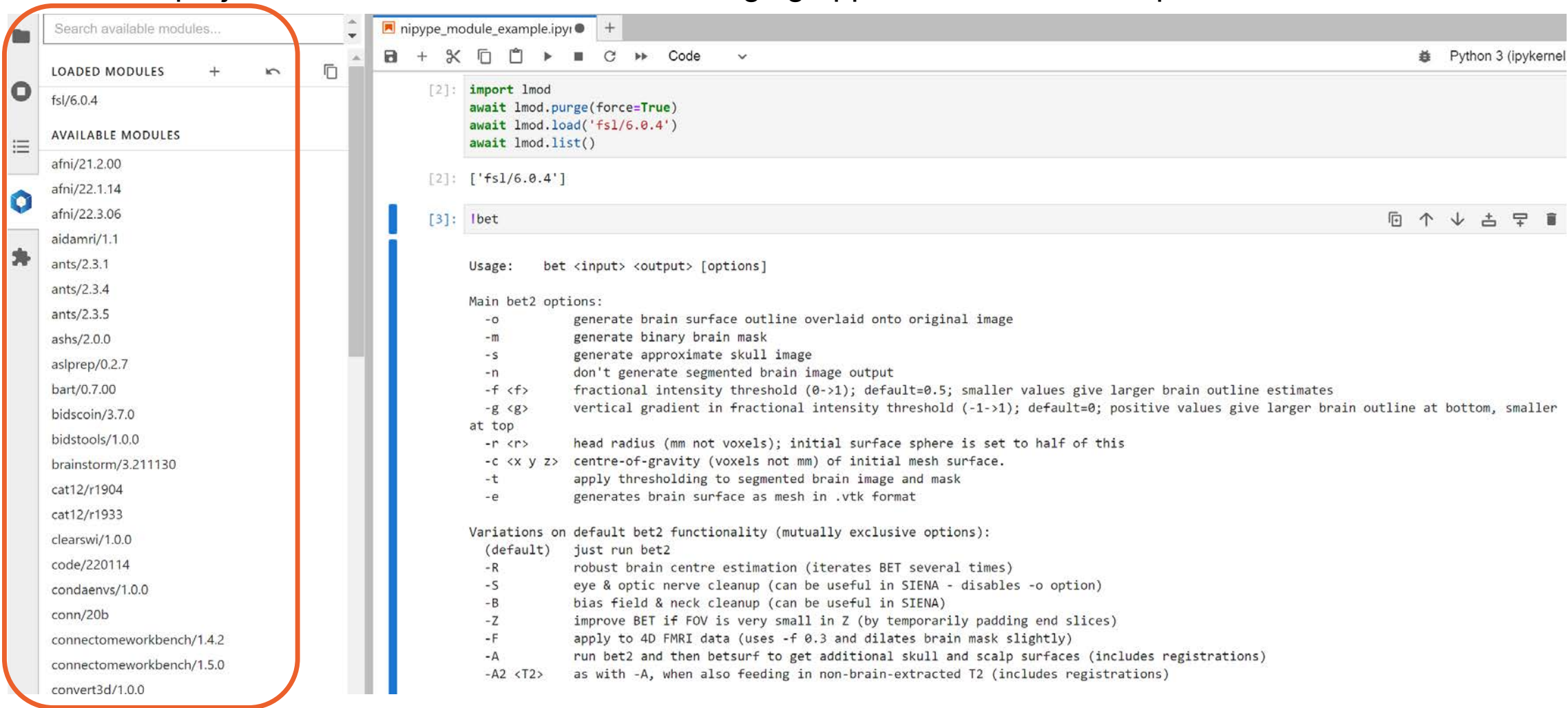


<https://elifesciences.org/labs/dc5acbde/welcome-to-a-new-era-of-reproducible-publishing>



# Neurodesk applications & Jupyter notebooks

Neurodesk project enables the use of all neuroimaging applications inside computational notebooks:



The screenshot displays a Jupyter notebook environment. On the left, a sidebar shows a search bar and two lists of modules: 'LOADED MODULES' (containing 'fsl/6.0.4') and 'AVAILABLE MODULES' (listing various neuroimaging tools like afni, ants, and bidscoin). The main notebook area shows a code cell with the following Python code:

```
[2]: import lmod
      await lmod.purge(force=True)
      await lmod.load('fsl/6.0.4')
      await lmod.list()
```

The output of the code cell is:

```
[2]: ['fsl/6.0.4']
```

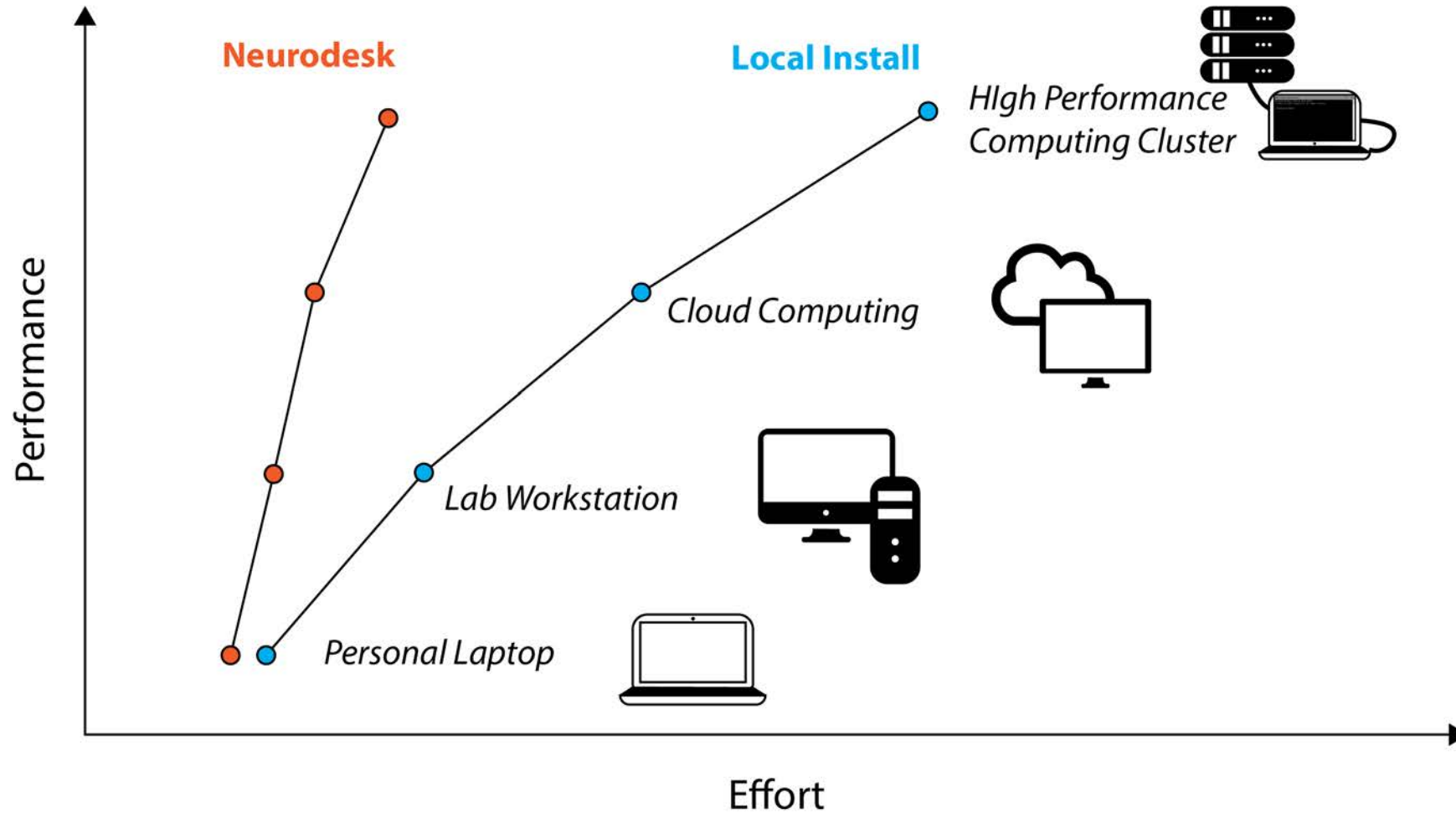
Below the code cell, the command 'lbet' is entered, and the help text for the 'bet' command is displayed:

```
Usage: bet <input> <output> [options]

Main bet2 options:
-o          generate brain surface outline overlaid onto original image
-m          generate binary brain mask
-s          generate approximate skull image
-n          don't generate segmented brain image output
-f <f>     fractional intensity threshold (0->1); default=0.5; smaller values give larger brain outline estimates
-g <g>     vertical gradient in fractional intensity threshold (-1->1); default=0; positive values give larger brain outline at bottom, smaller at top
-r <r>     head radius (mm not voxels); initial surface sphere is set to half of this
-c <x y z>  centre-of-gravity (voxels not mm) of initial mesh surface.
-t          apply thresholding to segmented brain image and mask
-e          generates brain surface as mesh in .vtk format

Variations on default bet2 functionality (mutually exclusive options):
(default)  just run bet2
-R         robust brain centre estimation (iterates BET several times)
-S         eye & optic nerve cleanup (can be useful in SIENA - disables -o option)
-B         bias field & neck cleanup (can be useful in SIENA)
-Z         improve BET if FOV is very small in Z (by temporarily padding end slices)
-F         apply to 4D FMRI data (uses -f 0.3 and dilates brain mask slightly)
-A         run bet2 and then betsurf to get additional skull and scalp surfaces (includes registrations)
-A2 <T2>  as with -A, when also feeding in non-brain-extracted T2 (includes registrations)
```

# Neurodesk at Scale

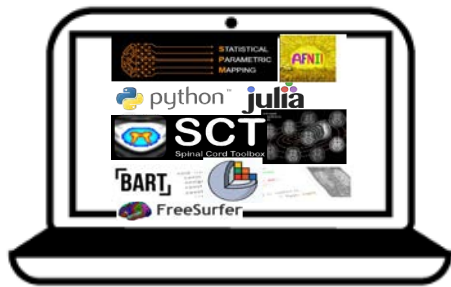


# Neurodesk brings ...



... a suite of neuroimaging tools ...

... on your notebook!



... on your lab workstation!



... on a cloud provider!



... on the university's high performance cluster!



# Roadmap

