

# Australian Electrophysiology Data Analytics PlaTform (AEDAPT)

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# The problem

We use the term electrophysiology for a range of related techniques including scalp electroencephalography (EEG), magnetoencephalography (MEG) and implanted electrodes and electrode arrays (iEEG, ECoG).

- Electrophysiology/EEG/MEG researchers have no advanced analysis solution in Australia
- EEG research groups are diverse: spanning industry and clinical settings, in the medical field and outside of it (AI/engineering to social and sports psychology)
  - many users unfamiliar with Linux
  - limited access & experience with supercomputers
  - locked-in to proprietary, hardware-based software
- In contrast, the open-source software offering for EEG analysis is expanding rapidly, especially around Python (e.g., MNE-Python) but also R and Matlab.
- Increasing focus on multimodal acquisition and analysis: MRI, electrophysiology, MEG, psychophysiology
- But how to make this easy, accessible, portable, reproducible?

# Key Questions

- Can we lower the barrier for users to analyze their data?
- Can we enable users to run the right analyses on the right hardware?
- Can we enable the re-use and sharing of data and analyses workflows?
- Can we build up a “library” of analysis workflows that are optimized for the data and instruments?
- Can we facilitate cross-modal data integration and analysis?



# AEDAPT approach

- AEDAPT aims to
  - foster the creation of **findable** structured data and **reproducible** analysis pipelines
  - make state of the art analysis tools highly **accessible** by researchers from diverse settings (regional universities/industry/clinical/labs with less-technical staff)
  - facilitate **interoperability** with other data storage and analysis platforms to allow scaling up of electrophysiology and multimodal neuroimaging research to
    - promote collaborative international research
    - address major challenges such as epilepsy, stroke, traumatic brain injury and dementia

# AEDAPT Core

A user-friendly desktop environment for electrophysiology and related behavioural and psychophysiological data analysis and processing.

Modular architecture consisting of:

- a linux desktop container that provides the interactive environment
- a continuous integration builder for automated building, testing and uploading containers to registries
- an installer tool that pulls and integrates user-selected containers into the environment
- integrated tools to convert from different electrophysiology formats to BIDS and manipulate, interrogate and share data in BIDS
- Integration with ACCS and Datalad for data and code provenance
- interoperable with other Australian and international platforms
  - Australian Imaging Service
  - Characterisation Virtual Laboratory
  - Australian Characterisation Commons at Scale
  - Brainlife.io
  - Neuroscience Without Borders

open, extensible, community-led

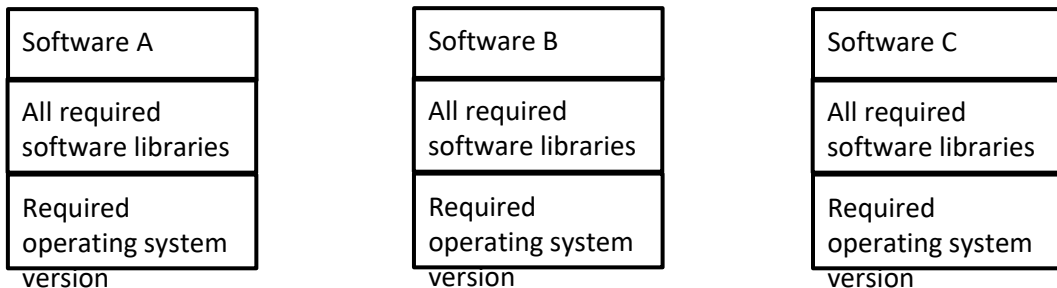
# Accessible: Easy

## Challenge

- Due to limited resources on part of the developers, academic open-source software is often **difficult to install**.
- Sometimes a **new software cannot be installed** due to conflicts with existing software or incompatibility with OS version.

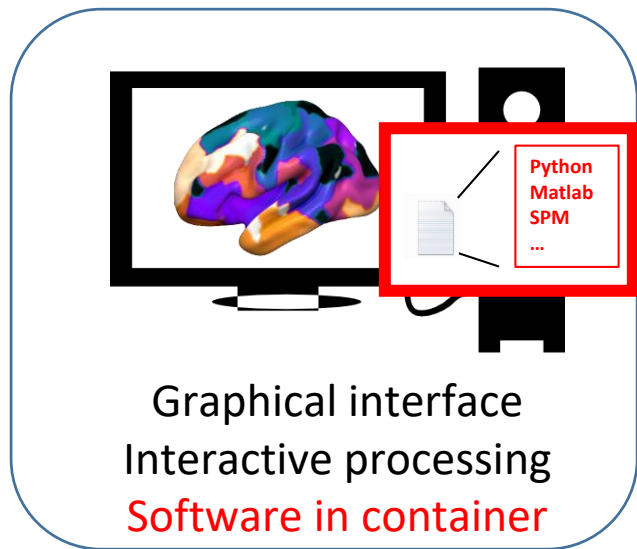
## Our approach

- All software packages come pre-installed, with a range of versions offered



Use <https://forms.gle/deKy85yniJLP4hDM8> to suggest more packages.

# Put working environment within a container



## Containers

- Can run on HPC
- Light
- Can be run on Linux/Mac/Windows
- Automatic download from registry
- Docker already comes with many OS installations
- Singularity can run on HPCs

Using docker-ubuntu-vnc-desktop

<https://github.com/fcwu/docker-ubuntu-vnc-desktop>

civier Update README.md 5df1819 7 hours ago

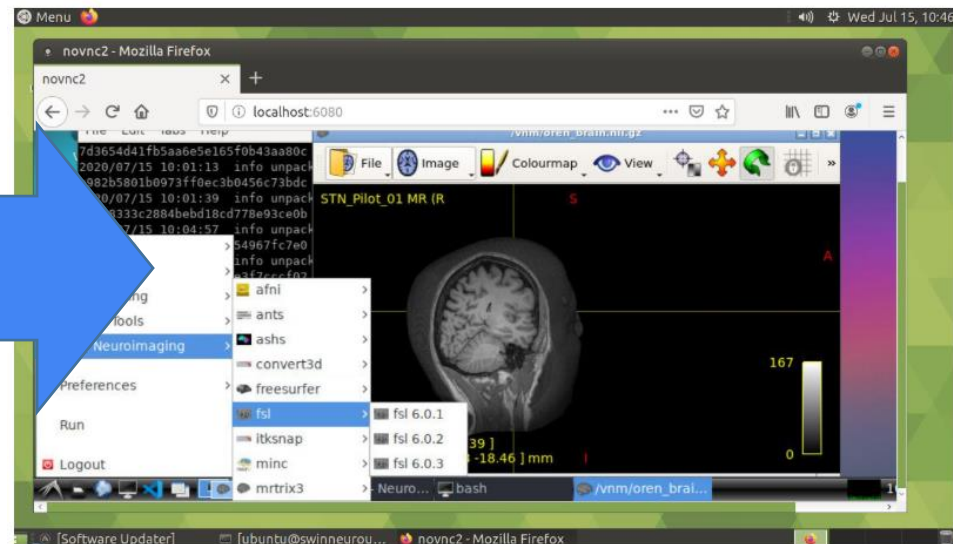
.github/workflows	Update docker-image.yml
config	added vnc port and made ml load message only appear when modul...
.gitattributes	refactor menu system to neurodesk repo
Dockerfile	Install basic popular linux utilities in main image
LICENSE	Initial commit
README.md	Update README.md
Screenshot.png	Add files via upload
build_run_stop.bat	menu generation is now in neurodesk repo
build_run_stop.sh	wrong message after closing container
logo-long-full.svg	Add files via upload
nif.png	Add files via upload
virtualneuromachine_logo_small.png	maded logo smaller

# Virtual Neuro Machine

A compact Docker container with a browser-accessible environment for reproducible neuroimaging analysis. Only the required software packages, already pre-installed, are downloaded from a public library (downloaded as containers).

Please complete the survey to help guide future additions to the software library:

<https://forms.gle/deKy85yniJLP4hDM8>

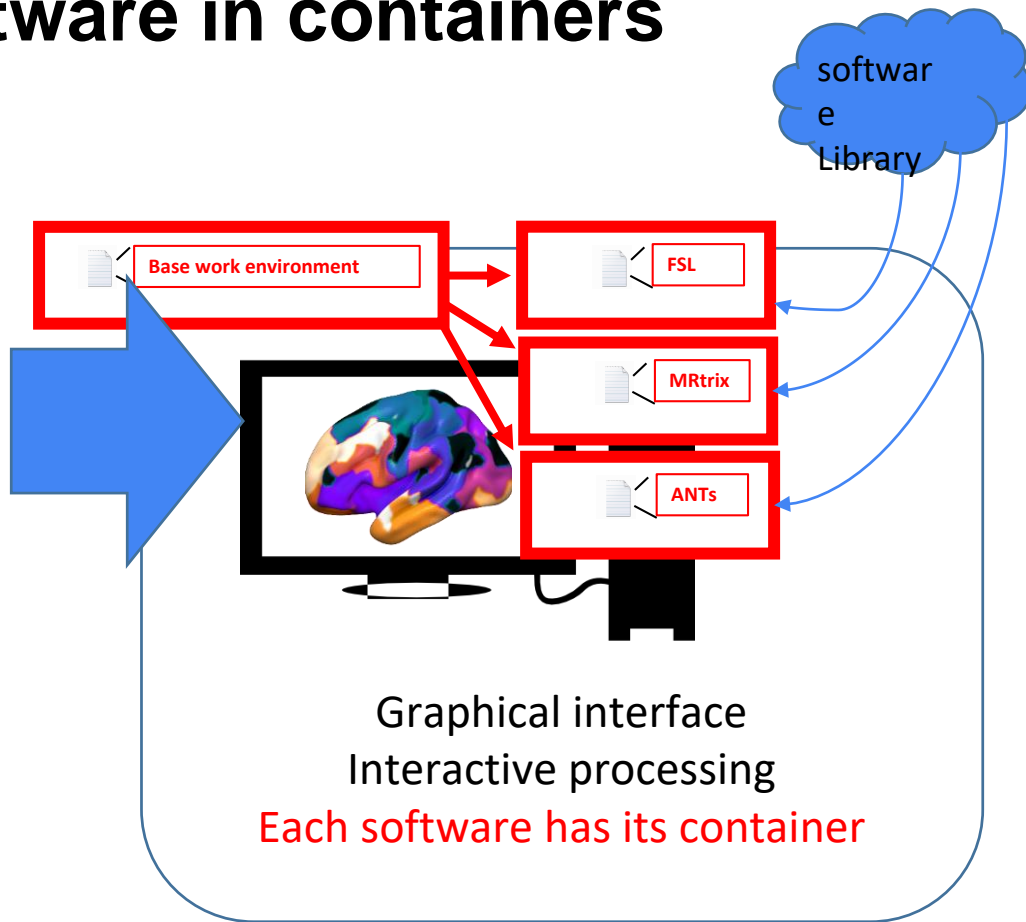
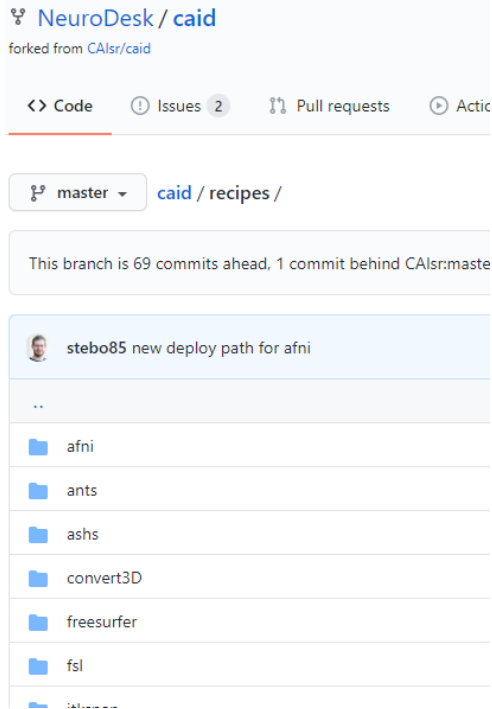


## Quickstart

1. Install Docker from here: <https://docs.docker.com/get-docker/> (Mac, Windows, Linux; for HPC/supercomputer: <https://github.com/NeuroDesk/transparent-singularity>)
2. Create a local folder where the downloaded software packages will be stored, e.g. ~/vnm in Mac and Linux, or C:\vnm in Windows



# Put all popular software in containers



# Put all popular software in containers

## Neurodocker

build **passing** docker pulls **406** docker pulls **17k** python **3.5 | 3.6 | 3.7 | 3.8** DOI **10.5281/zenodo.3753248**

*Neurodocker* is a command-line program that generates custom Dockerfiles and Singularity recipes for neuroimaging and minifies existing containers.

- Examples:
  - [Examples gallery](#)
  - [Canonical examples](#)
    - [Docker](#)
    - [Singularity](#)
  - [Minimize existing Docker image](#)
  - [Example of minimizing Docker image for FreeSurfer recon-all](#)
- [Known issues](#)

## Installation

Use the *Neurodocker* Docker image (recommended):

```
docker run --rm repronim/neurodocker:0.7.0 --help
```

The Docker images were recently moved to [repronim/neurodocker](#) from [kaczmarj/neurodocker](#).

## Neurodocker Supported Software

- AFNI
- ANTs
- Convert3D
- dcm2niix
- FreeSurfer
- FSL
- ITKsnap
- Matlab Compiler Runtime
- MINC
- Miniconda
- MRICron
- MRtrix3
- NeuroDebian
- PETPVC
- SPM12
- VNC

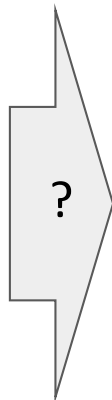
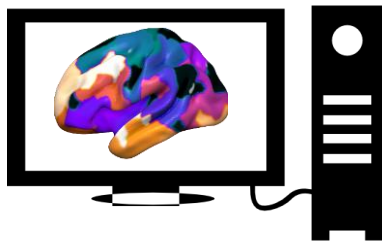
<https://github.com/ReproNim/neurodocker>

# Scalability - analyse many subjects in parallel

Initial analysis for study

Final analysis for study

- Only one subject
- Personal computer OR Cloud computing (AWS, NECTAR)
- Mac/Windows/Desktop Linux



- Many subjects
- Supercomputer (High-performance computing)
- Enterprise Linux



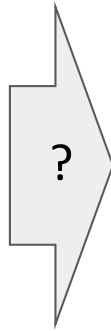
## AEDAPT/NeuroDesk:

Software packages are provided pre-installed, so no repeated installation on supercomputer. Owing to being cross-platform, NeuroDesk provides identical experience on both platforms.

# Reproducibility - Sharing a working version of pipelines

## Final analysis for study

- Supercomputer X



## Analysis by other scientists

- Supercomputer Y
- Personal computers
- Cloud computing (AWS, NECTAR)

Why do we need to share a working version of an analysis pipeline?

- Own use - to accurately repeat an analysis independently of hardware and OS upgrades
- Multi-site studies - require standardised analysis across sites
- Advancement of science - rapid dissemination of new pipelines
- **Scientific review - hands-on verification of analysis pipelines**



### AEDAPT/NeuroDesk:

**Desktop environment and software packages are pre-installed, so they can be provided as-is also for other scientists.**

# Automate/facilitate container building

Workflows New workflow

All workflows

Filter workflows

646 Results

- ✓ new deploy path for afni #56: Commit 626e6b6 pushed
- ✓ added afm02 on wieners #26: Commit 044f31a pushed
- ✓ added afm02 on wieners #53: Commit 044f31a pushed
- ✓ added afm02 on wieners #18: Commit 044f31a pushed
- ✓ added afm02 on wieners #98: Commit 044f31a pushed
- ✓ added afm02 on wieners #57: Commit 044f31a pushed
- ✓ added afm02 on wieners #9: Commit 044f31a pushed

singularity

convert3D

template

lshis

ashs

afni

ants

julia

mrtrix3

minc

freesurfer

Recipe Builder

Container Builder

fsl

## currently available tools:

<https://github.com/NeuroDesk/caid/packages>

- afni passing
- ants passing
- ashs passing
- convert3D passing
- freesurfer passing
- fsl passing
- itksnap passing
- julia passing
- lshis passing
- minc passing
- mrtrix3 passing

Docker

Singularity

dockerhub

Search for great content (e.g., myso)

Organizations vnmd Repositories

vnmd

Community Organization

Members Teams Repositories Settings

Search by repository name

NAME

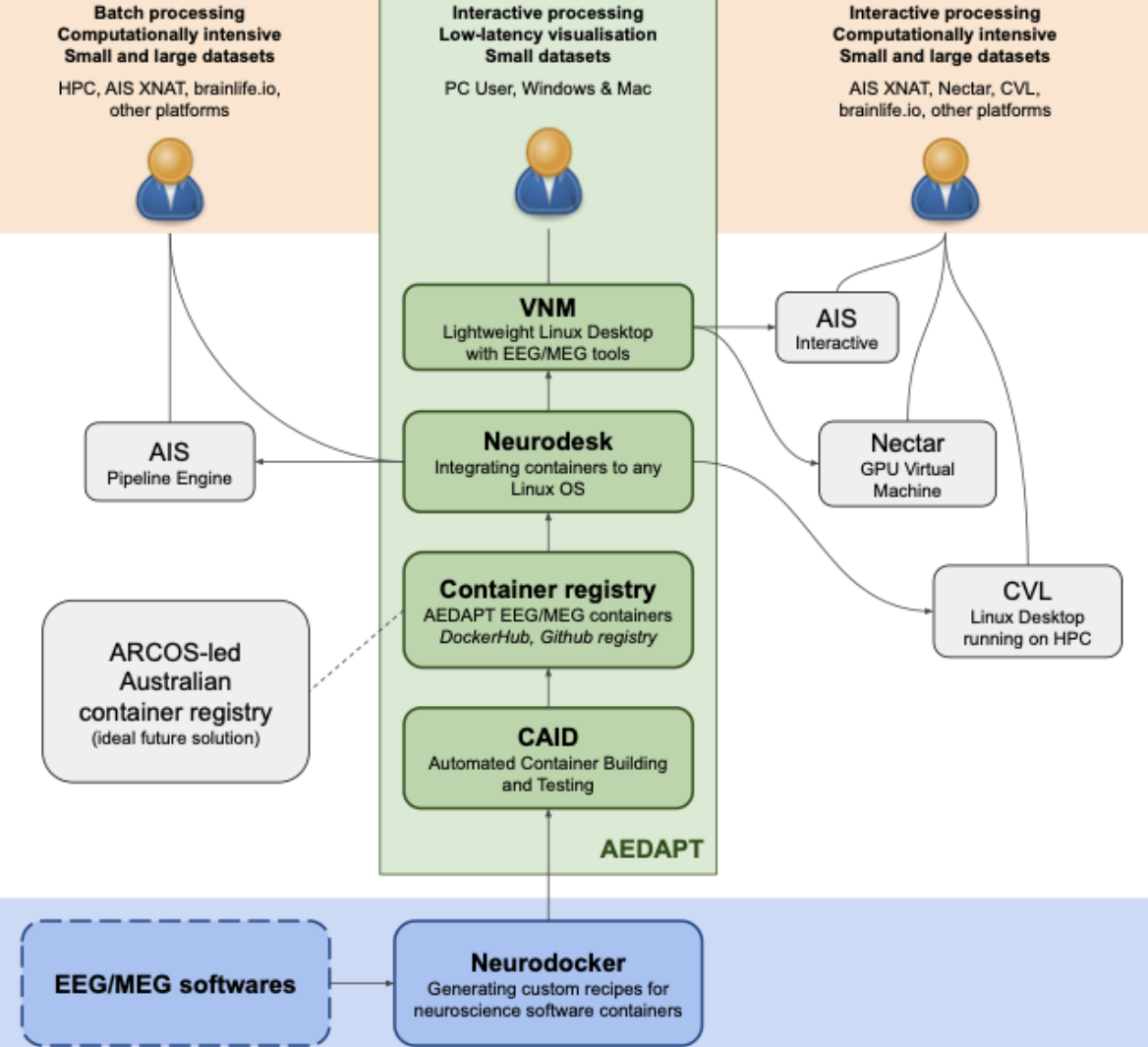
vnmd / afni\_20.2.11

vnmd / mrtrix3\_3.0.1

https://swift.rc.nectar.org.au/v1/AUTH...

This XML file does not appear to have any style information associated

```
<container name="singularityImages">
  <object>
    <name>afni_20.2.11_20200811.sif</name>
    <hash>d41d8c9f900b204e9800998ecf8427e</hash>
    <bytes>0</bytes>
    <content_type>application/octet-stream</content_type>
    <last_modified>2020-08-11T12:16:06.410370</last_modified>
  </object>
  <object>
    <name>ants_2.3.4_20200811.sif</name>
    <hash>5fbc3e465d7095c7304816da8913818c</hash>
    <bytes>669880512</bytes>
    <content_type>application/octet-stream</content_type>
    <last_modified>2020-08-11T08:09:30.049570</last_modified>
  </object>
```



## Standards:

- BIDS++ by default
- AIS/ACCS/CVL/Brainlife Interoperability
- ARCOS Container Library
- INCF/IBI/ARDC Meta-Data standards
  - [schema.org](https://schema.org) +

# Thank you

## AEDAPT CORE TEAM

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Australian Research Data Commons



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