



bio.tools and the ELIXIR Tools Platform


Scientific Software Registry Collaboration Workshop



Hervé Ménager, nov. 8th, 2019

www.elixir-europe.org

bio.tools: find tools

elixir
bio.tools

Topic: 'Comparative genomics' x Search bio.tools

110 tools

About

Login

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Sort by

Score

Updated

Added

Name




Citation Count

Publication Date

Display as

Compact

Detailed




i-ADHoRE |   

A highly sensitive software tool to detect degenerated homology relations within and between different genomes.

Comparative genomics

Sequence comparison

Command-line tool



PLAZA dicots |   

Access point for plant comparative genomics.

Comparative genomics

Analysis

Web application

BLSSPELLER |  

Exhaustive comparative discovery of conserved cis-regulatory elements.

Comparative genomics

Transcriptional regulatory element prediction

Command-line tool



bio.tools: access and modify tool descriptions

MAFFT (biotools:MAFFT)

<http://mafft.cbrc.jp/alignment/server/index.html>



Sequence analysis >

Mature BSD-Source-Code Free of charge Open access

Command-line tool Web application Python   

MAFFT (Multiple Alignment using Fast Fourier Transform) is a high speed multiple sequence alignment program.

Sequence alignment >
(FASTA)

Multiple sequence alignment >

Sequence alignment >
(FASTA)

Credits & Support

Contact Form
Primary contact | [Link](#) >

Documentation

[FAQ](#) >

Downloads

[Downloads page](#) >

Links

[Galaxy service](#) >

Publication details



Primary

DOI: 10.1007/978-1-62703-646-7_8



Other



DOI: 10.7490/f1000research.1114334.1


Update tool

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[Summary](#) [Function](#) [Labels](#) [Links](#) [Download](#) [Documentation](#) [Publications](#) [Credits & Support](#) [Relations](#) [JSON](#)

Miscellaneous scientific, technical and administrative details of the software, expressed in terms of controlled vocabularies. We recommend you specify at least the tool type, license, and one or more topics. See the [Curation Guidelines](#).

Tool type  Command-line tool 

Web application 



Add Tool type


Topic  Functional genomics  I don't know 

Filter



- Biology
- Biomedical science
- Chemistry
- Computational biology
- Computer science
- Experimental design and studies
- Informatics
- Laboratory techniques
- Literature and language
- Mathematics
- Medicine
- Omics
- Physics

Add topic



Operating system  Linux 



Mac 


Add operating system

Language  Python 

Add language

Maturity  Mature 

License  GPL-3.0 

Cost 

<https://biotools.readthedocs.io/en/latest/>



bio.tools data example (excerpts)

<https://biotoolsschema.readthedocs.io/en/latest/>

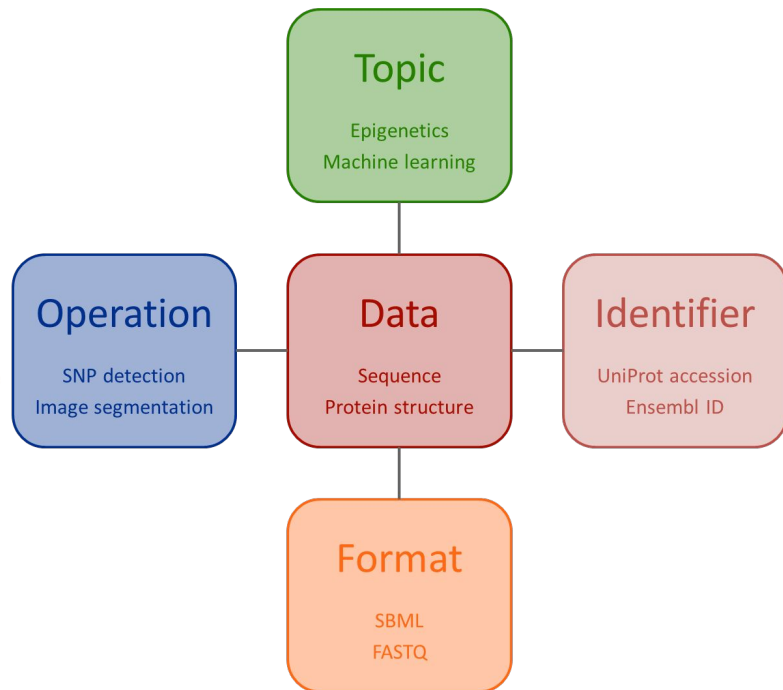
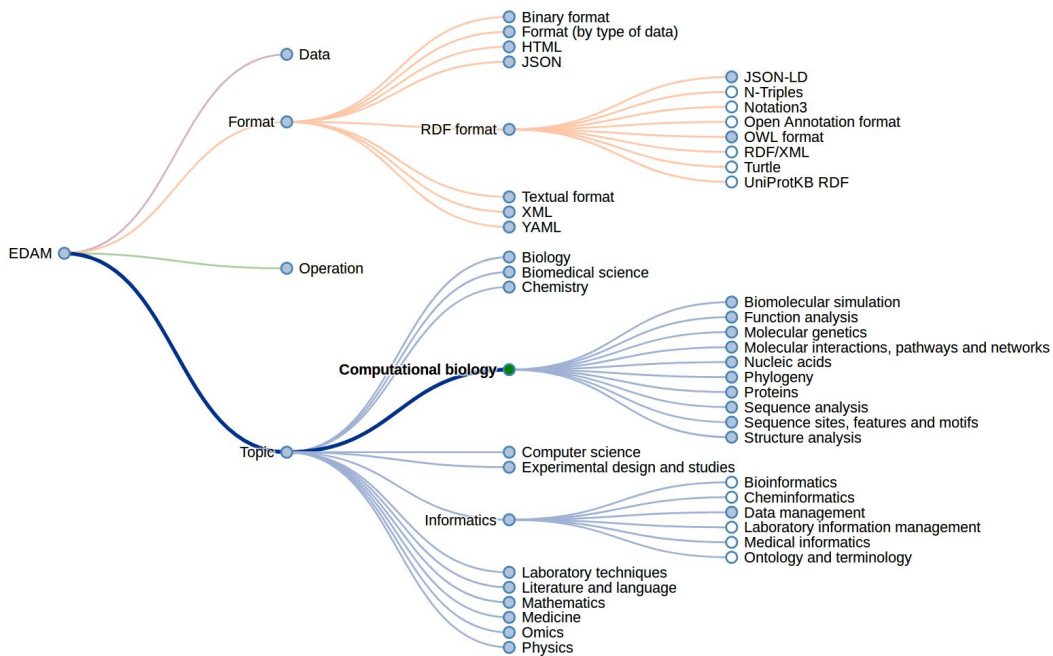
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  "description": "Fast, accurate, memory-efficient aligner for
short and long sequencing reads",
  "homepage": "http://bio-bwa.sourceforge.net",
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  "biotoolsCURIE": "biotools:bwa",
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        },
        {
          "uri":
"http://edamontology.org/operation_0292",
          "term": "Sequence alignment"
        }
      ],
      "input": [
        {
          "data": {
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"http://edamontology.org/data_2044",
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            {
              "uri":
```

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    "term": "Mapping"
  }
],
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  "Mac"
],
"language": [
  "C"
],
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"collectionID": [
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"maturity": "Mature",
"cost": null,
"accessibility": [],
"elixirPlatform": [],
"elixirNode": [],
"link": [],
"download": [
  {
    "url":
"https://gitlab.com/sibyllewohlgemuth/cwl_files/raw/master/bwa_index.
cwl",
    "type": "CWL file",
```



EDAM



<https://edamontologydocs.readthedocs.io/en/latest/>



Results and Stats

Contents

>13000 tools and services

See <https://bio.tools/stats>

Access

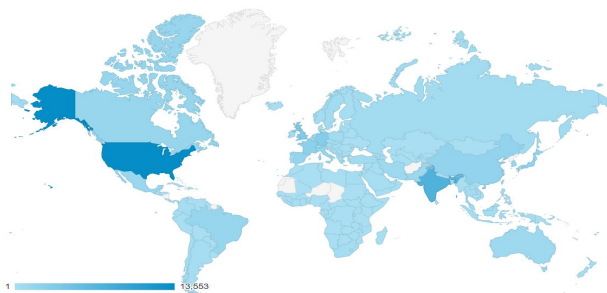
- 12,396 users/month (March 2019)
- 112,461 users and 223,557 page views
- world-wide usage

Availability

- Public API
- Contents: Creative Commons Attribution licence ([CC BY 4.0](https://creativecommons.org/licenses/by/4.0/)).
- Registry: [GPL v3](https://github.com/biodottools)
- And an ecosystem of tools and utilities:
<https://github.com/biodottools>

Trend of 30 Day Active Users

Mar 1, 2017–Apr 30, 2019



ELIXIR and the ELIXIR Tools Platform



Data



Compute



Interoperability



Training



discovery portal
for bioinformatics
software
information

Bio.tools



Software
packaging &
containers

BioConda/
BioContainers



scientific
benchmark and
technical
monitoring

OpenEBench



execution
platforms (e.g.
Galaxy) and
workflows

Galaxy,
CWL



software quality
and sustainability

software best
practices and
developing
training activities

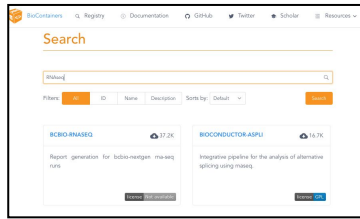
Tools Interoperability, guidelines and resources for guaranteeing platforms integration at the ELIXIR Tools platform ecosystem, with other platforms at ELIXIR and beyond.



Tools Platform: limitations



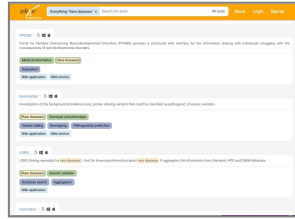
55,800 containers



BioContainers



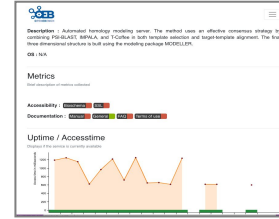
12,443 tools



bio.tools



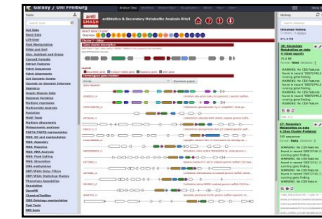
10+ Communities



OpenEBench



6,894 tools in
Galaxy tool shed

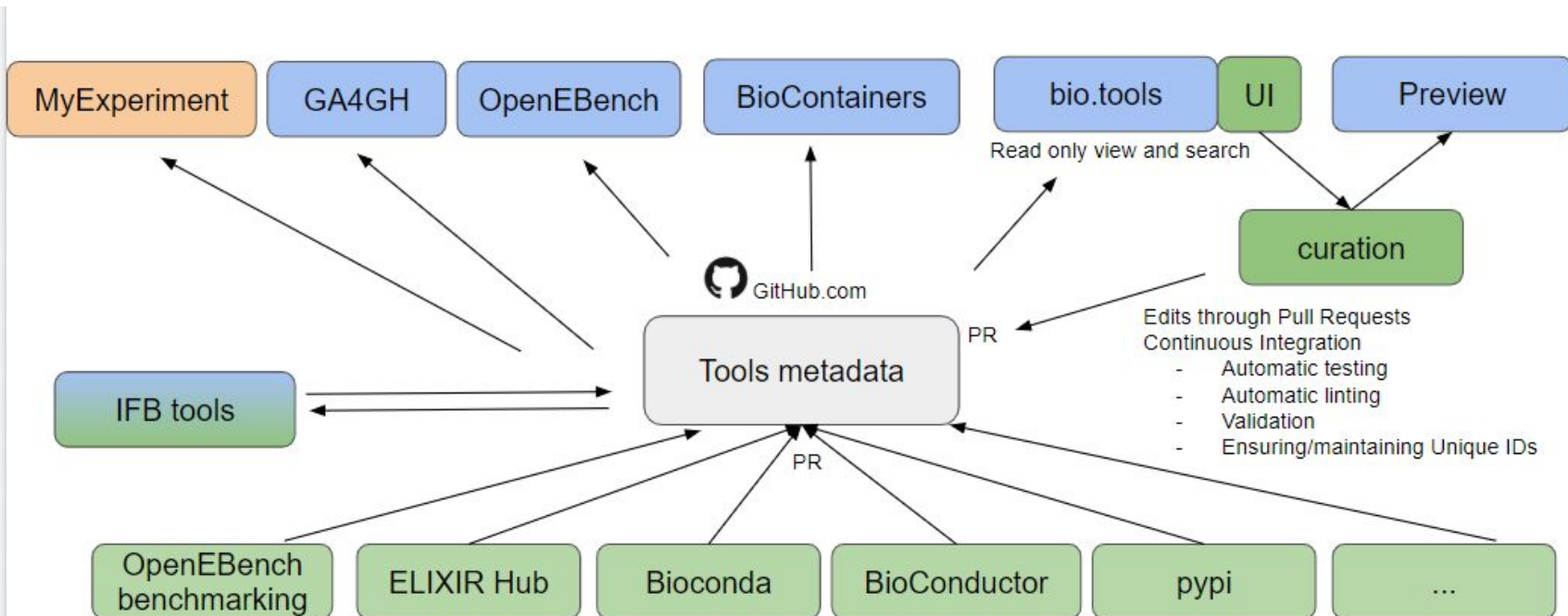


Galaxy

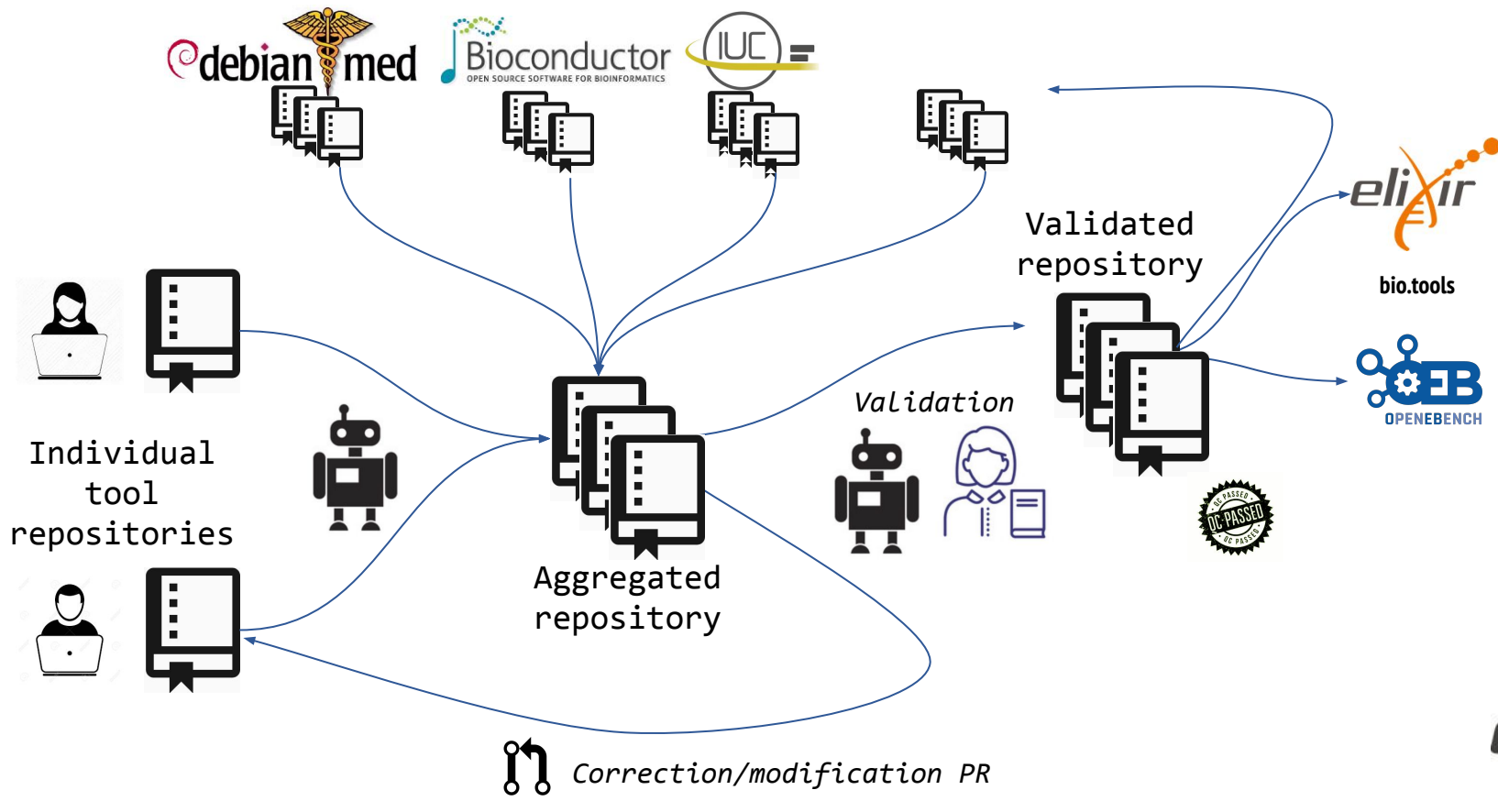
- Metadata (tool descriptions) **sharing** between these systems
- Metadata sharing with external community resources:
 - Debian-med
 - BioConductor
 - Other ELIXIR platforms
- **Simplify** the creation and **maintenance** of tool descriptions for **Tool authors**



The **new** Tools Platform Ecosystem (WIP)



The new Tools Platform Ecosystem architecture (WIP)



Credits, further information

Open Letter | [Open Access](#) | [Published: 12 August 2019](#)

The *bio.tools* registry of software tools and data resources for the life sciences

[Jon Ison](#) , [Hans Ienasescu](#), [...] [Søren Brunak](#)

[Genome Biology](#) 20, Article number: 164 (2019) | [Cite this article](#)

2237 Accesses | 1 Citations | 67 Altmetric | [Metrics](#)

Community curation of bioinformatics software and data resources

[Jon Ison](#) , [Hervé Ménager](#), [Bryan Brancotte](#), [Erik Jaaniso](#), [Ahto Salumets](#), [Tomáš Raček](#), [Anna-Lena Lamprecht](#), [Magnus Palmblad](#), [Matúš Kalaš](#), [Piotr Chmura](#) ... [Show more](#)

Briefings in Bioinformatics, bbz075, <https://doi.org/10.1093/bib/bbz075>

Jon Ison

Matúš Kalaš

Emil Rydza

Lukas Berger

Hans Ienasescu

Piotr Chmura

...

The Galaxy, CWL, and many other communities and contributors!

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Thank you!



www.elixir-europe.org

