

Galaxy for Bioinformatics tool developers

Galaxy is an open source, web-based platform for data intensive biomedical analysis. It is used in a broad range of biomedical research domains to make accessible bioinformatics applications to users lacking programming skills, and enabling them to easily build analysis workflows for NGS data.

This course is aimed at PhD students, computer scientists, bioinformaticians and developers who need to maintain/extend existing tools or develop new tools for Galaxy. The aim of this course is to make participants familiarize with the Galaxy platform and prepare them to work independently, using best practices guidelines for building, maintaining and installing Galaxy tools.

The course will be delivered using a mixture of lectures and computer based hands-on practical sessions. Lectures will provide an up-to-date overview of the practices for the most successful Galaxy tool development. During this 2 days course participants will learn a modern approach to create, configure and install their own tools into a Galaxy server.

Prerequisites:

Knowledge in a scripting language (bash, python, ...). Working knowledge of the Unix/Linux command line. Attendees should have access to a personal laptop.

<https://elixir-iib-training.github.io/website/>

<http://elixir-italy.org/en/>