



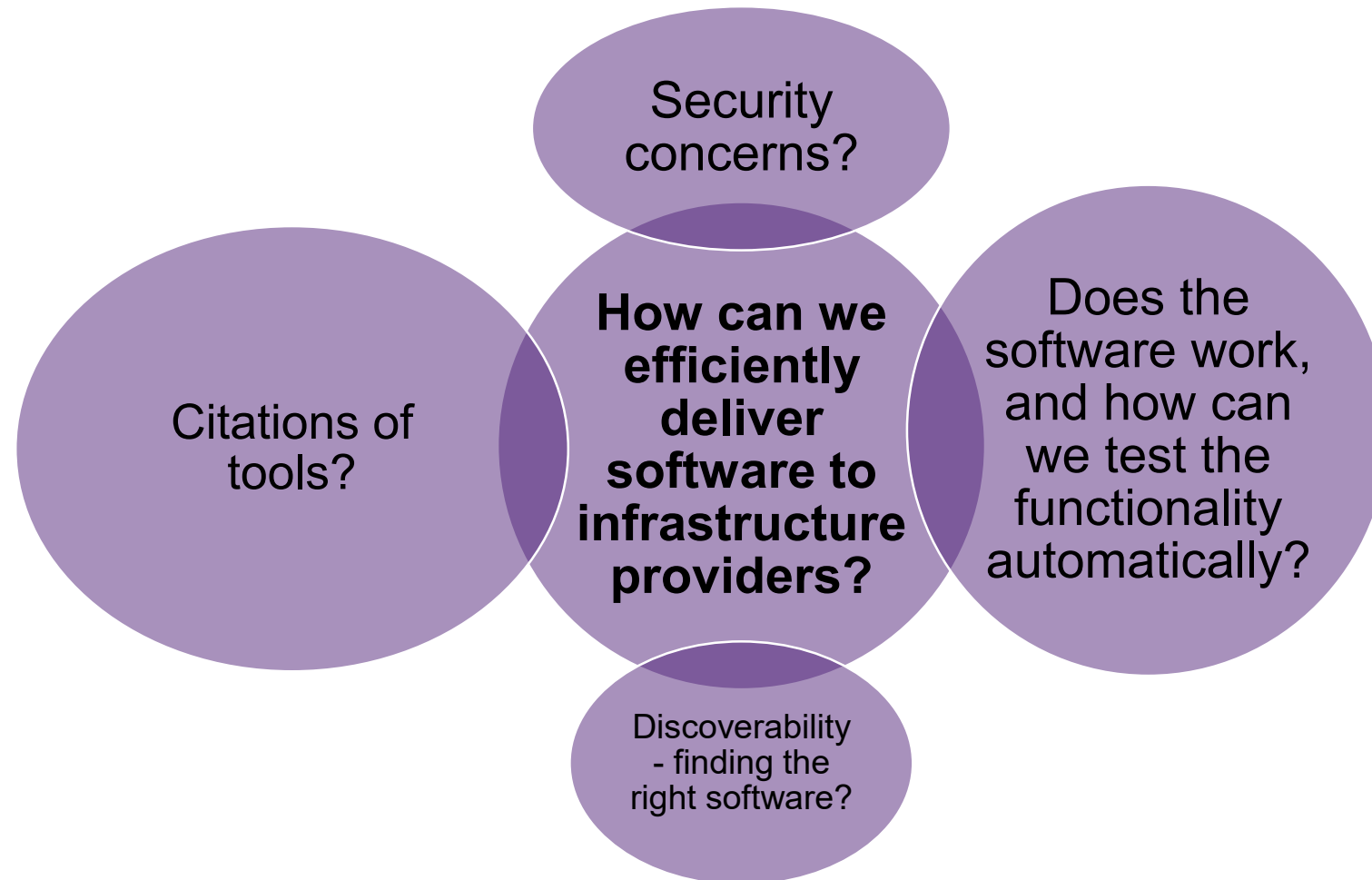
SCIDIR

A Scientific Software Distribution Repository

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- 1) University of Queensland
- 2) National Imaging Facility
- 3) Pawsey Supercomputing Research Centre
- 4) The Queensland Cyber Infrastructure Foundation (QCIF)
- 5) AARNet
- 6) Australian BioCommons

What is the problem?



History

- This proposal aims at bringing together various recent developments in different communities



Australian Biocommons Bring-Your-Own-Data Expansion Project

- Aimed at providing shared reference datasets and containers across different infrastructures

AEDAPT NeuroDesk platform project

- Neuroimaging containers automatically built via Github actions and distributed via CVMFS + Desktop environment for easy access

European Environment for Scientific Software Installations (EESSI)

- software layer with EasyBuild, Lmod and archspec; Gentoo Prefix compatibility layer; distribution via CVMFS

EESSI and DRA of Canada

- EESSI plans to build all applications available in easybuild and distribute via CMVFS
- DRA provides CVMFS servers with various software optimized for HPCs
- what they don't do:
 - provide software containers or workflows in containers (e.g. MRIQC)
 - less focused on reproducibility aspects (focus is on performance, no container archival, no citation of containers, no DOI for containers)

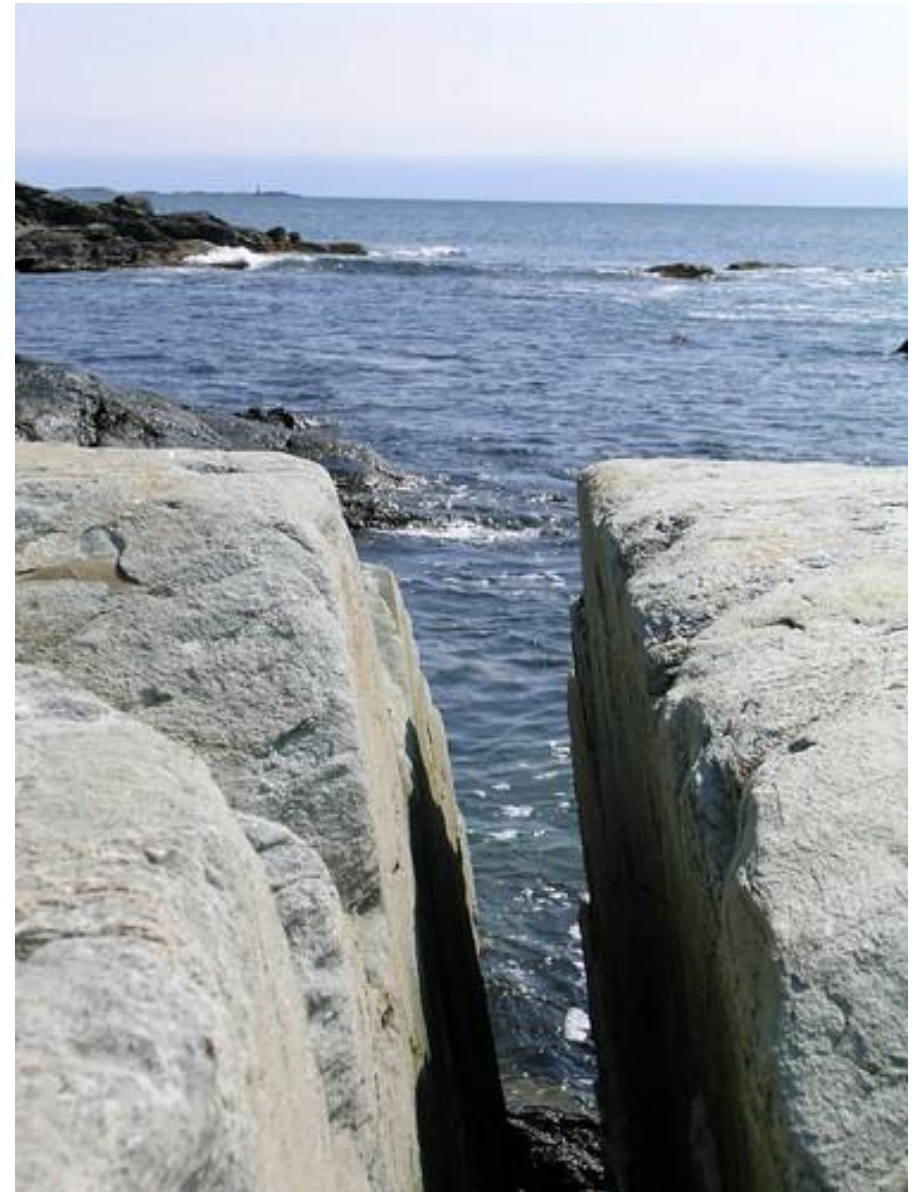


**Digital Research
Alliance** of Canada

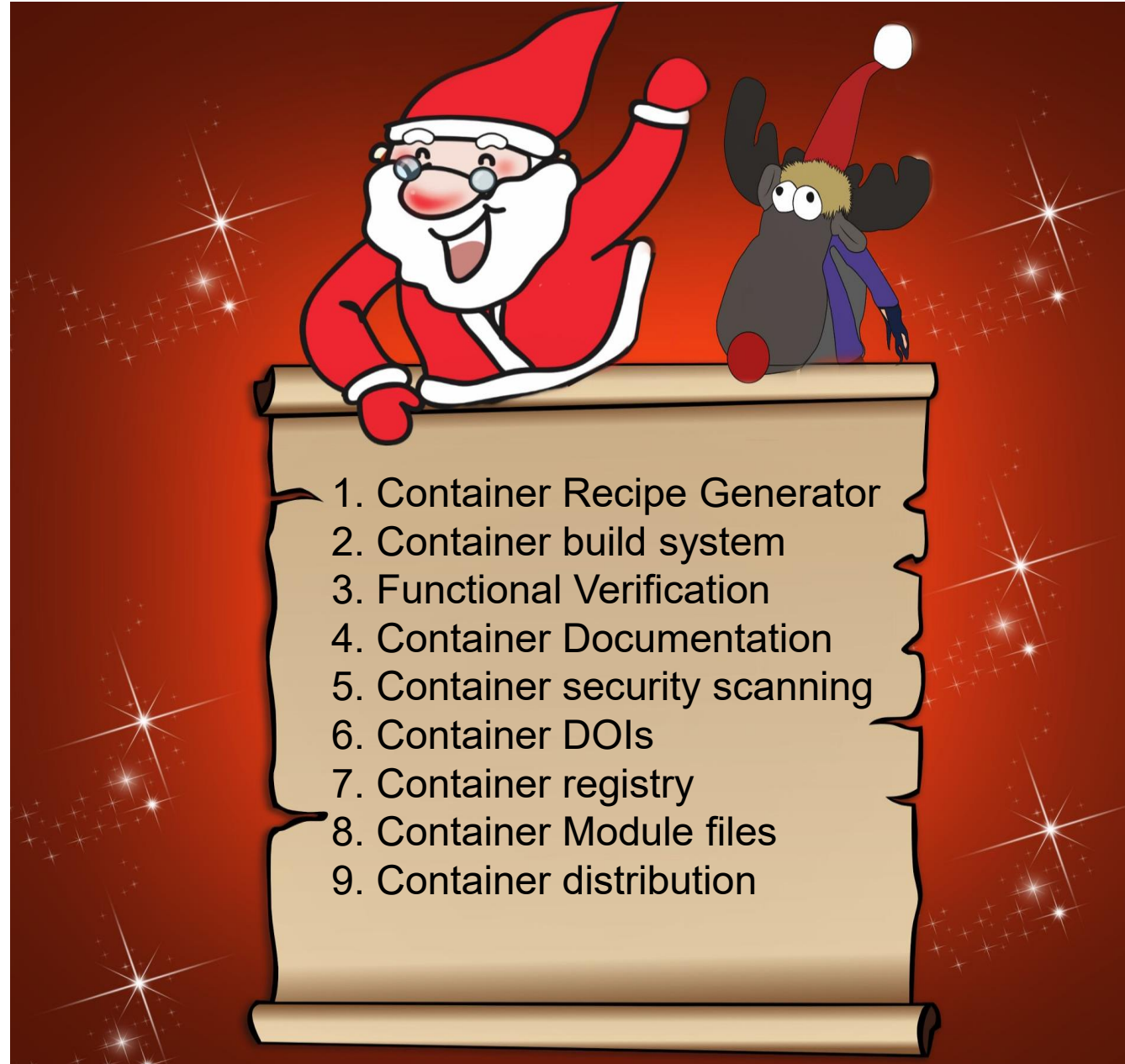
**Alliance de recherche
numérique** du Canada

The gap?

- current software distribution projects don't focus on containers
- scanning for vulnerabilities or testing for functional correctness currently not in focus
 - -> HPC admins struggle to allow these containers on their platforms, but users are already running it anyway
- software containers are not optimized for different hardware architectures
- no systematic mechanism to capture meta-data, discovery, or citation
- no production CVMFS deployment in Australia

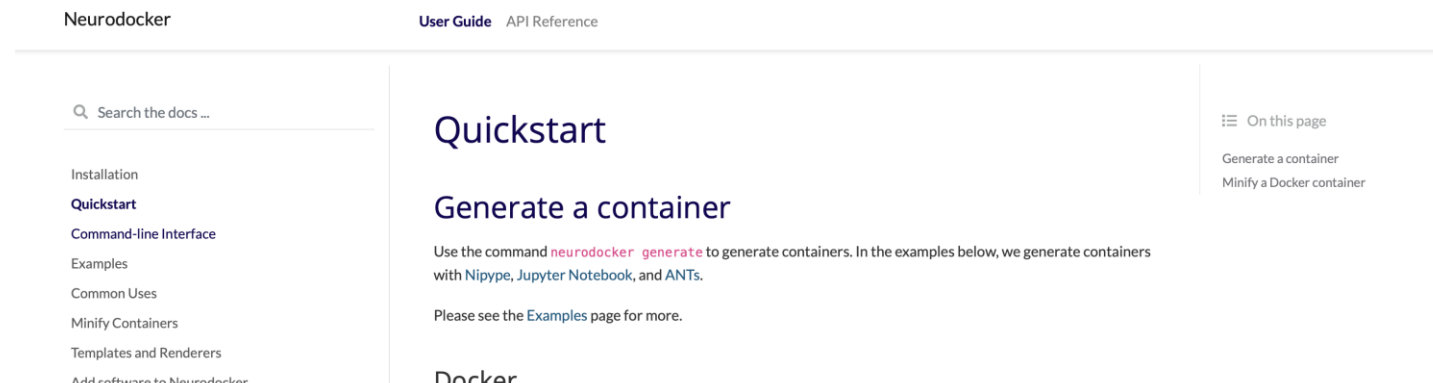


A wish list:



Container Recipe Generator / Template / Renderer


- Writing good docker recipes is tedious
- Domain specific recipe generators like neurodocker are a great help
- other domain agnostic tools
 - HPC Container Maker
 - Spack
 - Easybuild



The screenshot shows the Neurodocker website's 'Quickstart' page. The page title is 'Quickstart' and the main heading is 'Generate a container'. Below the heading, it says: 'Use the command `neurodocker generate` to generate containers. In the examples below, we generate containers with Nipype, Jupyter Notebook, and ANTs. Please see the Examples page for more.' On the right side, there is a sidebar with a search bar and a list of links: 'Generate a container' and 'Minify a Docker container'. The left sidebar contains a navigation menu with items like 'Installation', 'Quickstart', 'Command-line Interface', 'Examples', 'Common Uses', 'Minify Containers', and 'Templates and Renderers'.

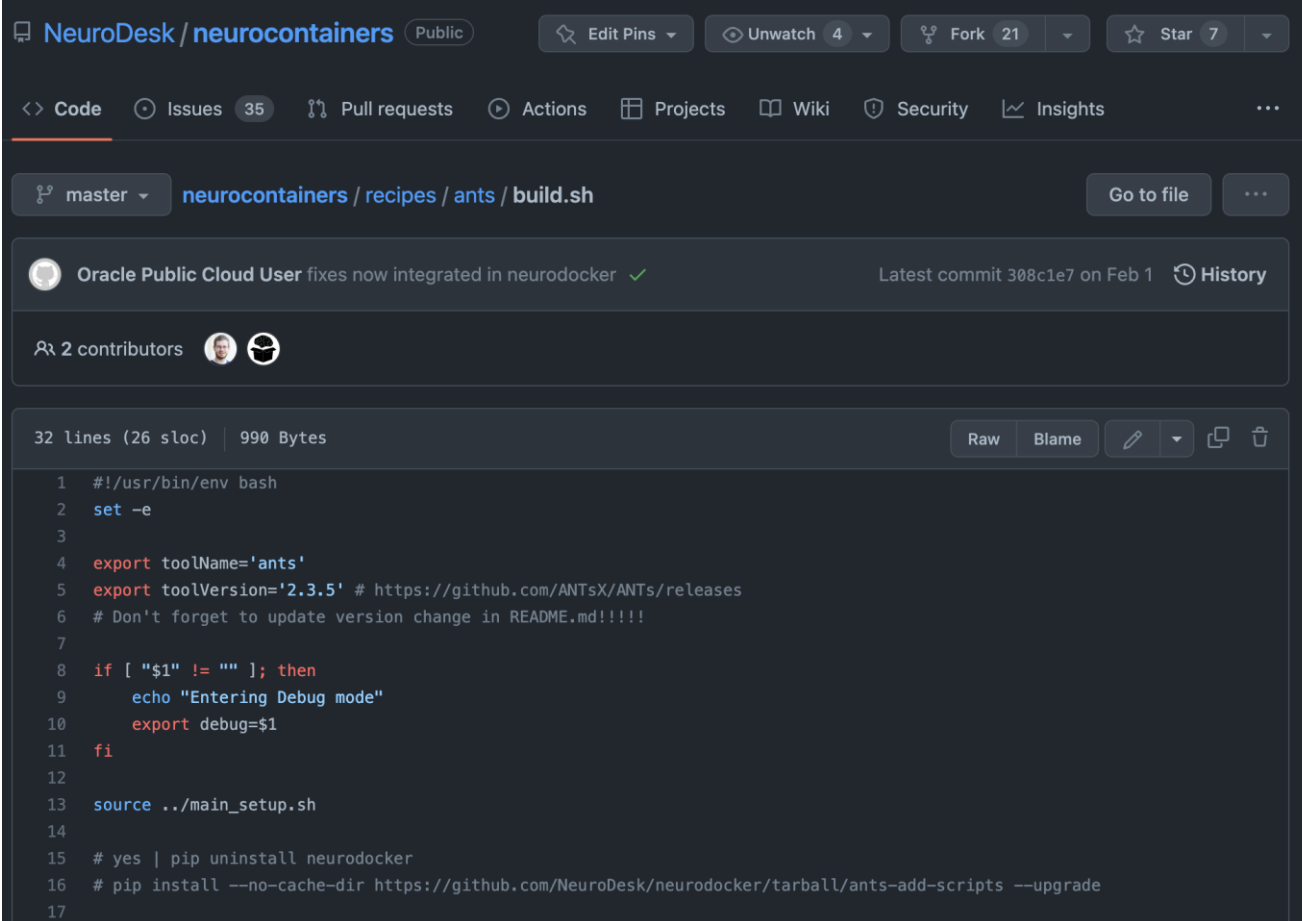
```
FROM ubuntu:16.04
RUN printf '#!/bin/bash\nls -la' > /usr/bin/ll
RUN chmod +x /usr/bin/ll
RUN mkdir /afm01 /afm02 /90days /30days /QRISdata /RDS /data /short /proc_temp /TMPDIR /nvme /local /gpfs1 /working
ENV ANTSPATH="/opt/ants-2.3.4/" \
    PATH="/opt/ants-2.3.4:$PATH"
RUN apt-get update -qq \
    && apt-get install -y -q --no-install-recommends \
    ca-certificates \
    curl \
    && rm -rf /var/lib/apt/lists/* \
    && echo "Downloading ANTs ..." \
    && mkdir -p /opt/ants-2.3.4 \
    && curl -fsSL https://dl.dropbox.com/s/gwf51ykkk5bifyj/ants-Linux-centos6_x86_64-v2.3.4.tar.gz \
    | tar -xz -C /opt/ants-2.3.4 --strip-components 1
ENV DEPLOY_PATH="/opt/ants-2.3.4/"
COPY ["README.md", \
    "/README.md"]
```

```
neurodocker generate ${neurodocker_buildMode} \
  --base-image ubuntu:16.04 \
  --pkg-manager apt \
  --ants version=${toolVersion} \
  > ${imageName}.Dockerfile
```



Automated Container build

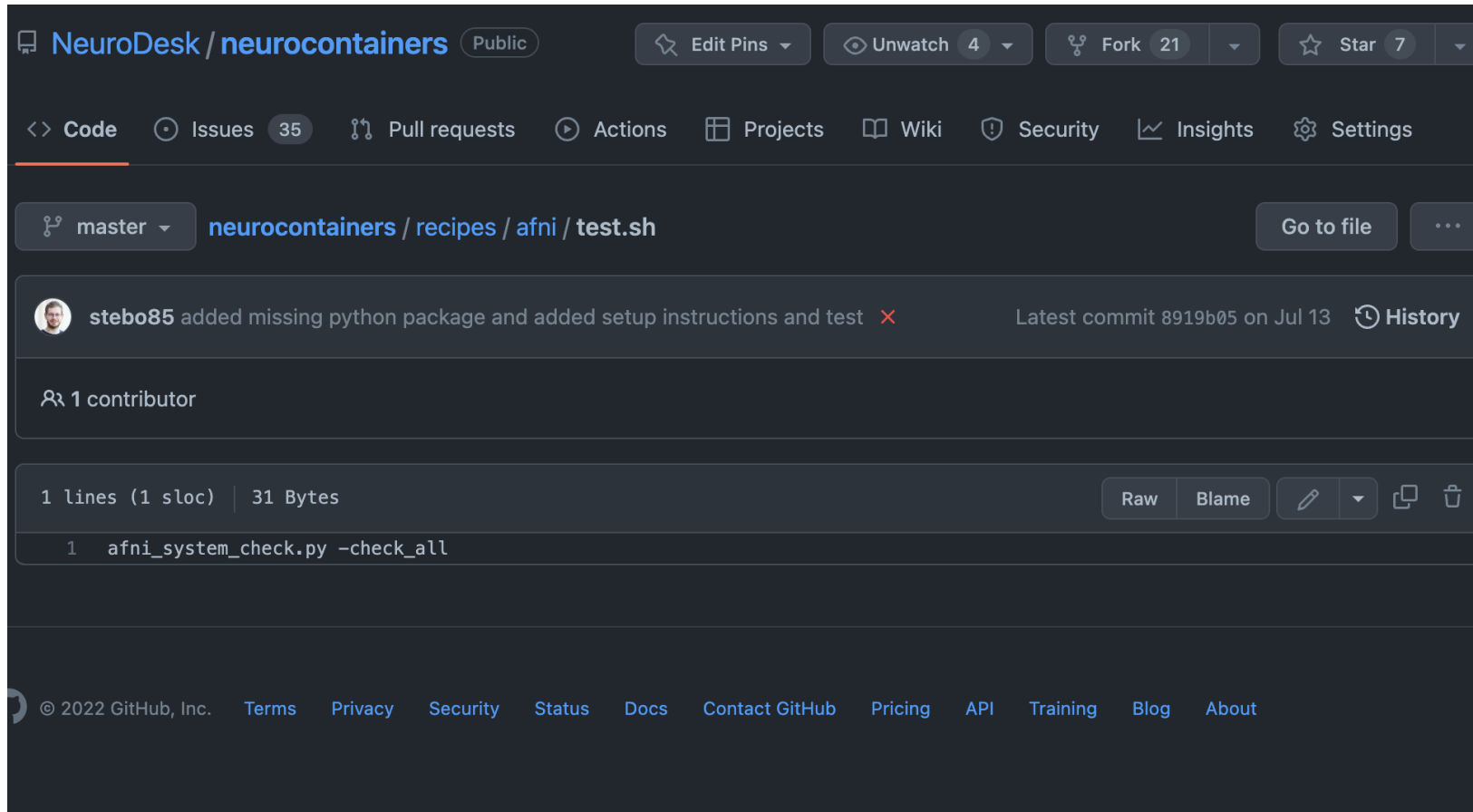
- Github repository that collects Docker recipes from contributors
- Recipes get build via github actions with custom runners + architecture specific builds via custom runners (e.g. ARM, AMD Milan ...)
- Periodic rebuilds for new versions?



```
1 #!/usr/bin/env bash
2 set -e
3
4 export toolName='ants'
5 export toolVersion='2.3.5' # https://github.com/ANTsX/ANTs/releases
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 # yes | pip uninstall neurodocker
16 # pip install --no-cache-dir https://github.com/NeuroDesk/neurodocker/tarball/ants-add-scripts --upgrade
17
```

Functional Verification

- test script with test data that we can run after the build process?



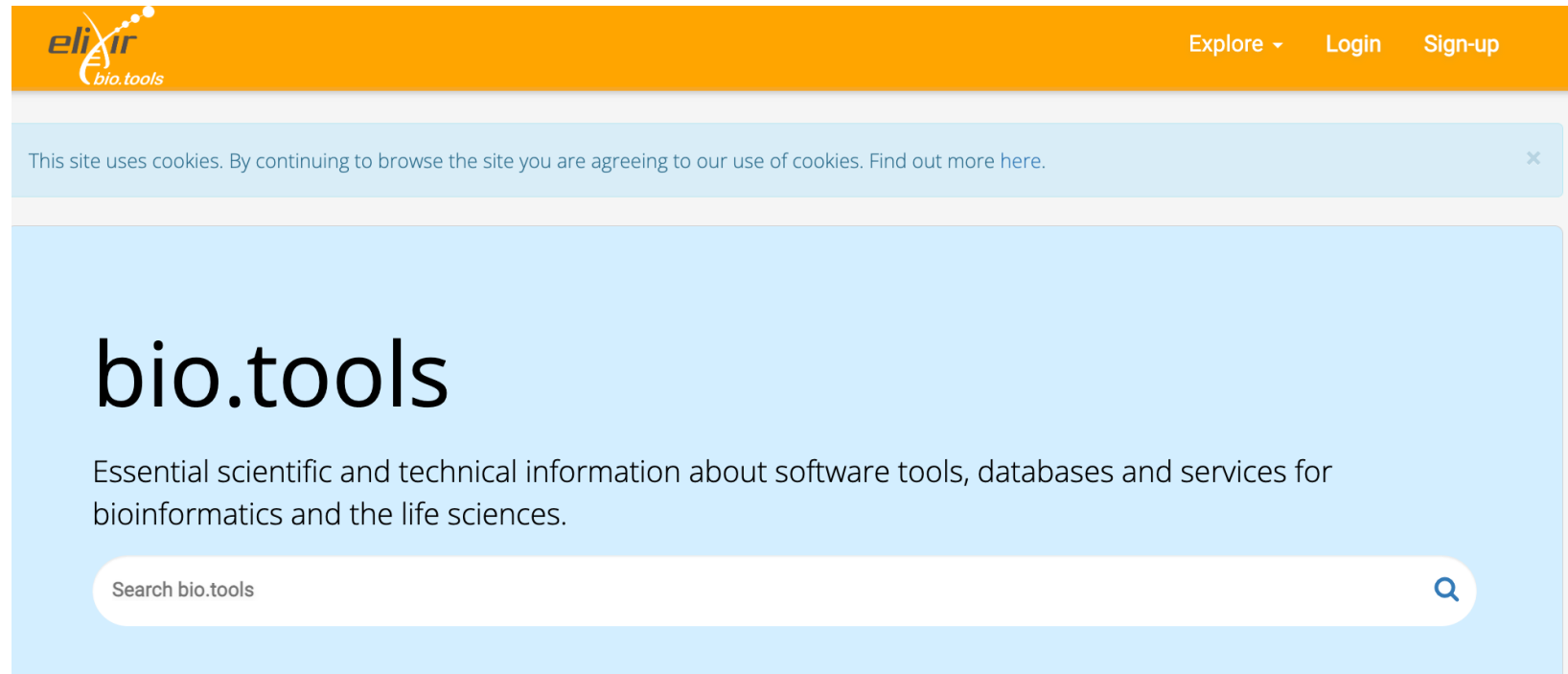
The screenshot shows the GitHub interface for the repository `NeuroDesk / neurocontainers`. The repository is public and has 21 forks and 7 stars. The navigation bar includes `Code`, `Issues` (35), `Pull requests`, `Actions`, `Projects`, `Wiki`, `Security`, `Insights`, and `Settings`. The current view is for the file `neurocontainers / recipes / afni / test.sh` on the `master` branch. A commit by `stebo85` is shown, with the message "added missing python package and added setup instructions and test" and the latest commit hash `8919b05` on July 13. The file content is displayed as follows:

```
1 lines (1 sloc) | 31 Bytes
1  afni_system_check.py -check_all
```

At the bottom of the page, the footer includes the copyright notice "© 2022 GitHub, Inc." and links for `Terms`, `Privacy`, `Security`, `Status`, `Docs`, `Contact GitHub`, `Pricing`, `API`, `Training`, `Blog`, and `About`.

Container Documentation

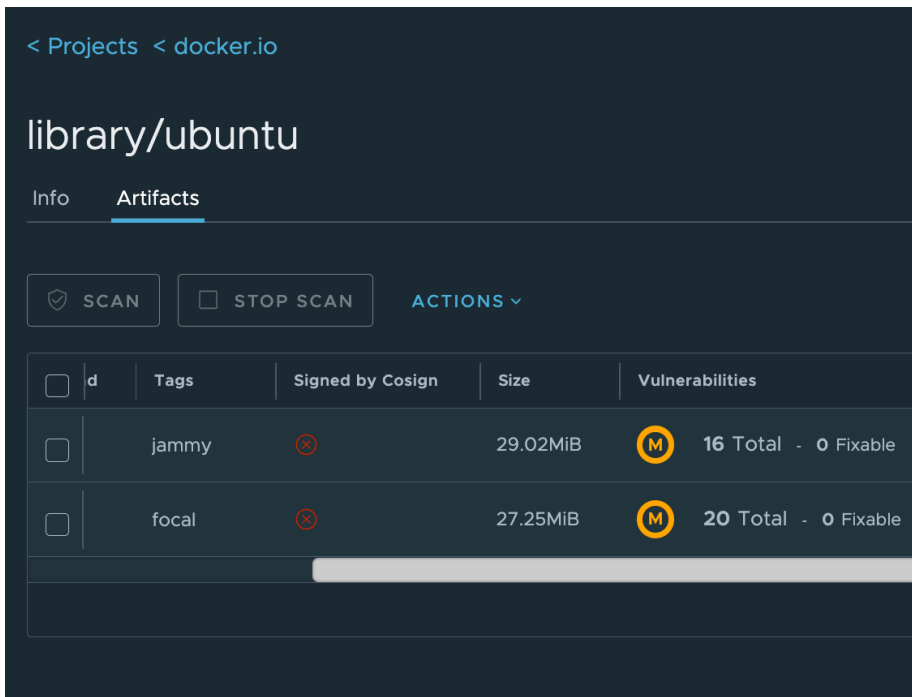
- EDAM / Bio.Tools ?
- Voting for new containers and discovering of what's there -> github issues ?
- how to find people who volunteer to build containers and test them?
- how to handle different hardware architectures / MPI versions ?



The screenshot shows the homepage of the bio.tools website. At the top, there is an orange navigation bar with the 'elixir bio.tools' logo on the left and 'Explore', 'Login', and 'Sign-up' links on the right. Below the navigation bar is a light blue banner with a cookie consent message: 'This site uses cookies. By continuing to browse the site you are agreeing to our use of cookies. Find out more here.' The main content area has a light blue background and features the 'bio.tools' logo in large black text. Below the logo is a subtitle: 'Essential scientific and technical information about software tools, databases and services for bioinformatics and the life sciences.' At the bottom of the main content area is a white search bar with the placeholder text 'Search bio.tools' and a magnifying glass icon on the right.

Container Security Scanning

- Scan after build using github action azure container scan
- Scan during storage in registry (e.g. Harbor)
- Regular scans on distribution infrastructure?



< Projects < docker.io

library/ubuntu

Info Artifacts

SCAN STOP SCAN ACTIONS ▾

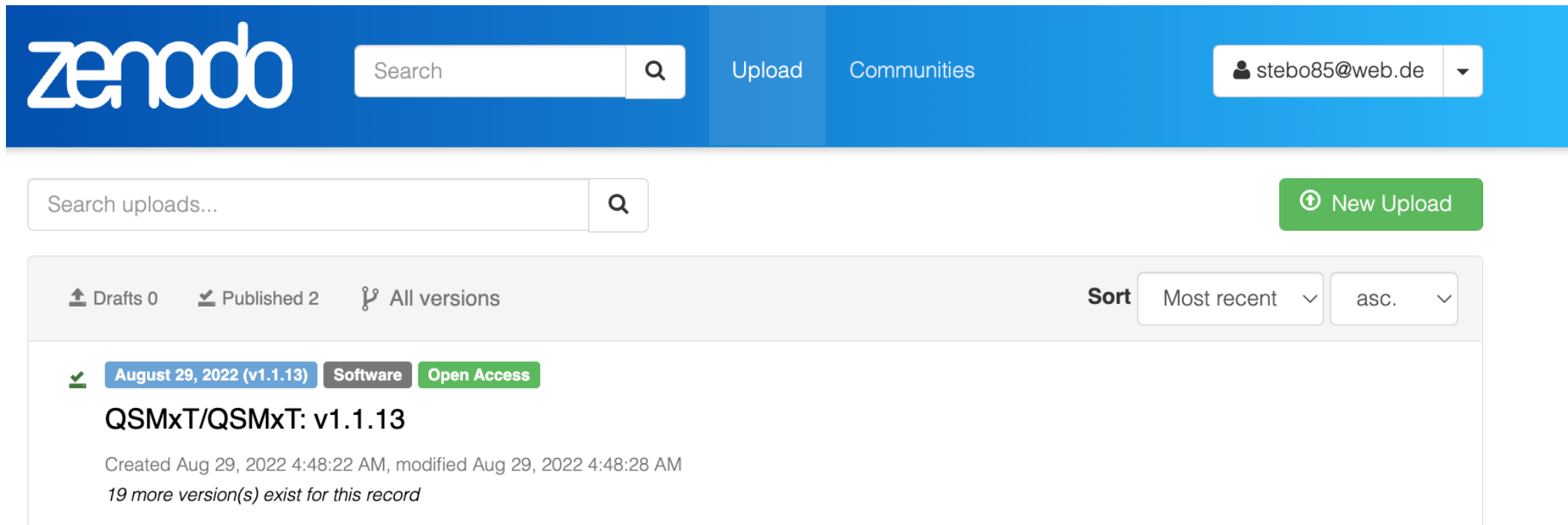
<input type="checkbox"/>	d	Tags	Signed by Cosign	Size	Vulnerabilities
<input type="checkbox"/>		jammy	⊗	29.02MiB	M 16 Total - 0 Fixable
<input type="checkbox"/>		focal	⊗	27.25MiB	M 20 Total - 0 Fixable

```
Container image scan 1m 18s

1 ▶ Run Azure/container-scan@v0.1
15 Could not find allowedlist file.
16 /usr/bin/tar --version
17 tar (GNU tar) 1.30
18 Copyright (C) 2017 Free Software Foundation, Inc.
19 License GPLv3+: GNU GPL version 3 or later
   <https://gnu.org/licenses/gpl.html>.
20 This is free software: you are free to change and redistribute it.
21 There is NO WARRANTY, to the extent permitted by law.
22
23 Written by John Gilmore and Jay Fenlason.
24 /usr/bin/tar xz --warning=no-unknown-keyword -C
   /home/runner/work/_temp/c9ee2594-0569-4bf1-8b17-050a7484098e -f
   /home/runner/work/neurodesktop/neurodesktop/_temp/tools/trivy
25 Scanning for vulnerabilities in image:
   ghcr.io/neurodesk/neurodesktop/neurodesktop
26 No vulnerabilities were detected in the container image
```

Making Containers citable

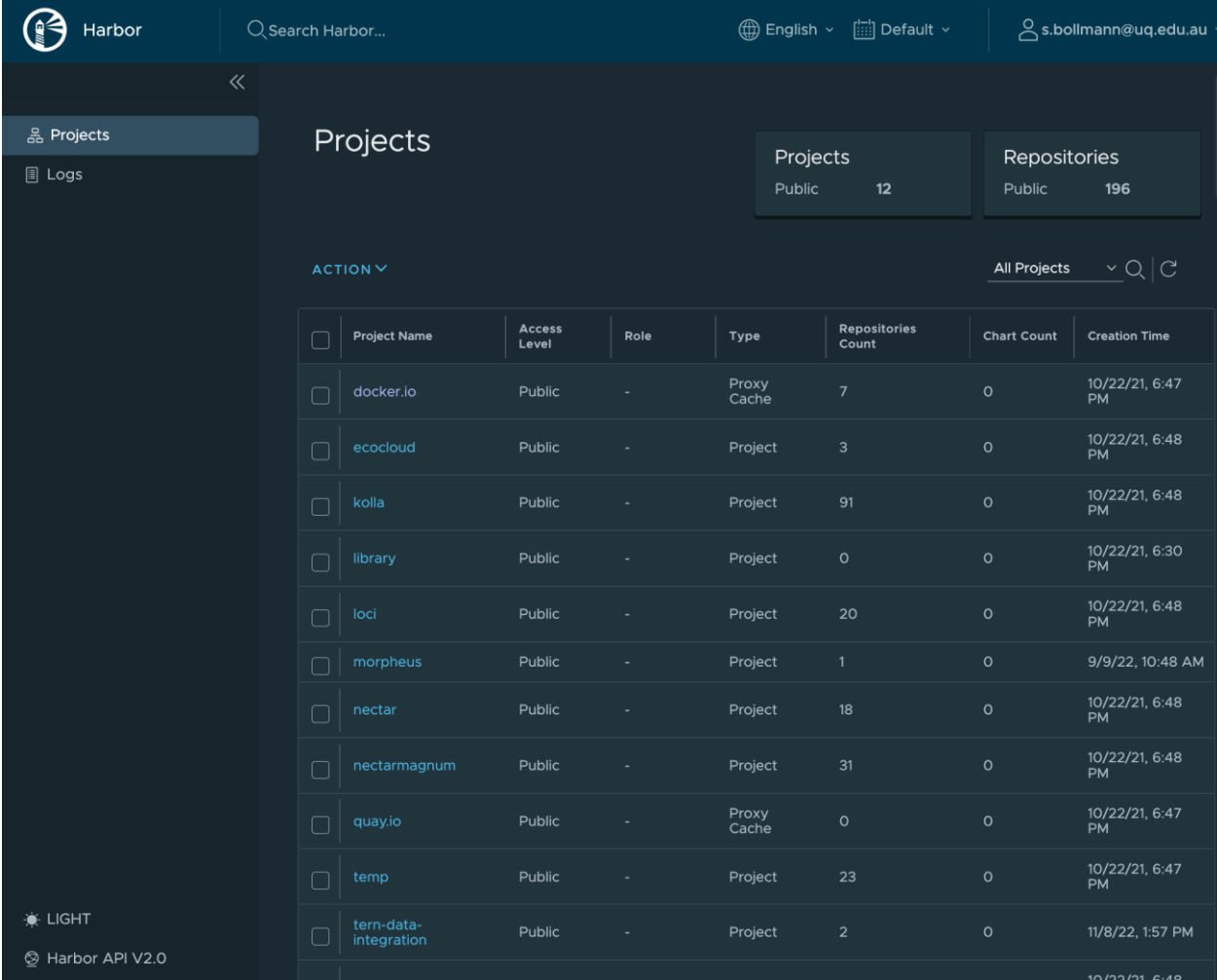
- Upload Singularity files to Zenodo and create DOI?
- Or can we mint our own DOIs and link these to nectar object storage?



The screenshot shows the Zenodo website interface. At the top, there is a blue navigation bar with the Zenodo logo on the left, a search bar, and buttons for 'Upload' and 'Communities'. On the right side of the navigation bar, the user's profile 'stebo85@web.de' is displayed with a dropdown arrow. Below the navigation bar, there is a search bar for uploads and a green 'New Upload' button. The main content area shows a list of uploads. The first upload is 'QSMxT/QSMxT: v1.1.13', which is marked as 'Software' and 'Open Access'. It was created on August 29, 2022, at 4:48:22 AM and modified at 4:48:28 AM. A note indicates that 19 more versions exist for this record.

Container Registry

<https://registry.rc.nectar.org.au/harbor>

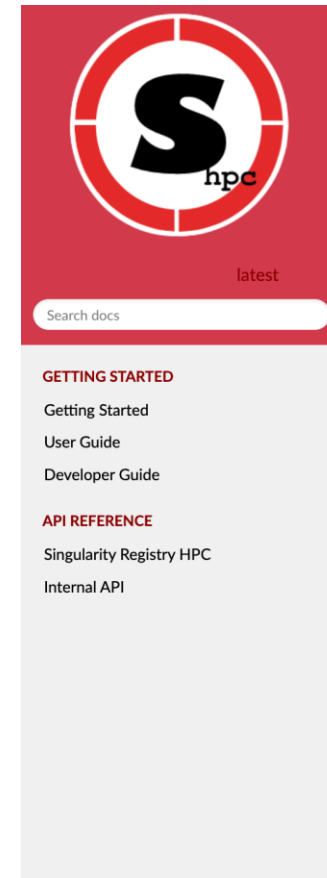


The screenshot displays the Harbor container registry interface. The top navigation bar includes the Harbor logo, a search bar, language and theme settings, and a user profile dropdown. The main content area is titled "Projects" and features summary cards for "Projects" (12 Public) and "Repositories" (196 Public). Below these is a table of projects with columns for Project Name, Access Level, Role, Type, Repositories Count, Chart Count, and Creation Time. The table lists several projects, including docker.io, ecocloud, kolla, library, loci, morpheus, nectar, nectarmagnum, quay.io, temp, and tern-data-integration.

<input type="checkbox"/>	Project Name	Access Level	Role	Type	Repositories Count	Chart Count	Creation Time
<input type="checkbox"/>	docker.io	Public	-	Proxy Cache	7	0	10/22/21, 6:47 PM
<input type="checkbox"/>	ecocloud	Public	-	Project	3	0	10/22/21, 6:48 PM
<input type="checkbox"/>	kolla	Public	-	Project	91	0	10/22/21, 6:48 PM
<input type="checkbox"/>	library	Public	-	Project	0	0	10/22/21, 6:30 PM
<input type="checkbox"/>	loci	Public	-	Project	20	0	10/22/21, 6:48 PM
<input type="checkbox"/>	morpheus	Public	-	Project	1	0	9/9/22, 10:48 AM
<input type="checkbox"/>	nectar	Public	-	Project	18	0	10/22/21, 6:48 PM
<input type="checkbox"/>	nectarmagnum	Public	-	Project	31	0	10/22/21, 6:48 PM
<input type="checkbox"/>	quay.io	Public	-	Proxy Cache	0	0	10/22/21, 6:47 PM
<input type="checkbox"/>	temp	Public	-	Project	23	0	10/22/21, 6:47 PM
<input type="checkbox"/>	tern-data-integration	Public	-	Project	2	0	11/8/22, 1:57 PM
<input type="checkbox"/>	test	Public	-	Project	0	0	10/22/21, 6:48 PM

Container Modules

- integration of containers in Module System in HPCs via Lmod
- SHPC?
 - can SHPC automatically expose individual binaries inside a container? Currently every binary needs a separate entry in the yaml?
- How to handle different sites?
 - every site has a subdirectory on distribution system with their own container subset and SHPC config?



» Singularity Registry (HPC)

[Edit on GitHub](#)

Singularity Registry (HPC)

Stars 70

Singularity Registry HPC (shpc) allows you to install containers as modules. Currently, this includes:

- [Lmod](#)
- [Environment Modules](#)

And container technologies:

- [Singularity](#)
- [Podman](#)
- [Docker](#)

And coming soon:

- [Shifter](#)
- [Sarus](#)

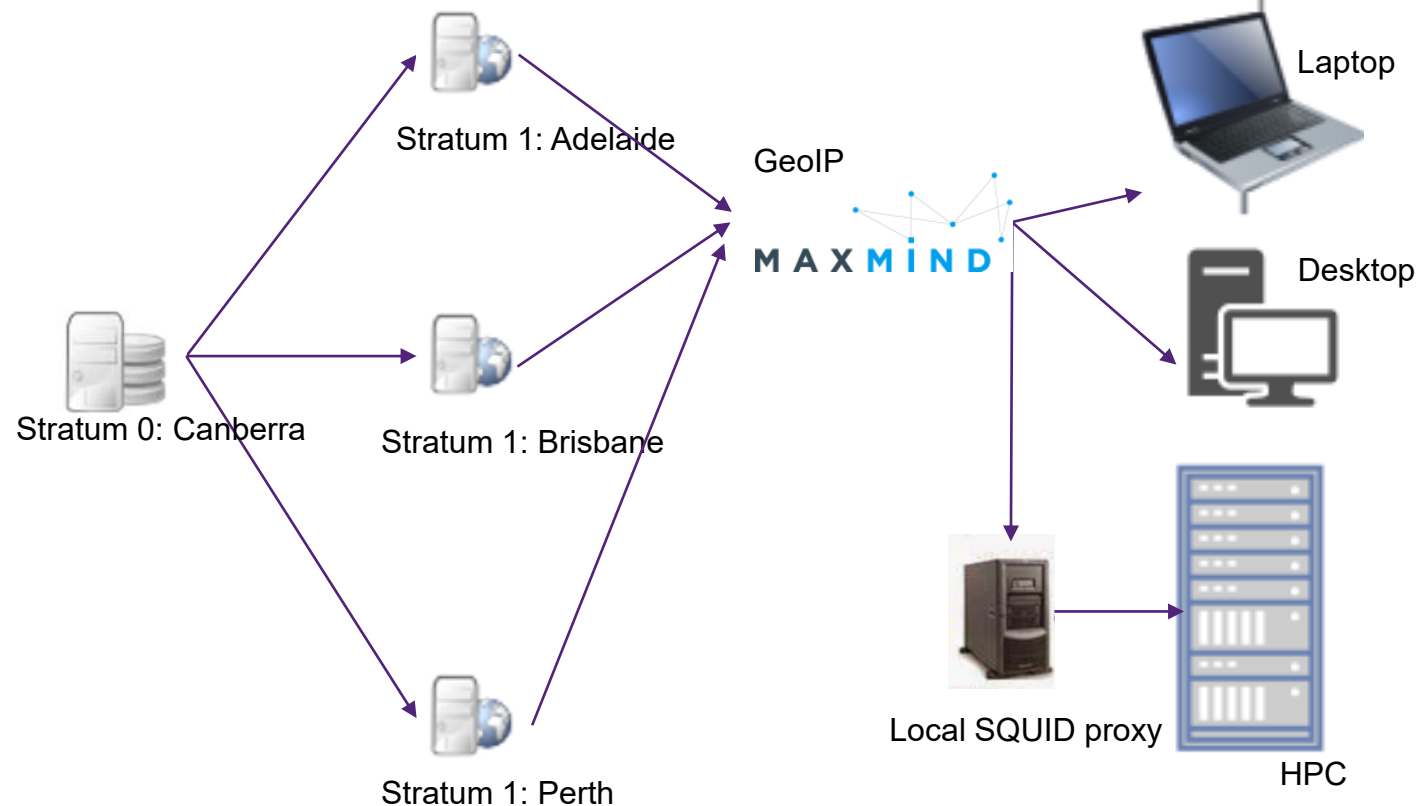
You can use shpc if you are:

1. a linux administrator wanting to manage containers as modules for your cluster
2. a cluster user that wants to maintain your own folder of custom modules
3. a cluster user that simply wants to pull Singularity images as GitHub packages.

The library contains a collection of module recipes that will install containers, so you can easily use them or write your own. To see the code, head over to the [repository](#). To browse modules available as containers, see [the library](#).

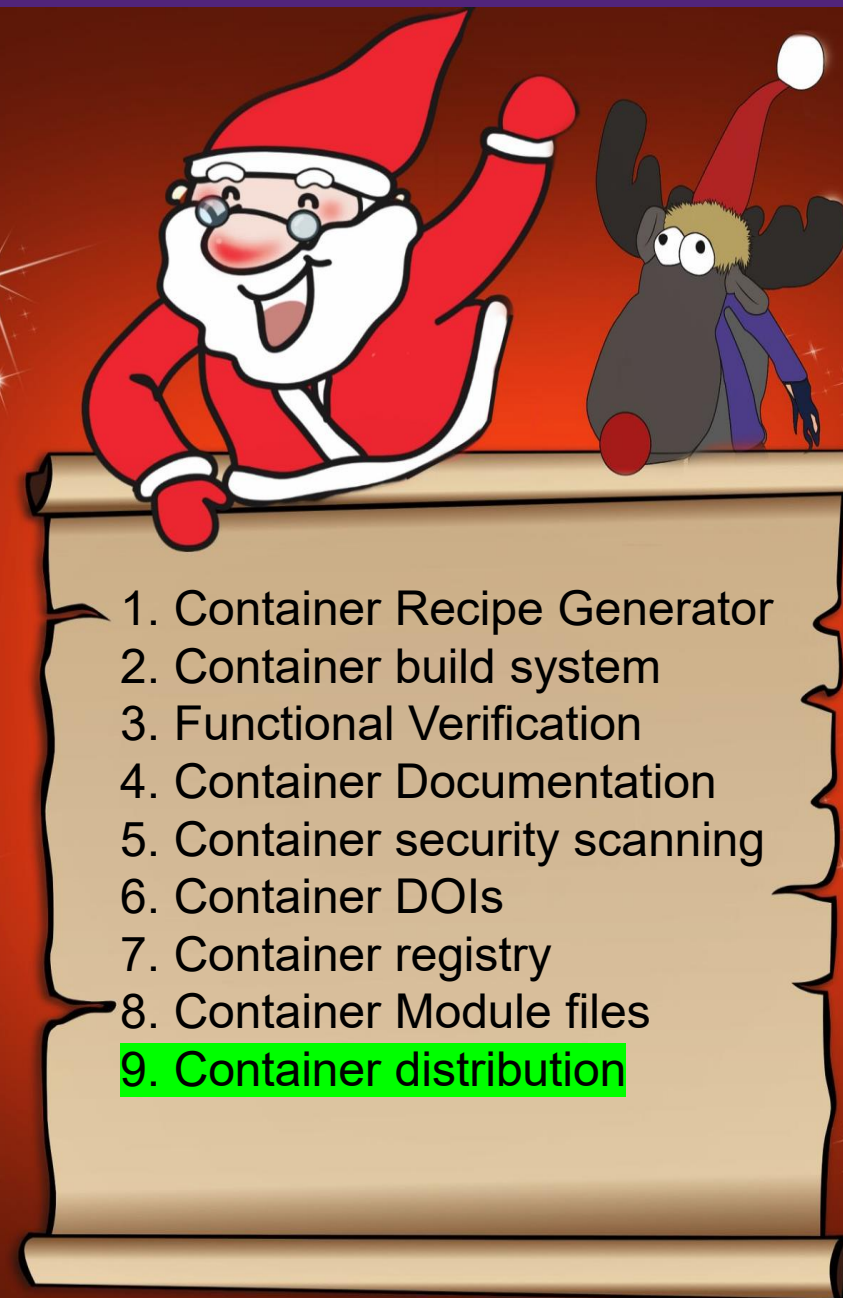
Distributing Singularity containers via CVMFS

- download and unpack singularity containers to CVMFS storage for distribution and on-demand access and distribute reference data
- every user-site has their own subset of containers that they offer to their users (e.g. architecture optimized)



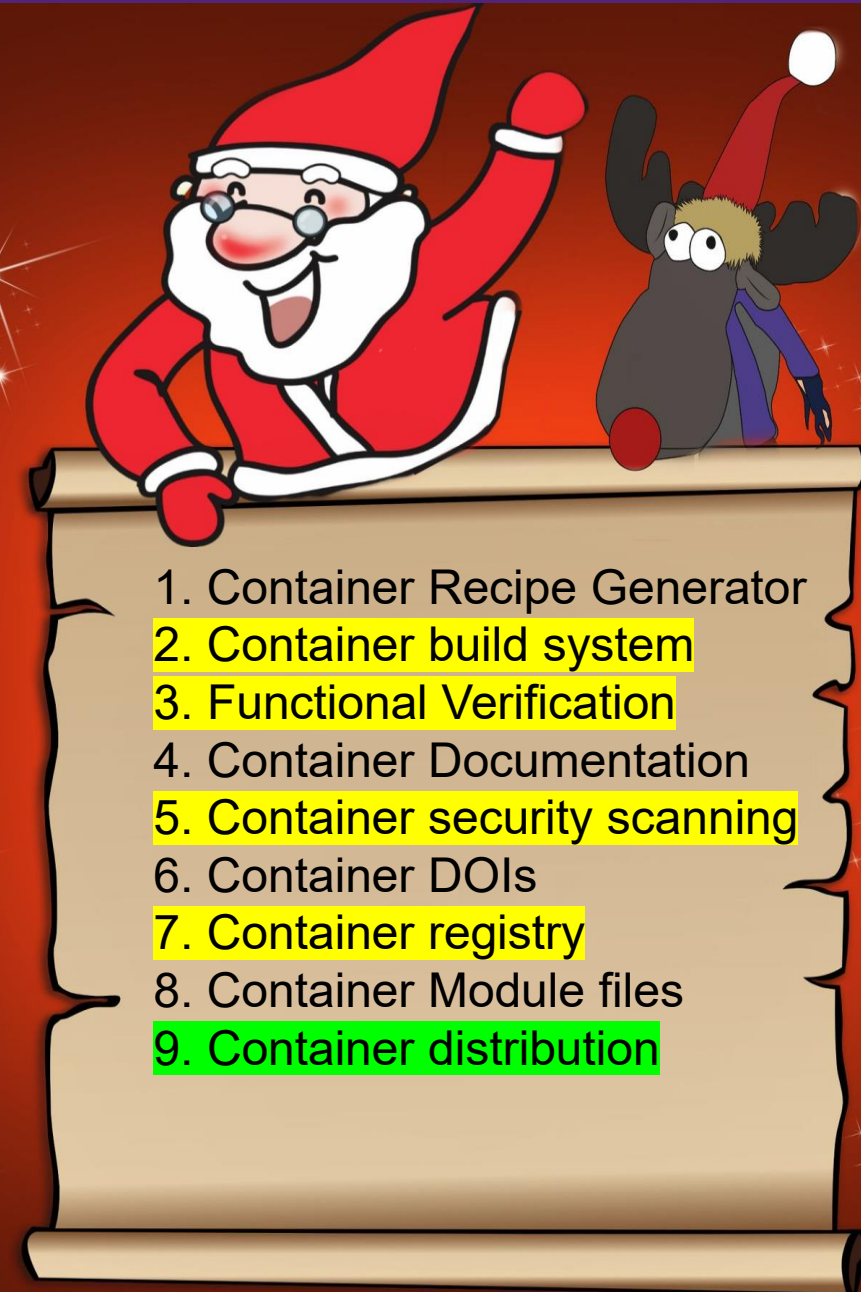
Proposed first phase

- Network of Stratum 1 servers in Australia hosted by AARNet & ARDC
 - These Stratum 1 servers distribute existing community operated Stratum 0 servers, such as
 - EESSI,
 - DRA,
 - Neurodesk,
 - Galaxy Project,
 - AARNet's Biocommons RNAseq repositories,
 - SHPC BioConda containers
- > Is there demand for a national service like this?



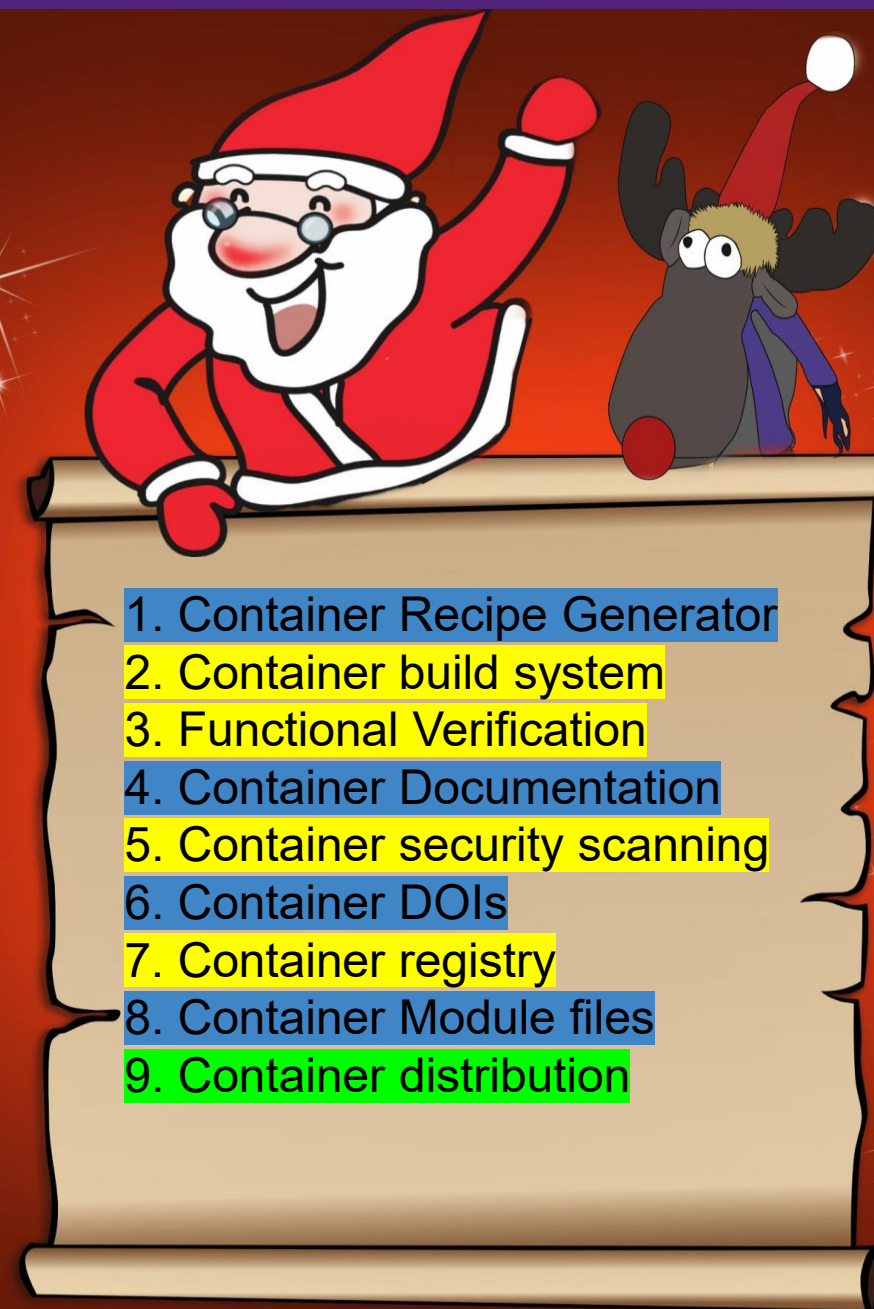
Proposed second phase

- building up a blueprint for a community to
- build and test (functional+security) their own containers using
- Github actions + Nectar Cloud + Nectar Harbour registry + cvmfs stratum 0 setup



Proposed third phase

- making it easier to generate container recipes
- enabling the long-term archival of containers and DOI minting
- building up a tool registry for hosting metadata about containers + discovery
- improve generation of module files for HPC use cases



Governance

- ARDC ARCOS Technical Working group for coordination between communities?
- joint working group between ARDC/AARNet/QCIF/community representatives



Join the discussion, Tuesday 17th, 14.15-15.15

Boulevard B2

Enabling Platforms &
Services

Aleem Uddin & Greg
D'arcy

BoF Session

Software Containers in
Australian Research
Sector: ARCOS
Community Building and
Collaboration on SciDir – a
Scientific Software
Distribution Project

Aleem Uddin, Greg D'arcy,
Steven Manos, Mark Gray,
David Powell, Paul
Coddington, Jake Yip, Ping
Chen



<https://bit.ly/scidirpoll>

