

# Computational workflow seminar: Understanding Docker, Singularity and containerization

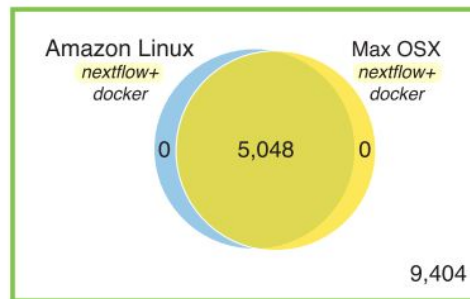
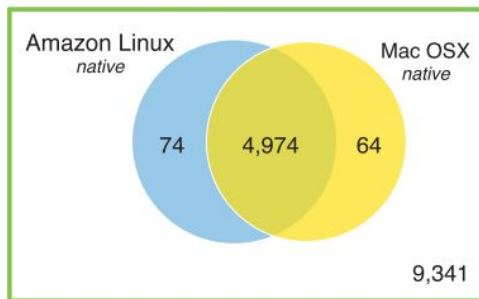
# Workflows and reproducibility

Number of differentially expressed genes  
without Nextflow and containerization

Number of differentially expressed genes  
with containerization

**C**

Transcript quantification and differential expression with Kallisto and Sleuth

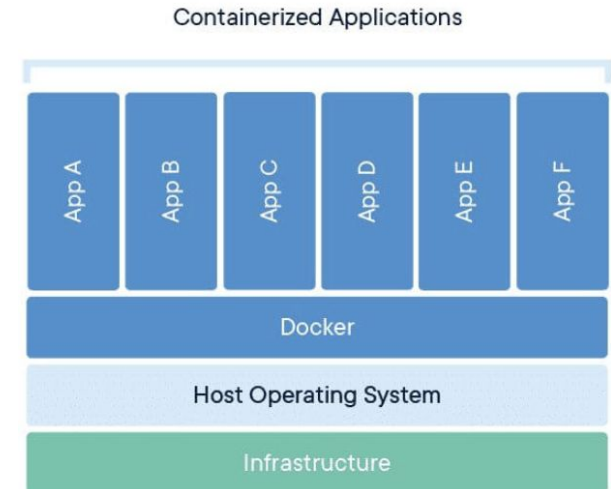


DI Tommaso, et al. (2017). Nextflow enables reproducible computational workflows. *Nature Biotechnology*.

# Containers



- Isolation of a runtime environment containing all tools and their dependencies and libraries with fixed versions
- Portable to any platform that supports a container engine
- **Container image**: portable snapshot of all dependencies, used to create a **container**
- Compared to Virtual Machines (VMs)
  - No guest OS, use the host's kernel
  - More lightweight, faster
  - Easier to ship

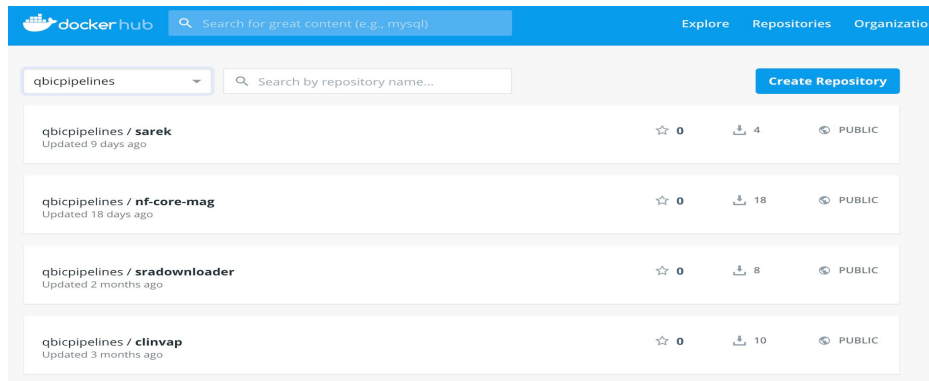
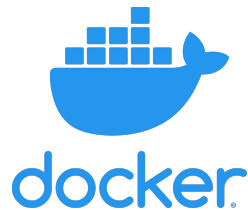




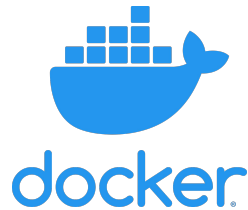
# Container engines

## Docker

- Since 2013, huge community
- Public repository for container sharing (DockerHub)
- Uses Dockerfiles
- Install Docker and you can run any docker container you want, without modifying it



# Container engines



## Docker

- Dockerfile, a recipe for building a container
- Example: Official Linux CentOS image:

```
FROM scratch
ADD centos-7-docker.tar.xz /
LABEL name="CentOS Base Image" \
      vendor="CentOS" \
      license="GPLv2" \
      build-date="20210630"

CMD ["/bin/bash"]
```

# Container engines

## Docker - Cons

- Requires a daemon (and a privileged user to set it up)
- Security risk because of the direct access to the host OS kernel
- Docker devs addressed many issues in the past, but misconfiguration can still present a surface for various attack types (Linux capabilities, Network, Kernel Security Systems)
- Alternatives: Singularity, Apptainer, Podman, Charliecloud, Shifter ...

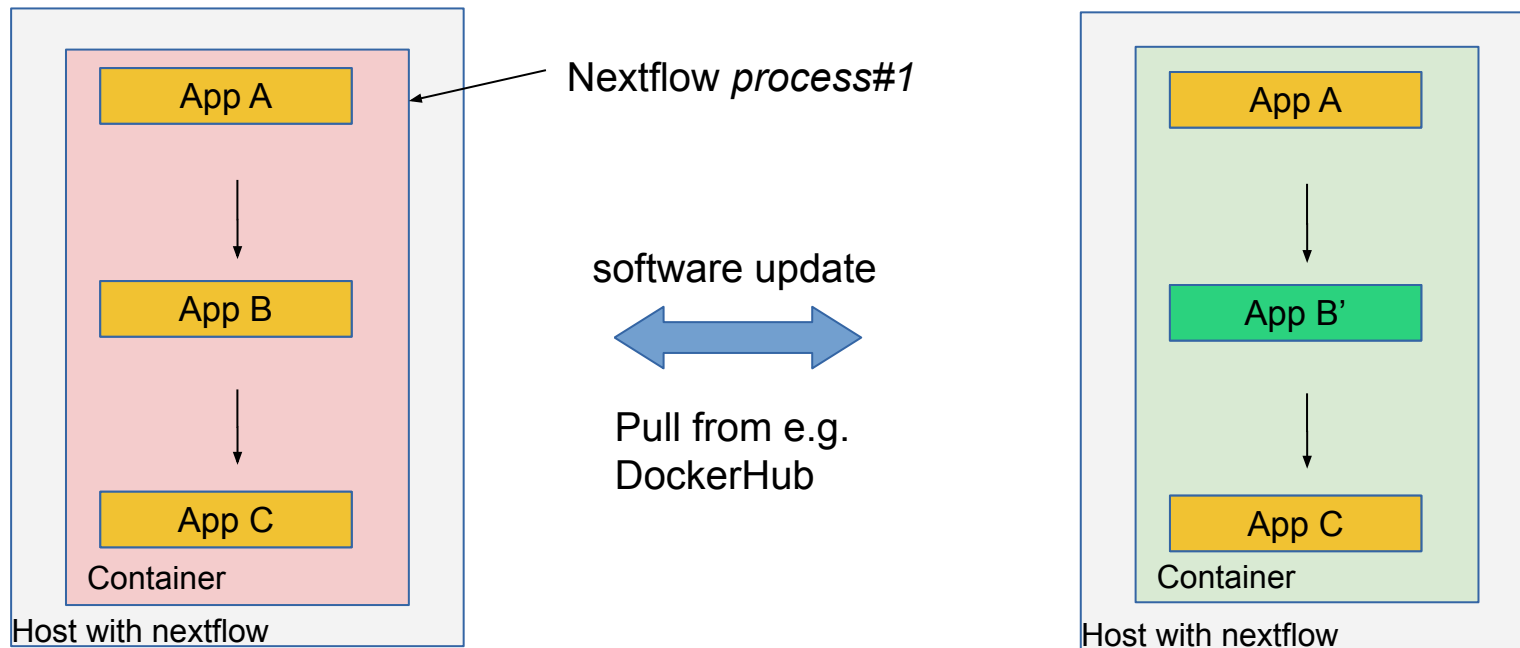


podman



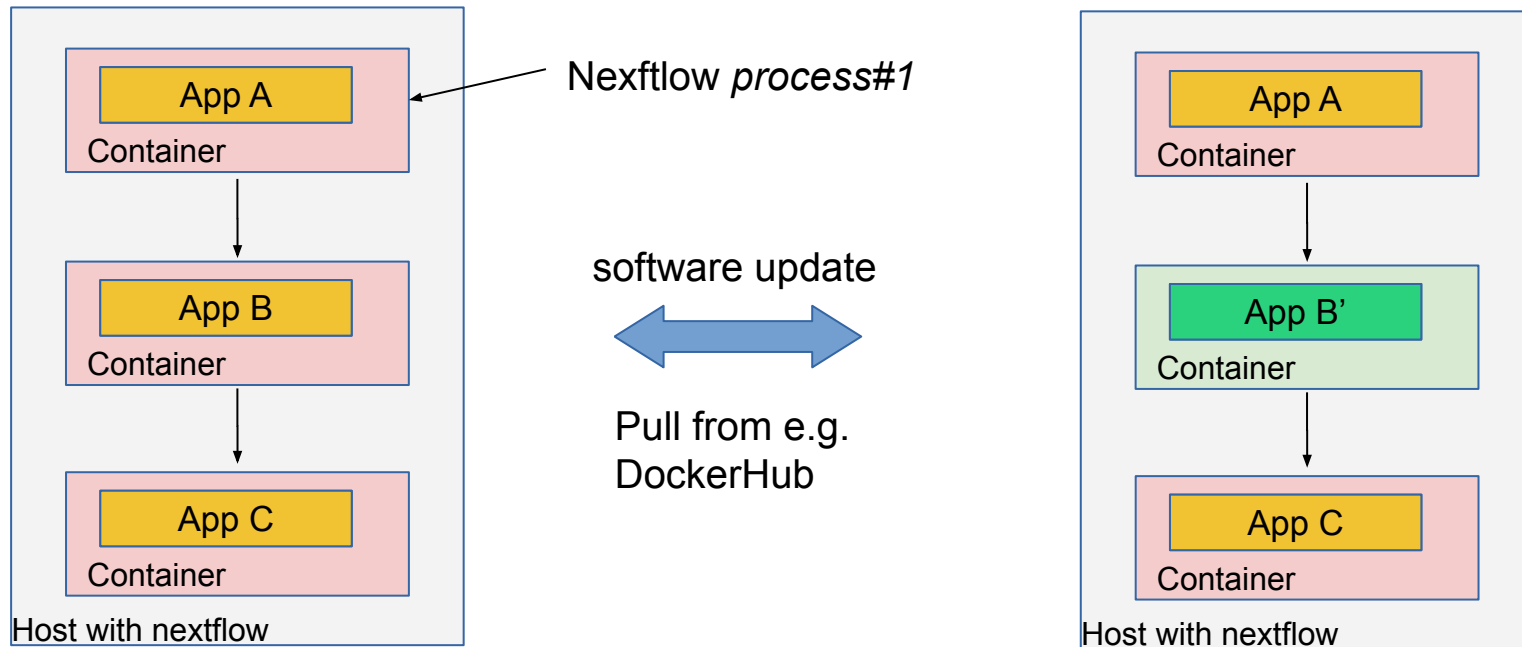
# Container engines

## Containers and Workflows – Fat container approach



# Container engines

## Containers and Workflows – Slim container approach





# BioContainers project

For each tool (and release) available at BioConda, a minimal container (docker and singularity) is automatically built

BIOCONDA®

## BioContainers Flow





# VM vs Containers

## Virtual Machines (VMs)

- Complete OS with its own kernel.
- Resource-heavy, slower startup, larger size.

## Containers

- Shared OS kernel with isolated user spaces.
- Lightweight, fast startup, smaller size.

Getting your Material for today

**Step 1:** Save your work to **your fork**

```
$ git add <file1> <file2>

$ git commit -m "adds files"

$ git push
```

**Step 2:** Get today's notebook **from upstream**

```
# pull from upstream

$ git pull upstream main

# To leave vi:
# ":" -> "q" -> "w" -> "enter"
```