

# FAIR Bioinfo 2022

Best practice in your bioinformatic projects



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UNIVERSITÉ  
Clermont @uvergne



This work is based on the IFB and I2BC formation offer

## Essay

# Why Most Published Research Findings Are False

John P.A. Ioannidis

## Summary

There is increasing concern that most current published research findings are false. The probability that a research claim is true may depend on study power and bias, the number of other studies on the same question, and, importantly, the ratio of true to no relationships among the relationships probed in each scientific field. In this framework, a research finding is less likely to be true when the studies conducted in a field are smaller; when effect sizes are smaller; when there is a greater number and lesser preselection of tested relationships; where there is greater flexibility in designs, definitions, outcomes, and analytical modes; when there is greater financial and other interest and prejudice; and when more teams are involved in a scientific field in chase of statistical significance. Simulations show that for most study designs and settings, it is more likely for a research claim to be false than true. Moreover, for many current scientific fields, claimed research findings may often be simply accurate measures of the prevailing bias. In this essay, I discuss the implications of these problems for the conduct and interpretation of research.

factors that influence this problem and some corollaries thereof.

## Modeling the Framework for False Positive Findings

Several methodologists have pointed out [9–11] that the high rate of nonreplication (lack of confirmation) of research discoveries is a consequence of the convenient, yet ill-founded strategy of claiming conclusive research findings solely on the basis of a single study assessed by formal statistical significance, typically for a *p*-value less than 0.05. Research is not most appropriately represented and summarized by *p*-values, but, unfortunately, there is a widespread notion that medical research articles

## It can be proven that most claimed research findings are false.

should be interpreted based only on *p*-values. Research findings are defined here as any relationship reaching formal statistical significance, e.g., effective interventions, informative predictors, risk factors, or associations. “Negative” research is also very useful.

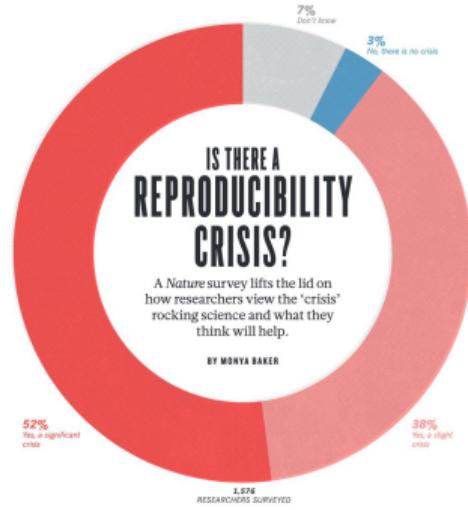
is characteristic of the field and can vary a lot depending on whether the field targets highly likely relationships or searches for only one or a few true relationships among thousands and millions of hypotheses that may be postulated. Let us also consider, for computational simplicity, circumscribed fields where either there is only one true relationship (among many that can be hypothesized) or the power is similar to find any of the several existing true relationships. The pre-study probability of a relationship being true is  $R/(R+1)$ . The probability of a study finding a true relationship reflects the power  $1-\beta$  (one minus the Type II error rate). The probability of claiming a relationship when none truly exists reflects the Type I error rate,  $\alpha$ . Assuming that *c* relationships are being probed in the field, the expected values of the  $2 \times 2$  table are given in Table 1. After a research finding has been claimed based on achieving formal statistical significance, the post-study probability that it is true is the positive predictive value, PPV. The PPV is also the complementary probability of what Wacholder et al. have called the false positive report probability [10]. According to the  $2 \times 2$  table, one gets  $PPV = (1 - \beta)R/(1 - \beta)R + \alpha(1 - R)$ .

## Crisis elements

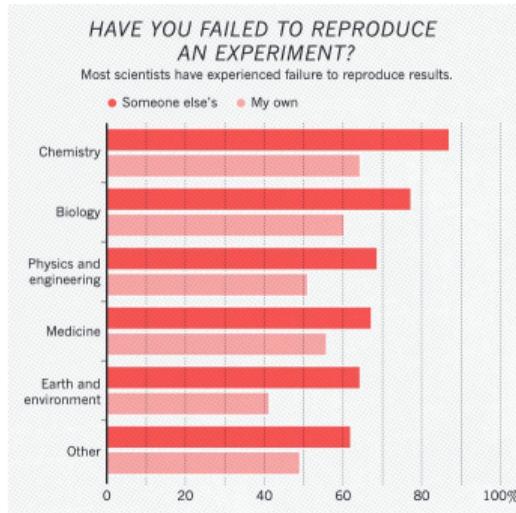
- Highlighted around 2005
- Since 2010 more articles related to the non reproducibility
- Medicine is one of the most impacted discipline

# Reproducibility crisis

2016

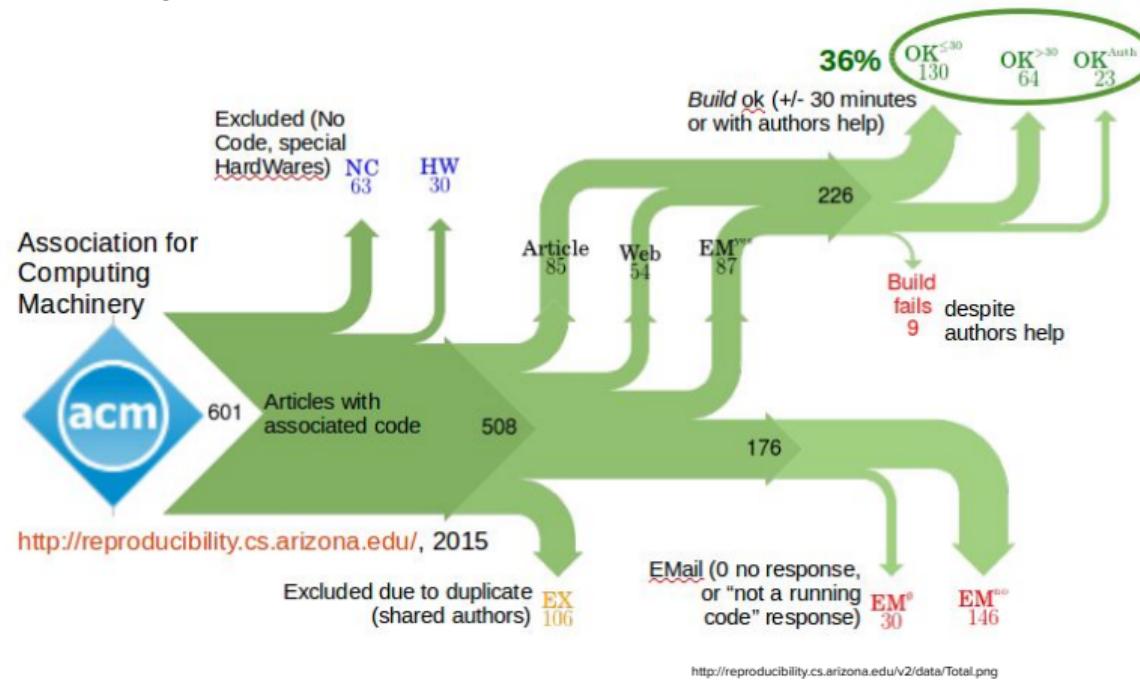


Baker, M. 1,500 scientists lift the lid on reproducibility. *Nature* 533, 452–454 (2016). <https://doi.org/10.1038/533452a>



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## Also in computer sciences



# Long term negative impact of retracted papers

Article	Year of retraction	Citing Articles before retraction	Citing Articles after retraction	Total cites (journals indexed by Web of Science)
1. Primary Prevention of Cardiovascular Disease with a Mediterranean Diet. N ENGL J MED; APR <b>2013</b> . Estruch R, et al.	2018	1919	816	2735
2. Ileal-lymphoid-nodular hyperplasia, non-specific colitis, and pervasive developmental disorder in children. LANCET; FEB 28 <b>1998</b> . Wakefield AJ, et al.	2010	642	867	1509
3. Visfatin: A protein secreted by visceral fat that mimics the effects of insulin. SCIENCE; JAN <b>2005</b> . Fukuhara A, et al.	2007	232	1192	1424
4. An enhanced transient expression system in plants based on suppression of gene silencing by the p19 protein of tomato bushy stunt virus. PLANT J; MAR <b>2003</b> . Voinnet O, et al.	2015	896	375	1271
5. Lysyl oxidase is essential for hypoxia-induced metastasis. NATURE; APR <b>2006</b> . Erler JT, et al.	2020	977	81	1058

Retraction Watch : Top 10 most highly cited retracted papers  
<https://retractionwatch.com/the-retraction-watch-leaderboard/top-10-most-highly-cited-retracted-papers/>

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# The consequences of a non FAIR practice

International Journal of Antimicrobial Agents 56 (2020) 105949

Contents lists available at ScienceDirect



International Journal of Antimicrobial Agents

journal homepage: [www.elsevier.com/locate/ijantimicag](http://www.elsevier.com/locate/ijantimicag)



Hydroxychloroquine and azithromycin as a treatment of COVID-19: results of an open-label non-randomized clinical trial <sup>☆</sup>

Philippe Gautret <sup>a,b,§</sup>, Jean-Christophe Lagier <sup>a,c,§</sup>, Philippe Parola <sup>a,b</sup>, Van Thuan Hoang <sup>a,b,d</sup>, Line Meddeb <sup>a</sup>, Morgane Mailhe <sup>a</sup>, Barbara Doudier <sup>a</sup>, Johan Courjon <sup>e,f,g</sup>, Valérie Giordanengo <sup>h</sup>, Vera Esteves Vieira <sup>a</sup>, Hervé Tissot Dupont <sup>a,c</sup>, Stéphane Honoré <sup>i,j</sup>, Philippe Colson <sup>a,c</sup>, Eric Chabrière <sup>a,c</sup>, Bernard La Scola <sup>a,c</sup>, Jean-Marc Rolain <sup>a,c</sup>, Philippe Brouqui <sup>a,c</sup>, Didier Raoult <sup>a,c,\*</sup>

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<sup>e</sup>Infectiologie Hôpital de l'Archet, Centre Hospitalier Universitaire de Nice, Nice, France

<sup>f</sup>Université Côte d'Azur, Nice, France

<sup>g</sup>U1065, Centre Méditerranéen de Médecine Moléculaire, C3RM, Virulence Microbienne et Signalisation Inflammatoire, INSERM, Nice, France

<sup>h</sup>Department of Virology, Biological and Pathological Center, Centre Hospitalier Universitaire de Nice, 06200 Nice, France

<sup>i</sup>Service Pharmacie Hôpital Timone, AP-HM, Marseille, France

<sup>§</sup>Laboratoire de Pharmacie Clinique, Aix Marseille Université, Marseille, France

## Citation score

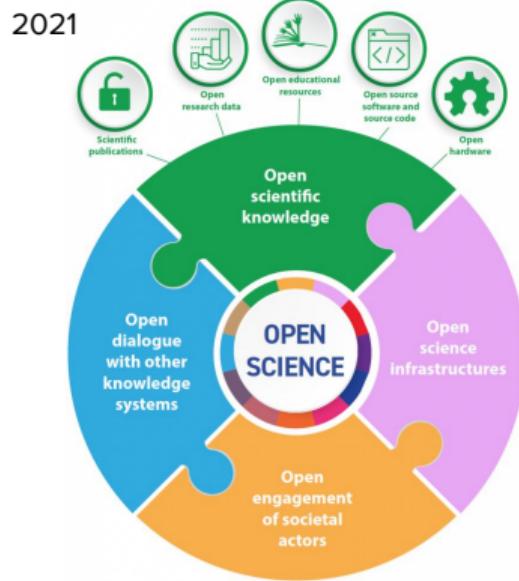
- 3522 citations (from journal)
- 6163 citation (from google)
- 66725 like, share and comments

## Social impact

- A part of the researchers focused on hydroxychloroquin
- Lost of time
- Lost of money
- scientific untruth

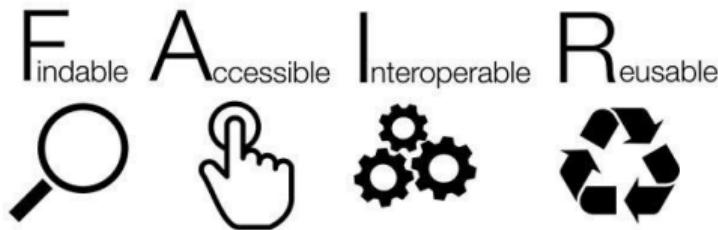
<https://doi.org/10.1016/j.ijantimicag.2020.105949>

# A way out: Open science and FAIR principles



Graphic on page 11. [UNESCO Recommendation on Open Science](#). CC BY IGO 3.0 C. Green

2016



Wilkinson, M., Dumontier, M., Aalbersberg, I. et al. The FAIR Guiding Principles for scientific data management and stewardship. *Sci Data* **3**, 160018 (2016).  
<https://doi.org/10.1038/sdata.2016.18>

By SangyaPundir - Own work, CC BY-SA 4.0, <https://commons.wikimedia.org/w/index.php?curid=53414052>

## FAIR history

- Born in 2016 with *The FAIR Guiding Principles for scientific data management and stewardship*
- How to build, stock, share, use and publish data
- Make criteria to better use our data

. <https://doi.org/10.1038/sdata.2016.18>

# SCIENTIFIC DATA

Amended: Addendum

OPEN

## SUBJECT CATEGORIES

- » Research data
- » Publication characteristics

Received: 10 December 2015

Accepted: 12 February 2016

Published: 15 March 2016

## Comment: The FAIR Guiding Principles for scientific data management and stewardship

Mark D. Wilkinson et al.<sup>#</sup>

There is an urgent need to improve the infrastructure supporting the reuse of scholarly data. A diverse set of stakeholders—representing academia, industry, funding agencies, and scholarly publishers—have come together to design and jointly endorse a concise and measurable set of principles that we refer to as the FAIR Data Principles. The intent is that these may act as a guideline for those wishing to enhance the reusability of their data holdings. Distinct from peer initiatives that focus on the human scholar, the FAIR Principles put specific emphasis on enhancing the ability of machines to automatically find and use the data, in addition to supporting its reuse by individuals. This Comment is the first formal publication of the FAIR Principles, and includes the rationale behind them, and some exemplar implementations in the community.

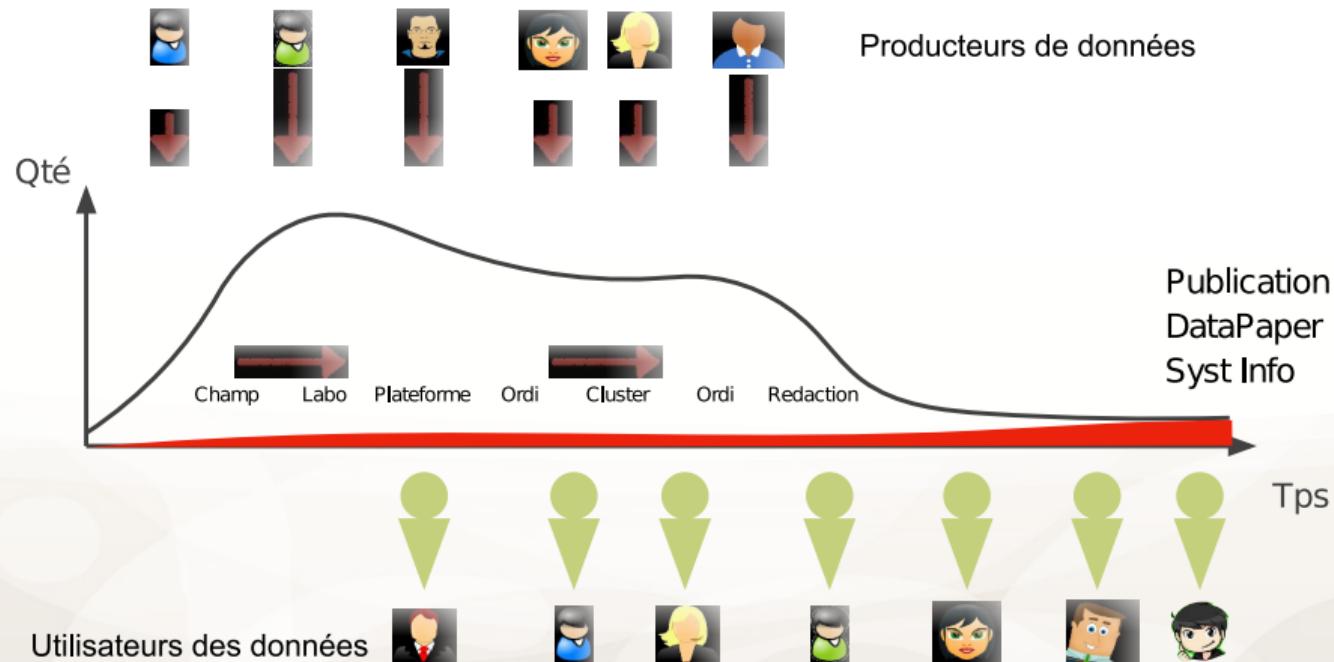
. <https://doi.org/10.1038/sdata.2016.18>

## Apply FAIR TO

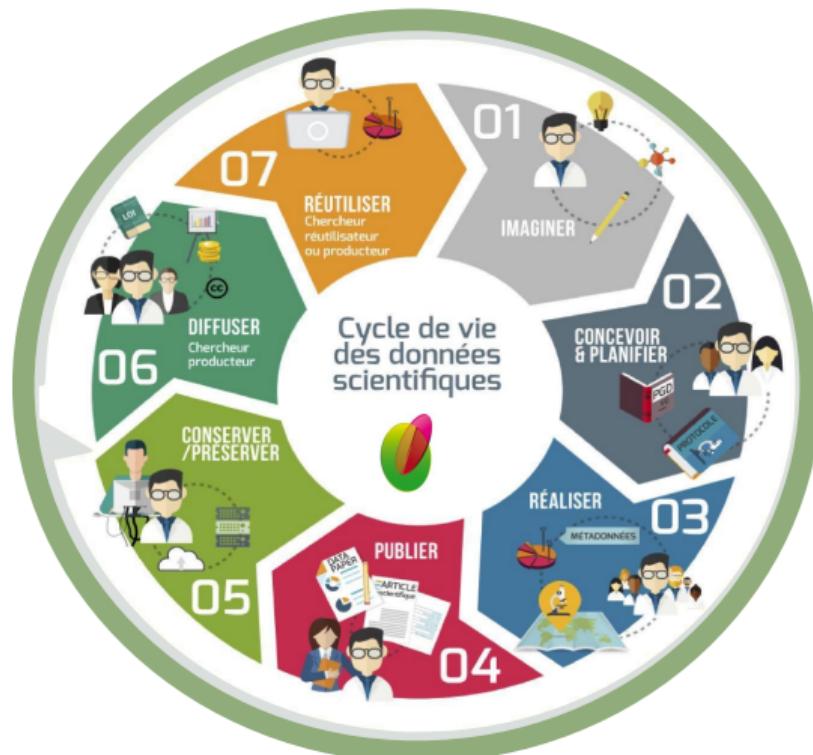
### ■ Your DATA

- Data lifecycle
- Data Management Plan (DMP)
- Metadata
- Data storage

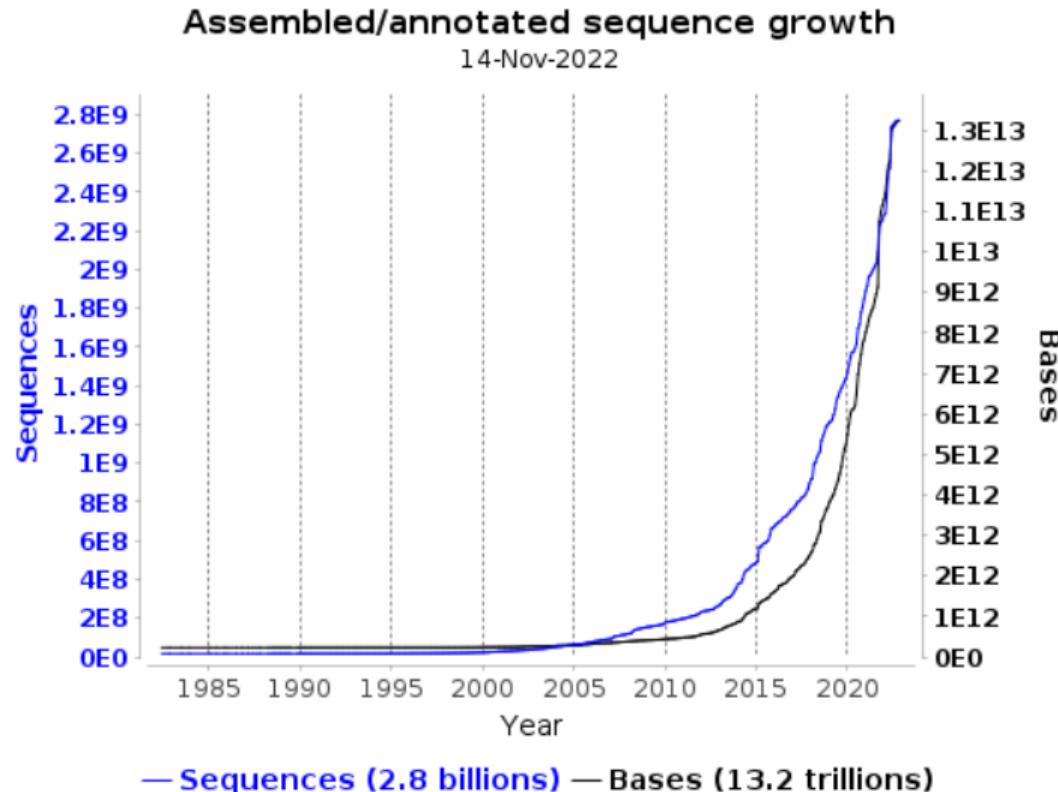
# Focus on the data lifecycle



# Focus on the data lifecycle



# Focus on the data lifecycle



<https://www.ebi.ac.uk/ena/browser/about/statistics>

# Focus on the data exchange

## Transfert de vos données de recherche



### Comment transmettre vos données ?





## Cost of not having FAIR research data

Cost-Benefit analysis for FAIR research data

## Apply FAIR TO

- Your DATA

- Data lifecycle
- Data Management Plan (DMP)
- Metadata
- Data storage

- Your scripts, environment...

- Objective of this training

# FAIR principles

F  
indable



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<https://commons.wikimedia.org/w/index.php?curid=88894774>

PID  
Repository

8

<https://doi.org/10.1038/sdata.2016.18>

# 404

This is not the  
web page you  
are looking for.



## To be Findable

- (meta)data are assigned a globally unique and persistent identifier
- data are described with rich metadata
- metadata clearly and explicitly include the identifier of the data it describes
- (meta)data are registered or indexed in a searchable resource

# FAIR principles

F  
indable



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<https://commons.wikimedia.org/w/index.php?curid=88894774>

A  
ccessible



<https://nitsfirstworldproblems.tumblr.com/post/147555650875/i-can-t-reach-the-top-shelves-of-the-kitchen>

PID  
Repository

Protocols  
(free, open, auth.)

9

<https://doi.org/10.1038/sdata.2016.18>

## To be Accessible

- (meta)data are retrievable by their identifier using a standardized communication protocol
- the protocol is open, free, and universally implementable
- the protocol allows for an authentication and authorization procedure, where necessary
- metadata are accessible, even when the data are no longer available

# FAIR principles

**F**indable



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<https://commons.wikimedia.org/w/index.php?curid=88894774>

**A**ccessible



<https://nitsfirstworldproblems.tumblr.com/post/147555650875/i-can-t-reach-the-top-shelves-of-the-kitchen>

**I**nteroperable



By Unknown author - Popular Science Monthly Volume 88, Public Domain  
<https://commons.wikimedia.org/w/index.php?curid=22614407>

PID  
Repository

Protocols  
(free, open, auth.)

Standards  
(format, vocabulary)

10  
<https://doi.org/10.1038/sdata.2016.18>

## To be Interoperable

- (meta)data use a formal, accessible, shared, and broadly applicable language for knowledge representation.
- (meta)data use vocabularies that follow FAIR principles
- (meta)data include qualified references to other (meta)data

# FAIR principles

**F**indable



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<https://commons.wikimedia.org/w/index.php?curid=88894774>

**A**ccessible



<https://nillsfirstworldproblems.tumblr.com/post/147555650875/i-can-t-reach-the-top-shelves-of-the-kitchen>

**I**nteroperable



By Unknown author - Popular Science Monthly Volume 88, Public Domain  
<https://commons.wikimedia.org/w/index.php?curid=22614407>

**R**eusable



By Sun Ladder - Own work, CC BY-SA 3.0,  
<https://commons.wikimedia.org/w/index.php?curid=5746428>

PID  
Repository

Protocols  
(free, open, auth.)

Standards  
(format, vocabulary)

Metadata  
License  
Origin

11  
<https://doi.org/10.1038/sdata.2016.18>

## To be Reusable

- (meta)data are richly described with a plurality of accurate and relevant attributes
- (meta)data are released with a clear and accessible data usage license
- (meta)data are associated with detailed provenance
- (meta)data meet domain-relevant community standard

# To be Reusable

## A point on the licences

- number different types of licences from proprietary to totally free AND open
- more than 50 different kinds
- No licence = authors' rights
- France = support for free and open data

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**Recherche dans GitHub par type de licence**

Vous pouvez filtrer les référentiels en fonction de leur licence ou famille de licences à l'aide du qualificateur `license` et du mot clé de licence exact :

Licence	Mot clé de licence
Academic Free License v3.0	afl-3.0
Licence Apache 2.0	apache-2.0
Licence Artistic 2.0	artistic-2.0
Licence logicielle Boost 1.0	bsl-1.0
Licence BSD « simplifiée » à 2 clauses	bsd-2-clause
Licence BSD « nouvelle » ou « révisée » à 3 clauses	bsd-3-clause

# To be Reusable

## A point on the licences

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The screenshot shows the homepage of the Joinup Licensing Assistant. At the top left is the European Commission logo. The top navigation bar includes links for "Interoperable Europe", "Interoperability Solutions", "Sign in", and "Get started". A search icon is also present. The main header features the text "Joinup Licensing Assistant" over a background of binary code. Below the header, there's a diagram illustrating the licensing process: a circular icon with a person head, a circular icon with a document and a star, a circular icon with a checkmark, and a circular icon with a folder labeled "Joinup Licensing Assistant". To the right of the diagram is a button labeled "SUBSCRIBE TO THIS SOLUTION". A small box indicates the topic is "EUPL". The bottom right corner features the logo of Université Clermont Auvergne.

# To be Reusable

## A point on the licences

- number different types of licences from proprietary to totally free AND open
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[Overview](#)

[Members](#)

[About](#)

[JLA - Compatibility Checker](#)

[JLA - Find and compare software licenses](#)

[REPORT ABUSIVE CONTENT](#)

A unique tool allowing everyone to compare and select open licences based on their content.

[Select licence terms below](#)

	Can	Must	Cannot	Compatible	Law	Support
Use/reproduce	Incl. Copyright	Hold liable	None N/A	EU/MS law	Strong Community	
Distribute	Royalty free	Use trademark	Permissive	US law	Governments/EU	
Modify/merge	State changes	Commerce	GPL	Licensor's law	OSI approved	
Sublicense	Disclose source	Modify	Other copyleft	Other law	FSF Free/Libre	

[Users' comments on the JLA](#)

[/ergne](#)

# To be Reusable

## A point on software archive

- Git-like (github, gitlab) are web services not archive
- Software are fragile

# To be Reusable

## A point on software archive

- Git-like (github, gitlab) are web services not archive
- Software are fragile

The screenshot shows the Software Heritage website. At the top, there is a navigation bar with links for Mission, Archive, Communauté, Grants, Soutien, A propos, and a search icon. The main header features the Software Heritage logo (a stylized orange and yellow starburst) and the text "Software Heritage". Below this, a sub-header reads "préserve le code source des logiciels, pour les générations actuelles et futures". To the right, there is a photograph of a modern library or archive interior with white bookshelves and a staircase. The central part of the page has a large red banner with the text "Nous construisons l'archive universelle des logiciels". At the bottom, there is a footer section with the Software Heritage logo and text about collecting and preserving software source code, followed by a "Collect Preserve Share" call-to-action.

Software Heritage

préserve le code source des logiciels, pour les générations actuelles et futures

Nous construisons l'archive universelle des logiciels

Collect  
Preserve  
Share

Nous collectons et préservons les logiciels sous forme de code source parce qu'ils sont le support indissociable des connaissances techniques et scientifiques de l'humanité tout entière et que nous ne pouvons pas prendre le risque de les perdre.

Nous conservons et rendons accessible tous les logiciels que nous collectons car c'est uniquement en les partageant que nous pouvons

UNIVERSITÉ Clermont Auvergne

# FAIR tools

**F**indable



**A**ccessible



**I**nteroperable



**R**eusable



Data

Software  
and  
analyses

[FAIRsharing.org](https://fairsharing.org)  
standards, databases, policies



**CeCILL**

# A complete integrated FAIR environment

The Galaxy project



# A complete integrated FAIR environment

The Galaxy project

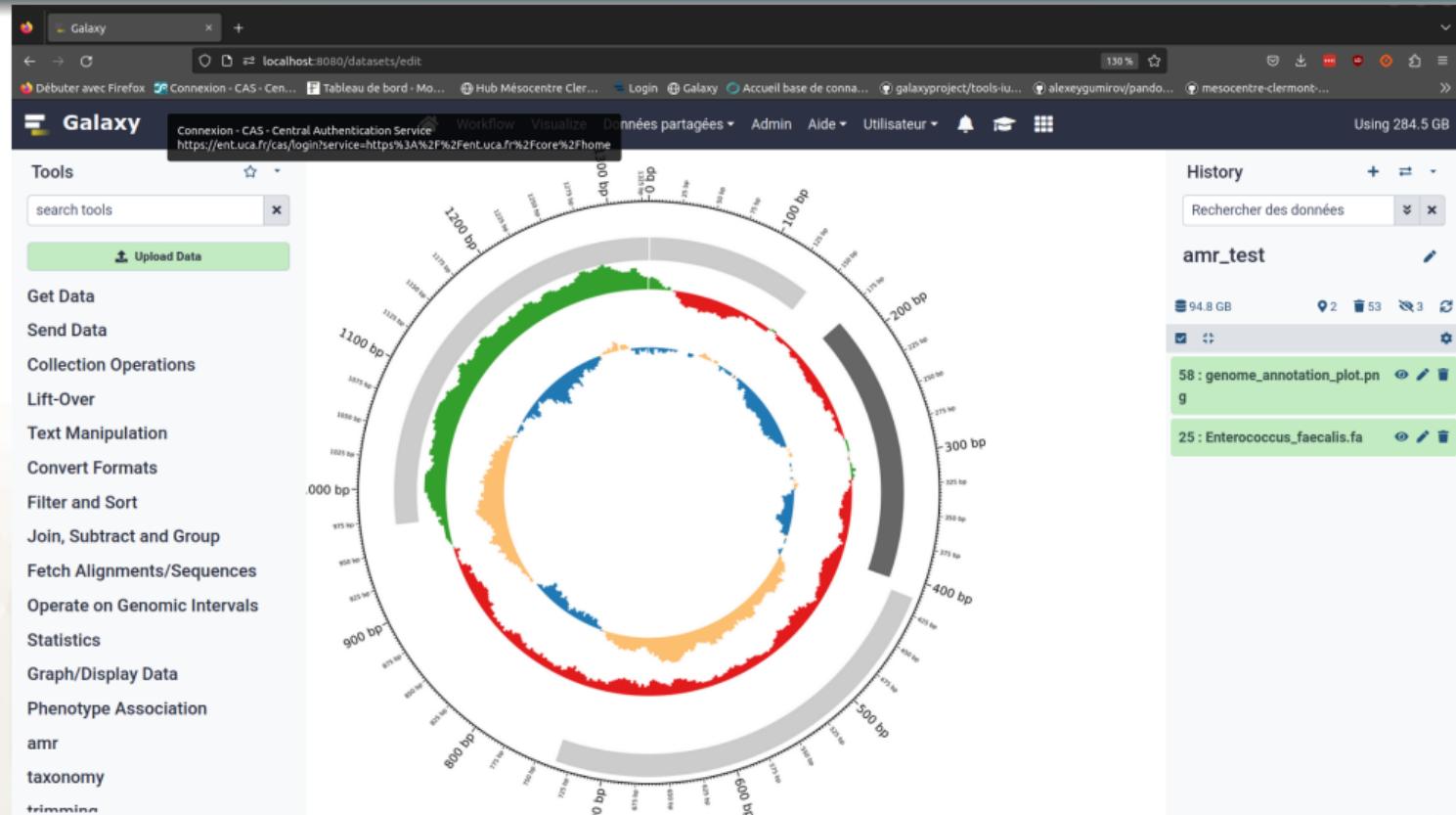
## Galaxy

Galaxy is an open-source platform for FAIR data analysis that enables users to :

- Use tools from various domains (that can be plugged into workflows) through its graphical web interface.
- Run code in interactive environments (RStudio, Jupyter...) along with other tools or workflows.
- Manage data by sharing and publishing results, workflows, and visualizations.
- Ensure reproducibility by capturing the necessary information to repeat and understand data analyses.

# A complete integrated FAIR environment

## The Galaxy project



# A complete integrated FAIR environment

## The Galaxy project

The screenshot shows the Galaxy web interface running on localhost:8080. The main panel displays a workflow titled "staramr" which scans genome assemblies against ResFinder, PlasmidFinder, and PointFinder databases for AMR genes. The workflow has a single step named "25: Enterococcus\_faecalis.fa". The interface includes a sidebar for "Tools" (blast), a "WORKFLOWS" section, and a "History" panel on the right containing "amr\_test" with files like "58 : genome\_annotation\_plot.png" and "25 : Enterococcus\_faecalis.fa". The "Advanced options" section at the bottom contains sliders for BLAST parameters: Percent identity threshold for BLAST (98.0), Percent length overlap of BLAST hit for ResFinder database (60.0), Percent length overlap of BLAST hit for PointFinder database (95.0), and Percent length overlap of BLAST hit for PlasmidFinder database (60.0).

# A complete integrated FAIR environment

## The Galaxy project

The screenshot shows the Galaxy web interface running a workflow titled "Workflow: abromics\_SR\_PE\_workflow". The workflow consists of nine steps:

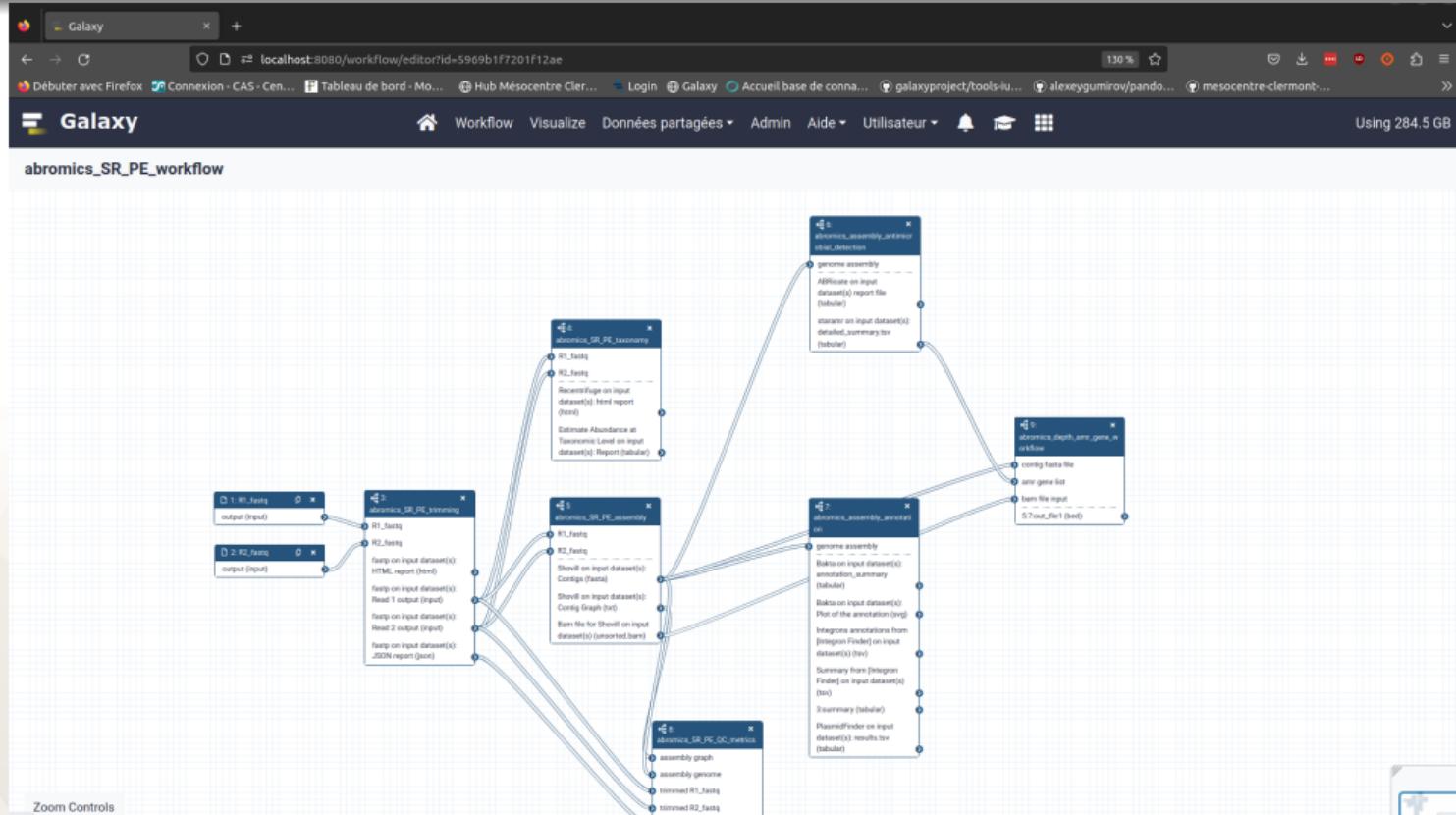
- 1: R1\_fastq
- 2: R2\_fastq
- 3: abromics\_SR\_PE\_trimming
- 4: abromics\_SR\_PE\_taxonomy
- 5: abromics\_SR\_PE\_assembly
- 6: abromics\_assembly\_antimicrobial\_detection
- 7: abromics\_assembly\_annotation
- 8: abromics\_SR\_PE\_QC\_metrics
- 9: abromics\_depth\_amr\_gene\_workflow

The "History" panel on the right shows a single history named "amr\_test" containing three items:

- 94.8 GB (9 items)
- 58 : genome\_annotation\_plot.png (1 item)
- 25 : Enterococcus\_faecalis.fa (1 item)

# A complete integrated FAIR environment

## The Galaxy project



# A FAIR approach at any level



*"One practice to rule them all, One practice to find them, One practice to bring them all and in the FAIR bind them."*

# A FAIR approach at any level



*"One practice to rule them all, One practice to find them, One practice to bring them all and in the FAIR bind them."*

## Improvement for who ?

At each level a good practice help you

- Long term efficiency to a bioinformatician
- stop wasting time for a beginner

# How to integrate FAIR concepts in my work ?

Some tools for reproducible research



# FAIR session with AuBi

## Objectives

- Discover FAIR practices
- Discover tools for best practices
- Learn tools and best practices

# FAIR session with AuBi

## Objectives

- Discover FAIR practices
- Discover tools for best practices
- Learn tools and best practices
- 5 sessions for courses and practices
  - Day 1 : Introduction to FAIR and building training environment
  - Day 2 : Code versioning with Git
  - Day 3 : Environment managment using conda and docker/singularity
  - Day 4 : Workflow managment using snakemake
  - Day 5 : Documentation using Rmarkdown or Jupyter

## Contents

- Introduction to FAIR practices

## Contents

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- Code control using Git 

  - Git environment
  - Gitlab and Github  

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## Contents

- Introduction to FAIR practices
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  - Conda environment and packages use 
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  - Reproducible workflow using snakemake 
- Literate programming and documentation
  - Markdown syntax 
  - Rmarkdown for R 
  - Jupyterlab for Python 

# Biosphere a virtual environment for training

The screenshot shows the login interface for the IFB Biosphere platform. At the top left is the IFB logo with the text "IFB Biosphere". To its right are links for "RAINBio", "myVM", and "DATA". On the far right are "Support", "[fr]", and "Se connecter". Below these, a "SE CONNECTER" button is visible. The main area features the IFB logo and the text "INSTITUT FRANÇAIS DE BIOINFORMATIQUE". A sub-instruction "Utilisez vos identifiants de votre organisme (CNRS, INRAE, Inserm, Universités...)" is followed by a "Se connecter" button. A note at the bottom states: "Nous utilisons la fédération d'identité européenne eduGAIN. Si votre organisme académique n'est pas dans cette fédération, vous pouvez utiliser un compte local avec votre adresse professionnelle.".



# Biosphere a virtual environment for training

The screenshot shows the IFB Biosphere homepage. At the top, there's a navigation bar with the IFB logo, "Biosphere", "RAINBio", "myVM", and "DATA". On the right side of the header, there are "Support" and user account icons. Below the header, a large blue banner says "WELCOME ON BIOSPHERE, IFB CLOUD FOR LIFE SCIENCES". Underneath the banner, a text block explains what Biosphere offers: "French Institute of Bioinformatics (IFB) provides life scientists with a federation of clouds, Biosphere, and bioinformatics cloud services to analyze life science data. Biosphere is used for scientific production in the life sciences, developments, and to support events like scientific training sessions, university courses, hackathons or workshops." A section titled "BIOSPHERE FEATURES" lists various capabilities, including a unified user portal, pre-defined environments, infrastructure as code, high availability, modular cloud environments, bring-your-own-tools, useful databases, and on-demand resources.

## BIOSPHERE FEATURES

With IFB-Biosphere, you get:

- A unified user portal ([Biosphere portal](#)) to deploy all bioinformatics environments on all clouds
  - Single sign-on, with your academic credentials ([Sign in](#)).
- Pre-defined bioinformatics environments, available with an one-click deployment from the [RAINBio catalogue](#)
- Infrastructure as Code: most configurations rely on public git repositories available in [Biosphere Commons](#).
- 8 cloud sites with more than 10,000 vCPU and 40 TB RAM ([System status](#))
  - High-availability thanks to the different sites usable equally.
- Modular cloud environments:
  - Single virtual machine (VM) to bunch of VMs.
  - Usual VM: up to 64 vCPUs-250 GB RAM.
  - BigMemory VM: up to 3 TB RAM.
  - HighFrequency VM : up to 3.8GHz vCPU.
  - ManyCores VM: up to 255 vCPUs in a VM
- Bring-Your-Own-Tools
  - Admin rights in the VM (all apps).
  - Deploy with your own container image (some apps).
  - Configure some apps with your own git repository (Infrastructure as Code).
- Useful public biological reference databases
- On-demand resources (CPU, RAM, storage, IFB experts) to support:
  - Training events, university courses, scientific schools, workshops, hackathons.
  - Scientific projects.

## BIOSPHERE PORTAL

The Biosphere portal provides high-level cloud interfaces:

# Biosphere a virtual environment for training

**IFB Biosphère RAINBio myVM DATA Support pierre.marin@uca.fr (edu) GAIN**

## RAINBIO - APPLIANCES BIOINFORMATIQUES DANS LE CLOUD

Catalogue des appliances bioinformatiques dans le cloud, filtrez-les en utilisant les termes présents dans l'ontologie EDAM, ou en langage naturel.

**App Store (59)** Appliances Outils Topics

<b>Galaxy</b> bioconda, Docker, Galaxy portal Informatics, Bioinformatics, Comparative genomics, Functional genomics	<b>AnalysesSV</b> bcftools, BEDTools, BWA, Jupyter, Matplotlib, pandas, SAMtools DNA polymorphism, Genetic variation, Genotyping experiments, GWAS analysis	<b>ANF MetaBioDiv</b> Bioconductor, DESeq2, devtools (R), ggplot2, gridExtra, phyloseq, r Bioinformatics, Computational biology, Data management, Taxonomy	<b>Askomics</b> AskOmics Data integration and warehousing, Data visualisation	<b>BactComparativeGenomics</b> ImageJ2, Jupyter, MACS2, Matlab, Nextflow, pandas, Prokka Imaging, Mathematics, Statistics and probability, CHP-seq, Workflows, Data archiving	<b>Bacterial Genomics</b> HMMER, Insygh, SGE - GridEngine, Ubuntu, Web interface Protein folds and structural domains, Sequence comparison, Sequence composition, comparative
<b>Bioimage</b> Bureau virtuel, Icy, ImageJ-Fiji, X2Go, Xfce Informatics, Data visualisation, OF, Imaging	<b>BioPipes</b> bioconda, cwltool, Docker, Nextflow, Snakemake Informatics, Bioinformatics, Workflows	<b>bistor</b> bioconda, Bowtie2, FastQC, Snakemake Bioinformatics, Genomics, Mapping, Sequence alignment, Data quality management	<b>CentOS 7</b> Ansible, bioconda, Docker Informatics, Bioinformatics	<b>CentOS 7 Desktop</b> Ansible, bioconda, Bureau virtuel, Docker Informatics, Bioinformatics	<b>CoursAnalysesNanoporeSG</b> bandage, Jupyter Data architecture, analysis and design, Mathematics, Statistics and probability
<b>Cytoscape</b> Bureau virtuel, Cytoscape, X2Go, Xfce Bioinformatics, Data visualisation, Molecular interactions, Pathway	<b>Debian 10</b> Ansible, bioconda, Docker Bioinformatics, Informatics	<b>Debian 11</b> Ansible, bioconda, Docker Bioinformatics, Informatics	<b>DRomics</b> Bioconductor, DESeq2, DRomics, R - base, RStudio, Shiny Bioinformatics, Computational biology, Data management, Taxonomy	<b>DRomicsInterpreter</b> Bioconductor, DESeq2, DRomics, R - base, RStudio, Shiny Bioinformatics, Computational biology, Data management, Taxonomy	<b>EBAME-2022 oDNA</b> BAMtools, BEDTools, bioconda, Bowtie2, metaDMG-cpp, python3, R Data management, Bioinformatics, Sequence alignment, Computer science, Sequencing
<b>EBAME-2022 MetaTOR</b> Bowtie2, CheckM, hicstrix, Pairix, SAMtools Sequence alignment, Phylogenetics, Population genomics	<b>EBAME-Anvio</b> Anvio	<b>EBAME-Quince</b> bam-readcount, BEDTools, BWA, CONCOCT, DESeq2, Diamond, FastQC Transcriptomics, Informatics	<b>ETBII AnalyseMultivariée</b> BioCStyle, Butcher, clusterProfiler, ComplexHeatmap, DESeq2, DT Literature and language, Transcriptomics	<b>ETBII Réseaux</b> BINGO (Cytoscape), Bureau virtuel, compositions (R), Cytoscape, igraph, Networkx Transcriptomics, Sequencing	<b>formation_CIRI</b> DESeq2, FastQC, HISAT2, RStudio, Trimomatic Transcriptomics, Whole genome sequencing

# Biosphere a virtual environment for training



**Biosphere**

RAINBio myVM DATA

[Support](#)

## VOS PARAMÈTRES

**Informations personnelles**

Adresse électronique	pierre.marin@uca.fr
Affiliation fournie par la fédération d'identité	
Prénom	Pierre
Nom	MARIN
Ville et code postal	63170
Formation initiale (optionnel)	<ul style="list-style-type: none"> <li>• Biology</li> <li>• Computer Science</li> </ul>
Pubkey	<ul style="list-style-type: none"> <li>• ssh-rsa AAAAAB3NzaC1yc2EAAAQABAAQDXgGQYRHqk4klU6XoeNqYVFqL14F5WkO3U2xSCDDQW8MpVQTCRqbzTq02GpIMF6014Q0gnC5-W-bTTJkZgnsigSziViug31MOdviZHj8oWKXW6c0TZ1InMrj0wjbgbUBdB7RApTmHL4Laihvz/EdtIASOTbKAQMLBtm4k3uL7l2RvFMdZcYVTKSbvcilEGShw8OHOHrclNEW3giiCIIUFSTZ5KEZ99/4KgarJRNcIXybzza+mtYGETfIQhJkyRD+R6DNrhvU8aJaagGpPdPwT/9ARVs9/avoF7e0JMUUdxWT9D139EPe44ony/s3k93HK4mpqGV piemari@hplogin01</li> <li>• ssh-rsa AAAAAB3NzaC1yc2EAAAQABAAQDXgGQCFgYeYkm6YwmhKbf+mcckwcqzJVBGvRTgZwfhGWeWwfLyJsgDM9fWV+4ZucxtXLrxja69d9r2309E+IdUDoFYRvVbLiQhX9X472DqbZ2duuDHvpVKtgYaAtK4rjhjhih32VuxSq7HeffrV5csTTbPJhunCTEsMIGLNVGH5rLjCwI-WtDVvaHYCdse2:YRAJeFsqAHtubRQucE2EPKpqRixzS5cg8q2T3kdiYjaquOvCvQBlzswfkNyvQldg38LMf4JDqOW26ls7WEtavMD1X3EKUEmxm+TldNoc1hnNjgg8XEN/h</li> </ul>

Connecté.e en tant que pierre.marin@uca.fr

Langues

[en] English

[fr] Français

**Paramètres**

Groups

Quota

Se déconnecter

<https://biosphere-france.bioinformatione.fr/cloudweb/account/settings/>

# SSH key use

## The principle

- Secure Shell (SSH)
- Securized protocol
- Encryption of informations between users
- Authentification without password
- Assymetric system based on keys

## The keys

- Paired key based
- A public key for everyone to share
- A private key for myself (never share)

# Installing a bash terminal

Git bash for non unix user



--distributed-even-if-your-workflow-isnt



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GUI Clients

Logos

[Community](#)

The entire [Pro Git book](#) written by Scott Chacon and Ben Straub is available to [read online for free](#). Dead tree versions are available on [Amazon.com](#).

## Downloads



macOS



Windows



Linux/Unix

Older releases are available and the [Git source repository](#) is on GitHub.

### GUI Clients

Git comes with built-in GUI tools ([git-gui](#), [gitk](#)), but there are several third-party tools for users looking for a platform-specific experience.



Latest source Release  
**2.40.0**

[Release Notes \(2023-03-12\)](#)

[Download for Linux](#)

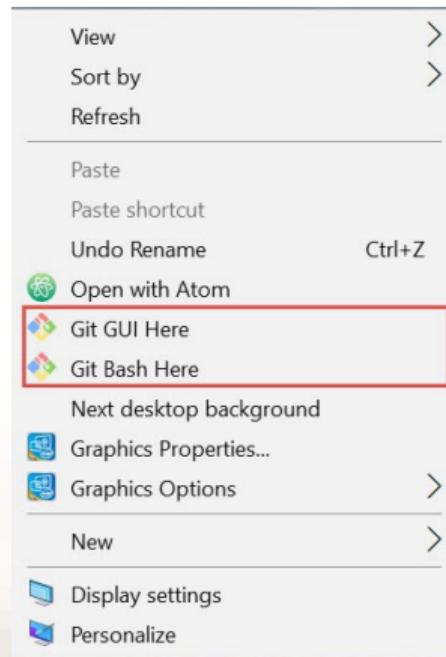
### Logos

Various Git logos in PNG (bitmap) and EPS (vector) formats are available for use in online and print projects.

[View Logos →](#)

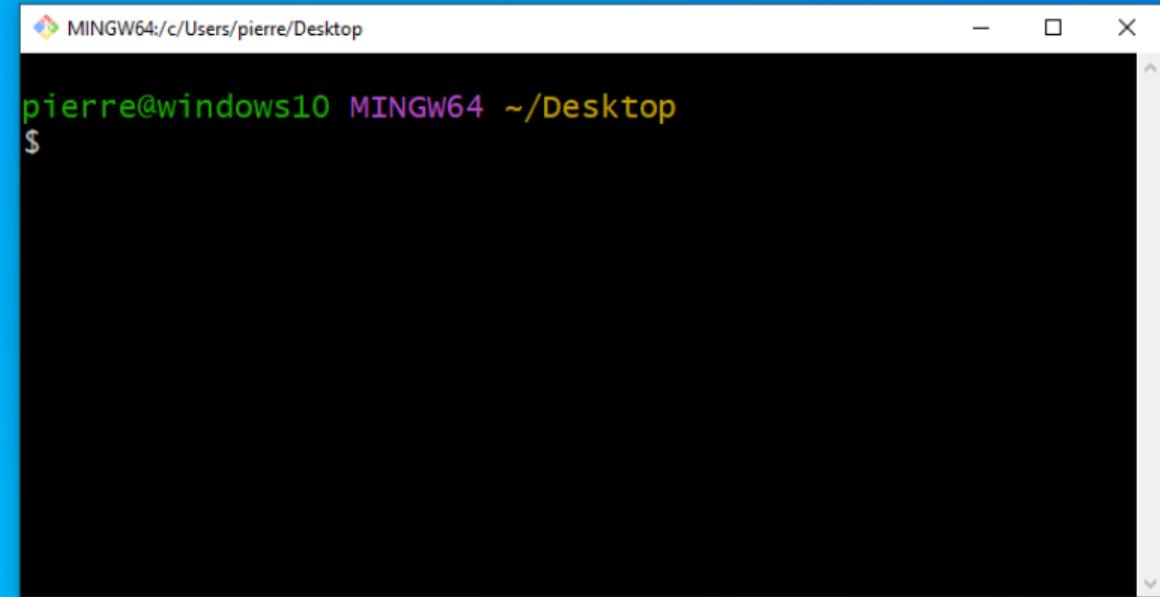
# Installing a bash terminal

Git bash for non unix user



# Installing a bash terminal

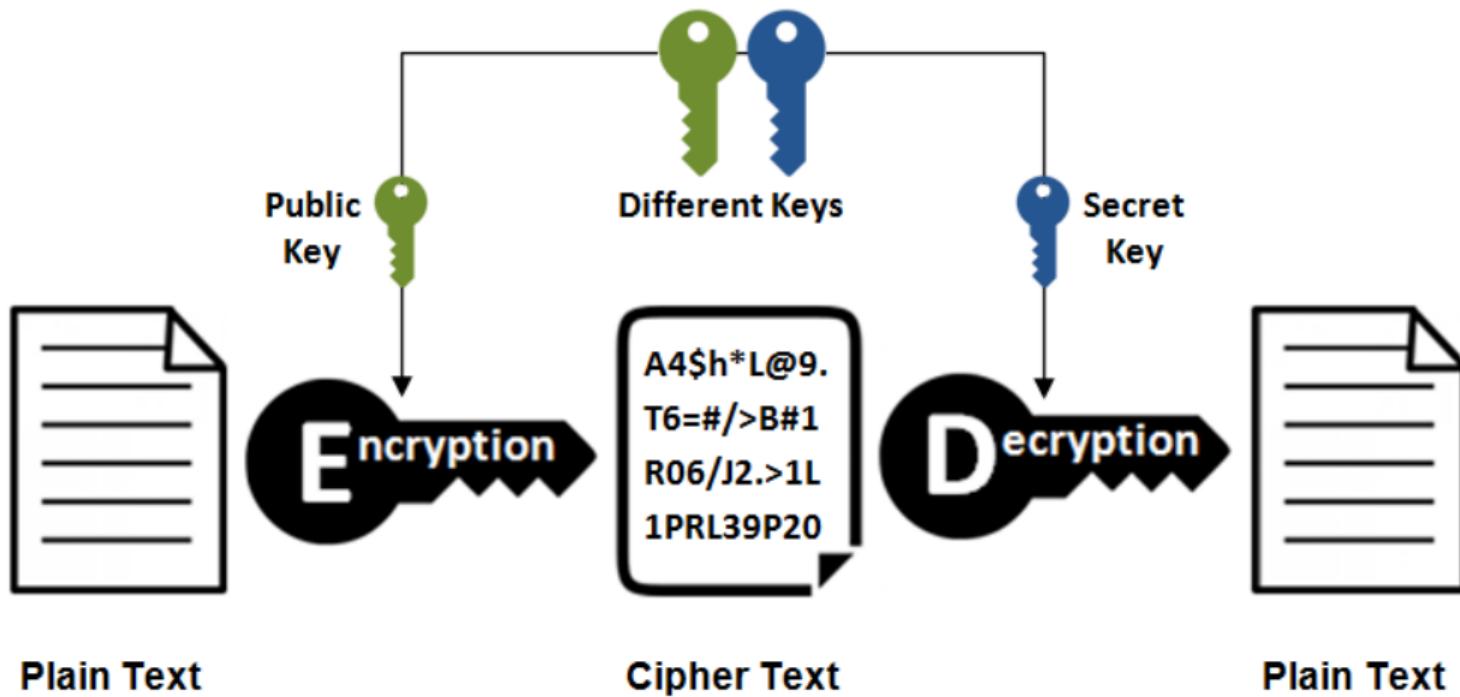
Git bash for non unix user



```
MINGW64:c/Users/pierre/Desktop
pierre@windows10 MINGW64 ~/Desktop
$
```

# SSH key use

## Asymmetric Encryption



Plain Text

Cipher Text

Plain Text

# SSH key use

```
ssh-keygen -t dsa
```



# SSH key use

```
ssh-keygen -t dsa
```

```
$ ssh-keygen -t dsa
```

Generating public/private dsa key pair.

Enter file in which to save the key (/Users/tdd/.ssh/id\_dsa): /Users/tdd/.ssh/id\_dsa\_

Enter passphrase (empty for no passphrase):

Enter same passphrase again:

Your identification has been saved in /Users/tdd/.ssh/id\_dsa\_ga.

Your public key has been saved in /Users/tdd/.ssh/id\_dsa\_ga.pub.

The key fingerprint is:

65:31:7e:ee:49:3a:66:cd:92:7b:02:2b:bf:b3:1a:79 tdd@CodeMagic.local

The key's randomart image is:

+--[ DSA 1024]----+

```
 |          |
 |          o   |
 |         . o  |
 |         + .  |
 |         o o  |
 |           S  o |
 |             o  |
```

# SSH key use

```
cat /home/pierre/.ssh/id_dsa_ga
```

# SSH key use

```
cat /home/pierre/.ssh/id_dsa_ga
```

```
$ cat ~/.ssh/id_dsa_ga
-----BEGIN DSA PRIVATE KEY-----
Proc-Type: 4,ENCRYPTED
DEK-Info: DES-EDE3-CBC,6ED59B013D8A361F
pB5eHHpvXxoz6i1jFz1KANv9W6SeHw664PV/1A90acR/Mw/ERQvTQKo3TaLaFhkb
NwhQFyxZZty2hn6xrv5UIAGTpjk+P2+waRmSno1Vg1x0epCp45kvFRv9AiXs0pt4
RgzPC5+a6kjPf8EtyozGoQ==
-----END DSA PRIVATE KEY-----
```

```
cat /home/pierre/.ssh/id_dsa_ga.pub
```

```
$ cat ~/.ssh/id_dsa_ga.pub
ssh-dss AAAAB3NzaC1kc3MAAACBAJhbQcZK81FMvpw7trbFj51Sqjd9nKBu2xkw/kvUAQ1PQPaIRL0iq92fx
```