

# Practical introduction to Singularity containers

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Tom Harrop

[tharrop@unimelb.edu.au](mailto:tharrop@unimelb.edu.au)

[melbournebioinformatics.org.au](http://melbournebioinformatics.org.au)

 [@MelBioInf](https://twitter.com/MelBioInf)

# Reproducibility

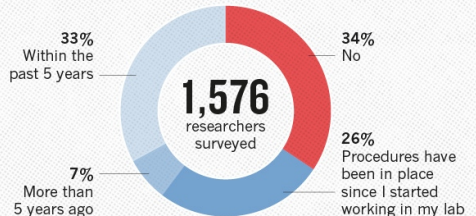
## IS THERE A REPRODUCIBILITY CRISIS?



©nature

## HAVE YOU ESTABLISHED PROCEDURES FOR REPRODUCIBILITY?

Among the most popular strategies was having different lab members redo experiments.



©nature

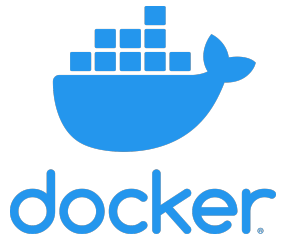
# Analysis practices

## Guidelines:

1. Don't modify raw data
2. Record the steps  
(with version control)
3. Capture the computing environment

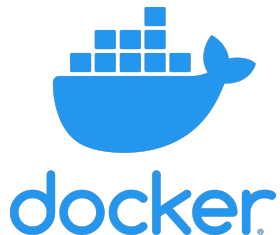
- ◆ Data management:
  - see Gayle Philip's slides
- ◆ Project management, source control:
  - Jessica Chung's slides
- ◆ Workflow management:
  - Bobbie Shaban's slides
- ◆ Reproducible computing:
  - use containers

# Why use containers?



**Motivation:** Use software without installing it

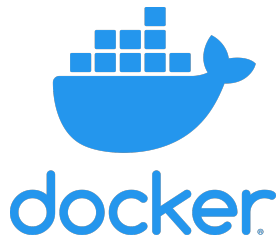
# Why use containers?



**Motivation:** Use software without installing it

**Benefits:** Portability, reproducibility

# Why use containers?



**Motivation:** Use software without installing it

**Benefits:** Portability, reproducibility

**Drawbacks:** Effort

# Use software without installing it

## On my computer:

```
# not provided for my OS  
guppy_basecaller --version
```

guppy\_basecaller: command not found

## Using a container:

```
singularity exec guppy_5.0.16.sif \  
guppy_basecaller --version
```

: Guppy Basecalling Software, (C) Oxford Nanopore

# Get the version you need

## On my computer:

```
# installed by my OS package manager  
samtools --version
```

```
samtools 1.13  
Using htlib 1.13+ds  
Copyright (C) 2021 Genome Research Ltd.
```

## Using a container:

```
singularity exec samtools_1.12.sif \  
samtools --version
```

```
samtools 1.12  
Using htlib 1.12  
Copyright (C) 2021 Genome Research Ltd.
```



## Avoid tricky software installations

### Dependencies

Funannotate has a lot of dependencies. However, it also comes with a few tools to help you get everything installed. The first is that of `funannotate check`. You'll see in the output below that the `fastx` tool is missing, which is Bill Pearson's `fastx` a dependency of the PAGA pipeline. Also the `STAR` and `SRANIMATE` variables are not set, that is because on this particular machine they are not installed. I.e. Funannotate will alert you at runtime if it is missing a dependency.

[illegible]

- lots of dependencies



🧩 not all dependencies are listed

## Avoid tricky software installations

### Dependencies

Farmanote has a lot of dependencies. However, it also comes with a few tools to help you get everything installed. The first is that of `farmanote check`. You'll see in the output below that the `twine` tool is missing, which is Bill Pearson's `twine` a dependency of the RASA pipeline. Also the `SHASOME` and `FRONTTRIM` variables are not set, that is because on this particular machine they are not installed. I.e. Farmanote will alert you at runtime if it is missing a dependency.

[illegible]

- lots of dependencies
- not all dependencies are listed
- need specific versions
- package managers don't always help

## Avoid tricky software installations

## Dependencies

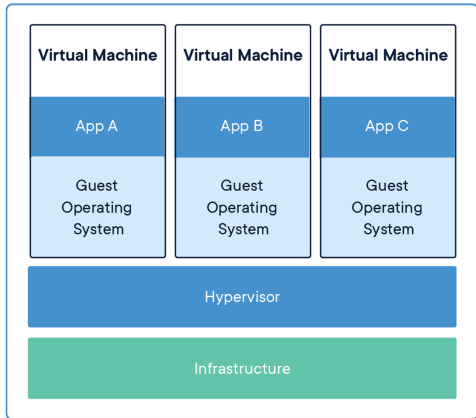
Farmanote has a lot of dependencies. However, it also comes with a few tools to help you get everything installed. The first is that of `funannotate check`. You'll see in the output below that the `twisto` tool is missing, which is Bill Pearson's `twisto` a dependency of the PASA pipeline. Also the `SHORE` and `SRKSTRIM` variables are not set, that is because on this particular machine they are not installed. I.e. Farmanote will alert you at runtime if it is missing a dependency.

[illegible]

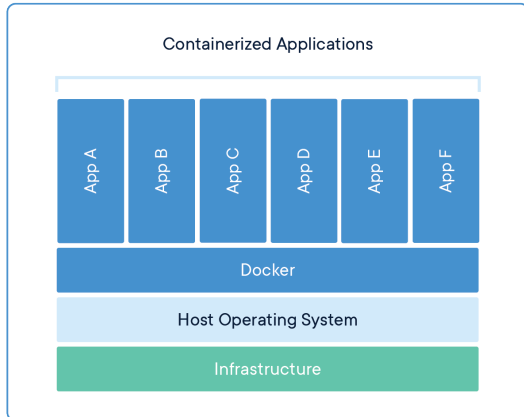
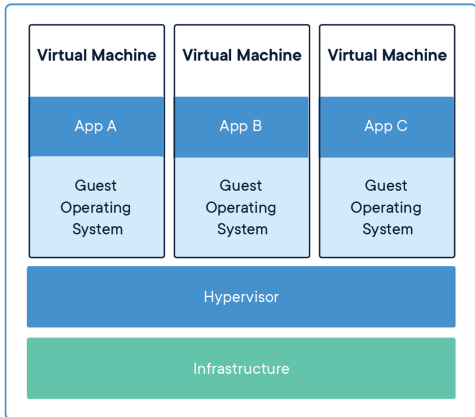
- lots of dependencies
- not all dependencies are listed
- need specific versions
- package managers don't always help

```
singularity run docker://nextgenusfs/funannotate
```

# What is a container?



# What is a container?



# Docker, or Singularity?

## Docker

- popular on cloud platforms
- effectively requires root to run\*
- doesn't respect job schedulers\*

\* may have been fixed

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- runs on HPC
- popular in research / edu?
- **supports Docker containers**

# Docker, or Singularity?

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## 📦 Singularity

- runs on HPC
- popular in research / edu?
- **supports Docker containers**

\* may have been fixed

**Suggested workflow:** build (or obtain) your containers in Docker format and use Singularity to run them



# How to use Singularity

## 1. Install Singularity

- 💡 not too hard to install locally
- 💡 HPCs often have it installed
- 💡 you can ask the admin to install it

e.g. on Spartan:

```
$ module load singularity/3.7.3  
$ singularity --version  
singularity version 3.7.3
```

# How to use Singularity

## 1. Install Singularity

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e.g. on Spartan:

```
$ module load singularity/3.7.3
$ singularity --version
singularity version 3.7.3
```

## 2. Run a container

- 💡 detailed instructions at [singularity.hpcng.org](https://singularity.hpcng.org)
- 💡 basic commands is  
`singularity exec {container URL} \`  
`{command} {args}`
- 💡 usually need some options, e.g.
  - `-B` binds paths to make files available in the container
  - `--nv` enables GPU support

# Workflow managers support containers

## Snakefile:

```
rule trim_adaptors:
    input:          'data/raw_reads.fastq'
    output:         'output/trimmed.fastq'
    container:      'docker://my_repos/trim_adaptors:1.7'
    shell:          'trim_adaptors --raw_reads={input} > {output}'

rule run_assembly:
    input:          'output/trimmed.fastq'
    output:         'output/assembly.fasta'
    container:      'docker://my_repos/tidy_assembler:2.9'
    shell:          'tidy_assembler --reads={input} > {output}'
```

# Workflow managers support containers

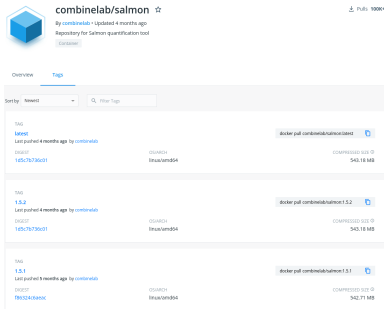
## Snakefile:

```
rule trim_adaptors:
    input:          'data/raw_reads.fastq'
    output:         'output/trimmed.fastq'
    container:      'docker://my_repos/trim_adaptors:1.7'
    shell:          'trim_adaptors --raw_reads={input} > {output}'
rule run_assembly:
    input:          'output/trimmed.fastq'
    output:         'output/assembly.fasta'
    container:      'docker://my_repos/tidy_assembler:2.9'
    shell:          'tidy_assembler --reads={input} > {output}'
```

## Run the workflow:

```
snakemake --use-singularity \
    --singularity-args ...
```

# Where to find containers



combinelab/salmon ☆

By combinelab • Updated 4 months ago  
Repository for Salmon quantification tool

1000+

Overview Tags

Sort by: Newest

Filter tags


TAG	DIGEST	OS/ARCH	COMPRESSED SIZE
latest	1d5c7b739cd1	linux/amd64	543.18 MB
1.5.2	1d5c7b739cd1	linux/amd64	543.18 MB
1.5.1	f85324ba00c	linux/amd64	542.71 MB



Some developers provide docker containers

```
singularity pull \  
docker://combinelab/salmon:1.1.0
```

# You can search for images on [hub.docker.com](https://hub.docker.com)

 **docker**hub

[Explore](#) [Pricing](#) [Sign In](#) [Sign Up](#)

 Docker Containers Plugins**Filters**1 - 16 of 16 results for **trinityrnaseq**. [Clear search](#)

Best Match

☐ **Verified Publisher** ⓘ

☐ **Official Images** ⓘ  
*Official Images Published By Docker*

**Categories** ⓘ☐ Analytics☐ Application Frameworks☐ Application Infrastructure☐ Application Services☐ Base Images **trinityrnaseq/trinityrnaseq-wdl** **50K+** **0**  
Downloads Stars  
By [trinityrnaseq](#) • Updated a year ago  
Container Linux x86-64 **trinityrnaseq/trinityrnaseq** **10K+** **4**  
Downloads Stars  
By [trinityrnaseq](#) • Updated 2 months ago  
Trinity Docker  
Container Linux x86-64

13 / 22

# Check with the software developer

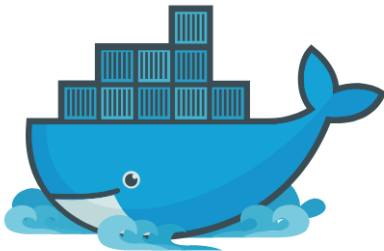
trinityrnaseq / trinityrnaseq Public

<> Code 29 Issues Pull requests 3 Actions Projects Wiki Security Insights

## Trinity in Docker

Brian Haas edited this page on 1 Apr 2020 · 13 revisions

## Run Trinity Using Docker



If you have [Docker](#) installed, you can pull [our image from DockerHub](#), which contains Trinity and all software used for downstream analyses supported within the larger Trinity framework.

# Build them yourself!

TomHarrop / container-flye Public

generated from [deardenlab/container-build-template](#)

Unwatch 1

Star 0

Fork 0

<> Code

Issues

Pull requests

Actions

Projects

Wiki

Security

Insights

Settings

main 1 branch 2 tags

Go to file

Add file

Code

TomHarrop Create README.md

✓ d8caa3a 16 days ago 11 commits

.github/workflows	Initial commit	16 days ago
Dockerfile.2.9	certificates	16 days ago
README.md	Create README.md	16 days ago
VERSION	2.9	16 days ago

README.md

Singularity and Docker containers for [Flye](#).

About

No description, website, or topics provided.

Readme

Releases 2

Release v2.9 Latest

16 days ago

+ 1 release

Packages 1


container-flye

Languages

Roff 100.0%




# Build them yourself!


 **TomHarrop** / **container-flye** Public

generated from [deardenlab/container-build-template](#)

Unwatch 1 Star 0 Fork 0

[Code](#) [Issues](#) [Pull requests](#) [Actions](#) [Projects](#) [Wiki](#) [Security](#) [Insights](#) [Settings](#)

 **container-flye**

 Install from the command line: [Learn more](#)

```
$ docker pull ghcr.io/tomharrop/container-flye:2.9
```

### Recent tagged image versions

2.9 ↓ 6


Published 16 days ago · Digest ...


[View and manage all versions](#)


README.md

Singularity and Docker containers for [Flye](#).

### Details

 TomHarrop

 container-flye

 Readme

Last published

**16 days ago**

Issues


**0**

Total downloads

**9**

Collaborators

1

 TomHarrop Tom Harrop

[Open an issue](#)

[Package settings](#)

# Some barriers to container usage

- ❖ Building containers yourself can be painful
- ❖ Duplication of effort
- ❖ Some software **shouldn't** go in a container because of “unfortunate licensing issues”
  - DTU software e.g. rnammer, tmhmm
  - GATech: GeneMark
  - GIRInst's RepBase
- ❖ Getting Singularity installed

# When to use containers

**Modules:**

**Conda, venv, *etc.*:**

**Containers:**

# When to use containers

## Modules:

```
module load \  
  samtools/1.12
```

## Conda, venv, etc.:

## Containers:

- 📦 installed by the sysadmin
- 📦 properly configured
- 📦 easy

# When to use containers

## Modules:

```
module load \  
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## Conda, venv, etc.:

```
conda install -c \  
  bioconda samtools
```

- ❖ latest packages
- ❖ testing in a specific environment

## Containers:

# When to use containers

## Modules:

```
module load \  
  samtools/1.12
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- ❖ installed by the sysadmin
- ❖ properly configured
- ❖ easy

## Conda, venv, etc.:

```
conda install -c \  
  bioconda samtools
```

- ❖ latest packages
- ❖ testing in a specific environment

## Containers:

```
singularity run \  
  samtools.sif
```

- ❖ reproducibility
- ❖ collaboration
- ❖ portability
- ❖ performance?

# Get started with containers

## ◆ How I use containers:

1. **Write Docker recipes** (one tool, one recipe)
2. Remotely build Docker image store it permanently
3. Use with Singularity via a workflow manager

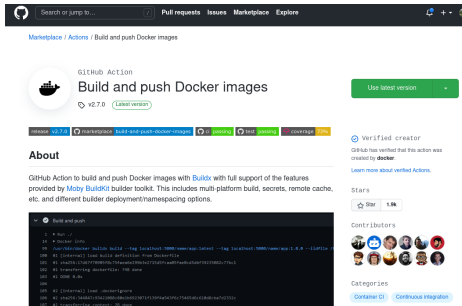
## ◆ Singularity has good documentation: [quick start](#)

## ◆ Docker documentation is ... extensive: [Best practices for writing Dockerfiles](#)

## ◆ Integrating with workflow managers is easy

# Building containers on GitHub

## TomHarrop/container-build-template



The screenshot shows the GitHub Actions marketplace page for the 'Build and push Docker images' action, created by Docker. The page has a dark header with navigation links: 'Search or jump to...', 'Pull requests', 'Issues', 'Marketplace', and 'Explore'. Below the header, the breadcrumb trail reads 'Marketplace / Actions / Build and push Docker images'. The main content area features the action's logo (a Docker ship icon), the title 'Build and push Docker images', and the version 'v2.7.0' with a 'Latest version' badge. A green button labeled 'Use latest version' is on the right. Below this, a row of badges includes 'Release v2.7.0', 'Marketplace build-and-push-docker-images', 'Docker', 'Linux', 'macOS', and 'Coverage 100%'. The 'About' section explains that the action uses Buildx with full support for features provided by the Moby BuildKit builder toolkit, including multi-platform build, secrets, remote cache, and different builder deployment/namespacing options. A code block shows a sample workflow for building and pushing Docker images. On the right, the 'Verified creator' section states that GitHub has verified the action was created by Docker, with a link to 'Learn more about verified Actions'. Below this are 'Stars' (1.5k) and 'Contributors' (a grid of 12 avatars). The 'Categories' section lists 'Container CI' and 'Continuous Integration'.

GitHub Action

### Build and push Docker images

v2.7.0 Latest version

[Release v2.7.0](#) [Marketplace build-and-push-docker-images](#) [Docker](#) [Linux](#) [macOS](#) [Coverage 100%](#)

#### About

GitHub Action to build and push Docker images with [Buildx](#) with full support of the features provided by [Moby BuildKit](#) builder toolkit. This includes multi-platform build, secrets, remote cache, etc. and different builder deployment/namespacing options.

```
name: Build and push
on:
  push
jobs:
  build:
    runs-on: ubuntu-latest
    steps:
      - name: Checkout
        uses: actions/checkout@v2
      - name: Set up Docker Buildx
        uses: docker/setup-buildx-action@v1
      - name: Login to Docker Hub
        uses: docker/login-action@v1
      - name: Build and push
        uses: docker/build-push-action@v2
        with:
          context: .
          file: Dockerfile
          push: true
          tags: myusername/myimage:latest
```

**Verified creator**  
GitHub has verified that this action was created by [Docker](#).  
[Learn more about verified Actions.](#)

**Stars**  
1.5k

**Contributors**  
12

**Categories**  
[Container CI](#) [Continuous Integration](#)



# Docker and Singularity example

TomHarrop/container-flye

- 💡 generally use the Docker container in Singularity
- 💡 some old versions can't login to GHCR

## Is this useful?

*In your experience do developers appreciate pull requests so that everyone has access to the container from the official page - or do containers take a bit of time to maintain so developers would be less keen?*

*- question from Alistair Legione*

- ◆ do enough people use these setups?
- ◆ is Conda preferred?
- ◆ PRs back to the software developer?