On the web, right now

useGalaxy.
or | .eu | .org.au

120+ Public Servers

On cloud services

aws | Azure | Google Cloud

galaxyproject.org/use

Docker & Virtual Machines

Over 35 Docker and VM images with fully functional pre-populated Galaxy instances on them, that you can setup and run on your laptop in minutes

Visualization, Epigenomics, metagenomics, RNA-Seq, BLAST+, ChIP-Seq, Exome-Seq, Image Analysis, Mass Spec ...

Learn: Everyone

Hands-on tutorials, slides, training datasets, exercises, ...

See Poster P141: The Galaxy Training Network: A Community Based Training Resource

Ask: Support

help.galaxyproject.org

gitter.im/galaxyproject

Enable: Providers

getgalaxy.org

Publish: Tool Devs

The Galaxy ToolShed contains over 7,000 tools, datatypes, & workflows, all defined for Galaxy, and easy to install. Wrapping your tools for Galaxy makes them easy to deploy and use.

Workflows are created from scratch, or extracted from past analyses.

Individual tools through entire analyses can be rerun. Galaxy saves every dataset, tool, and tool parameter.

Galaxy supports sharing and publishing analyses.

Repeat, Share, Publish

BCC Bioinformatics Community Conference

BlackDuck Open Hub: Over the past twelve months, 157 developers contributed new code to Galaxy. This is one of the largest open-source teams in the world,

galaxyproject.org