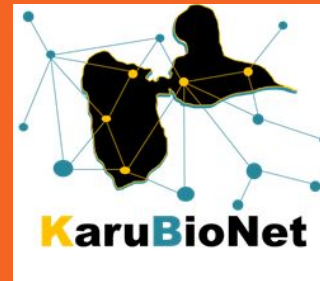




Présentation générale



Un peu d'histoire depuis ses débuts en 2005...

PENNSYLVANIA STATE UNIVERSITY



EMORY
UNIVERSITY



JOHNS HOPKINS
UNIVERSITY



Qu'est ce que Galaxy ?

- Un outil d'intégration et d'analyse de données
- Un portail web libre d'accès incluant un nombre important de programmes/outils...
- Une application web écrite en Python et "Open source"
- Devise: Making computation accessible; Ensuring reproducibility; Promoting transparency



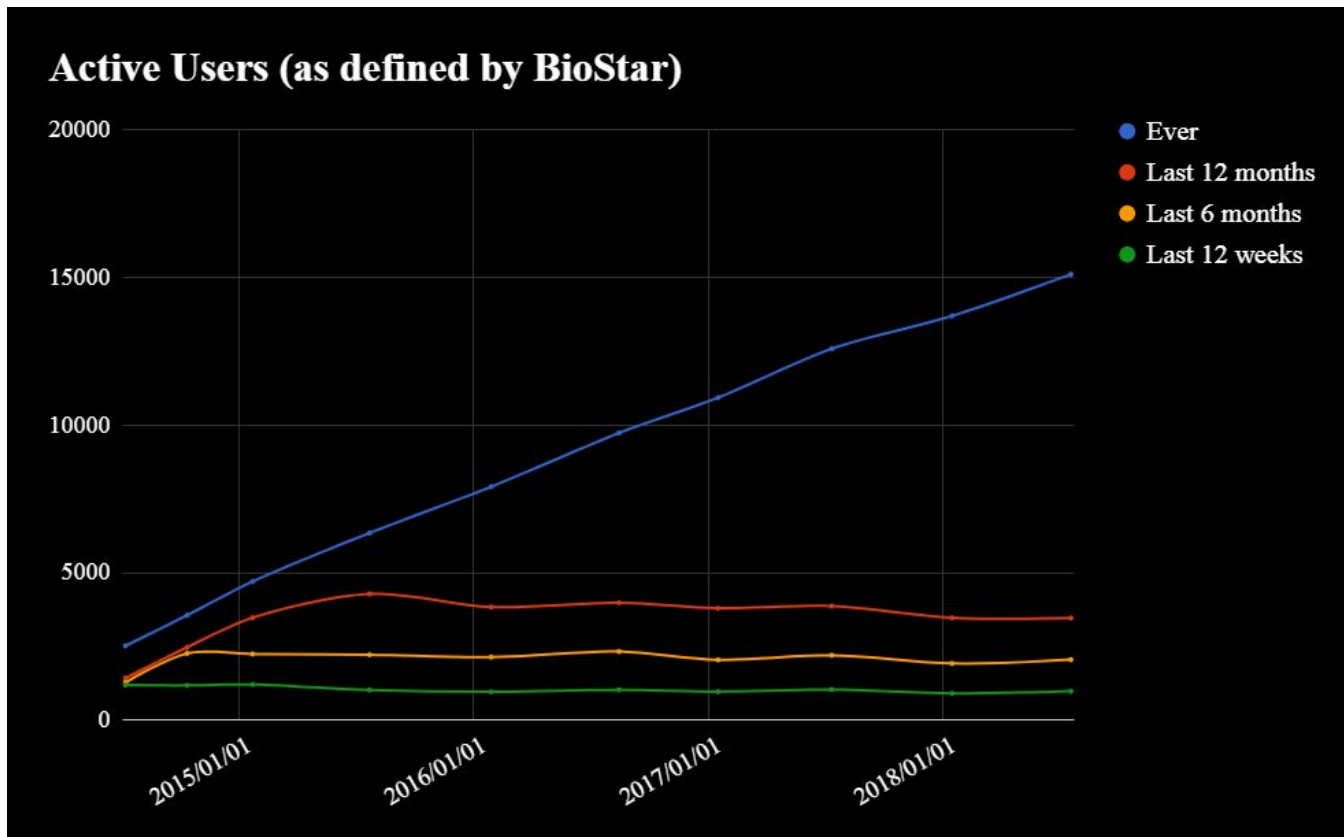
Analyze Data

Workflow

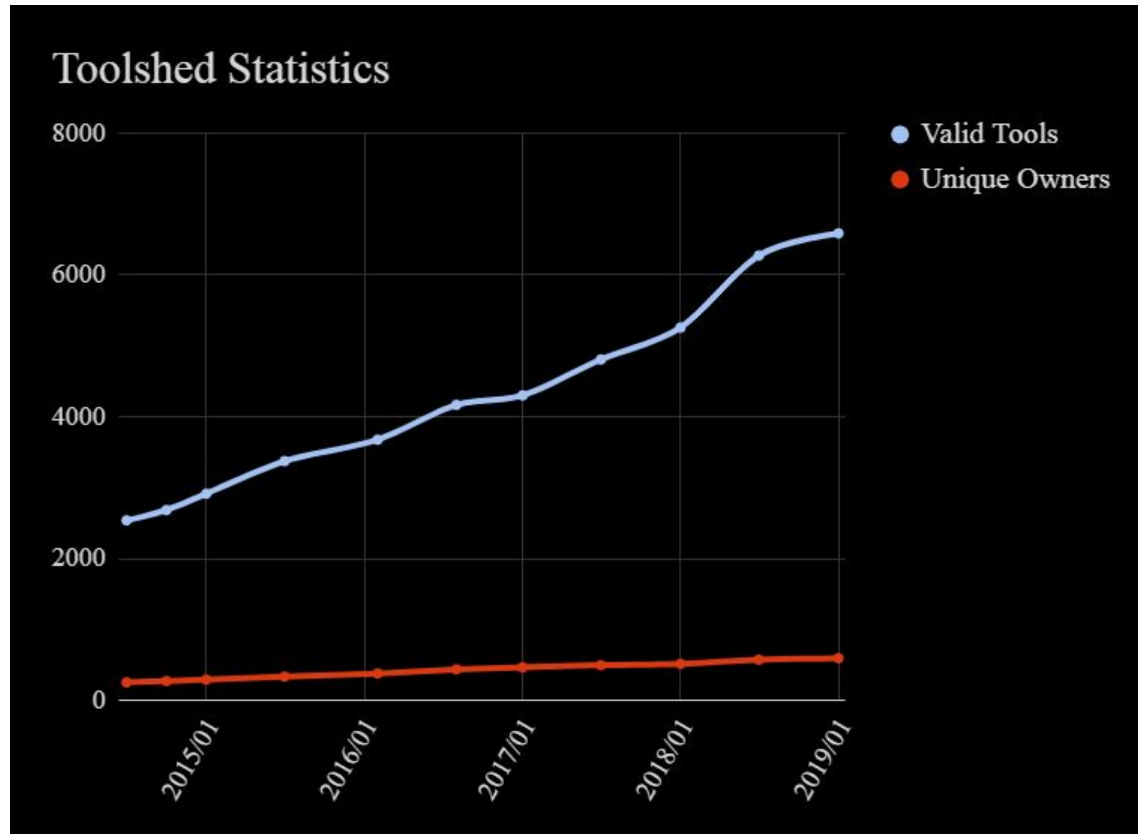
Visualize ▾

Shared Data ▾

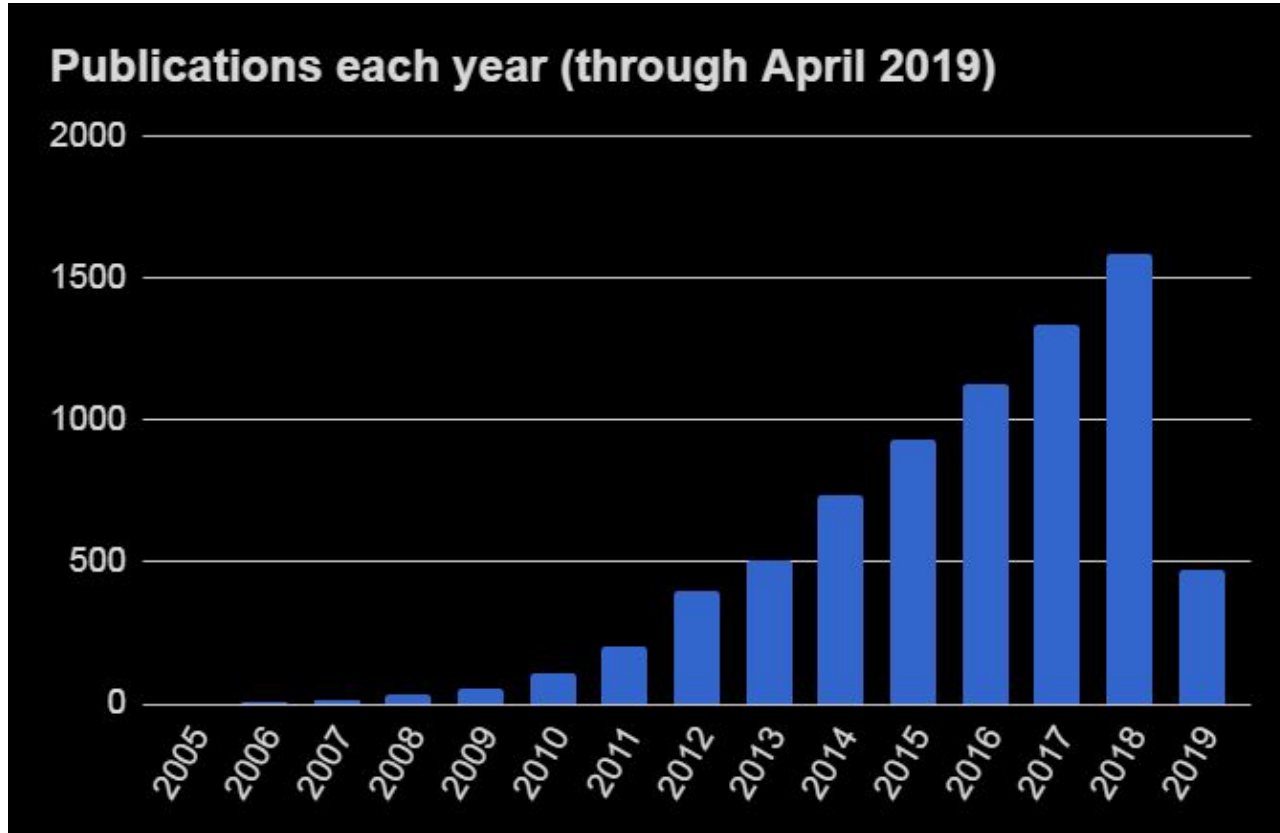
Quelques statistiques



Quelques statistiques



Quelques statistiques



Source : <https://galaxyproject.org/galaxy-project/statistics/>

Structure globale



Menus

The screenshot displays the Galaxy web interface. At the top, the browser address bar shows 'localhost:8080'. The main navigation bar includes 'Galaxy' and a menu with options: 'Analyze Data', 'Workflow', 'Visualize', 'Shared Data', 'Admin', 'Help', and 'User'. The user's session is identified as 'Using 11.1 MB'.

Tools Menu (Left):

- Tools
- Get Data
- Send Data
- Collection Operations
- Lift-Over
- Text Manipulation
- Convert Formats
- Filter and Sort
- Join, Subtract and Group
- Fetch Alignments/Sequences
- Operate on Genomic Intervals
- Statistics
- Graph/Display Data
- Phenotype Association
- Sequence Alignment
- Phylogeny
- Annotation
- NGS: Mapping
- Workflows
- All workflows

Main Content Area:

Hello, Galaxy is running!

To customize this page edit [steps.html](#) or [new.html](#)

Configuring Galaxy | **Installing Tools**

Take an interactive tour: [Galaxy UI](#) | [History](#) | [Screenshot](#)

KaruBioNet

Galaxy is an open platform for supporting data intensive research. Galaxy is developed by The Galaxy Team with the support of many contributors.

History Panel (Right):

test

13 shown, All deleted

16.26 MB

43: Map with BWA-MEM on data.15, data.16, and data.14 (mapped reads in BAM format).	🔍	✏	✕
44: Map with BWA-MEM on data.15, data.16, and data.14 (mapped reads in BAM format).	🔍	✏	✕
18: Map with BWA-MEM on data.15, data.16, and data.14 (mapped reads in BAM format).	🔍	✏	✕
17: sequence.fasta	🔍	✏	✕
16: FC2_raw_R1.fasta	🔍	✏	✕
15: FC2_raw_R2.fasta	🔍	✏	✕
14: Reference.fasta	🔍	✏	✕
13: PhyML Stdout: phylo.conversion	🔍	✏	✕
12: PhyML Statistic: phylo.conversion.stats.txt	🔍	✏	✕
11: PhyML Newick tree: phylo.conversion.nwk	🔍	✏	✕
10: phylo.conversion	🔍	✏	✕
9: phylo.conversion.log	🔍	✏	✕
4: MUSCLE on data.2: log	🔍	✏	✕
3: MUSCLE on data.2: aligned_sequences	🔍	✏	✕

Barre
horizontale

The screenshot shows the Galaxy Tools menu. At the top, it says "Galaxy" and "Tools" with an upload icon. Below is a search bar labeled "search tools". The menu is organized into several sections: "Get Data", "Send Data", "Lift-Over", "Text Manipulation", "Filter and Sort", "Join, Subtract and Group", "Convert Formats", "Extract Features", "Fetch Sequences", "Fetch Alignments", "Get Genomic Scores", "Statistics", "Graph/Display Data", "Phenotype Association", "NGS TOOLBOX BETA", "NGS: QC and manipulation", "NGS: Mapping", "Assembly", "NGS: RNA analysis", "Multiple Alignments", "BLAST+", "Alignment", "SAM tools", "VCF tools", and "ValidateSamFile assess validity of SAM/BAM dataset".

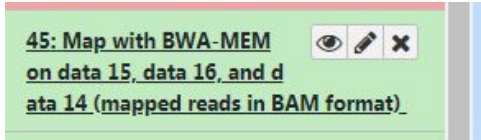
Menu de gauche (outils)

Espace de visualisation
principale

The screenshot shows the Galaxy History panel. At the top, it says "History" with refresh, settings, and window icons. Below is a search bar labeled "search datasets". The panel shows a list of datasets with the following details: "test", "20 shown, 46 deleted", and "117.99 MB". The list contains several entries, each with a red 'x' icon, a name, and a file type. The entries are: "65: MUSCLE on data 2: log.", "64: MUSCLE on data 2: aligned sequences.", "61: Prokka on data 1 7: log.", "60: Prokka on data 1 7: gff.", "45: Map with BWA-MEM on data 15_data 16_and data 14 (mapped reads in BAM format).", "44: Map with BWA-MEM on data 15_data 16_and data 14 (mapped reads in BAM format).", "18: Map with BWA-MEM on data 15_data 16_and data 14 (mapped reads in BAM format).", "17: sequence.fasta", "17: sequence.fasta", "16: RC2_raw R1.fastq", "15: RC2_raw R2.fastq", "14: Reference.fasta", and "13: PhyML Stdout: ph". Each entry has an eye icon, a pencil icon, and a red 'x' icon.

Menu de droite (historique)

Quelques fonctionnalités



Les outils liés à l'analyse lancée (dataset)

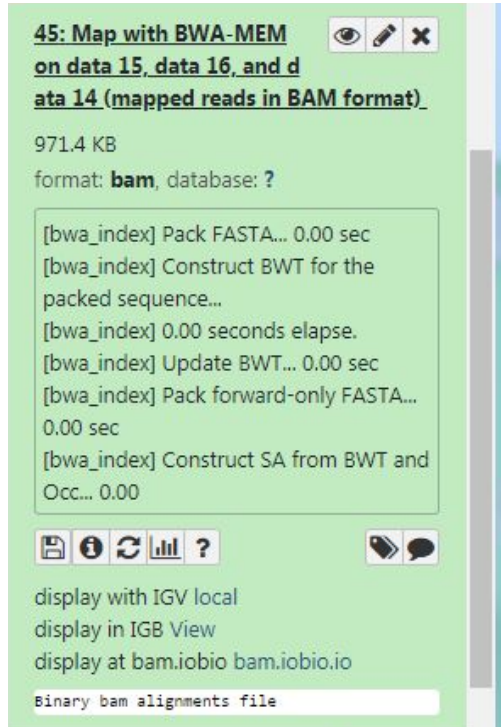





Visualiser sur l'espace principal

Éditer les attributs : nom,
référence/database, type,
outils de conversion ...

Supprimer

Quelques fonctionnalités










45: Map with BWA-MEM   

on data 15, data 16, and data 14 (mapped reads in BAM format)

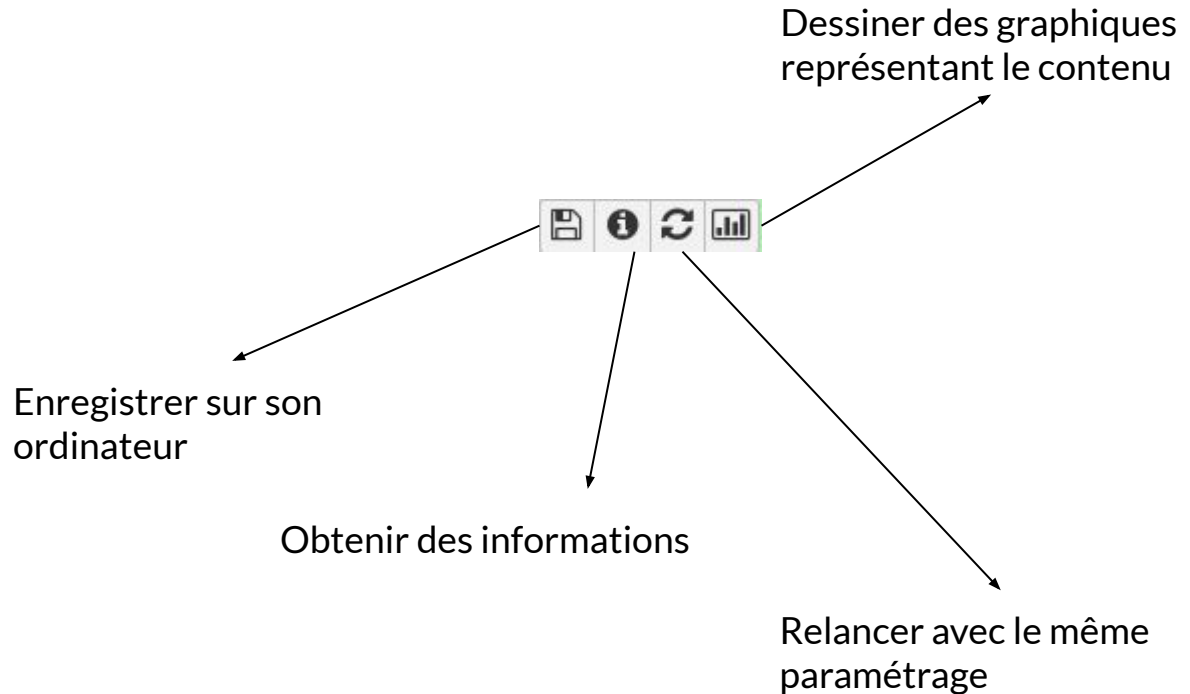
971.4 KB
format: **bam**, database: ?

```
[bwa_index] Pack FASTA... 0.00 sec  
[bwa_index] Construct BWT for the packed sequence...  
[bwa_index] 0.00 seconds elapse.  
[bwa_index] Update BWT... 0.00 sec  
[bwa_index] Pack forward-only FASTA... 0.00 sec  
[bwa_index] Construct SA from BWT and Occ... 0.00
```

display with IGV local
display in IGB View
display at bam.iobio bam.iobio.io

Binary bam alignments file



Merci pour votre attention!





Bibliographie

Galaxy project : <https://galaxyproject.org/>

Utiliser directement Galaxy : <https://usegalaxy.org/>

Publication récente : Afgan et al., 2016 (DOI:
<https://doi.org/10.1093/nar/gkw343>)

Exemples d'instance Galaxy:

- <http://galaxy.southgreen.fr/galaxy/>
- <https://galaxy.pasteur.fr/>

Vidéo d'exemple: <https://www.youtube.com/watch?v=3aVNAlIJ8sg>

Demonstration....