



Using clouds and VMs in bioinformatics training

European Life Sciences Infrastructure for Biological Information

www.elixir-europe.org



Background: typical bioinformatics course

- 2-3 day course with 20-30 life scientists
- Computer classrooms are not always available
- Need to install many analysis programs and their dependencies
 - Programs run typically on Linux
- Need data and reference data, both can be sizeable
- Analysis programs and reference data need to be updated often
- Some programs need more memory and CPU
- All participants run the same analysis jobs at the same time
- Participants need identical environment after the course
- Need to run the same course in different cities / countries

The goals of this workshop

- Learn when and how to make use of clouds, virtual machine images and Docker
- Hear how these things are done in different countries, can we learn from each other?
- Guideline document for EXCELERATE Train-the-Trainer task



ISMB 2016

Orlando, Florida,
July 8 - July 12

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Workshop 02 (WK02): Workshop on Education in Bioinformatics (WEB) - Exploiting Cloud and Virtual Resources for Training