



### Outro

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### Outline for the 2 hours

- Introduction
- Install worker on your laptop (hands on)
- Introduction into CWL and Docker
- 2 Workflows examples (hands on)
- Results and Outlook

# Why all of this?

- data is becoming cheaper and bigger
- analysis is complex
- needs many steps and often many machines for analysis
- building tool chains (aka pipelines, aka workflows) is hard
- what did I run last month?

## Geek Speak explained

- Workflow
- CWL
- Container
- Docker
- Singularity
- Provenance
- Reproducibility



#### Are there ...

- existing CWL workflows?
  YES: e.g. MG-RAST amplicon, MG-RAST shotgun, EBI MGnify assembly (metahitm, metaspades), EBI MGnify annotate, EBI MGnify amplicon, CheckM, GroupM, Prokka, QIIME, MGTap, ...
- existing tool definitions for CWL?
  YES! BLAST, SAMtools, BWA, spades, metaspades, velvet, metahit, cutadpt, diamond, ....
- other users:

YES: Pasteur, Galaxy, MG-RAST, EBI MGnify, Broad, Harvard, ISB, ELIXIR, Seven Bridges Genomics, Cyverse, CERN, Sanger Institute, ...

#### How can I...?

- Convince my local SysAdmin to install Singularity?
  - I need 15+ tools and approx. 150 libraries installed on MANY machines. When can you install this by? Or would you rather install Singularity for me
- use pre-existing containers?
  - https://hub.docker.com/
- learn about Containers/Docker?
  - use e.g. <a href="https://stackify.com/docker-tutorial/">https://stackify.com/docker-tutorial/</a>
- create my own Docker or Singularity containers?
  - see above
- integrate this with my institutes systems?
  - see the skyport2 repository on github or the CWL web page
- use whatever local mechanism exists?
  - depends on the amount of work "translating" the workflows and installing software

# What is a good solution?

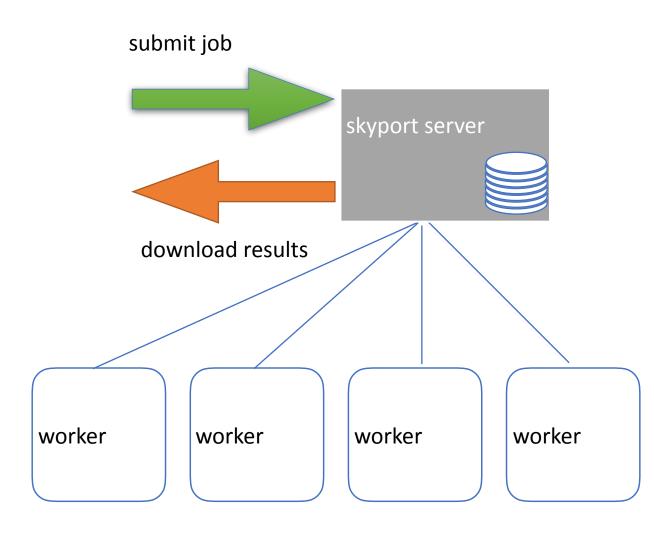
- setup a single static server
- dynamically add e.g. AWS nodes ("cloud")
- use existing cluster start aweworker job

or

 use LSF-toil to run CWL jobs inside LSF

or

• ...



## Questions comments