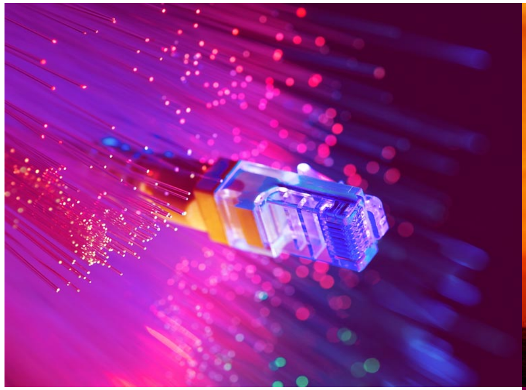


CSC

Containers and Workflows in Bioinformatics


CSC – Suomalainen tutkimuksen, koulutuksen, kulttuurin ja julkishallinnon ICT-osaamiskeskus

Course Preliminaries

- About instructors
- Course Theme
- Course expectations, organisation, overview and hands-on environment
- Getting started with course

Setting Expectations for Course

- Basics of HPC environment and containers
- Container essentials for running bioinformatics software
- Data persistence in containers
- HPC containers /singularity
- Workflows

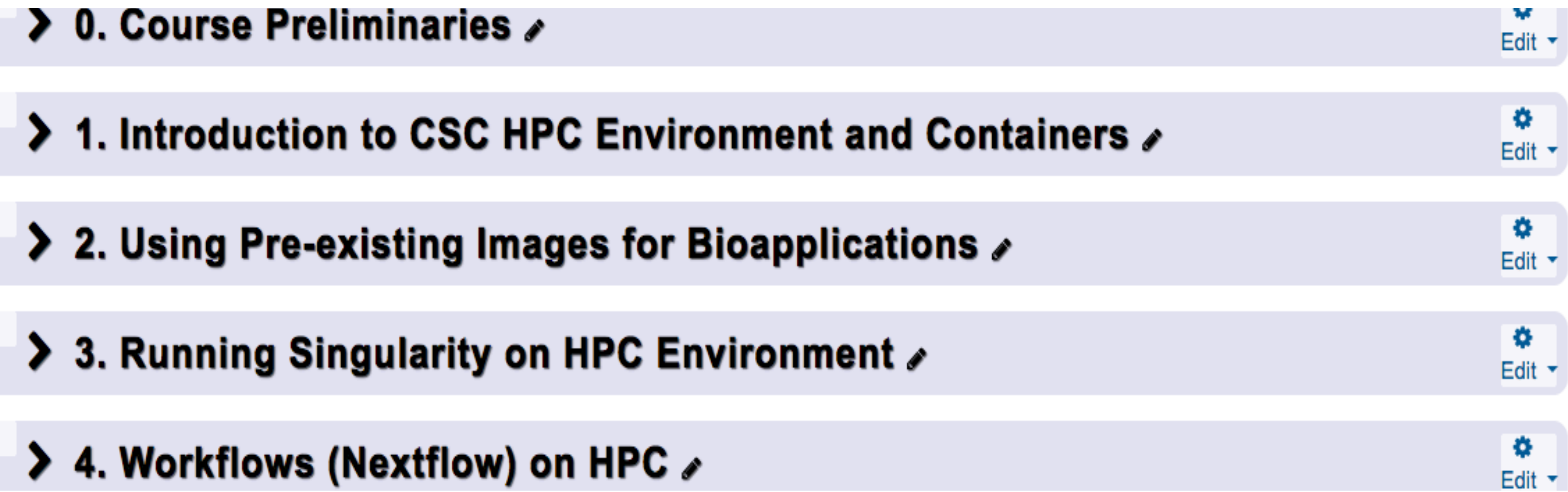
Organisation of course

Lectures

Optional Demos

Hands-on tutorials

Course Overview



0. Course Preliminaries

1. Introduction to CSC HPC Environment and Containers

2. Using Pre-existing Images for Bioapplications

3. Running Singularity on HPC Environment

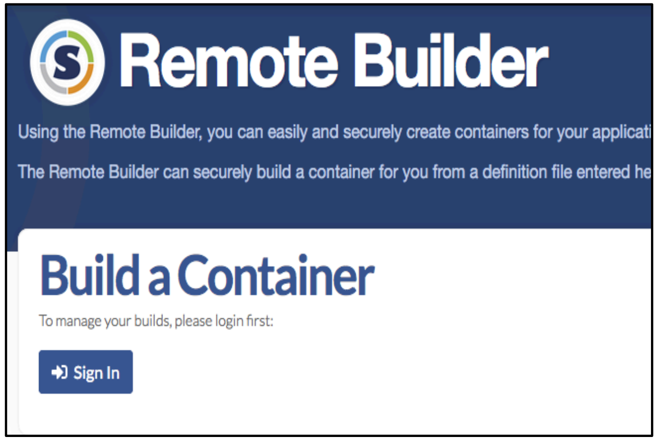
4. Workflows (Nextflow) on HPC

Hands-on Environment for Course


Play with Docker

A simple, interactive and fun playground to learn Docker

In-browser PWD


Remote Builder

Using the Remote Builder, you can easily and securely create containers for your applicati

The Remote Builder can securely build a container for you from a definition file entered he

Build a Container

To manage your builds, please login first:

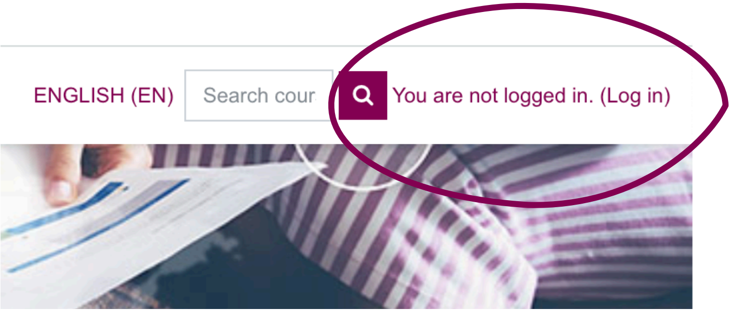
Syllabs remote builder

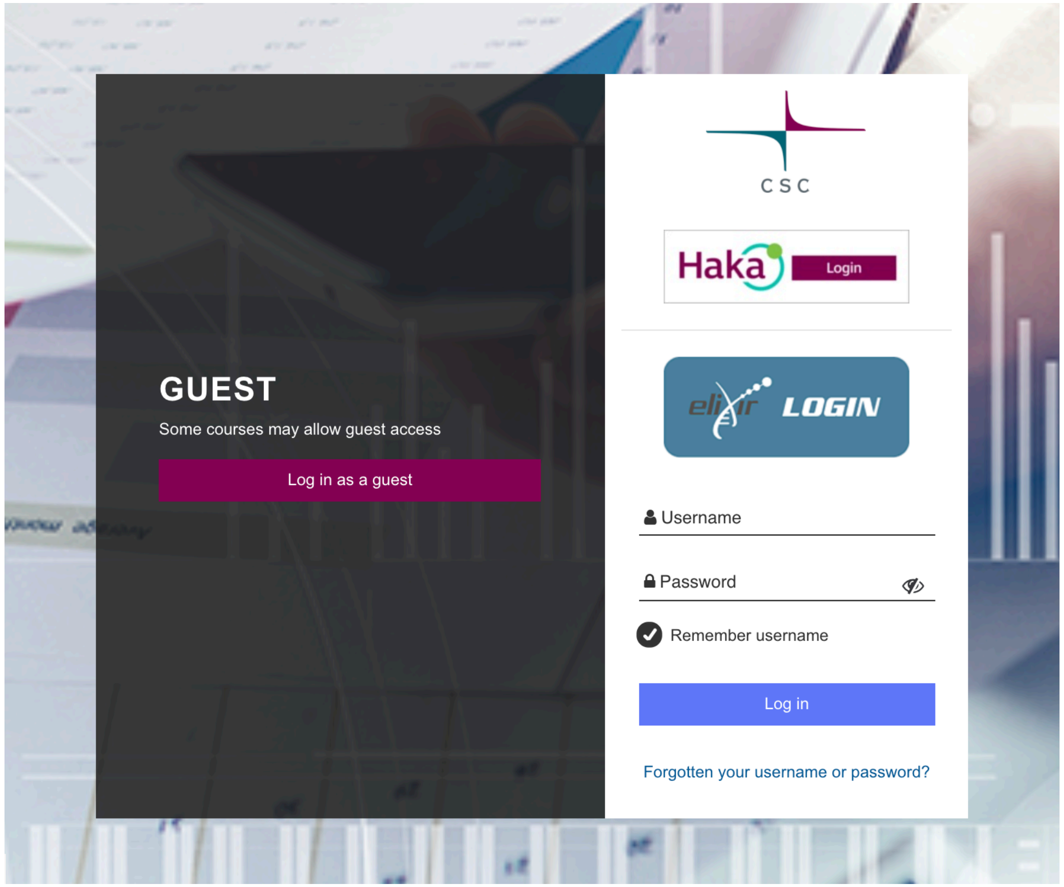
Puhti supercomputer
(Main environment)

Getting Started with Course

Sign in to e-Lena & enrol to course

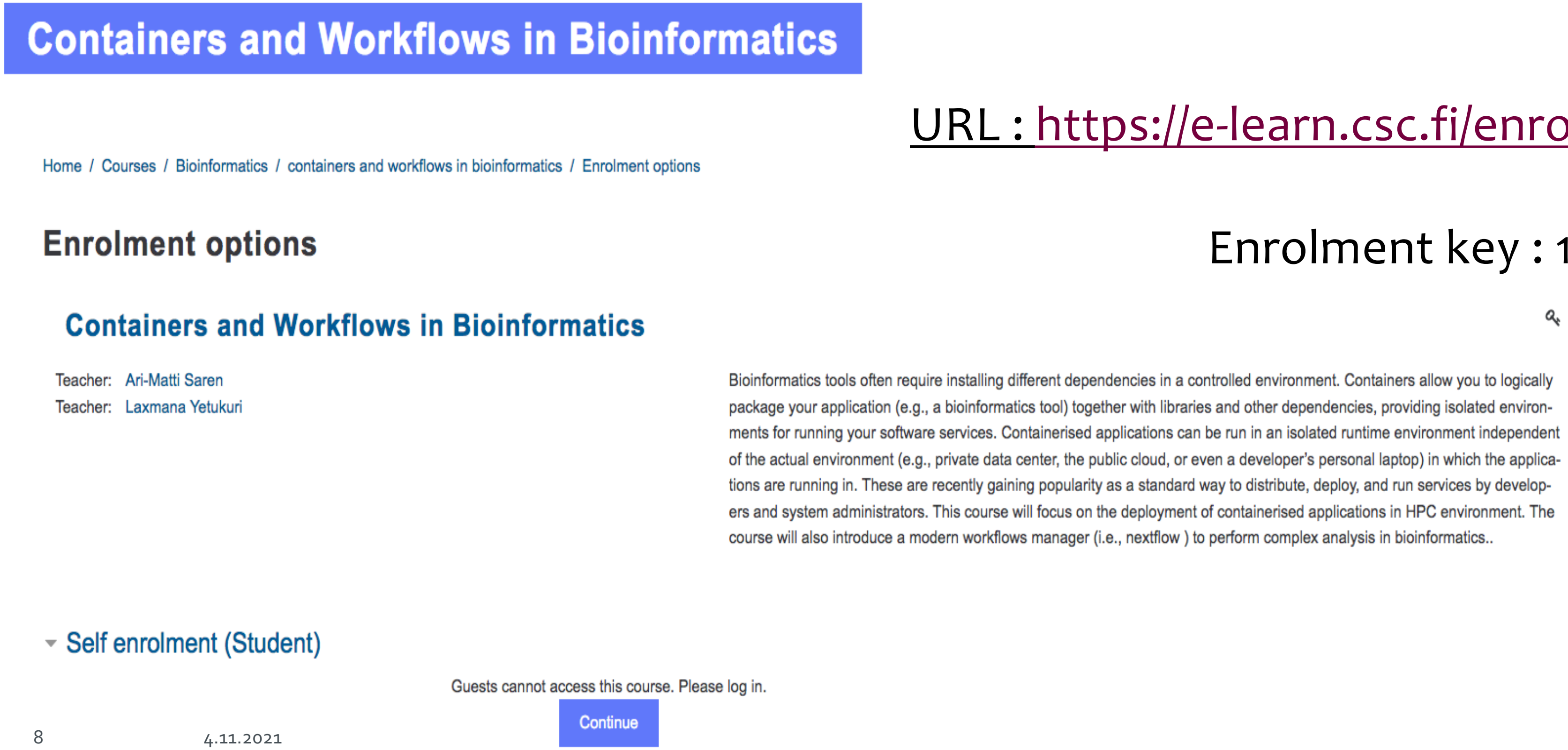
https://e-learn.csc.fi/login




GUEST

Some courses may allow guest access

Sign in to e-Lena & enrol to course



Containers and Workflows in Bioinformatics

Enrolment options

Containers and Workflows in Bioinformatics

Teacher: Ari-Matti Saren
Teacher: Laxmana Yetukuri

Bioinformatics tools often require installing different dependencies in a controlled environment. Containers allow you to logically package your application (e.g., a bioinformatics tool) together with libraries and other dependencies, providing isolated environments for running your software services. Containerised applications can be run in an isolated runtime environment independent of the actual environment (e.g., private data center, the public cloud, or even a developer's personal laptop) in which the applications are running in. These are recently gaining popularity as a standard way to distribute, deploy, and run services by developers and system administrators. This course will focus on the deployment of containerised applications in HPC environment. The course will also introduce a modern workflows manager (i.e., nextflow) to perform complex analysis in bioinformatics..

Guests cannot access this course. Please log in.

URL : https://e-learn.csc.fi/enrol/index.php?id=73

Enrolment key : 1234