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ReGaTE: Registration of Galaxy Tools in Elixir

Olivia Doppelt-Azeroual1,∗,†, Fabien Mareuil1,†, Eric Deveaud1, Matúš Kalaš2, Nicola Soranzo3, Marius van den Beek4, Björn Grüning5, Jon Ison6 and Hervé Ménager1

1Centre de Bioinformatique, Biostatistique et Biologie Intégrative (C3BI, USR 3756 Institut Pasteur et CNRS), 25 rue du Docteur Roux, Paris, France, 2Computational Biology Unit, Department of Informatics, University of Bergen, Thormøhlensgate 55, Bergen, Norway, 3Earlham Institute, Norwich Research Park, NR4 7UG Norwich, United Kingdom, 4Institut de Biologie Paris-Seine, Université Pierre et Marie Curie, Paris, France, 5Department of Computer Science, Albert-Ludwigs-University, Center for Biological Systems Analysis (ZBSA), University of Freiburg, Freiburg, Germany and 6Department of Systems Biology, Center for Biological Sequence Analysis, Technical University of Denmark, Building 208, 2800 Kongens Lyngby, Denmark.

∗Correspondence address. Centre de Bioinformatique, Biostatistique et Biologie Intégrative (C3BI, USR 3756 Institut Pasteur et CNRS), 25 rue du Docteur Roux, Paris, France. Tel: +33626045763; Fax: +33626045763; E-mail olivia.doppelt@pasteur.fr
†Equal contribution

Abstract

Background: Bioinformaticians routinely use multiple software tools and data sources in their day-to-day work and have been guided in their choices by a number of cataloguing initiatives. The ELIXIR Tools and Data Services Registry (bio.tools) aims to provide a central information point, independent of any specific scientific scope within bioinformatics or technological implementation. Meanwhile, efforts to integrate bioinformatics software in workbench and workflow environments have accelerated to enable the design, automation, and reproducibility of bioinformatics experiments. One such popular environment is the Galaxy framework, with currently more than 80 publicly available Galaxy servers around the world. In the context of a generic registry for bioinformatics software, such as bio.tools, Galaxy instances constitute a major source of valuable content. Yet there has been, to date, no convenient mechanism to register such services en masse. Findings: We present ReGaTE (Registration of Galaxy Tools in Elixir), a software utility that automates the process of registering the services available in a Galaxy instance. This utility uses the BioBlend application program interface to extract service metadata from a Galaxy server, enhance the metadata with the scientific information required by bio.tools, and push it to the registry. Conclusions: ReGaTE provides a fast and convenient way to publish Galaxy services in bio.tools. By doing so, service providers may increase the visibility of their services while enriching the software discovery function that bio.tools provides for its users. The source code of ReGaTE is freely available on Github at https://github.com/C3BI-pasteur-fr/ReGaTE.

Keywords: Galaxy; bio.tools; bioinformatics services

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Introduction

Over the recent years, various initiatives have aimed at cata-
logging bioinformatics tools and services [1–6]. In particular, the
ELIXIR Tools and Data Services Registry (bio.tools) [7] offers
a community-curated information portal whose goals are com-
prehensive coverage and consistent description of bioinformat-
ics tools and services. Another ongoing trend is the integration
of bioinformatics software in workbench and workflow environ-
ments, which allows data analysts to design, automate, and re-
produce bioinformatics experiments.

The Galaxy framework [8–10] is one of the most popu-
lar of such environments, with currently more than 80 pub-
licly available Galaxy servers (see https://wiki.galaxyproject.org/
PublicGalaxyServers) around the world. The registration and
maintenance of entries in the bio.tools registry is based on a
“federated curation model” whereby the maintenance of re-
source entries is handled by their owners. Current efforts to
automatically register tools and services in resource catalogs
mostly target programming language–specific catalogs, such as
the Python package index (see http://pypi.python.org/pypi), and
seldom domain–specific catalogs, with a few notable exceptions
such as BioS [11], the BioGems registry [12], and BioMOBY [13].
In contrast, ReGaTE is a solution for owners of Galaxy server in-
estances to easily register their tools on a resource catalog that is
not specific to any programming language or technical require-
ment. The scientists browsing the bio.tools server can therefore
search and compare resources independently of any technologi-
ical implementation. In the context of a generic registry for bioin-
formatics software, such as bio.tools, Galaxy instances consti-
tute a major source of valuable content. The ReGaTE utility is
a software component that automates the registration of the
bioinformatics tools installed on a Galaxy server. We will present
in the following sections the major aspects of its implementa-
tion, its architecture, and finally the mapping of tool metadata
from Galaxy to bio.tools.

Implementation

ReGaTE pulls tool descriptions from a Galaxy server, augments
the information, and pushes it to the bio.tools registry.

A Galaxy server is a framework that supports users to con-
figure and run a range of bioinformatics tools and workflows
and that gathers many other features for the sharing, visu-
alization, and reproducibility of analyses. The user interface
and execution of tools are based on a tool definition in an
eXtensible Markup Language (XML) file (detailed documenta-
tion of this format is available at https://wiki.galaxyproject.org/
Admin/Tools/ToolConfigSyntax). Each file describes the bioinfor-
matics tool in a detailed way, including the tool parameters, in-
puts, and outputs. This allows the display of their sometimes
complex configuration options in a graphical user interface, pri-
marily to enable tool parameterization and its execution. Such
tool definitions are loaded by the Galaxy server and are acces-
sible through the Galaxy RESTful interface. The BioBlend library
[14] allows convenient access to the Galaxy application program
interface (API) from Python. Here, we have used BioBlend to ex-
tract Galaxy tool definitions from remote Galaxy instances.

Bio.tools [7] is a web portal provided by ELIXIR – the
European infrastructure for biological information for the ex-
ploration of bioinformatics resources including software pack-
ages, web services, and database portals. Through a dedicated
graphical interface, users can search for and compare resources.
Thus, bioinformatics resource providers can use bio.tools to en-
hance the visibility of their services. The description and regis-
tration of a resource can be done manually via a web user in-
terface, or resources may be registered using the registry API.
Registry entries follow a model that is formalized in biotoolsS-
chema (the biotoolsSchema format definition is available at
https://github.com/bio-tools/biotoolsSchema/), an XML schema
that defines a resource description model for bioinformatics
with a mandatory core of 10 attributes.

ReGaTE fetches the Galaxy tool definitions, enhances them
with additional annotations, and converts them into the
biotoolsSchema-based JSON format, using the mapping mech-
anism described in the next section, before pushing them to
bio.tools. This process can be triggered at once or step by step,
first extracting the tool metadata, and second pushing enhanced
metadata to bio.tools. A ReGaTE user needs to have an account
on the targeted Galaxy and retrieve his API key to extract the
tool definitions and an account on the bio.tools server to push
the registry entries.

ReGaTE Architecture

ReGaTE is a Python script coupled with a configuration file
and mapping of semantics used by Galaxy and bio.tools. An overview
of its architecture is shown in Fig. 1.

The configuration file includes the Galaxy server uniform re-
source locator, an API key, and a directory to store the generated
tool files uploadable to bio.tools. Suffix and prefix variables, for
tagging the names of the tools extracted by ReGaTE, may also be
specified. For example, the name of the tool SARTools DESeq2
[15], implemented at Institut Pasteur, can be named SARTools
DESeq2-IP.

Tool Metadata Mapping

A biotools-Schema file describes a given software application, covering different properties:

- scientific properties, such as the domain catered for and de-
scription of the type of task(s) done by a tool;
- technical properties, such as the type of software and its
interface(s), e.g., command line tool, web application, web
service, etc.;
- credit, e.g., the references that need to be cited when refer-
ing to this work;
- administrative information, such as the license used in the
software.

Some of these properties are described using the EMBRACE
Data and Methods (EDAM) ontology [16]. Development of the
EDAM ontology is driven by community requests via GitHub,
mailing lists, and community-based hackathons (more informa-
tion on contributions can be found at https://github.com/
edamontology/edamontology/blob/master/HOW_TO_CONTRIBU-
TE.md). It currently includes 3280 concepts with regular (at least quarterly) major releases. EDAM includes the following
common bioinformatics concepts:

- topics, i.e., scientific disciplines or domains covered by the
resource;
- specific operations performed by a tool or service;
- types of input and output data;
- formats in which inputs and outputs are available.

The mapping from a Galaxy tool definition file (de-
tailed documentation of this format is available at
https://wiki.galaxyproject.org/Admin/Tools/ToolConfigSyntax)
to a bio.tools file is handled by the ReGaTE code, taking advantage of the important number of common properties between such workbench wrappers and registry entries [17]. A few properties are not natively available in the Galaxy tool files retrieved by BioBlend; these missing data are provided by the ReGaTE configuration files.

The mapping of Galaxy tool properties to EDAM concepts is a key component. This translation is handled by yet another markup language mapping files included in the ReGaTE distribution that handle the conversion of Galaxy datatypes to EDAM data and format concepts, and that also allow EDAM topics and operations to be specified.

Conclusions and Future Work

The bio.tools registry allows Galaxy server maintainers to increase the visibility of their services, set in context of offerings from other providers. The ReGaTE utility is a fast and convenient solution to enhance, publish, and maintain the services provided by a Galaxy server in the registry. Furthermore, ReGaTE can prove a valuable contribution toward providing bio.tools with more comprehensive coverage of the community resources.

Current work on ReGaTE is focused on migration of the core functionality and tool semantics to the Galaxy Project itself. This integration will rely on the direct annotation of Galaxy datatypes with EDAM format and data concepts (see https://github.com/galaxyproject/galaxy/pull/2387 and https://github.com/galaxyproject/galaxy/pull/2428), as well as the possibility to specify an EDAM topic (see https://github.com/galaxyproject/galaxy/pull/2397) and operational concepts (see https://github.com/galaxyproject/galaxy/pull/2379) directly in Galaxy tool definitions (see https://github.com/galaxyproject/galaxy/pull/3221).

The use of EDAM as a standard for describing bioinformatics resources can provide a backbone to improve interoperability and guide users to connect and compose Galaxy tools [18], extending potentially to external components and environments that share this common vocabulary. A future priority will therefore be to exploit EDAM annotations in these ways for the benefit of Galaxy users and providers.

Abbreviations

API: application program interface; EDAM: EMBRACE Data and Methods; URL: Uniform Resource Locator; XML: eXtensible Markup Language; YAML: Yet Another Markup Language.

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Availability and requirements

Project name: ReGaTE
Project home page: https://github.com/C3BI-pasteur-fr/ReGaTE
Operating system(s): Unix-based operating systems
Programming language: Python
License: GPLv2
Any restrictions to use by non-academics: None

Availability of supporting data

A snapshot of the version of the ReGaTE source code used in this paper is archived in the GigaScience database GigaDB [19].

Conflicts of interest

The authors declare that they have no competing interests.

Author’s contributions

ReGaTE was designed by contributions of all authors. The development was done by O.D., F.M., and H.M. The paper was written by all of the authors, who read and approved the final manuscript.
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