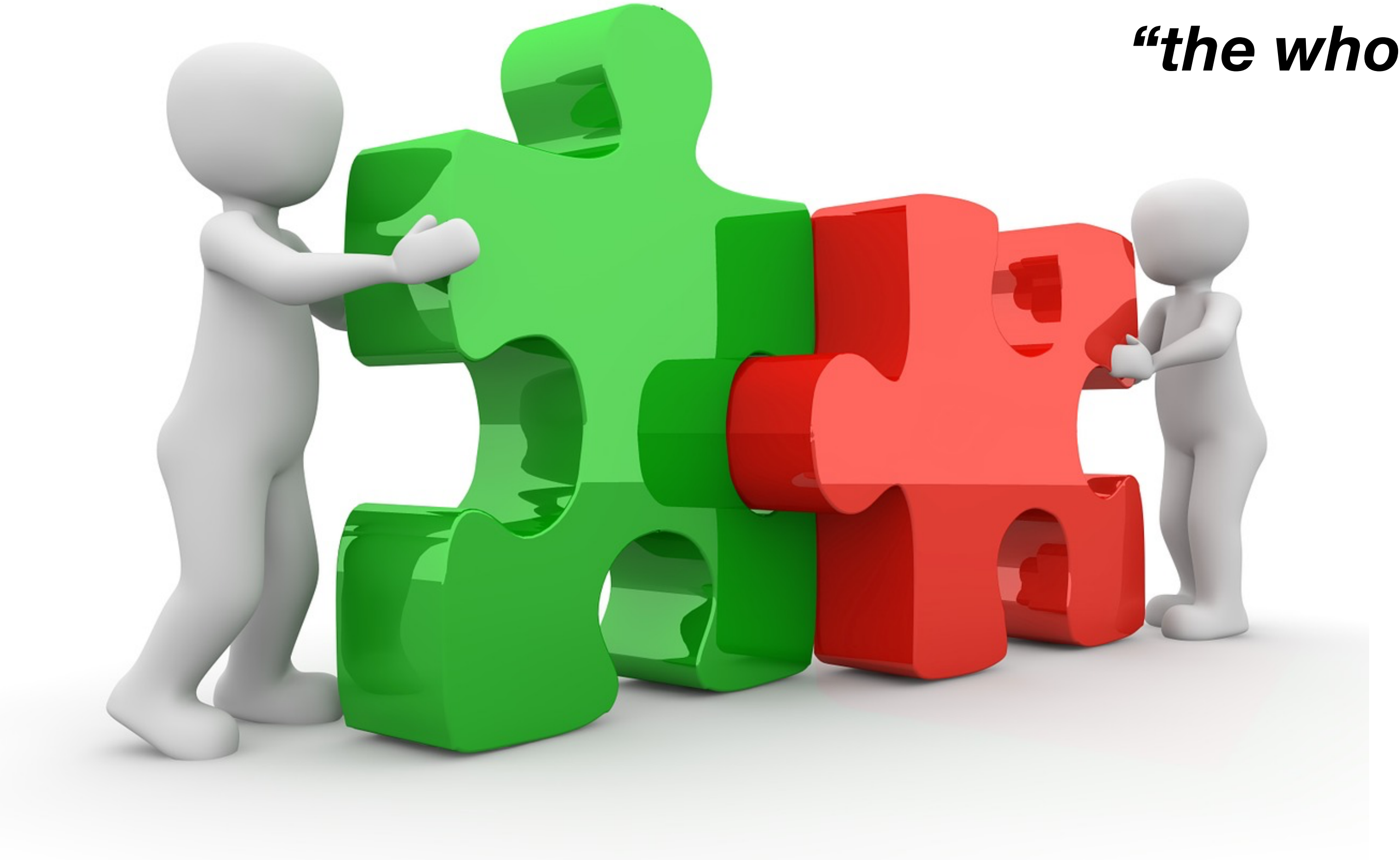
NBIS
NATIONAL BIOINFORMATICS INFRASTRUCTURE SWEDEN

SciLifeLab

Stockholm University

# Interdisciplinary collaboration

***"the whole is greater than the sum of its parts"***
~ *Aristotele*



Olga Dethlefsen
olga.dethlefsen@nbis.se

# Introduction: talking from experience

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*Can I ask you a question? I'm trying to understand the results of this copy number variations analysis and I'd thought I would ask you as you have been working with EVERYTHING (~ NBIS colleague)*

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MSc internship, FR

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KI, Sweden & RIKEN, Japan

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Medical Statistician, Oxford, UK

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- at NBIS since 2015
- "bioinformatics expert"
- 40+ projects
- across multiple omics
- medical focus

# Introduction: session’s aim

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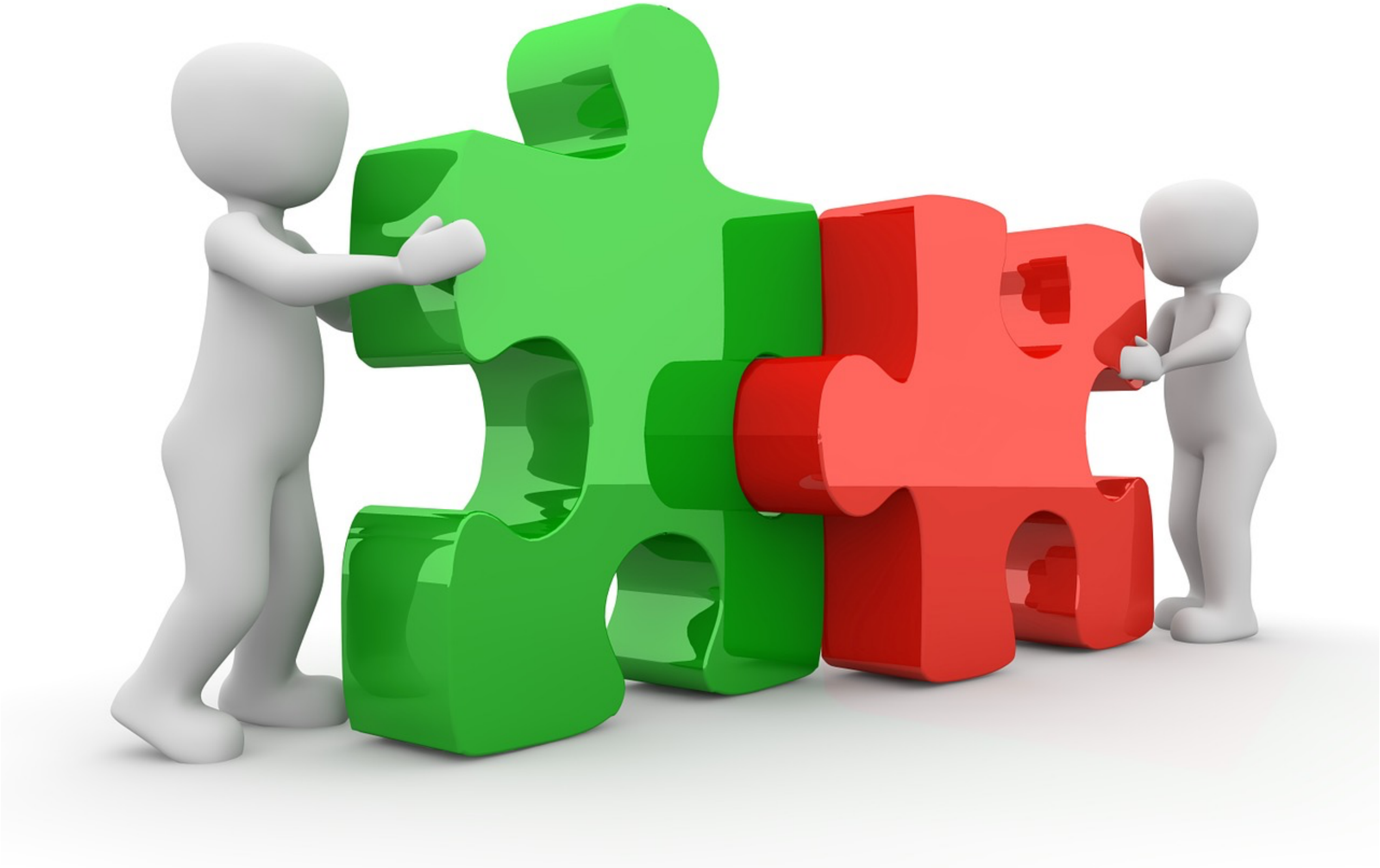

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Show,
don’t tell

- to highlight and discuss some of the collaboration aspects worth thinking about

- to introduce “reproducibility” concepts covered more in day 2

- to prepare a first draft of a “Good collaboration checklist”

# Introduction: theory

**https://docs.google.com/document/d/1MpefgEuklXooeo86Q5bX_wjD4RQxMHT9OlY1jEQA2q4/edit?usp=sharing**

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***“the act of working together with other people or organisations to create or achieve something“***

*– Cambridge Dictionary*

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- **trust**
- **attachment**
- **clarity and alignment**
- **speed**
- **technology, geography and culture**

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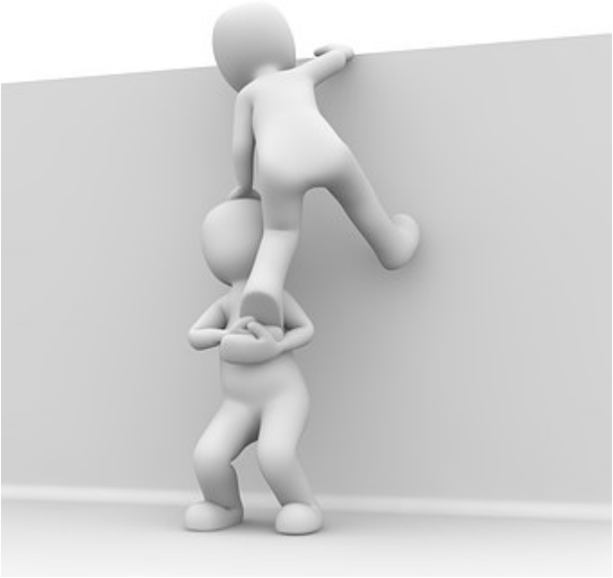
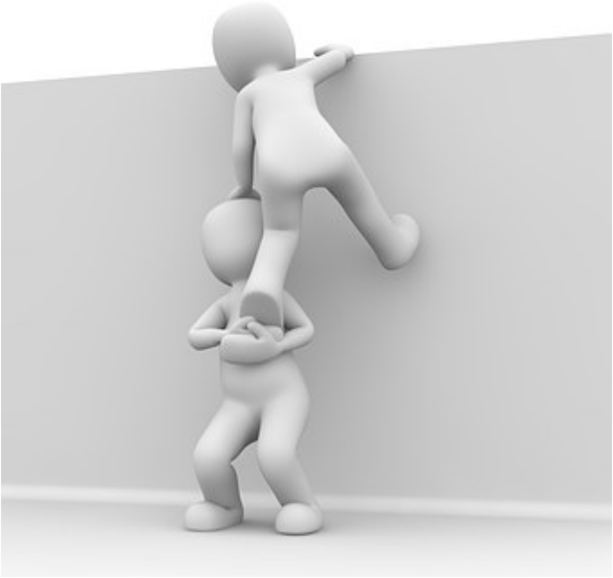
- **diversity**
- **speed**
- **engagement**
- **productivity**



## Alignment on a collective goal

- missing details
- conflicting incentives
- conflicting prioritisation
- conflict avoidance



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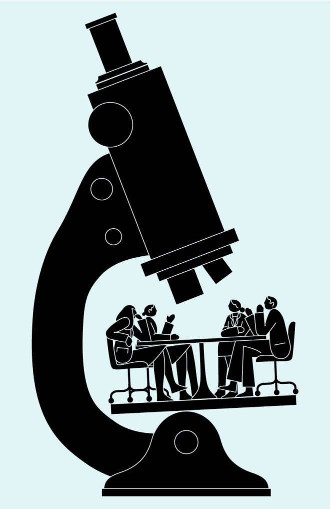
## Team players

- core team
- others joining as needed
- roles and responsibilities
  - e.g. facilitators, evaluators
  - e.g. coordinators, communicators
- engage leadership support
- setting the team for success



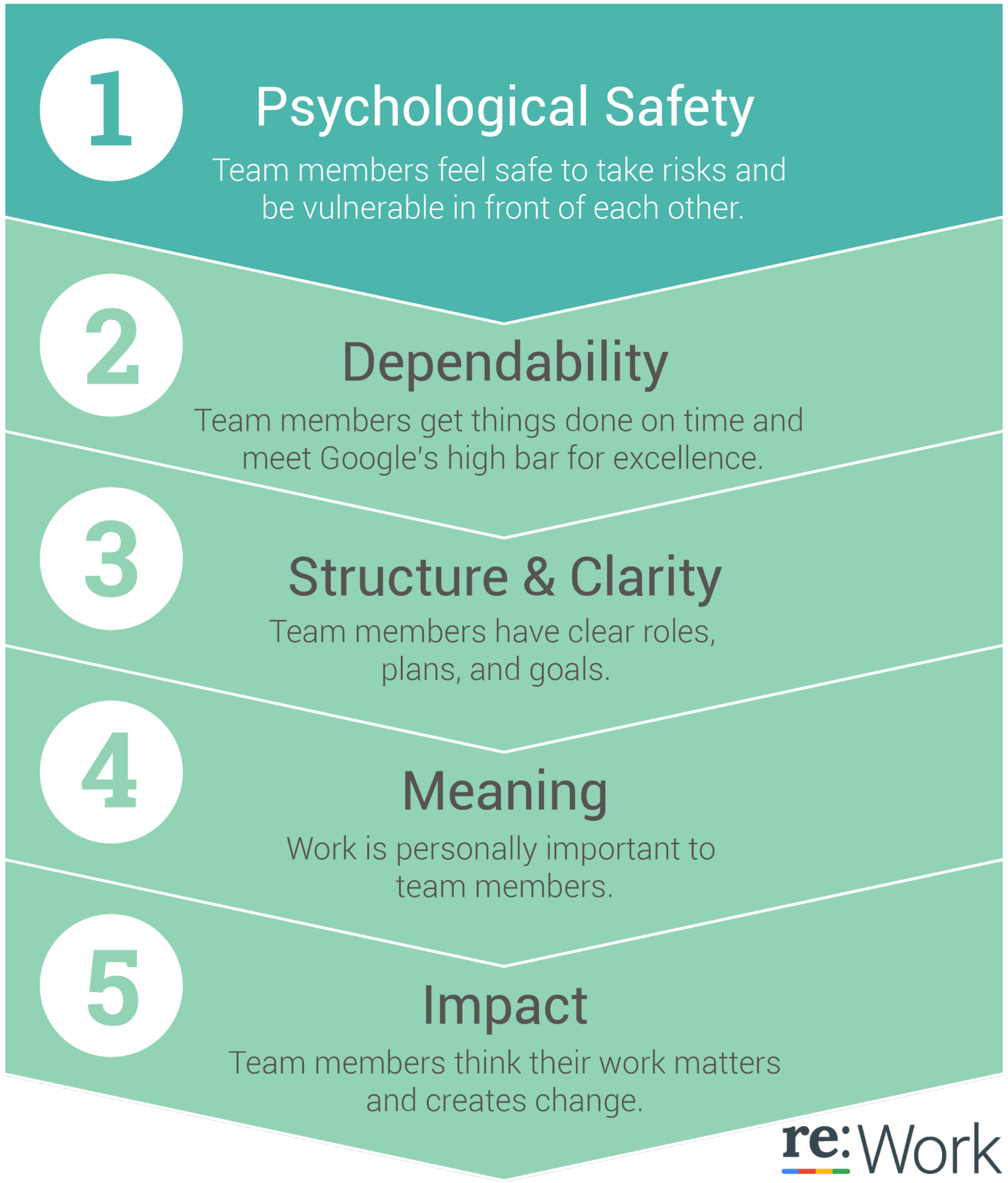
Google

THE WORK ISSUE

# What Google Learned From Its Quest to Build the Perfect Team

New research reveals surprising truths about why some work groups thrive and others falter.

- Equality of distribution of conversational turn-talking
- Highly average social sensitivity



1 Psychological Safety
Team members feel safe to take risks and be vulnerable in front of each other.

2 Dependability
Team members get things done on time and meet Google's high bar for excellence.

3 Structure & Clarity
Team members have clear roles, plans, and goals.

4 Meaning
Work is personally important to team members.

5 Impact
Team members think their work matters and creates change.

re:Work

https://rework.withgoogle.com/print/guides/5721312655835136/

https://www.nytimes.com/2016/02/28/magazine/what-google-learned-from-its-quest-to-build-the-perfect-team.html?smid=pl-share

## Project management main steps

- ☑ defining project
- ☑ listing tasks
- ☑ estimate times and costs
- ☑ assess risk and prepare action plans
- ☑ monitor progress & costs
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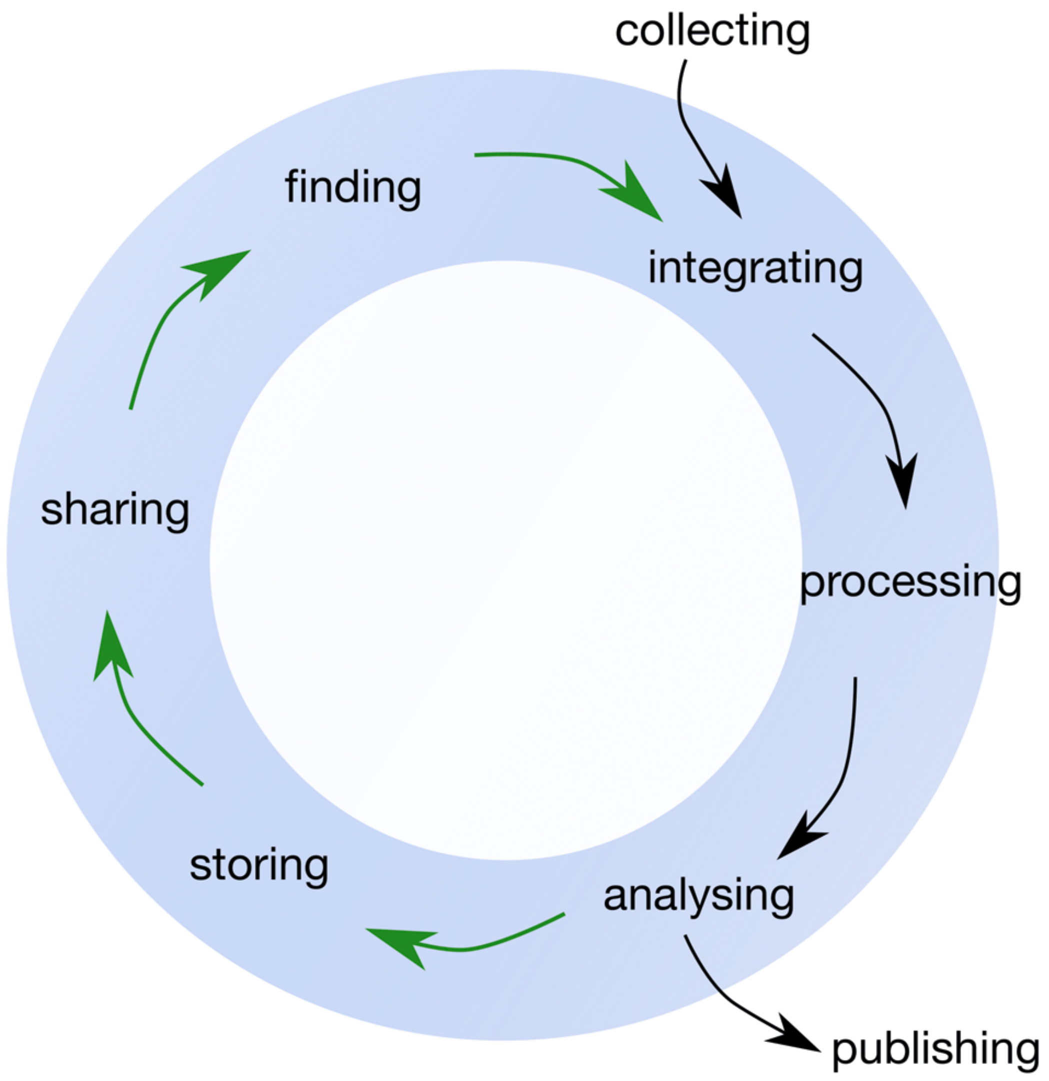
**Simplified Data Life Cycle framework for bioscience, biomedical and bioinformatics data**



Griffin PC, Khadake J, LeMay KS et al. Best practice data life cycle approaches for the life sciences [version 2; peer review: 2 approved]. F1000Research 2018, 6:1618 (https://doi.org/10.12688/f1000research.12344.2)

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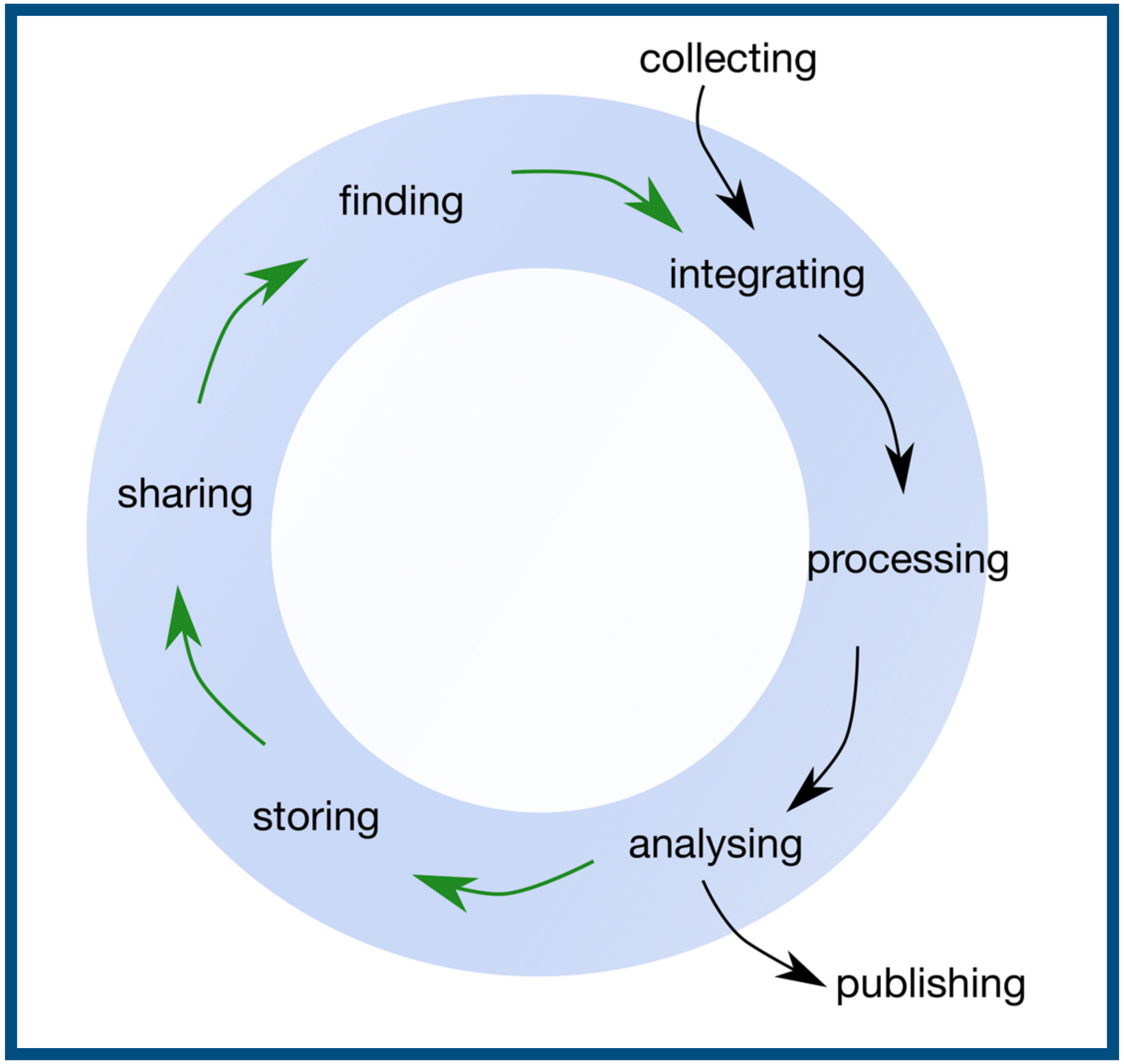
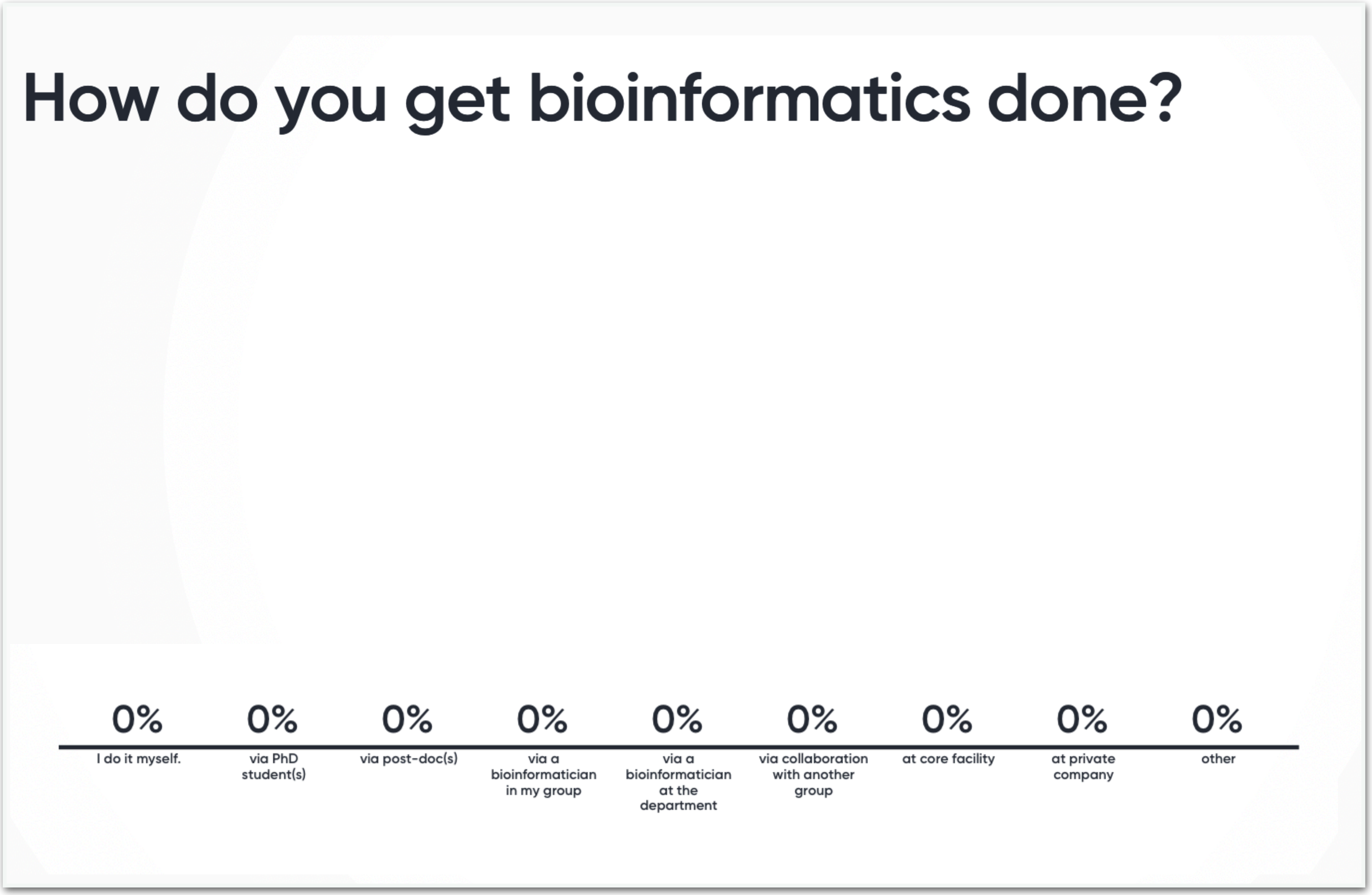


**potential bioinformatics needs**

Griffin PC, Khadake J, LeMay KS et al. Best practice data life cycle approaches for the life sciences [version 2; peer review: 2 approved]. F1000Research 2018, 6:1618 (https://doi.org/10.12688/f1000research.12344.2)

Go to www.menti.com and use the code 50 54 91



How do you get bioinformatics done?

0%
I do it myself.
0%
via PhD student(s)
0%
via post-doc(s)
0%
via a bioinformatician in my group
0%
via a bioinformatician at the department
0%
via collaboration with another group
0%
at core facility
0%
at private company
0%
other

https://docs.google.com/document/d/
1MpefgEukIXooeo86Q5bX_wjD4RQxMHT9OIY1jEQA2q4/edit?usp=sharing

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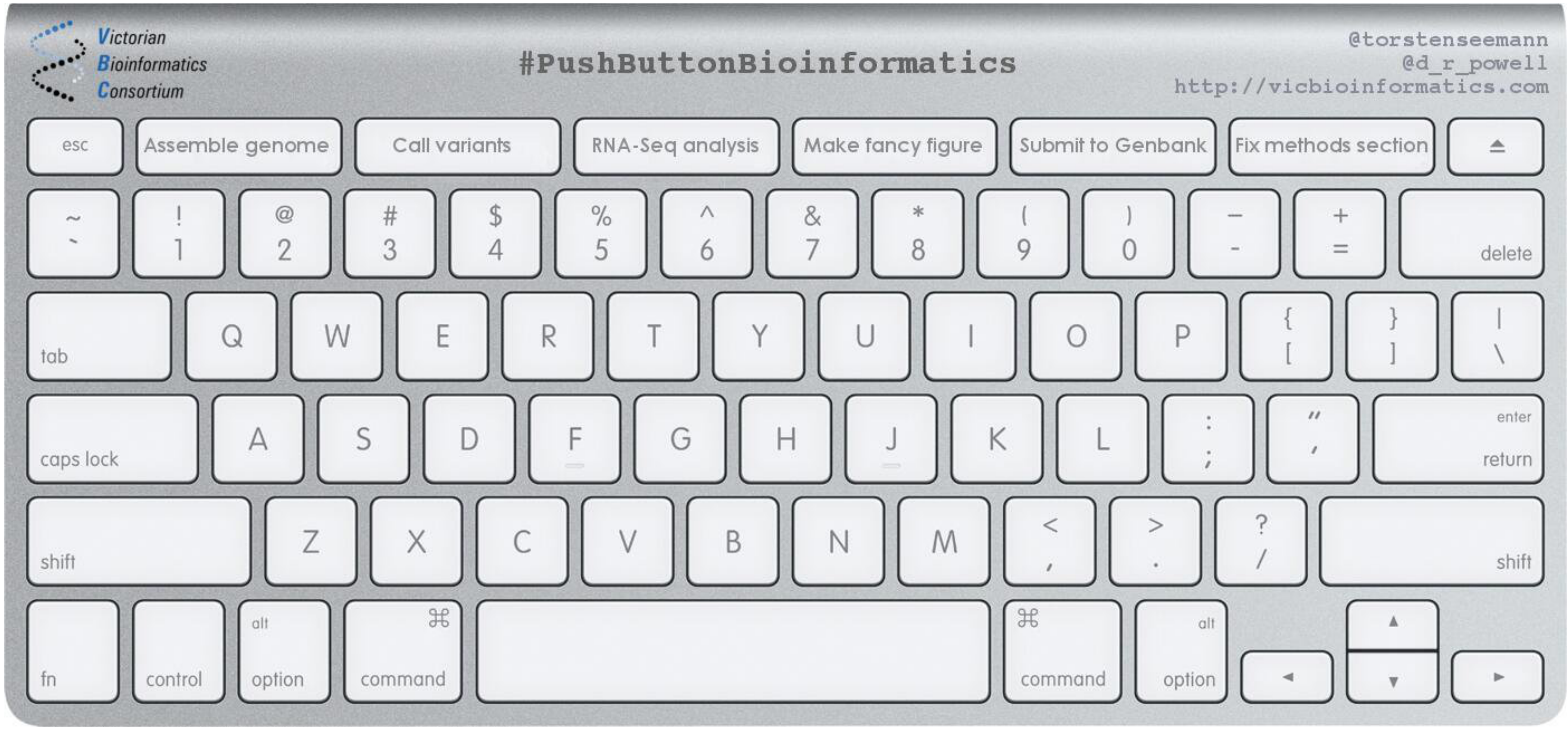
| at an external company | will you ever see the code and be able to explain M&M? |

# NO

#PushButtonBioinformatics

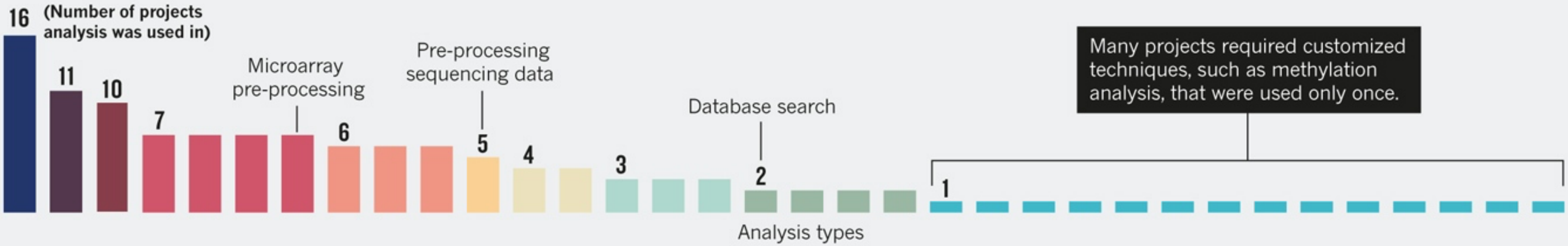


Victorian
Bioinformatics
Consortium
#PushButtonBioinformatics
@torstenseemann
@d_r_powell
http://vicbioinformatics.com
esc
Assemble genome
Call variants
RNA-Seq analysis
Make fancy figure
Submit to Genbank
Fix methods section
~ ` ! 1 @ 2 # 3 $ 4 % 5 ^ 6 & 7 * 8 ( 9 ) 0 – - + = delete
tab Q W E R T Y U I O P { [ } ] | \
caps lock A S D F G H J K L : ; " ' enter return
shift Z X C V B N M < , > . ? / shift
fn control alt option ⌘ command ⌘ command alt option

***"Biological data will continue to pile up unless those who analyse it are recognised as creative collaborators in need of career paths"***

*– Jeffrey Chang, 2015*

Over 18 months, 46 data-analysis projects undertaken at the bioinformatics core of the University of Texas Health Science Center at Houston required 34 different types of analysis — most were used infrequently. Each project demanded unique combinations of analyses, demonstrating how bioinformaticians must be versatile, creative and collaborative.



Core services: Reward bioinformaticians; *Nature* **520,** 151–152 (09 April 2015) doi:10.1038/520151a

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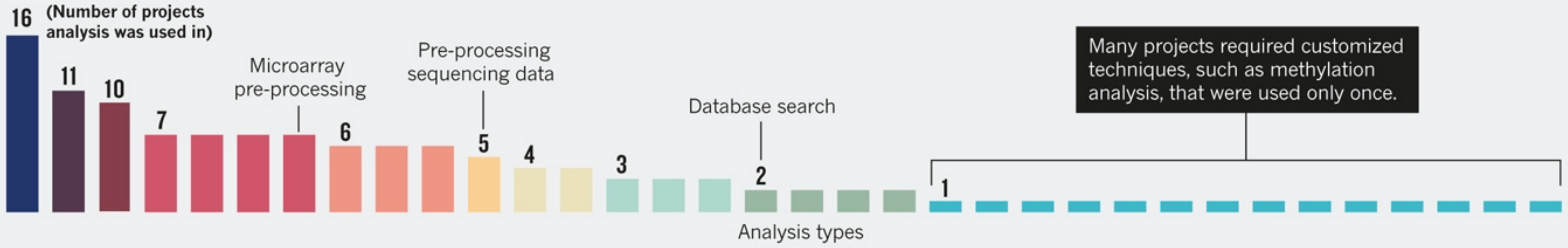


Many projects required customized techniques, such as methylation analysis, that were used only once.

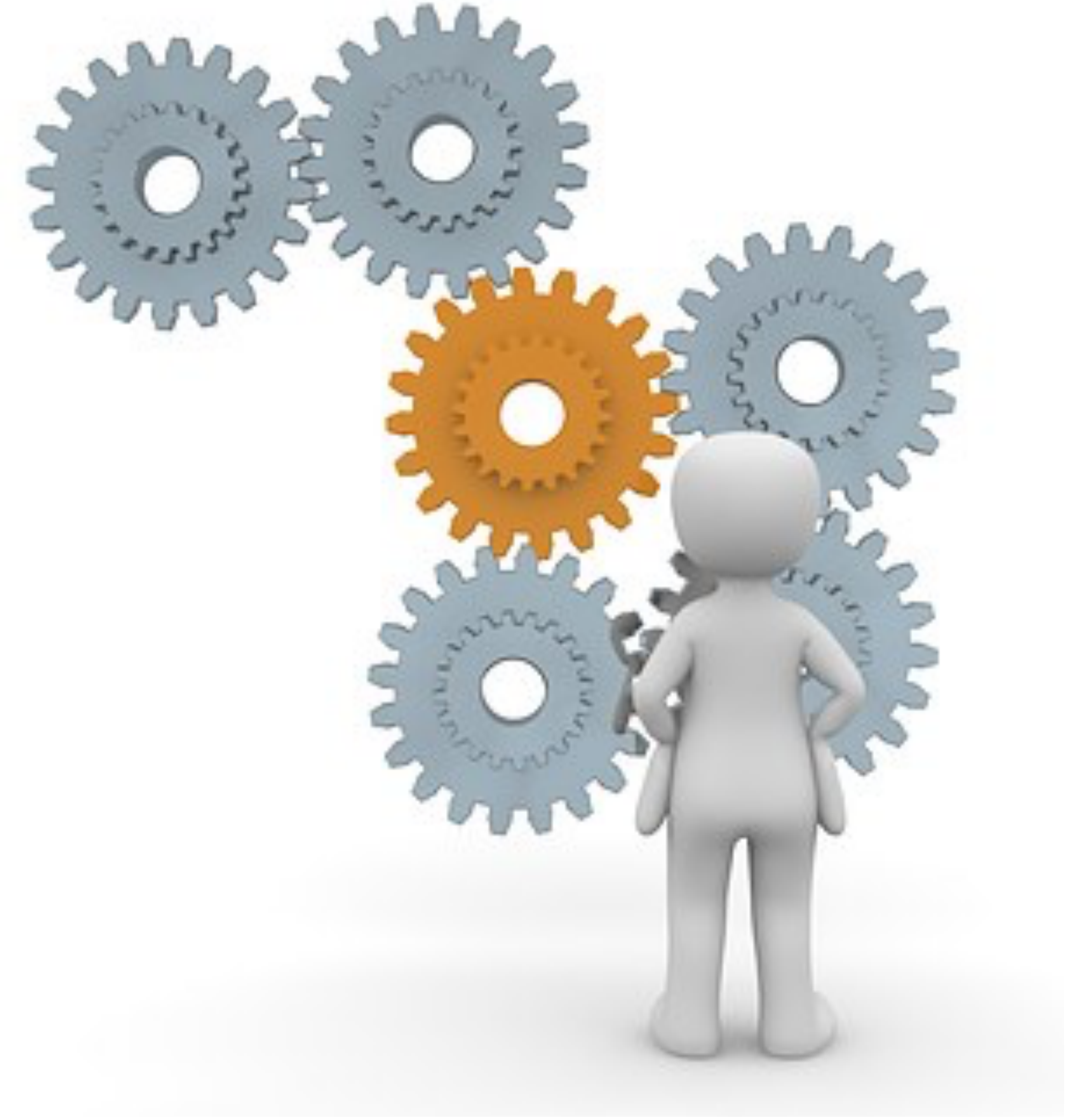
Core services: Reward bioinformaticians; *Nature* **520,** 151–152 (09 April 2015) doi:10.1038/520151a

***“87% of analysis time was spent on projects that had the characteristics of research…These findings suggest that to foster team-based multidisciplinary research, institutions must adopt policies that recognise contributions to research by applied bioinformatics scientists.”***

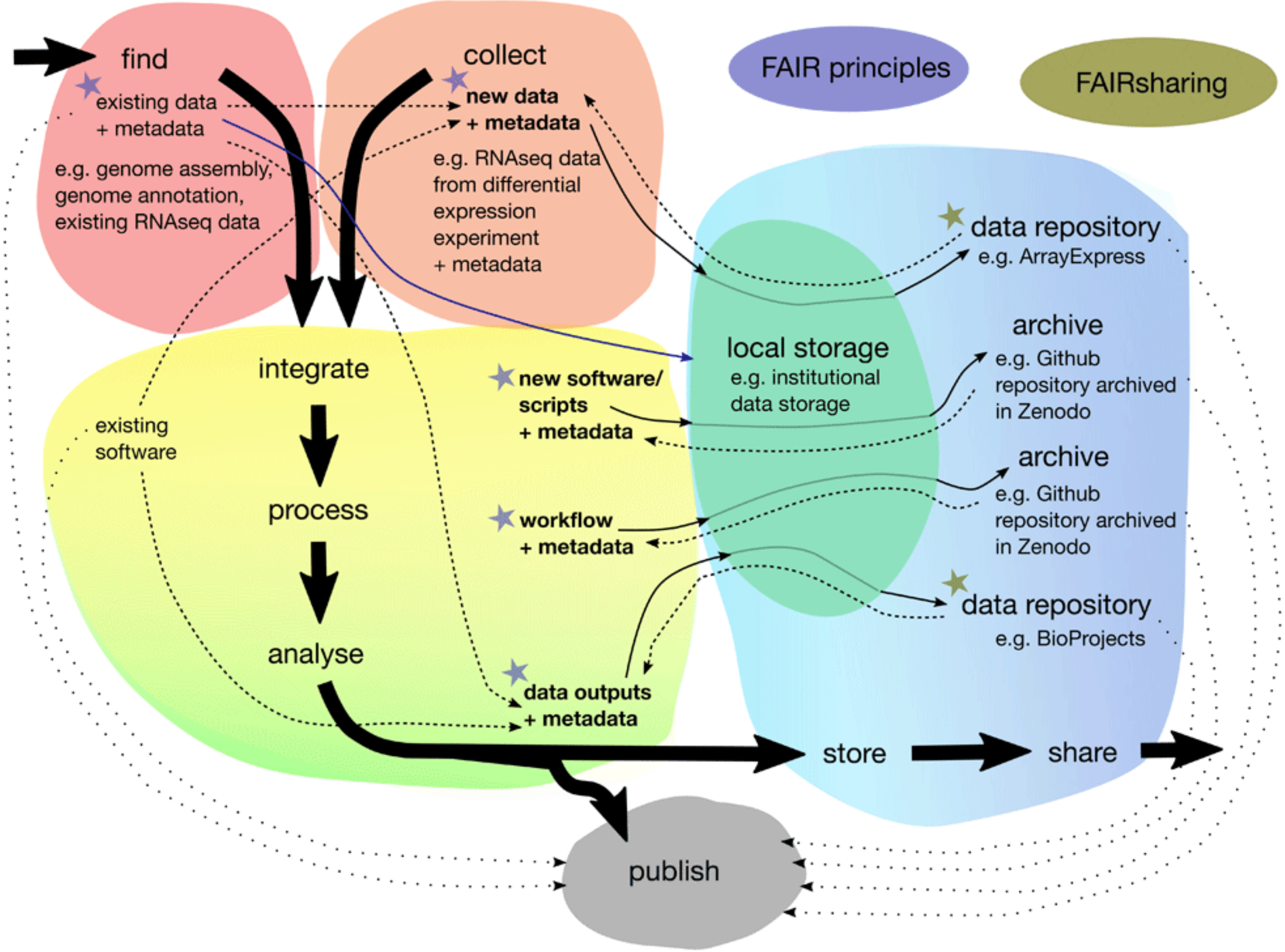
*– Jeffrey Chang, 2019*

Bioinformatics service center projects go beyond service; https://doi.org/10.1016/j.jbi.2019.103192

# Practicalities: key aspects



A short intro to how we work & reproducibility



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# ✱ DATA

**Sharing data with a statistician / bioinformatician**

- The raw data
- The tidy / clean dataset
- A code book describing each variable and its values in the tidy data set
- An explicit and exact recipe to go from 1 to 2 and 3

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- ❖ The tidy / clean dataset
- ❖ A code book describing each variable and its values in the tidy data set
- ❖ An explicit and exact recipe to go from 1 to 2 and 3

### Expecting back

- ❖ An analysis script that performs each of the analyses
- ❖ The exact computer code
- ❖ All output files and figures generated

Read more: https://github.com/jtleek/datasharing

# ✱ Bioinformatics File Formats

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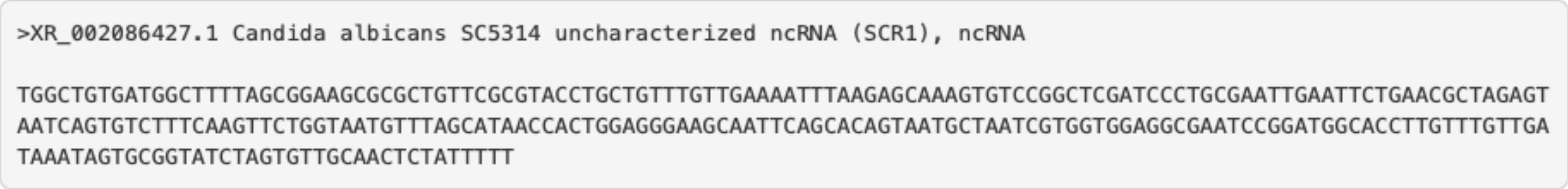
**FASTA**
***.fa, *fasta, *.sa**

A simple way to represent nucleotide of amino acid sequences of nucleic acids and proteins; 2 lines per entry



```
>XR_002086427.1 Candida albicans SC5314 uncharacterized ncRNA (SCR1), ncRNA

TGGCTGTGATGGCTTTTAGCGGAAGCGCGCTGTTCGCGTACCTGCTGTTTGTTGAAAATTTAAGAGCAAAGTGTCCGGCTCGATCCCTGCGAATTGAATTCTGAACGCTAGAGT
AATCAGTGTCTTTCAAGTTCTGGTAATGTTTAGCATAACCACTGGAGGGAAGCAATTCAGCACAGTAATGCTAATCGTGGTGGAGGCGAATCCGGATGGCACCTTGTTTGTTGA
TAAATAGTGCGGTATCTAGTGTTGCAACTCTATTTTT
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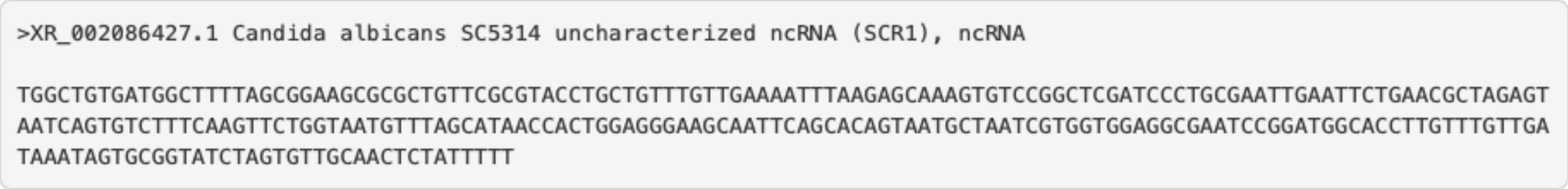

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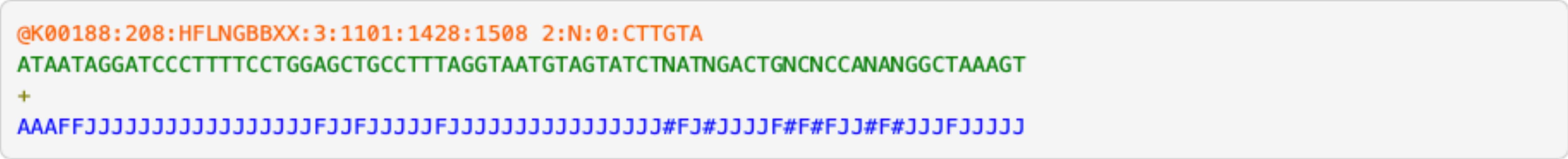
AATCAGTGTCTTTCAAGTTCTGGTAATGTTTAGCATAACCACTGGAGGGAAGCAATTCAGCACAGTAATGCTAATCGTGGTGGAGGCGAATCCGGATGGCACCTTGTTTGTTGA
TAAATAGTGCGGTATCTAGTGTTGCAACTCTATTTTT
```

**FASTQ**
*.fastq, *fq, *sanfastq

Puts together sequence and its quality score Q; 4 lines per entry



```
@K00188:208:HFLNGBBXX:3:1101:1428:1508 2:N:0:CTTGTA
ATAATAGGATCCCTTTTCCTGGAGCTGCCTTTAGGTAATGTAGTATCTNATNGACTGNCNCCANANGGCTAAAGT
+
AAAFFJJJJJJJJJJJJJJJJJFJJFJJJJJFJJJJJJJJJJJJJJJJ#FJ#JJJJF#F#FJJ#F#JJJFJJJJJ
```

source: https://bioinformatics.uconn.edu/resources-and-events/tutorials-2/file-formats-tutorial/#

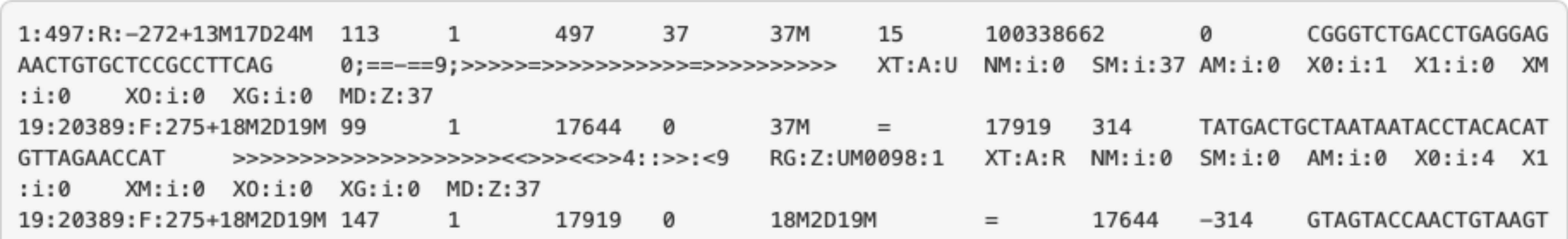
https://samtools.github.io/hts-specs/SAMv1.pdf

# SAM / BAM
# *.sam, *.bam

Sequence Alignment Map, generated following mapping of the reads to reference sequence; BAM a binary equivalent; header lines (@) followed by 1 line per entry

Example :

QNAME FLAG RNAME POS MAPQ CIGAR RNEXT PNEXT TLEN SEQ



```
1:497:R:-272+13M17D24M  113     1       497     37      37M     15      100338662       0       CGGGTCTGACCTGAGGAG
AACTGTGCTCCGCCTTCAG     0;==-==9;>>>>>=>>>>>>>>>>>=>>>>>>>>>>   XT:A:U  NM:i:0  SM:i:37 AM:i:0  X0:i:1  X1:i:0  XM
:i:0    XO:i:0  XG:i:0  MD:Z:37
19:20389:F:275+18M2D19M 99      1       17644   0       37M     =       17919   314     TATGACTGCTAATAATACCTACACAT
GTTAGAACCAT     >>>>>>>>>>>>>>>>>>>><<>>><<>>4::>>:<9   RG:Z:UM0098:1   XT:A:R  NM:i:0  SM:i:0  AM:i:0  X0:i:4  X1
:i:0    XM:i:0  XO:i:0  XG:i:0  MD:Z:37
19:20389:F:275+18M2D19M 147     1       17919   0       18M2D19M        =       17644   -314    GTAGTACCAACTGTAAGT
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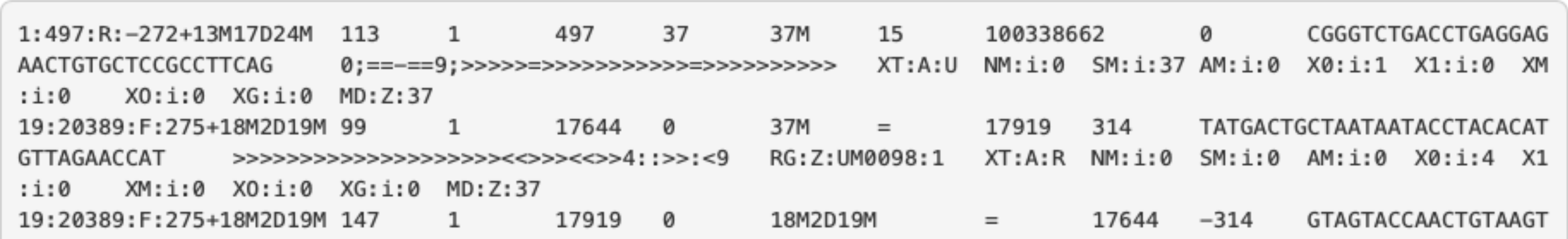
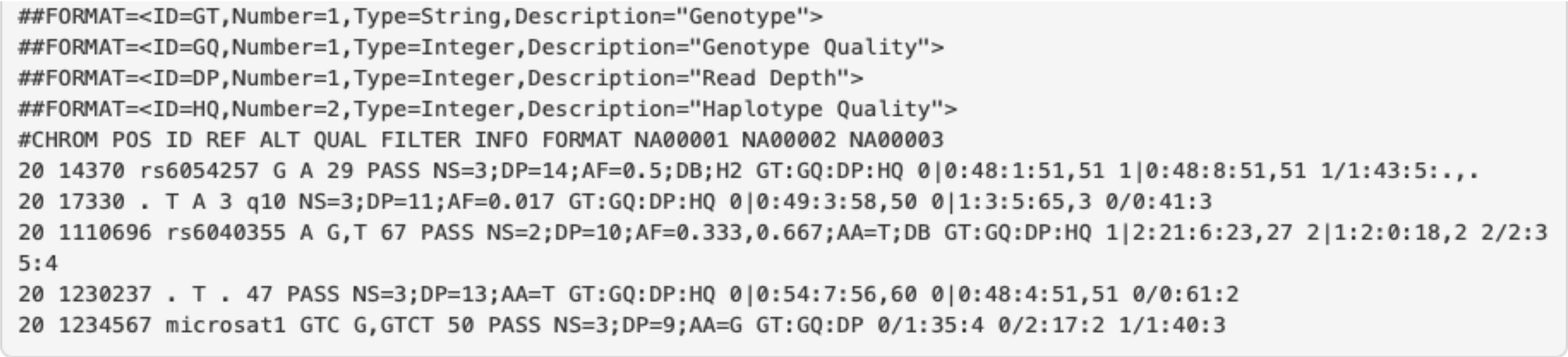


```
1:497:R:-272+13M17D24M  113     1       497     37      37M     15      100338662       0       CGGGTCTGACCTGAGGAG
AACTGTGCTCCGCCTTCAG     0;==-==9;>>>>>=>>>>>>>>>>>>=>>>>>>>>>    XT:A:U  NM:i:0  SM:i:37 AM:i:0  X0:i:1  X1:i:0  XM
:i:0    XO:i:0  XG:i:0  MD:Z:37
19:20389:F:275+18M2D19M 99      1       17644   0       37M     =       17919   314     TATGACTGCTAATAATACCTACACAT
GTTAGAACCAT     >>>>>>>>>>>>>>>>>>>><<>>><<>>4::>>:<9   RG:Z:UM0098:1   XT:A:R  NM:i:0  SM:i:0  AM:i:0  X0:i:4  X1
:i:0    XM:i:0  XO:i:0  XG:i:0  MD:Z:37
19:20389:F:275+18M2D19M 147     1       17919   0       18M2D19M        =       17644   -314    GTAGTACCAACTGTAAGT
```

https://samtools.github.io/hts-specs/VCFv4.2.pdf

## VCF
## *.vcf

Variant Calling Format/File, used to store gene sequence variations, header lines (##) followed by 1 liner per entry



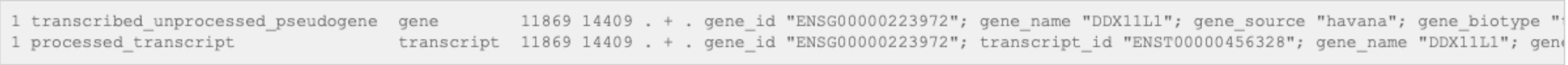
```
##FORMAT=<ID=GT,Number=1,Type=String,Description="Genotype">
##FORMAT=<ID=GQ,Number=1,Type=Integer,Description="Genotype Quality">
##FORMAT=<ID=DP,Number=1,Type=Integer,Description="Read Depth">
##FORMAT=<ID=HQ,Number=2,Type=Integer,Description="Haplotype Quality">
#CHROM POS ID REF ALT QUAL FILTER INFO FORMAT NA00001 NA00002 NA00003
20 14370 rs6054257 G A 29 PASS NS=3;DP=14;AF=0.5;DB;H2 GT:GQ:DP:HQ 0|0:48:1:51,51 1|0:48:8:51,51 1/1:43:5:.,.
20 17330 . T A 3 q10 NS=3;DP=11;AF=0.017 GT:GQ:DP:HQ 0|0:49:3:58,50 0|1:3:5:65,3 0/0:41:3
20 1110696 rs6040355 A G,T 67 PASS NS=2;DP=10;AF=0.333,0.667;AA=T;DB GT:GQ:DP:HQ 1|2:21:6:23,27 2|1:2:0:18,2 2/2:3
5:4
20 1230237 . T . 47 PASS NS=3;DP=13;AA=T GT:GQ:DP:HQ 0|0:54:7:56,60 0|0:48:4:51,51 0/0:61:2
20 1234567 microsat1 GTC G,GTCT 50 PASS NS=3;DP=9;AA=G GT:GQ:DP 0/1:35:4 0/2:17:2 1/1:40:3
```

# GFF/GTF

# *.gff, *.gff2, *.gff3, *.gtf

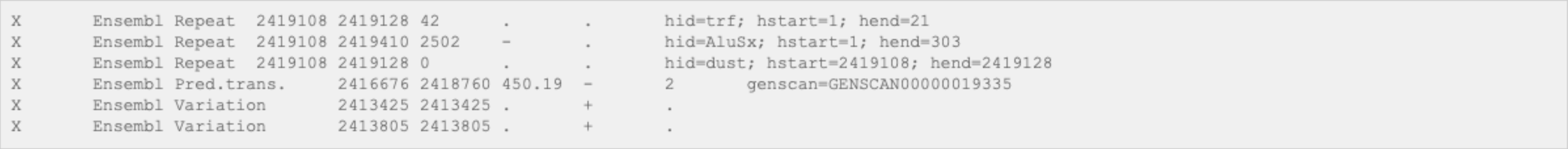
General Feature Format / Gene Transfer Format, used for describing genes and other features of DNA, RNA and protein sequences

## GTF

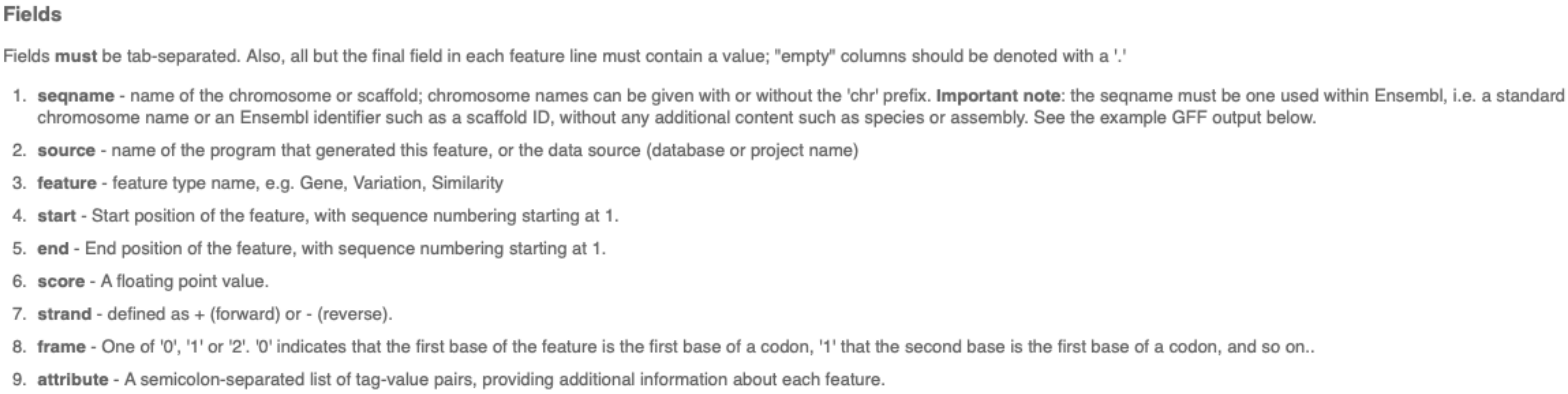


```
1 transcribed_unprocessed_pseudogene  gene        11869 14409 . + . gene_id "ENSG00000223972"; gene_name "DDX11L1"; gene_source "havana"; gene_biotype "
1 processed_transcript                transcript  11869 14409 . + . gene_id "ENSG00000223972"; transcript_id "ENST00000456328"; gene_name "DDX11L1"; gen
```

## GFF



```
X       Ensembl Repeat  2419108 2419128 42      .       .       hid=trf; hstart=1; hend=21
X       Ensembl Repeat  2419108 2419410 2502    -       .       hid=AluSx; hstart=1; hend=303
X       Ensembl Repeat  2419108 2419128 0       .       .       hid=dust; hstart=2419108; hend=2419128
X       Ensembl Pred.trans.     2416676 2418760 450.19  -       2       genscan=GENSCAN00000019335
X       Ensembl Variation       2413425 2413425 .       +       .
X       Ensembl Variation       2413805 2413805 .       +       .
```



### Fields

Fields **must** be tab-separated. Also, all but the final field in each feature line must contain a value; "empty" columns should be denoted with a '.'

1. **seqname** - name of the chromosome or scaffold; chromosome names can be given with or without the 'chr' prefix. **Important note**: the seqname must be one used within Ensembl, i.e. a standard chromosome name or an Ensembl identifier such as a scaffold ID, without any additional content such as species or assembly. See the example GFF output below.
2. **source** - name of the program that generated this feature, or the data source (database or project name)
3. **feature** - feature type name, e.g. Gene, Variation, Similarity
4. **start** - Start position of the feature, with sequence numbering starting at 1.
5. **end** - End position of the feature, with sequence numbering starting at 1.
6. **score** - A floating point value.
7. **strand** - defined as + (forward) or - (reverse).
8. **frame** - One of '0', '1' or '2'. '0' indicates that the first base of the feature is the first base of a codon, '1' that the second base is the first base of a codon, and so on..
9. **attribute** - A semicolon-separated list of tag-value pairs, providing additional information about each feature.

source: https://www.ensembl.org/info/website/upload/gff.html

**Let’s discuss: share your experiences in any of the following**

- locating data
- describing data (metadata)
- coding data (continous, ordinal, categorical, missing, censored)
- sharing data

## Unix-like operating systems

Unix, 1960s, Bell Labs

“Unix philosophy” of creating small, modular utilities that do one thing and do them well.

*Commonly used for: working with files and directories; checking file sizes, previewing data, summary statistics*

```
# List directory content
[olga@rackham3 Fastq]$ ls -lh
total 23G
-rw-rw---- 1 5.8G Sep 10 09:18 P12516_101_R1.fastq
-rw-rw---- 1 5.8G Sep 10 09:18 P12516_101_R2.fastq
-rw-rw---- 1 5.4G Sep 10 09:18 P12516_102_R1.fastq
-rw-rw---- 1 5.4G Sep 10 09:18 P12516_102_R2.fastq
```

```
# Output the first part of files
head P12516_101_R1.fastq
@A00187:119:H72F7DRXX:2:1101:1072:1000 1:N:0:ATTACTCG
CAATGTTCTGCATGGTTATCGATCCGGAGGCTGCTAGCTTTCCAGCCAGAC
+
FFFFFFFFFFFFFFFFFFFFF::FFFFFFFFFFFFFFFFFFFFFFFFFFFF
```

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FFFFFFFFFFFFFFFFFFFFF::FFFFFFFFFFFFFFFFFFFFFFFFFFFF
```

## ✱ High-performance computers & large-scale storage

Tetralith, NSC, Linköping University

**e.g. https://www.uppmax.uu.se**

**UPPMAX (*Uppsala Multidisciplinary Center for Advanced Computational Science*) is Uppsala University's resource of high-performance computers, large-scale storage and know-how of high-performance computing (HPC)**

*Commonly used as: computational infrastructure and project/temporary data storage*

## Bioinformatics tools

e.g. FastQC, SAMtools, BEDTools

```
# Use samtools to generate stats
samtools stats example.sam
```

```
# Sort bed file
bedutils sort example.bed
```

```
# Mapping reads to a reference
star --genomeDir /proj/uppstore2019092/NBIS/Index/Star --readFilesIn /proj/snic2019-8-218/private/NBIS/Cutad
apt/v03/Out/FC5_9.trim8.fastq.gz --readFilesCommand zcat --outFileNamePrefix /proj/uppstore2019092/NBIS/Star
/Out/v03/FC5_9/FC5_9_ --runThreadN 4 --outFilterMultimapNmax 999 --outFilterMismatchNmax 3 --outSAMtype SAM
--outSAMunmapped Within --outFilterMultimapScoreRange 1 --seedSearchStartLmax 15
```

## Bioinformatics tools

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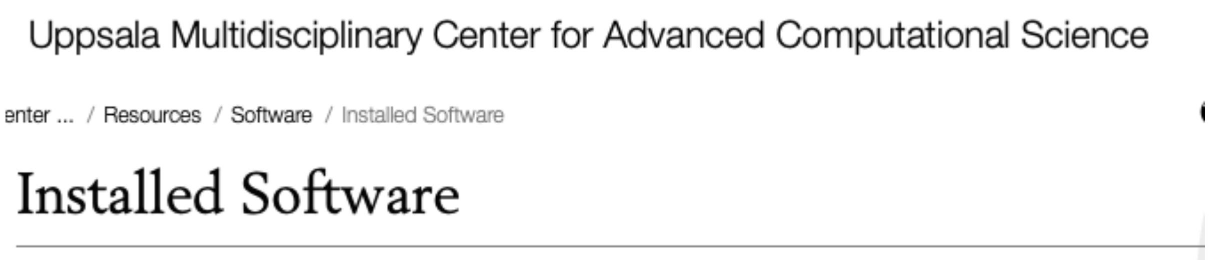
apt/v03/Out/FC5_9.trim8.fastq.gz --readFilesCommand zcat --outFileNamePrefix /proj/uppstore2019092/NBIS/Star
/Out/v03/FC5_9/FC5_9_ --runThreadN 4 --outFilterMultimapNmax 999 --outFilterMismatchNmax 3 --outSAMtype SAM
--outSAMunmapped Within --outFilterMultimapScoreRange 1 --seedSearchStartLmax 15
```



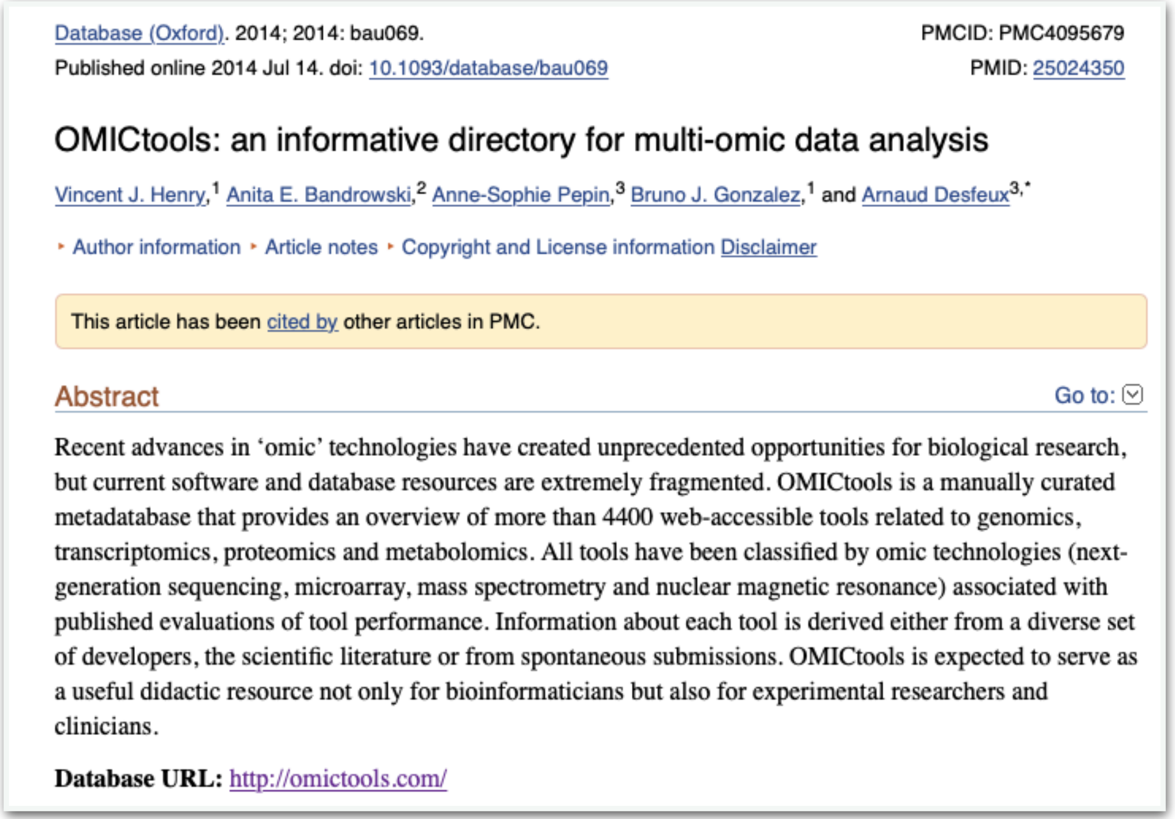
Uppsala Multidisciplinary Center for Advanced Computational Science

enter ... / Resources / Software / Installed Software

Installed Software

https://www.uppmax.uu.se/resources/software/installed-software/

elixir bio.tools



Database (Oxford). 2014; 2014: bau069.
Published online 2014 Jul 14. doi: 10.1093/database/bau069

PMCID: PMC4095679
PMID: 25024350

OMICtools: an informative directory for multi-omic data analysis

Vincent J. Henry,[1] Anita E. Bandrowski,[2] Anne-Sophie Pepin,[3] Bruno J. Gonzalez,[1] and Arnaud Desfeux[3,*]

‣ Author information ‣ Article notes ‣ Copyright and License information Disclaimer

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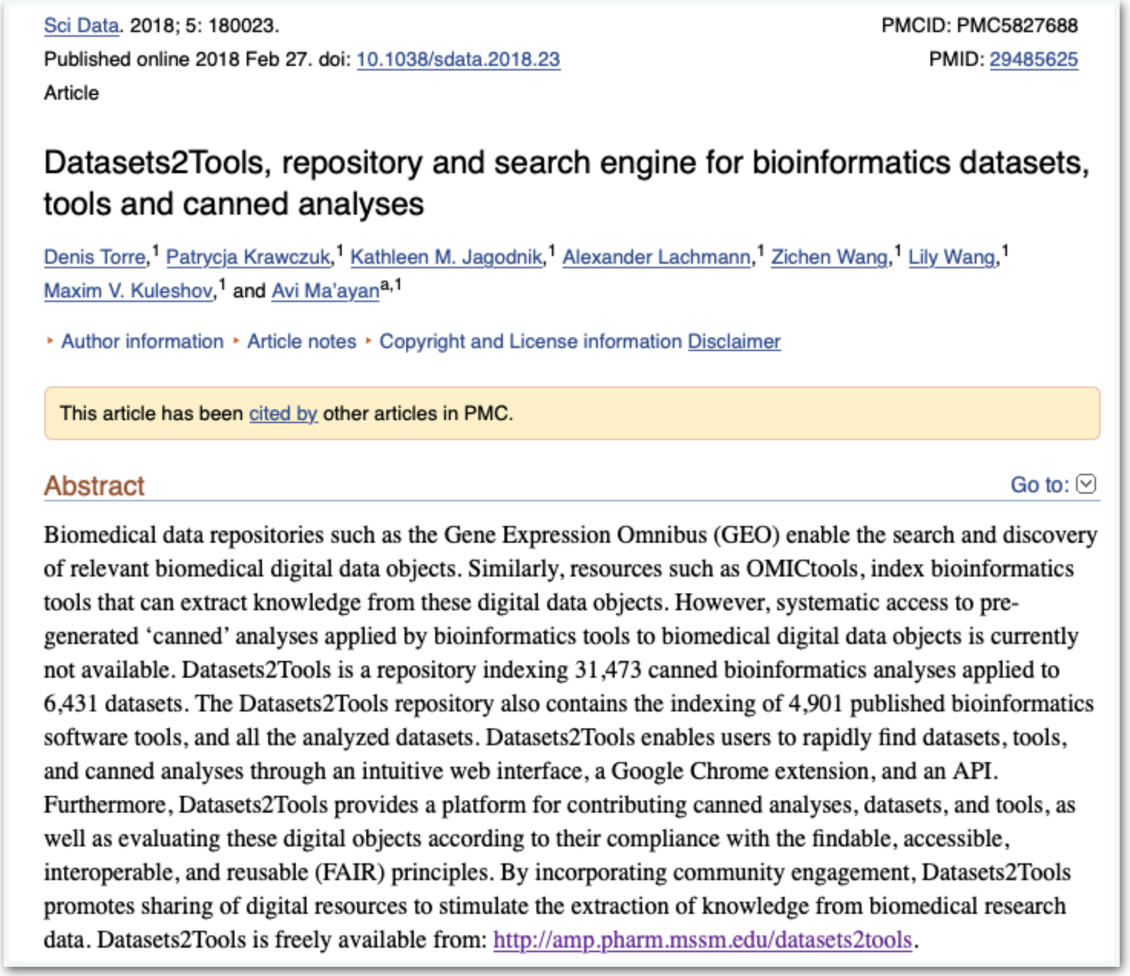
Abstract

Recent advances in 'omic' technologies have created unprecedented opportunities for biological research, but current software and database resources are extremely fragmented. OMICtools is a manually curated metadatabase that provides an overview of more than 4400 web-accessible tools related to genomics, transcriptomics, proteomics and metabolomics. All tools have been classified by omic technologies (next-generation sequencing, microarray, mass spectrometry and nuclear magnetic resonance) associated with published evaluations of tool performance. Information about each tool is derived either from a diverse set of developers, the scientific literature or from spontaneous submissions. OMICtools is expected to serve as a useful didactic resource not only for bioinformaticians but also for experimental researchers and clinicians.

**Database URL:** http://omictools.com/

https://omictools.com



Sci Data. 2018; 5: 180023.
Published online 2018 Feb 27. doi: 10.1038/sdata.2018.23

PMCID: PMC5827688
PMID: 29485625

Article

Datasets2Tools, repository and search engine for bioinformatics datasets, tools and canned analyses

Denis Torre,[1] Patrycja Krawczuk,[1] Kathleen M. Jagodnik,[1] Alexander Lachmann,[1] Zichen Wang,[1] Lily Wang,[1] Maxim V. Kuleshov,[1] and Avi Ma'ayan[a,1]

‣ Author information ‣ Article notes ‣ Copyright and License information Disclaimer

This article has been cited by other articles in PMC.

Abstract

Biomedical data repositories such as the Gene Expression Omnibus (GEO) enable the search and discovery of relevant biomedical digital data objects. Similarly, resources such as OMICtools, index bioinformatics tools that can extract knowledge from these digital data objects. However, systematic access to pre-generated 'canned' analyses applied by bioinformatics tools to biomedical digital data objects is currently not available. Datasets2Tools is a repository indexing 31,473 canned bioinformatics analyses applied to 6,431 datasets. The Datasets2Tools repository also contains the indexing of 4,901 published bioinformatics software tools, and all the analyzed datasets. Datasets2Tools enables users to rapidly find datasets, tools, and canned analyses through an intuitive web interface, a Google Chrome extension, and an API. Furthermore, Datasets2Tools provides a platform for contributing canned analyses, datasets, and tools, as well as evaluating these digital objects according to their compliance with the findable, accessible, interoperable, and reusable (FAIR) principles. By incorporating community engagement, Datasets2Tools promotes sharing of digital resources to stimulate the extraction of knowledge from biomedical research data. Datasets2Tools is freely available from: http://amp.pharm.mssm.edu/datasets2tools.

http://amp.pharm.mssm.edu/datasets2tools/

## ✱ Scripts and programs

putting commands together

BASH
THE BOURNE-AGAIN SHELL
python™
R
Bioconductor
OPEN SOURCE SOFTWARE FOR BIOINFORMATICS
perl
Programming Language
Ruby
Java
Programming
C++
biopython
THE
C
PROGRAMMING
LANGUAGE
php
JavaScript
BioPerl

## ✱ Scripts and programs

putting commands together

***Main three (interpreted)***

CRAN
The Comprehensive R Archive Network
Bioconductor
OPEN SOURCE SOFTWARE FOR BIOINFORMATICS
biopython
BioPerl

## ✱ Scripts and programs

putting commands together

*Main three (interpreted)*

*Compiled languages*

CRAN
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biopython
BioPerl

## ✱ Scripts and programs
putting commands together

BASH THE BOURNE-AGAIN SHELL

python™

R

*Main three (interpreted)*

perl Programming Language

Ruby

PHP

JavaScript

*Website development*

Java Programming

C++

C#

THE C PROGRAMMING LANGUAGE

*Compiled languages*

CRAN The Comprehensive R Archive Network

Bioconductor OPEN SOURCE SOFTWARE FOR BIOINFORMATICS

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BioPerl

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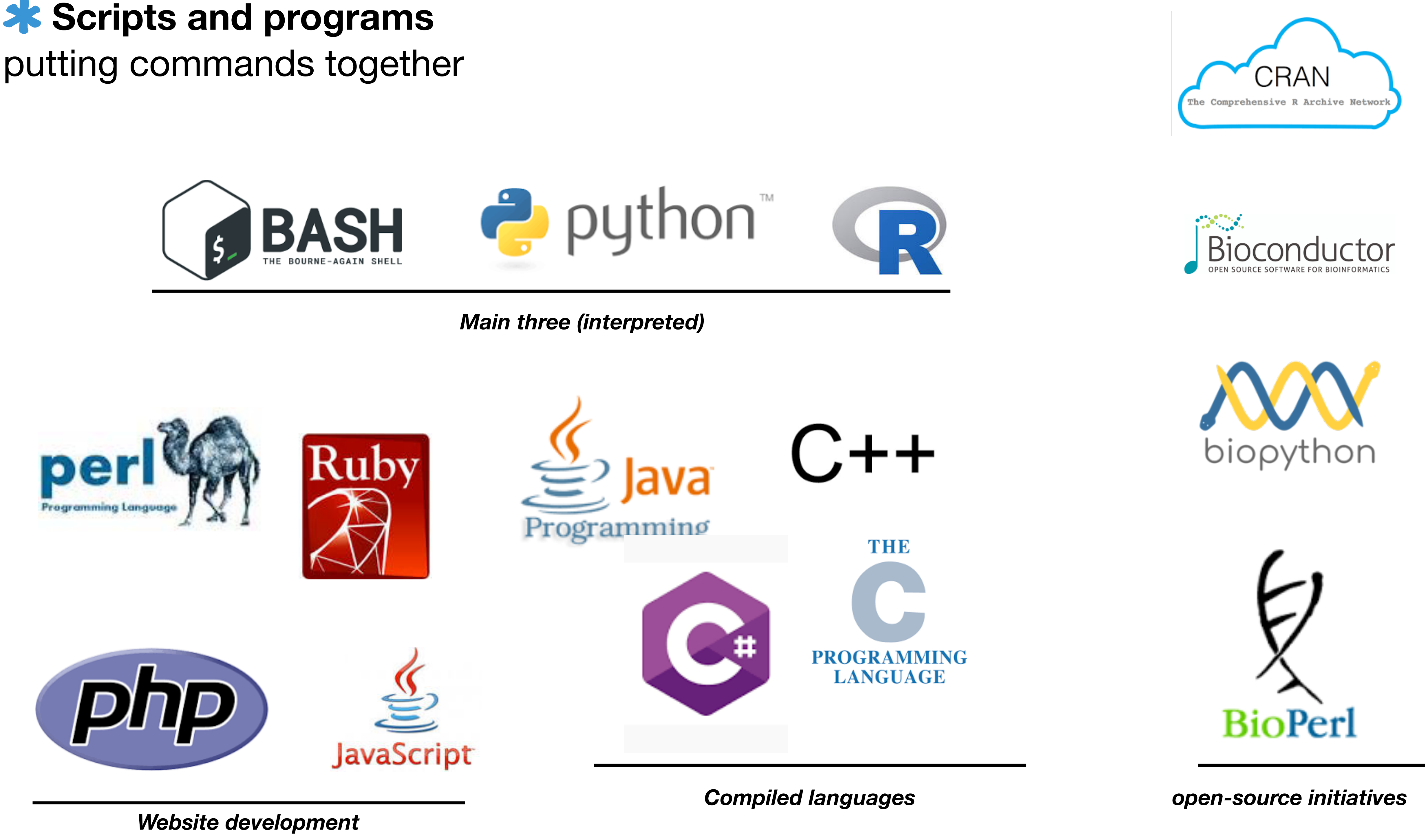


*Main three (interpreted)*

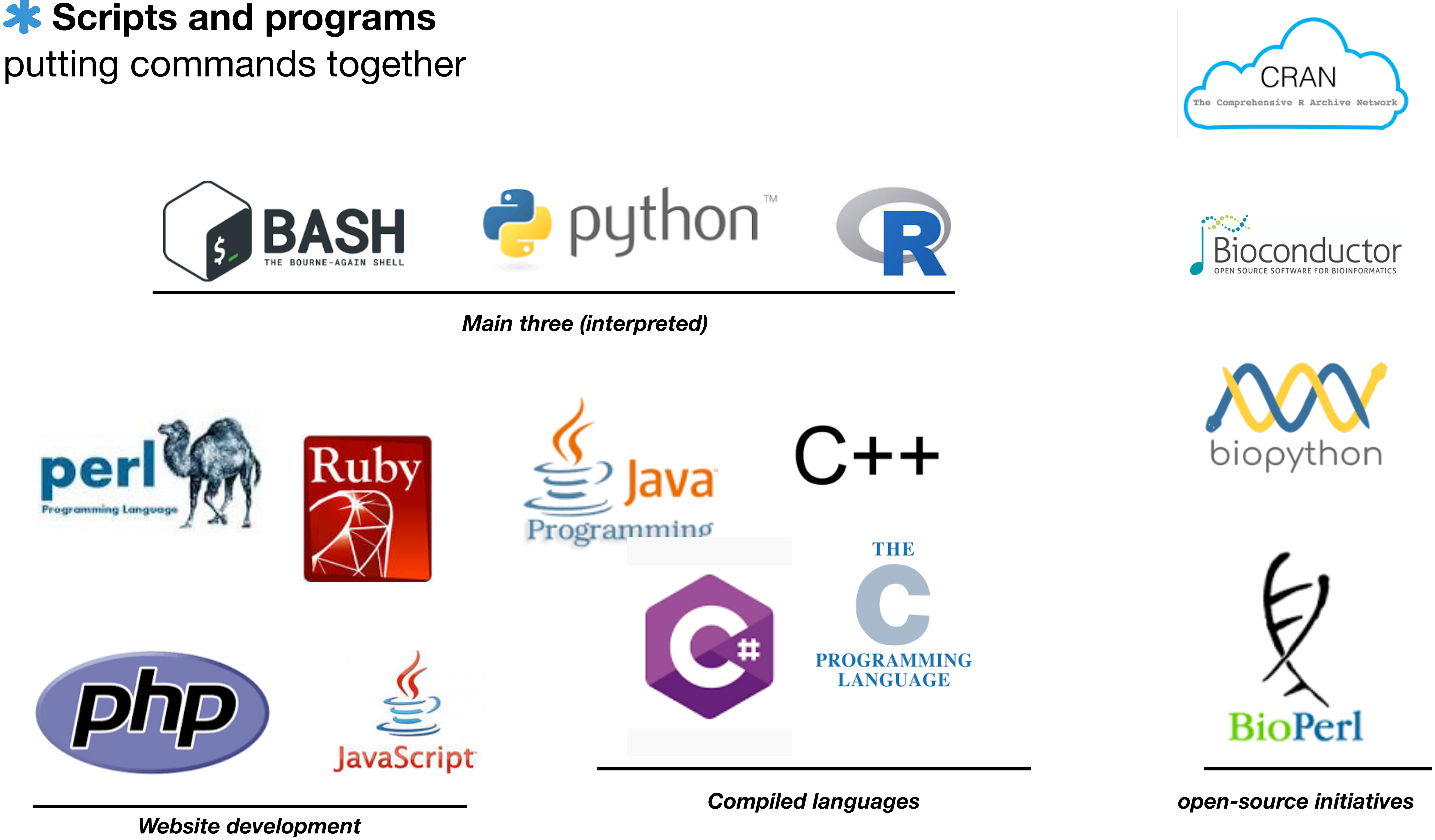
*Website development*

*Compiled languages*

*open-source initiatives*

## ✱ Scripts and programs

putting commands together



*Main three (interpreted)*

*Website development*

*Compiled languages*

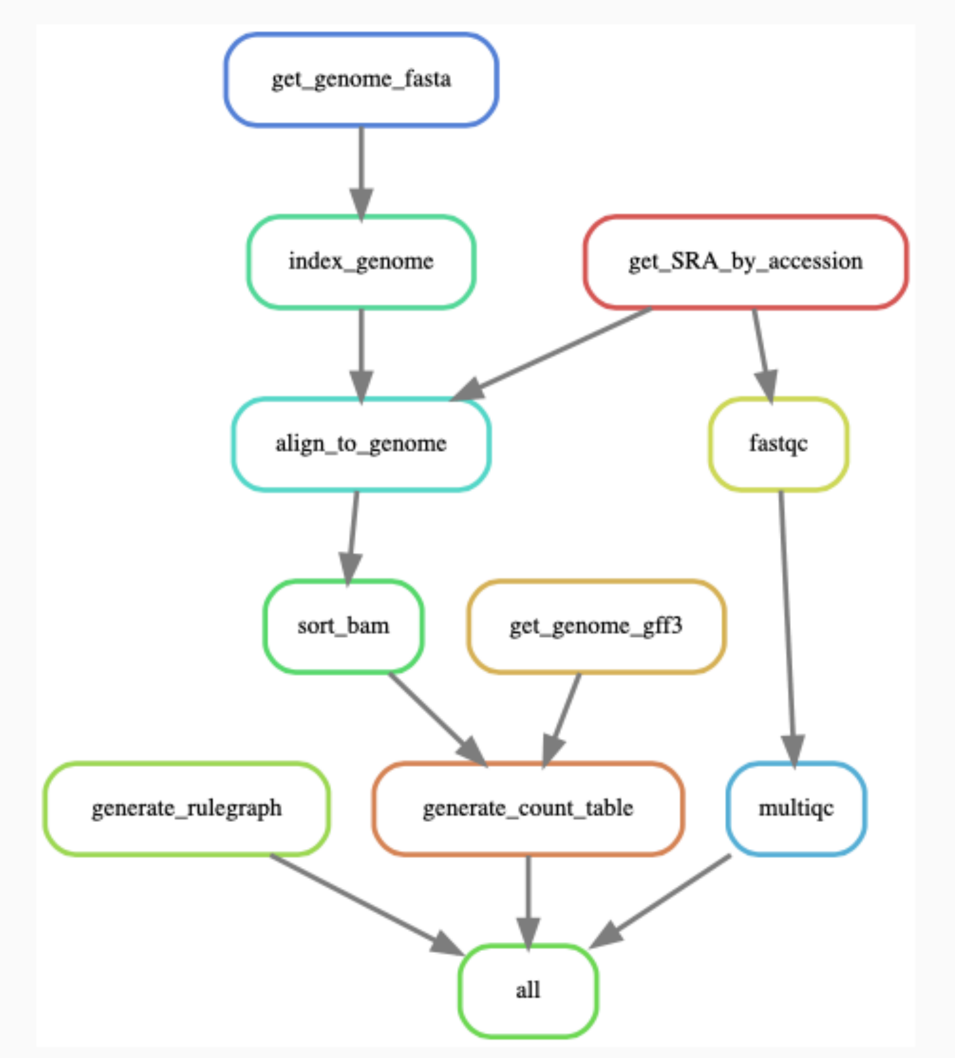
*open-source initiatives*

- ❖ **Interpreted vs. compiled languages**
- ❖ **Script vs. program vs. tool vs. software**

Read more:
http://omgenomics.com/programming-languages/
https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2267699/

## ✱ Workflows

automating tasks
tracking provenance



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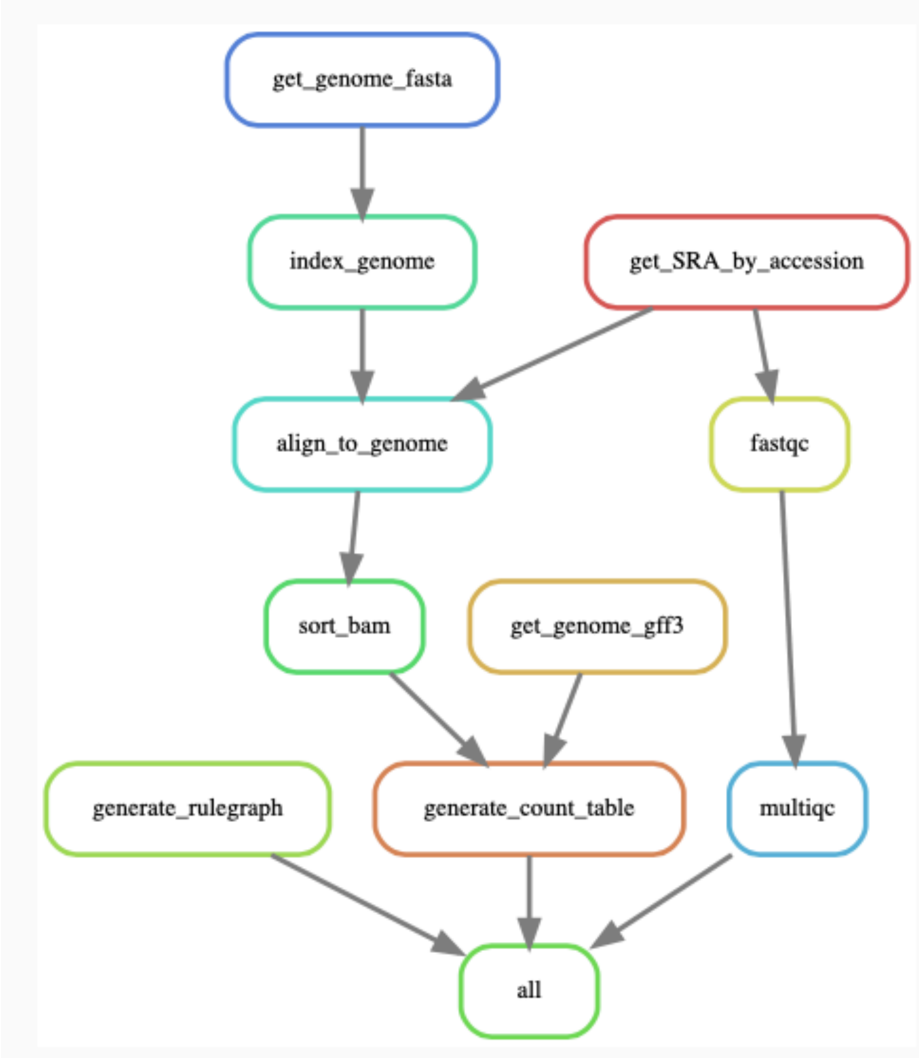
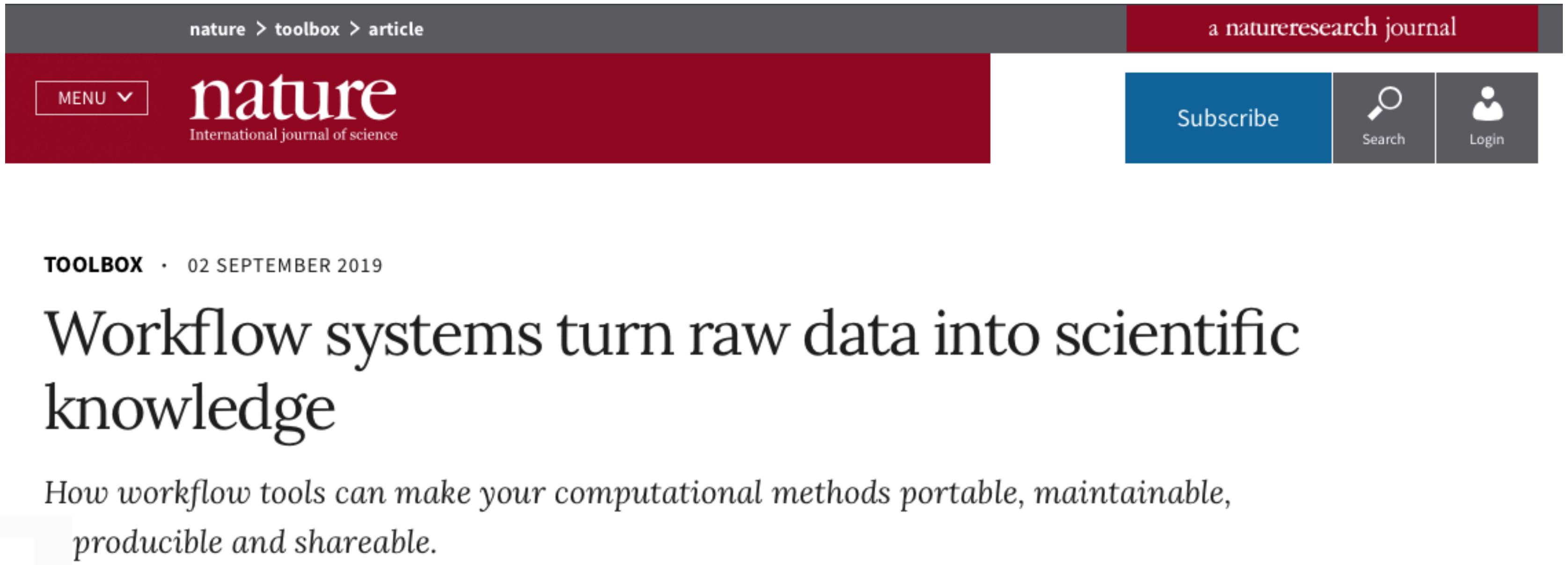
tracking provenance





TOOLBOX · 02 SEPTEMBER 2019

Workflow systems turn raw data into scientific knowledge

*How workflow tools can make your computational methods portable, maintainable, producible and shareable.*

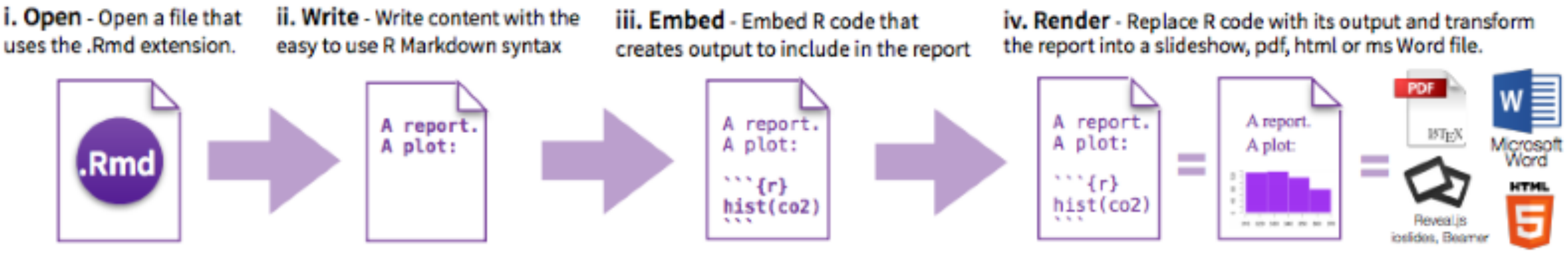
Snakemake

nextflow

Galaxy

## ✱ Literate computing & authoring

writing self-contained documents that include narrative and code used to generate both text and graphical results



**i. Open** - Open a file that uses the .Rmd extension.

**ii. Write** - Write content with the easy to use R Markdown syntax

**iii. Embed** - Embed R code that creates output to include in the report

**iv. Render** - Replace R code with its output and transform the report into a slideshow, pdf, html or ms Word file.

.Rmd
A report.
A plot:
A report.
A plot:
```{r}
hist(co2)
```
A report.
A plot:
```{r}
hist(co2)
```
=
A report.
A plot:
=
PDF
LaTeX
Microsoft Word
HTML
Reveal.js
ioslides, Beamer

The LaTeX Project

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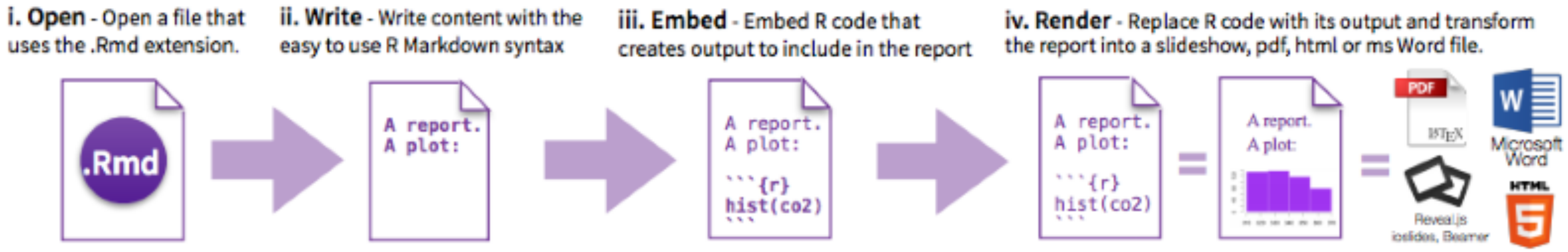

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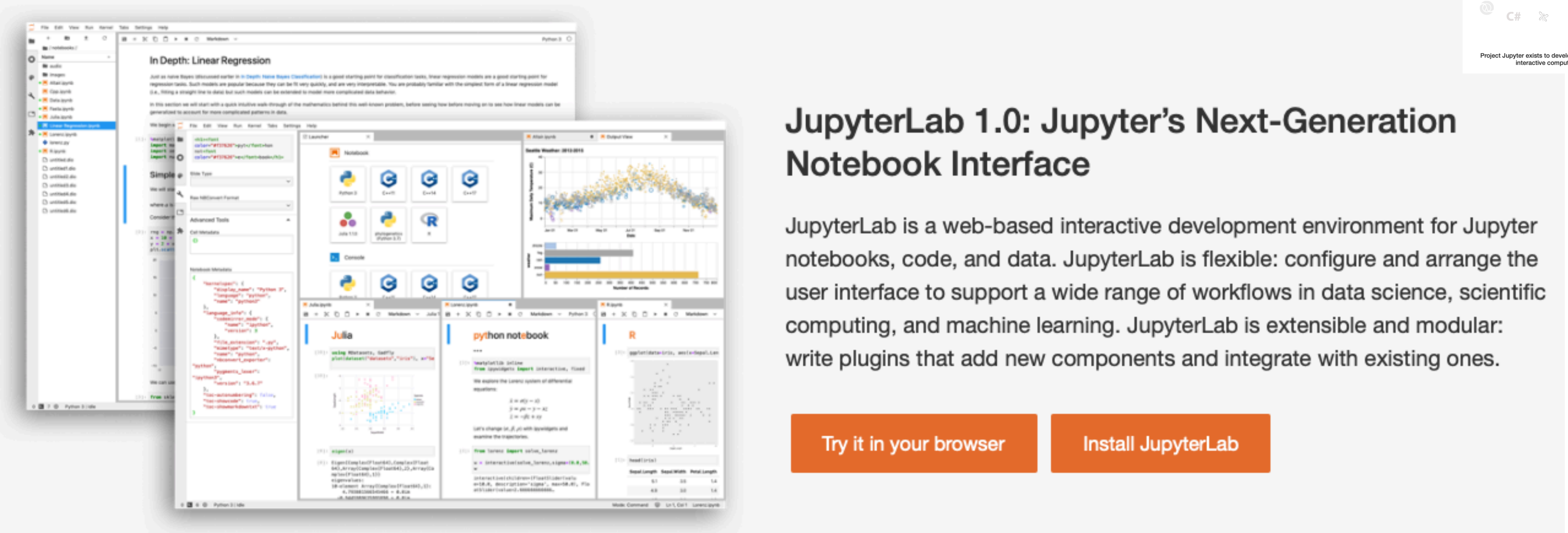
ioslides, Beamer

Project Jupyter exists to develop open-source software, open-standards, and services for interactive computing across dozens of programming languages.

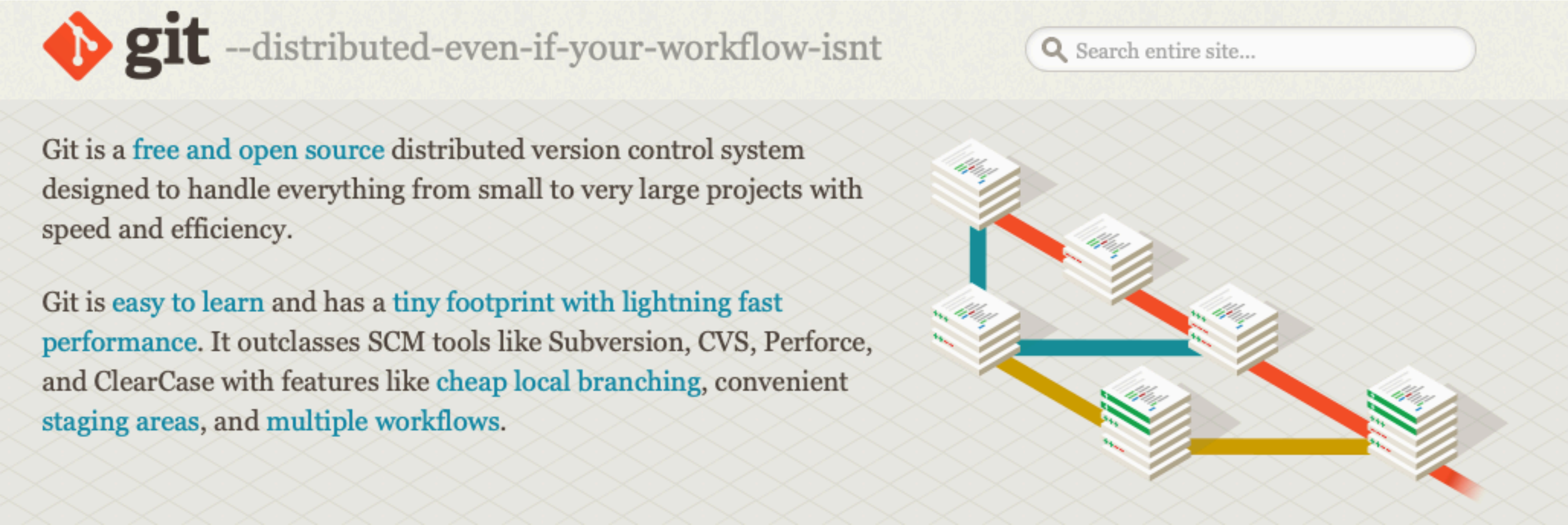


### JupyterLab 1.0: Jupyter's Next-Generation Notebook Interface

JupyterLab is a web-based interactive development environment for Jupyter notebooks, code, and data. JupyterLab is flexible: configure and arrange the user interface to support a wide range of workflows in data science, scientific computing, and machine learning. JupyterLab is extensible and modular: write plugins that add new components and integrate with existing ones.

## ✱ Version control

keeping a record of file changes over time
collaborating on a code development



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

Git is a free and open source distributed version control system designed to handle everything from small to very large projects with speed and efficiency.

Git is easy to learn and has a tiny footprint with lightning fast performance. It outclasses SCM tools like Subversion, CVS, Perforce, and ClearCase with features like cheap local branching, convenient staging areas, and multiple workflows.

https://git-scm.com

Git repository hosting services

GitHub Bitbucket GitLab

## ✱ Capturing the computational environment

CONDA

BIOCONDA®

**Package and environment manager**

- As a package it enables installing a wide range of tools using one command `conda install`
- As an environment manager it allows creating and managing multiple different environments, e.g. different versions of the same package

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### Containers

- Full control of environment. Can be used to package entire scientific workflows, software, libraries and data, by isolating everything in a “container"

# Summary

**Team work and project planning**

- **align on a common goal**
- **value team members**
- **communicate**

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**Data sharing & bioinformatics**

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**Team work and project planning**

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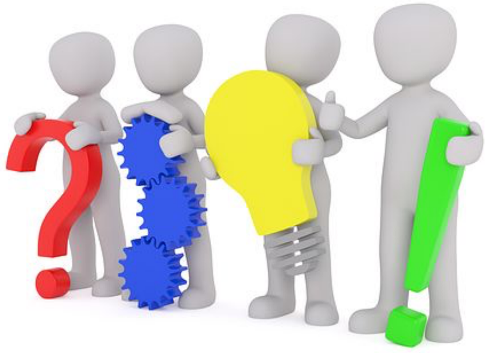

**Planning ahead:**

- **reproducible research**
- **reproducible publications**
- **sustainability and long-term growth**

# “Good collaboration checklist”

**https://docs.google.com/document/d/1MpefgEuklXooeo86Q5bX_wjD4RQxMHT9OlY1jEQA2q4/edit?usp=sharing**

**Thank you!**