ELIXIR-ITA and Cineca are pleased to announce that applications are open for our pilot Call "ELIXIR-ITA HPC@CINECA" starting on 18 April 2016.

Cineca is one of the key technological partners of ELIXIR-ITA and with this pilot project we are exploring possible actions to further exploit the wealth of resources and expertise provided by this institution, sharing valuable computational services with European life scientists and bioinformaticians.

The ELIXIR-ITA HPC@CINECA Call offers computational resources to researchers from ELIXIR-ITA, other ELIXIR Nodes and any European research institution. Resources are provided through the Cineca web and command line High Performance Computing (HPC) platforms for bioinformatic data analysis.

Command line platform

Cineca has developed a standard unix module bioinformatics environment supporting data analysis for several organisms on its Pico architecture. It is continuously updated and complemented with all the public data (reference genomes and annotations, software indexes, etc..) necessary to carry on an efficient, reliable and consistent bioinformatic analysis. The whole list of software is available at Pico data and software resources. In the near future this bioinformatics software environment will be accessible also through a standard web-based Galaxy instance.

To learn more on Pico:

Pico user's guide

Automated pipelines

Cineca provides the following NGS pipelines implemented with a user-friendly web interface:
1. Deep targeted exome sequencing;
2. RNA sequencing (transcriptome analysis);
3. Whole exome sequencing;
4. Identification of DNA protein interactions by ChiP-seq;
5. RNA editing prediction by RNA-seq.

"ELIXIR-ITA HPC@CINECA" has a total resource budget of 2,000,000 core hours and 200 TB of storage, with each approved application having at its disposal 50,000 core hours and 5 TB of storage (any special needs may be discussed).

A scientific and technical evaluation board appointed by ELIXIR-ITA will assess the scientific soundness and technical feasibility of each application. Projects will be evaluated with a "first

come, first served” policy until the total resources budget will be assigned. Each application will be evaluated within 7 working days from submission. Approved applications will have access to the computational resources within 7 working days from acceptance.

Successful applicants are requested to acknowledge the “ELIXIR-ITA HPC@CINECA” Call in any scientific publication including data analysed with resources made available by this Call.

Applications must be submitted using this form.

For any further info please contact Federico Zambelli for ELIXIR-ITA or hpc-bioinformatics@cineca.it for Cineca.