



# Dry Bench Skills for the Researcher

## Day 3

## Conda and Docker

## 2020 Dec 7

# What are we doing here?

We are taking you through the steps to create reproducible science



DATA

INSIGHT & PUBLICATION

DATA PROCESSING - REUSE & DEVELOPMENT

DATA PROCESSING - EXECUTION

RESULTS

Code  
versioning

Container-  
ization

Workflow  
Deployment

High  
performance  
computing

Cloud  
infrastructure

Reasoning

Reuse code  
Modify code  
Share &  
Collaborate

Conda and  
environments  
  
Containerize  
separate  
processes

Stitch them  
together into  
a unified  
workflow to  
accomplish  
the analysis

Provision &  
manage a HPC  
cluster to analyse  
the large volumes  
of genomics data

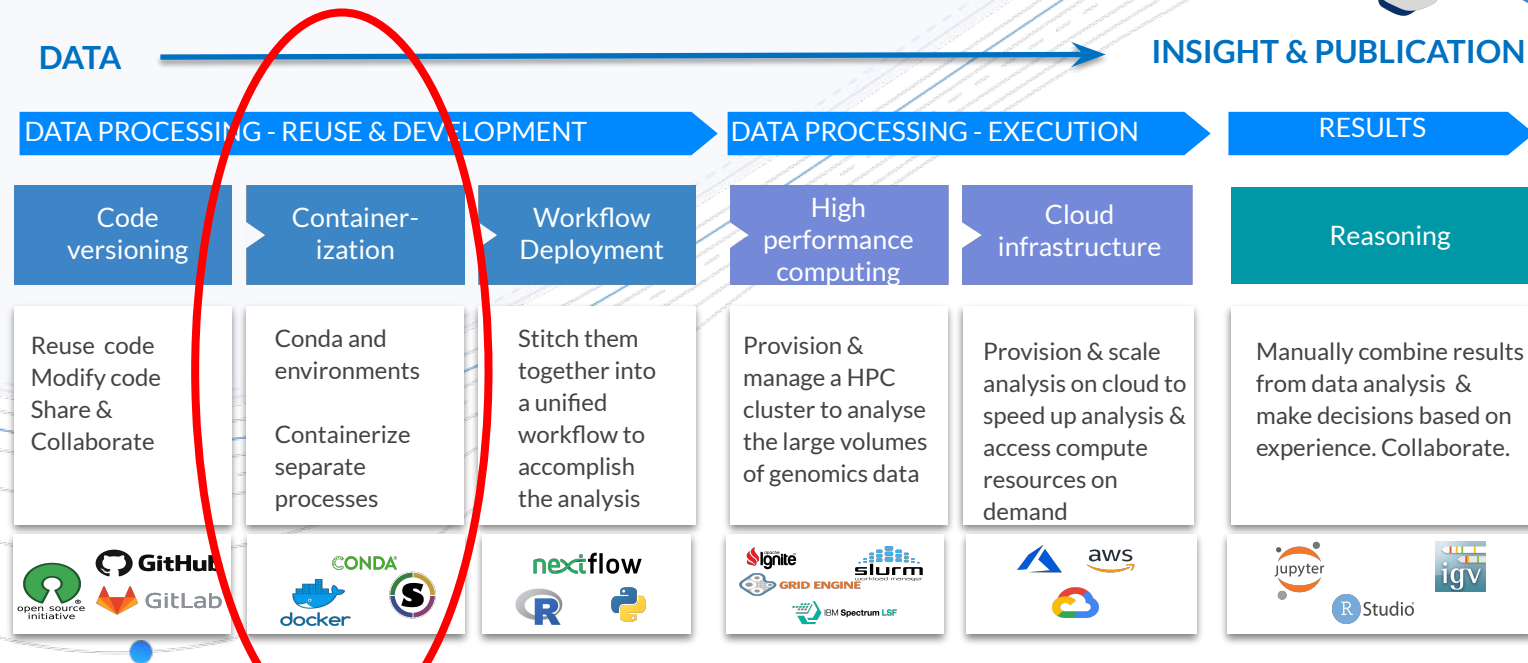
Provision & scale  
analysis on cloud to  
speed up analysis &  
access compute  
resources on  
demand

Manually combine results  
from data analysis &  
make decisions based on  
experience. Collaborate.



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# Dry Bench Skills Roadmap

Intro to Command  
line in the  
JupyterLab  
Interface

## Day 1

Bash skills intro  
R  
JupyterLab  
Volcano plot  
Zenodo

Git and  
Collaboration

## Day 2

Git  
GitHub for Teamwork  
JupyterLab  
Volcano plot

Introduction Conda  
and Docker

## Day 3

Conda  
Docker  
JupyterLab  
Volcano plot  
Prepping for Nextflow

Nextflow

## Day 4

Nextflow

Putting it all  
together  
RNASeq  
Nextflow &  
Jupyter Notebook

## Day 5

Best Practices  
RNASeq workflow



# Dry Bench Skills Agenda - Day 3



## Managing software dependencies

Conda and Docker in the service of reproducible scientific workflows

### Agenda for the day:

Time	Programme
12.00 - 12.05	Workspace set up and agenda for the day 
12.05 - 12.30	1. What is Conda, what is Docker and why do I need those for my research?
12.30 - 13.15	2. Introduction to dependencies management with conda
13.15 - 13.25	 Short break
13.25 - 14.00:	3. Build, test, share and re-use a docker image



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HM Government  
**G-Cloud**  
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# • Thank you

*...from everyone at*



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