Contribution ID: 26 Type: Tutorial

Running Chipster data analysis platform in EGI Federated Cloud

Wednesday, 11 November 2015 11:00 (1h 30m)

Chipster is a bioinformatics environment that includes over 350 analysis tools for high-throughput sequencing and microarray data. The tools are complemented with a comprehensive collection of reference datasets, such as genome indexes for the Tophat and BWA aligners. The tools can be used on command line or via an intuitive GUI, which offers also interactive visualizations and workflow functionality. Chipster is open source and the server environment is available as a virtual machine image free of charge.

In this tutorial session you will learn how virtual Chipster servers can be launched in the EGI Federated Cloud. The development and support work done by the EGI Federated Cloud community has made launching a Chipster server easy: The rOCCI client, needed to connect EGI Federated Cloud, is first installed to Linux or OSX machine. In addition you need to join chipster.csc.fi virtual organization.

After these preliminary steps, you can use a simple utility tool. With the FedCloud_chipster_manager, Chipster VM image is automatically downloaded form the EGI AppDB, launched in the EGI Federated Cloud environment and linked to the required reference data sets and applications using the CVMFS system.

More in-depth demonstrations about actually using Chipster for analyzing biological data will be shown in the NGS data analysis tuoral.

Requirements: 1. Linux machine with rOCCI client, 2. Chipster.csc.fi VO membership.

Primary authors: SCARDACI, Diego (EGI.eu/INFN); MATTILA, Kimmo (CSC)

Co-authors: CONDURACHE, Catalin (STFC); ANTONACCI, Marica (INFN)

Presenter: MATTILA, Kimmo (CSC)

Session Classification: Tutorial: Running Chipster in the EGI FedCloud