University of Warsaw
Faculty of Mathematics, Informatics and Mechanics

Architecture of large projects in bioinformatics (ADP)

Lecture 10

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Outline

1. Data formats in bioinformatics,
2. Popular software libraries (BioPerl, BioPython)
3. Most important bioinformatics databases (UniProt, PDB, RefSeq, GenBank, ENA, InterPro, etc.)
4. Software licensing for scientific purposes. Free-software licensing. Patents.

5. Generic model Organism database (GMOD) project - assumptions, history and usage

6. Genome browsers, problem description and state of the solutions

7. Version control systems (CVS, SVN, git), and online collaboration ad distribution platforms (github, sourceforge).

8. Software testing, automated testing frameworks.

9. Scientific workflow systems - taverna and galaxy. MyExperiment platform. Reproducible research.

10. Literate programming idea and sweave, markdown, software documentation.

11. Interactive scripting platforms, Rstudio, Jupyter.

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Scientific workflow systems

https://en.wikipedia.org/wiki/Scientific_workflow_system

Anduril, bioinformatics and image analysis

- Apache Airavata, a general purpose workflow management system
- Apache Airflow, a general purpose workflow management system
- BioBIKE, a cloud-based bioinformatics platform
- Bioclipse, a graphical workbench, with a scripting environment that lets you perform complex actions as a kind of workflow.
- Common Workflow Language, a community-developed YAML-based workflow language, supported by multiple engine implementations.
- Cuneiform, a functional workflow language.
- CLC bio, a bioinformatics analysis and workflow management platform from QIAGEN Digital Insights.
- Discovery Net, one of the earliest examples of a scientific workflow system
- **Galaxy**, initially targeted at genomics
- GenePattern, a powerful scientific workflow system that provides access to hundreds of genomic analysis tools
- …

More than 280 computational data analysis workflow systems have been identified, although the distinction between data analysis workflows and scientific workflows is fluid, as not all analysis workflow systems are used for scientific purposes.

Scientific workflow systems

Taverna

Galaxy

Taverna Workbench v1.7.1.0

Design | Results | T2 Activity palette preview | Discover | Taverna 2 preview | myExperiment (beta)

Search | Watch loads

- Available Processors
  - Local Services
  - Biomart service @ http://www.biomart.org/biomart/martservice
  - Soaplab @ http://www.ebi.ac.uk/soaplab/emboss4/services/
  - WSDL @ http://www.ebi.ac.uk/ws/services/urn:Dbfetch?wsdl
  - WSDL @ http://soap.genome.jp/KEGG.wsdl
  - WSDL @ http://eutils.ncbi.nlm.nih.gov/entrez/eutils/soap/eutils.wsdl
  - WSDL @ http://soap.bind.ca/wsdl/bind.wsdl
  - WSDL @ http://www.ebi.ac.uk/xembl/XEMBL.wsdl
  - Biomoby @ http://moby.ucalgary.ca/moby/MOBY-Central.pl

Advanced model explorer

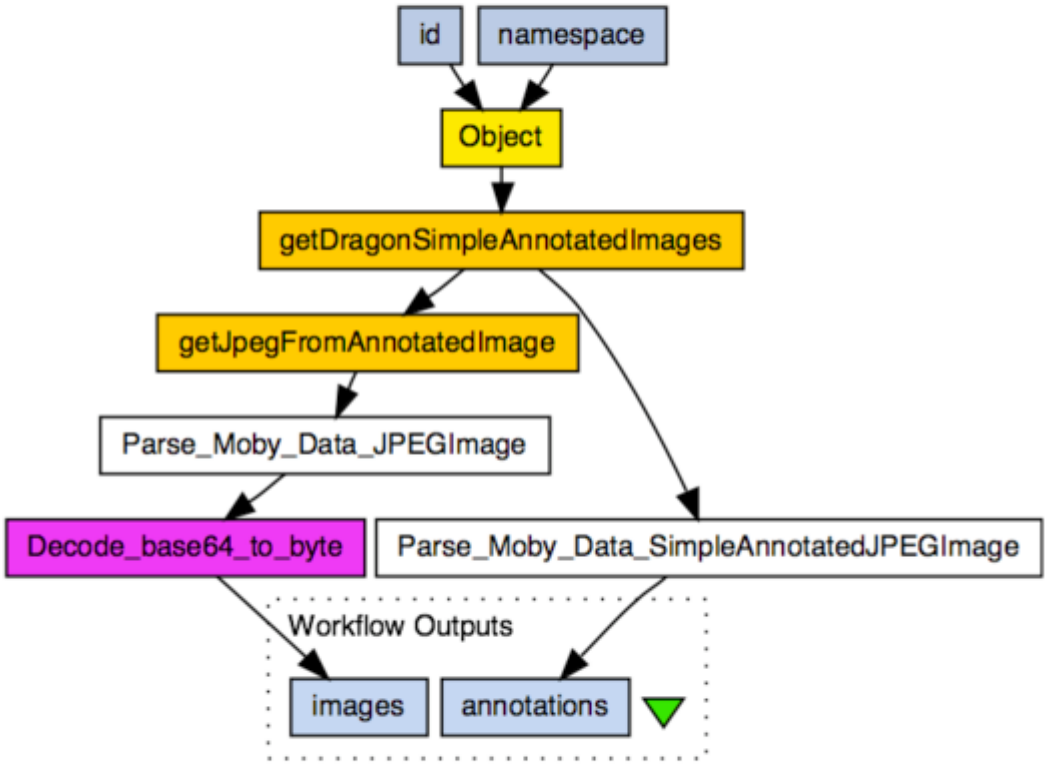
Workflow | Object properties

Add Nested Workflow | Offline

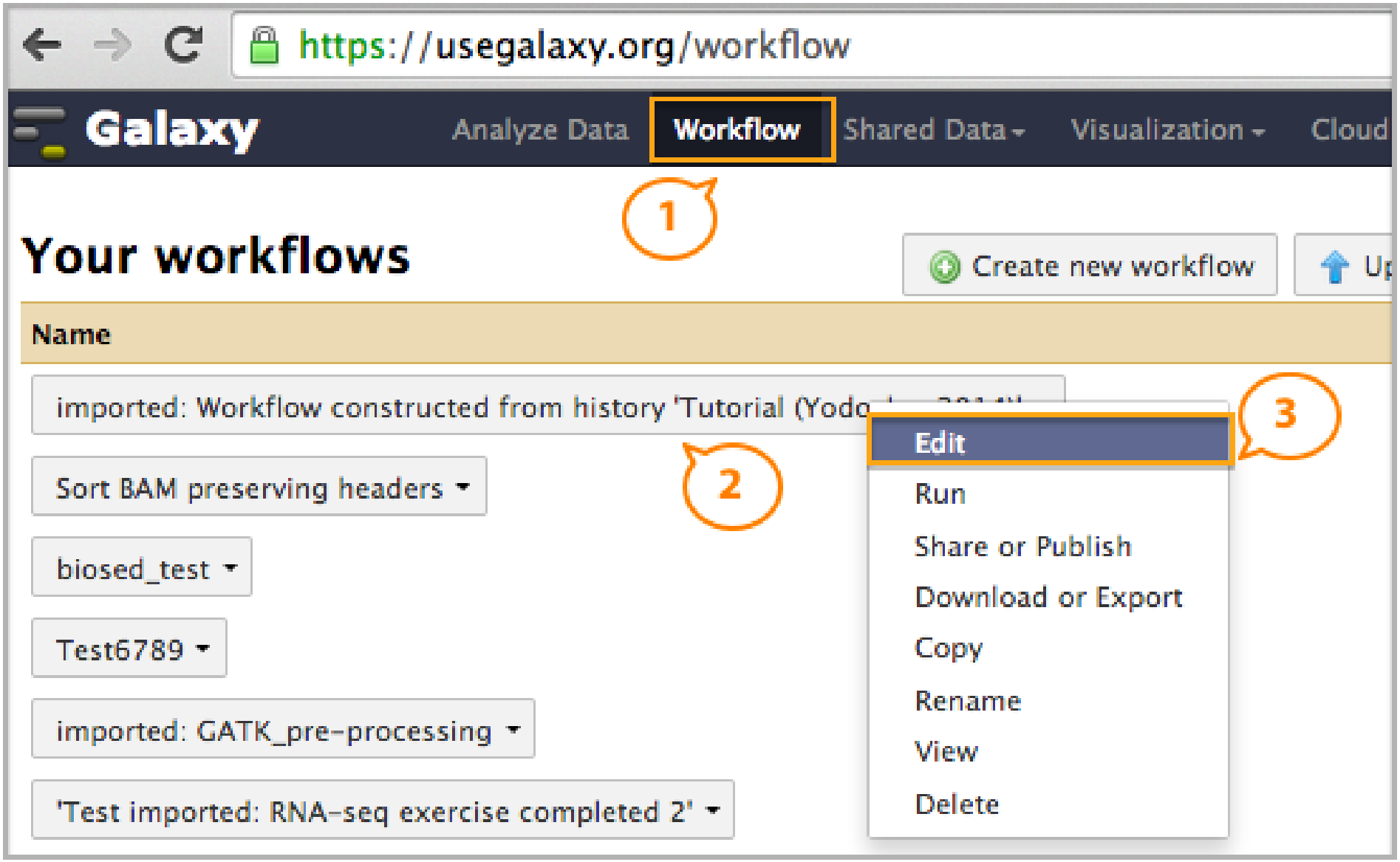
Workflow object	Retries	Delay	Backoff	Threads	Critical
Fetch Dragon images from BioMoby					
Workflow inputs					
Workflow outputs					
images					
annotations					
Processors					
id : cho	0	0	1	1	
namespace : DragonDB:Allele	0	0	1	1	
Decode_base64_to_byte	0	0	1	1	
getJpegFromAnnotatedImage	0	0	1	1	
getDragonSimpleAnnotatedImages	0	0	1	1	
Object	0	0	1	1	
Parse_Moby_Data_JPEGImage	0	0	1	1	
Parse_Moby_Data_SimpleAnnotatedJPEGImage	0	0	1	1	
Data links					
Decode_base64_to_byte:bytes-images					

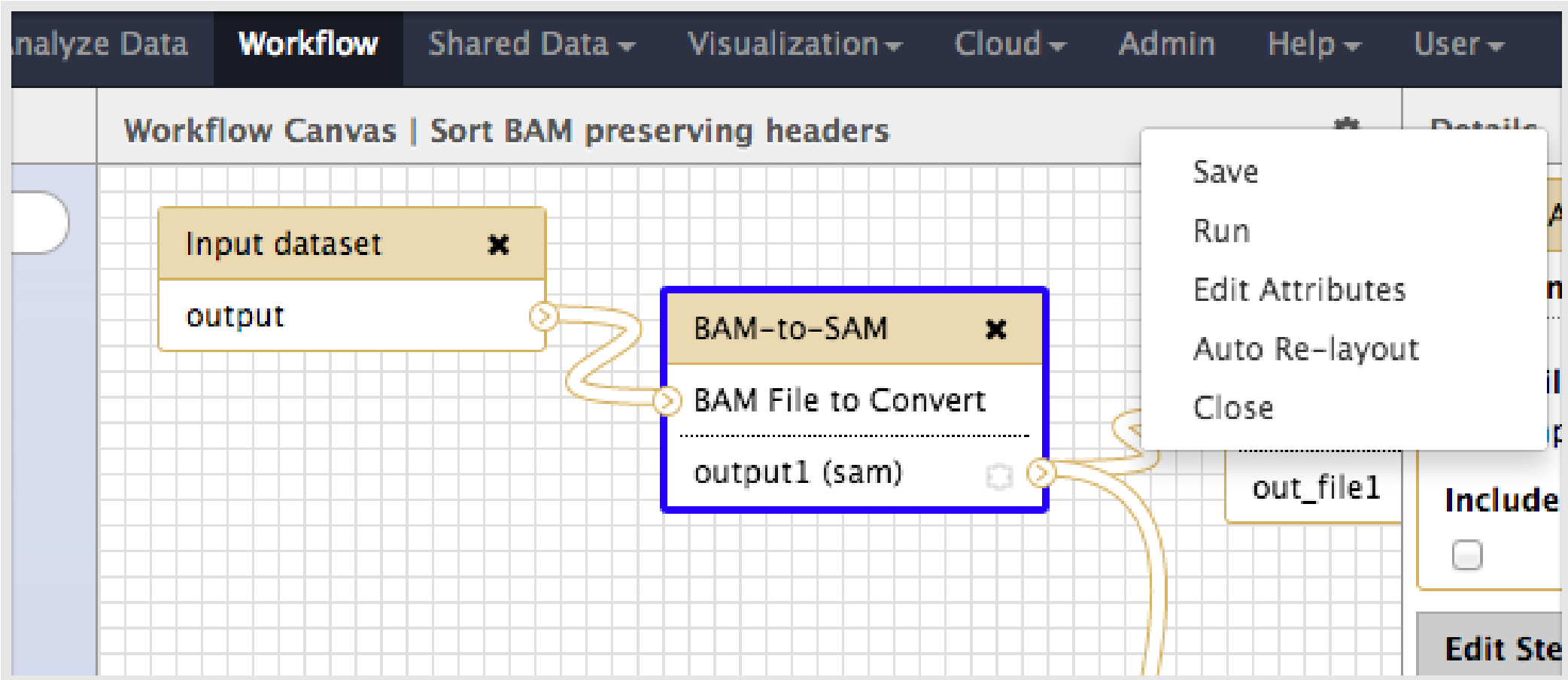
Graphical | Interactive (experimental)

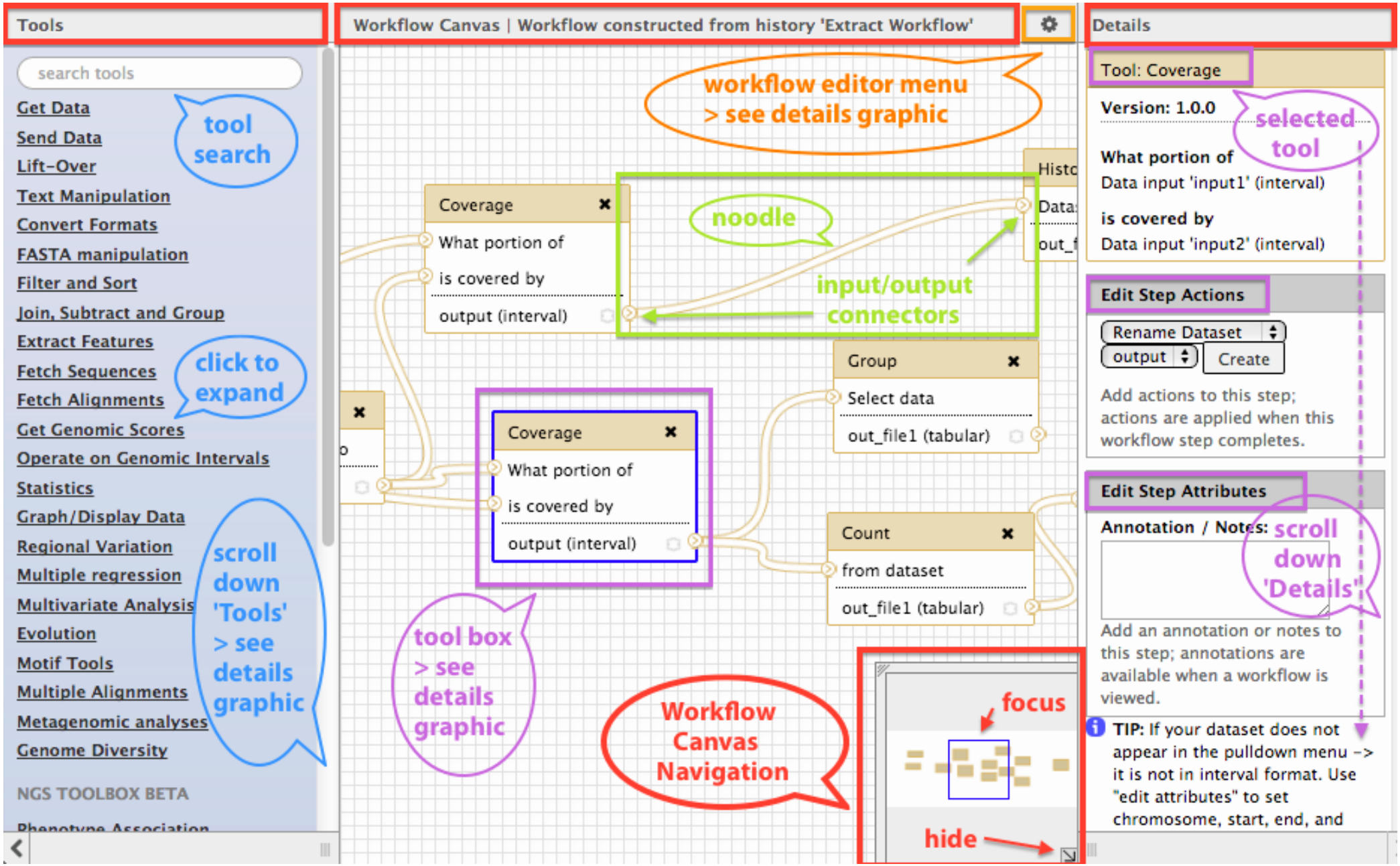
Save diagram | Refresh | Configure diagram



Rendering done.


https://usegalaxy.org/workflow
Galaxy
Analyze Data
Workflow
Shared Data
Visualization
Cloud
1
Your workflows
Create new workflow
Name
imported: Workflow constructed from history 'Tutorial (Yodo
2
3
Edit
Run
Share or Publish
Download or Export
Copy
Rename
View
Delete
Sort BAM preserving headers
biosed_test
Test6789
imported: GATK_pre-processing
'Test imported: RNA-seq exercise completed 2'


nalyze Data
Workflow
Shared Data
Visualization
Cloud
Admin
Help
User
Workflow Canvas | Sort BAM preserving headers
Input dataset
output
BAM-to-SAM
BAM File to Convert
output1 (sam)
Save
Run
Edit Attributes
Auto Re-layout
Close
out_file1
Include
Edit Ste


Tools
search tools
Get Data
Send Data
Lift-Over
Text Manipulation
Convert Formats
FASTA manipulation
Filter and Sort
Join, Subtract and Group
Extract Features
Fetch Sequences
Fetch Alignments
Get Genomic Scores
Operate on Genomic Intervals
Statistics
Graph/Display Data
Regional Variation
Multiple regression
Multivariate Analysis
Evolution
Motif Tools
Multiple Alignments
Metagenomic analyses
Genome Diversity
NGS TOOLBOX BETA
tool search
click to expand
scroll down 'Tools' > see details graphic
Workflow Canvas | Workflow constructed from history 'Extract Workflow'
workflow editor menu > see details graphic
Coverage
What portion of
is covered by
output (interval)
noodle
input/output connectors
Group
Select data
out_file1 (tabular)
Count
from dataset
out_file1 (tabular)
tool box > see details graphic
Workflow Canvas Navigation
focus
hide
Details
Tool: Coverage
Version: 1.0.0
selected tool
What portion of
Data input 'input1' (interval)
is covered by
Data input 'input2' (interval)
Edit Step Actions
Rename Dataset
output
Create
Add actions to this step; actions are applied when this workflow step completes.
Edit Step Attributes
Annotation / Notes:
scroll down 'Details'
Add an annotation or notes to this step; annotations are available when a workflow is viewed.
TIP: If your dataset does not appear in the pulldown menu -> it is not in interval format. Use "edit attributes" to set chromosome, start, end, and

Details

toolbox detail "B-1"

Tool: Coverage

Version: 1.0.0

1

What portion of

Data input 'input1' (interval)

2

is covered by

Data input 'input2' (interval)

Edit Step Actions

Rename Dataset

output Create

3

Add actions to this step; actions are applied when this workflow step completes.

Edit Step Attributes

Annotation / Notes:

4

Add an annotation or notes to this step; annotations are available when a workflow is viewed.

TIP: If your dataset does not appear in the pulldown menu -> it is not in interval format. Use "edit attributes" to set chromosome, start, end, and strand columns.

Find the coverage of intervals in the first dataset on intervals in the second dataset. The coverage is added as two columns, the first being bases covered, and the second being the fraction of bases covered by that interval.

5

Screencasts!

toolbox detail "B-2"

Screencasts!

See Galaxy Interval Operation Screencasts (right click to open this link in another window).

Example

5

if **First dataset** are genes

```
chr11 5203271 5204877 NM_000518 0 -
chr11 5210634 5212434 NM_000519 0 -
chr11 5226077 5227663 NM_000559 0 -
chr11 5226079 5232587 BC020719  0 -
chr11 5230996 5232587 NM_000184 0 -
```

and **Second dataset** are repeats:

```
chr11      5203895 5203991 L1MA6      500 +
chr11      5204163 5204239 A-rich     219 +
chr11      5211034 5211167 (CATATA)n  245 +
chr11      5211642 5211673 AT_rich     24 +
chr11      5226551 5226606 (CA)n      303 +
chr11      5228782 5228825 (TTTTTG)n  208 +
chr11      5229045 5229121 L1PA11     440 +
chr11      5229133 5229319 MER41A    1106 +
chr11      5229374 5229485 L2         244 -
chr11      5229751 5230083 MLT1A      913 -
chr11      5231469 5231526 (CA)n      330 +
```

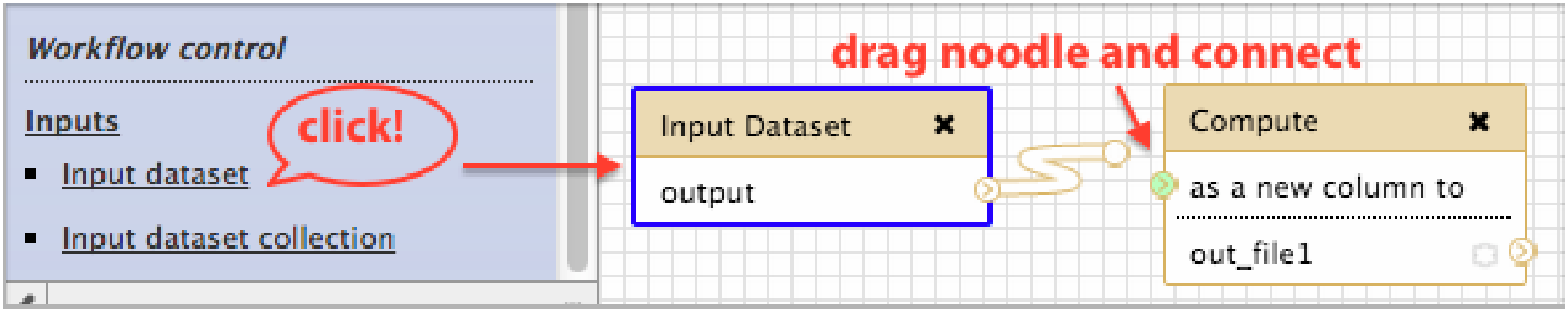
the Result is the coverage density of repeats in the genes:

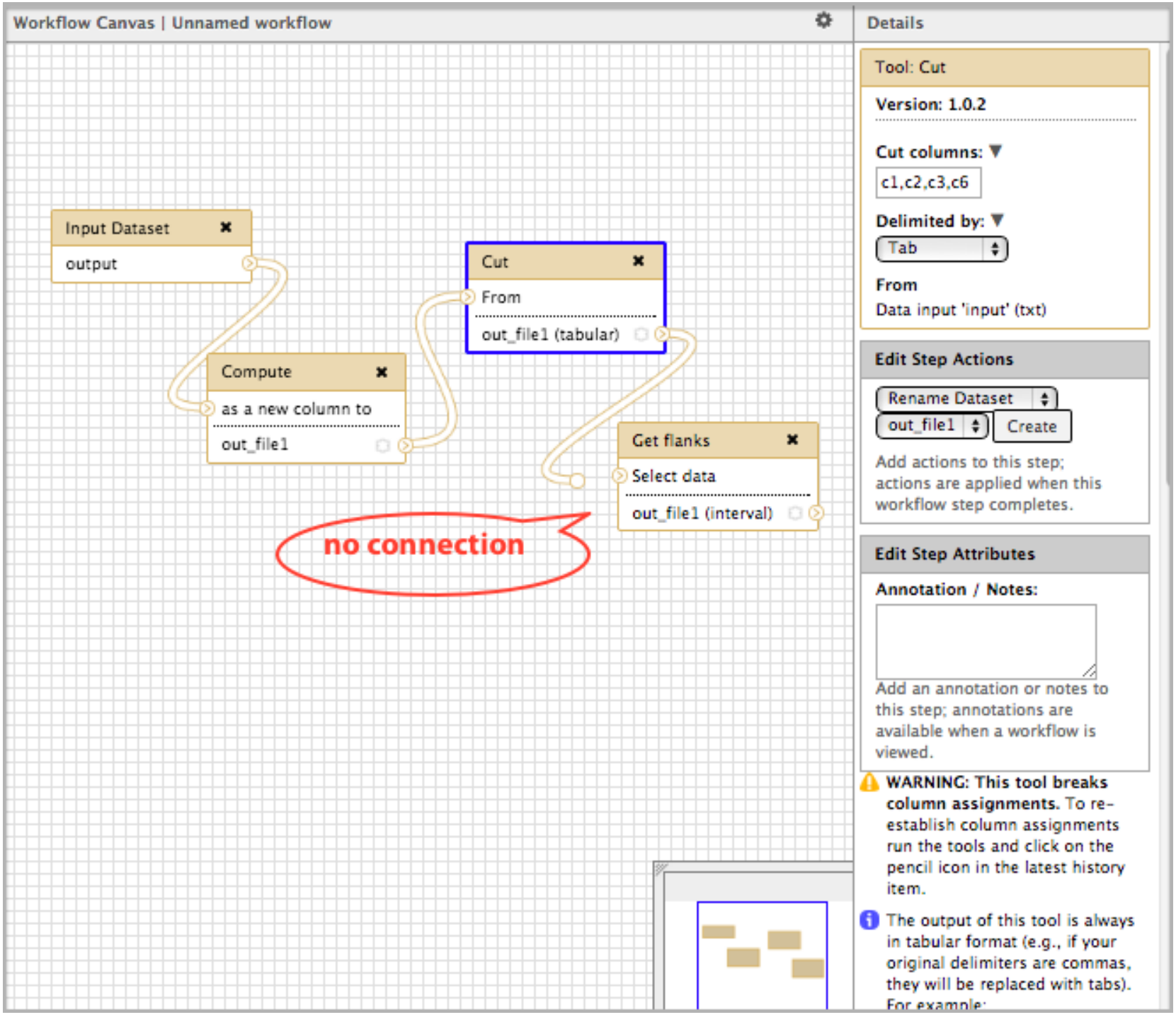
```
chr11 5203271 5204877 NM_000518 0 - 172   0.107098
chr11 5210634 5212434 NM_000519 0 - 164   0.091111
chr11 5226077 5227663 NM_000559 0 -  55   0.034678
chr11 5226079 5232587 BC020719  0 - 860   0.132145
chr11 5230996 5232587 NM_000184 0 -  57   0.035827
```

For example, the following line of output:

```
chr11 5203271 5204877 NM_000518 0 - 172   0.107098
```

implies that 172 nucleotides accounting for 10.7% of the this interval (chr11:5203271-5204877) overlap with repetitive elements.


Workflow control
Inputs
click!
Input dataset
Input dataset collection
drag noodle and connect
Input Dataset
output
Compute
as a new column to
out_file1


Workflow Canvas | Unnamed workflow
Input Dataset
output
Compute
as a new column to
out_file1
Cut
From
out_file1 (tabular)
Get flanks
Select data
out_file1 (interval)
no connection
Details
Tool: Cut
Version: 1.0.2
Cut columns:
c1,c2,c3,c6
Delimited by:
Tab
From
Data input 'input' (txt)
Edit Step Actions
Rename Dataset
out_file1
Create
Add actions to this step; actions are applied when this workflow step completes.
Edit Step Attributes
Annotation / Notes:
Add an annotation or notes to this step; annotations are available when a workflow is viewed.
WARNING: This tool breaks column assignments. To re-establish column assignments run the tools and click on the pencil icon in the latest history item.
The output of this tool is always in tabular format (e.g., if your original delimiters are commas, they will be replaced with tabs). For example:

https://github.com/galaxyproject 80%

Search or jump to… / Pull requests Issues Marketplace Explore

Galaxy Project

Galaxy is an open, web-based platform for data-intensive research.

http://galaxyproject.org/ outreach@galaxyproject.org

Repositories 98 Packages People 31 Projects 14

Pinned repositories

galaxy
Data intensive science for everyone.
Python 835 682

galaxy-hub
Galaxy Community Hub
Pug 47 164

training-material
A collection of Galaxy-related training material
HTML 200 483

tools-iuc
Tool Shed repositories maintained by the Intergalactic Utilities Commission
HTML 105 281

bioblend
A Python library for interacting with Galaxy and CloudMan APIs
Python 73 97

planemo
Command-line utilities to assist in developing Galaxy and Common Workflow Language artifacts - including tools, workflows, and training materials.
Python 65 68

Find a repository… Type Language Sort

training-material

A collection of Galaxy-related training material

training tutorial materials ngs metagenomics rnaseq proteomics

Top languages

Python HTML Shell Ruby Jinja

Data
Data
Data
BLAST
SAM Tools
BWA
BAM
FastQC
Velvet
RNA-SEQ
GFF
GALAXY
Results
Results
Results

Galaxy

Analyze Data | Workflow | Visualize | Shared Data | Help | User

Using 69%

Tools

search tools

Upload Data

Get Data
Collection Operations

GENERAL TEXT TOOLS

Text Manipulation
Filter and Sort
Join, Subtract and Group
Datamash

GENOMIC FILE MANIPULATION

FASTA/FASTQ
FASTQ Quality Control
SAM/BAM
BED
VCF/BCF
Nanopore
Convert Formats
Lift-Over

COMMON GENOMICS TOOLS

Interactive tools
Operate on Genomic Intervals
Fetch Sequences/Alignments

GENOMICS ANALYSIS

Assembly
Annotation

TOOLS

Galaxy is an open source, web-based platform for data intensive biomedical research. If you are new to Galaxy start here or consult our help resources. You can install your own Galaxy by following the tutorial and choose from thousands of tools from the Tool Shed.

JXTX

James P. Taylor Foundation

Design by Rebekka Paisner

James Taylor (1979-2020) believed that scientific progress can best be sustained through the mentoring of students and junior faculty.

To ensure implementation of this vision, the Galaxy community has established a foundation—JXTX: The James P. Taylor Foundation for Open Science. The JXTX Foundation's mission is to (1) assist graduate students to participate in computational biology and data science conferences, and (2) organize and host mentoring sessions between senior and junior faculty members at high-profile meetings.

To make this happen we are accepting contributions. More details can be found on **the @jxtx page in the Galaxy Hub**. Please, help us continue what James has started.

MAIN

Donate Now

Want to learn the best practices for the analysis of SARS-CoV-2 data using Galaxy? Visit the Galaxy SARS-CoV-2 portal at **covid19.galaxyproject.org**

PennState | Johns Hopkins University | Oregon Health & Science University | TACC | CyVerse

The Galaxy Team is a part of the Center for Comparative Genomics and Bioinformatics at Penn State, the Department of Biology at Johns Hopkins University and the Computational Biology Program at Oregon Health & Science University.

This instance of Galaxy is utilizing infrastructure generously provided by CyVerse at the Texas Advanced Computing Center, with support from the National Science Foundation.

History

search datasets

Galaxy introduction

(empty)

This history is empty. You can **load your own data** or **get data from an external source**

HISTORY

https://toolshed.g2.bx.psu.edu

Galaxy Tool Shed

Repositories Groups Help User

8140 valid tools on Apr 02, 2021

Search

Search for valid tools

Valid Galaxy Utilities

Tools

Custom datatypes

Repository dependency definitions

Tool dependency definitions

All Repositories

Browse by category

Available Actions

Login to create a repository

Repositories by Category

search repository name, description

Name	Description	Repositories
Assembly	Tools for working with assemblies	161
ChIP-seq	Tools for analyzing and manipulating ChIP-seq data.	75
Climate Analysis	Tools for analyzing climate data	5
Combinatorial Selections	Tools for combinatorial selection	9
Computational chemistry	Tools for use in computational chemistry	161
Constructive Solid Geometry	Tools for constructing and analyzing 3-dimensional shapes and their properties	11
Convert Formats	Tools for converting data formats	124
Data Export	Tools for exporting data to various destinations	10
Data Managers	Utilities for Managing Galaxy's built-in data cache	79
Data Source	Tools for retrieving data from external data sources	89
Ecology	Tools related to ecological studies	46
Entomology	Tools that involve insect studies	4

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Galaxy

Analyze Data | Workflow | Visualize | Shared Data | Help | User

Using 69%

Tools

search tools

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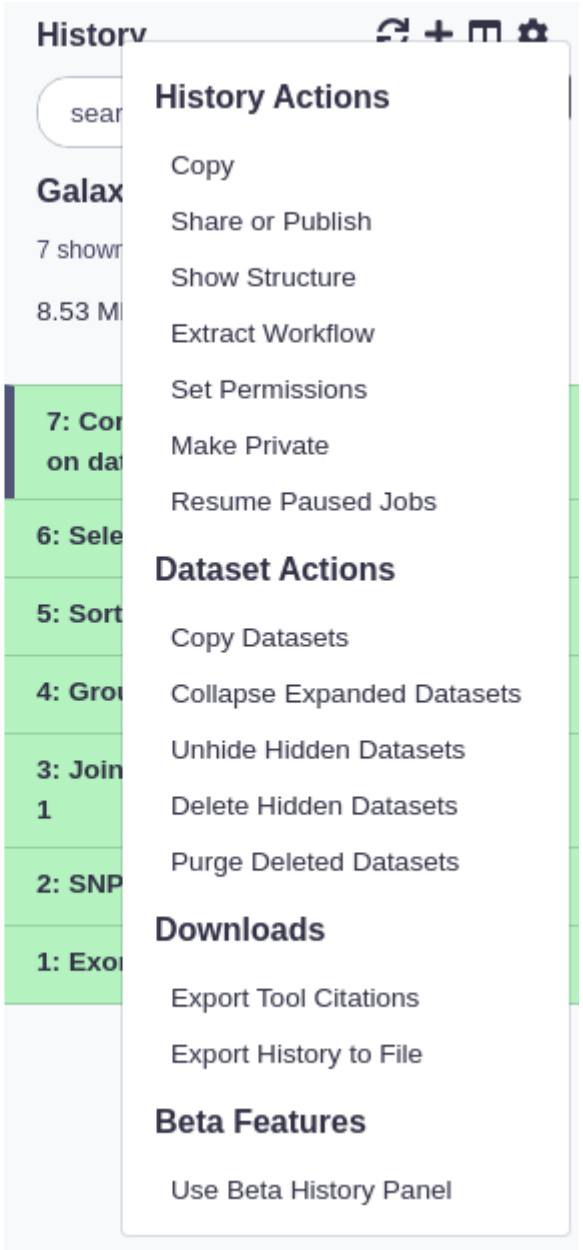
search datasets

Galaxy introduction

(empty)

This history is empty. You can **load your own data** or **get data from an external source**

HISTORY


History
sear
Galax
7 shown
8.53 M
7: Cor
on dat
6: Sele
5: Sort
4: Grou
3: Join
1
2: SNP
1: Exo
History Actions
Copy
Share or Publish
Show Structure
Extract Workflow
Set Permissions
Make Private
Resume Paused Jobs
Dataset Actions
Copy Datasets
Collapse Expanded Datasets
Unhide Hidden Datasets
Delete Hidden Datasets
Purge Deleted Datasets
Downloads
Export Tool Citations
Export History to File
Beta Features
Use Beta History Panel

Workflow name

Find exons with the highest number of SNPs

Create Workflow | Check all | Uncheck all

Tool		History items created
UCSC Main *This tool cannot be used in workflows*	▶	**1 Exons** ☑ Treat as input dataset Exons
UCSC Main *This tool cannot be used in workflows*	▶	**2 SNPs** ☑ Treat as input dataset SNPs
Join ☑ Include "Join" in workflow	▶	**3 Join on data 2 and data 1**
Group ☑ Include "Group" in workflow	▶	**4 Group on data 3**
Sort ☑ Include "Sort" in workflow	▶	**5 Sort on data 4**
Select first ☑ Include "Select first" in workflow	▶	**6 Select first on data 5**
Compare two Datasets ☑ Include "Compare two Datasets" in workflow	▶	**7 Compare two Datasets on data 6 and data 1**

Search Workflows

+ Create

Import

Name	Tags	Updated	Sharing	Bookmarked
Find exons with the highest number of SNPs		a few seconds ago		

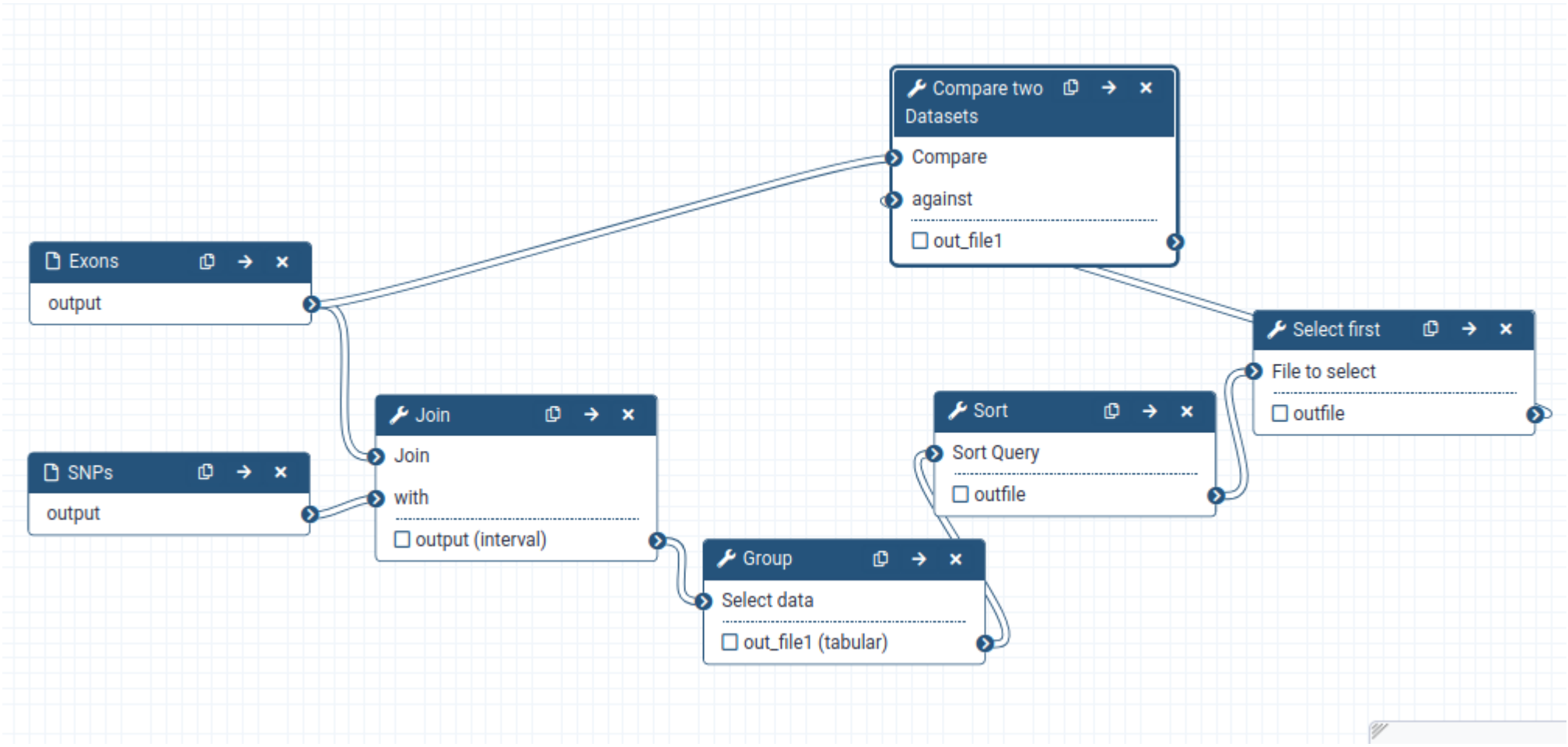
Search Workflows

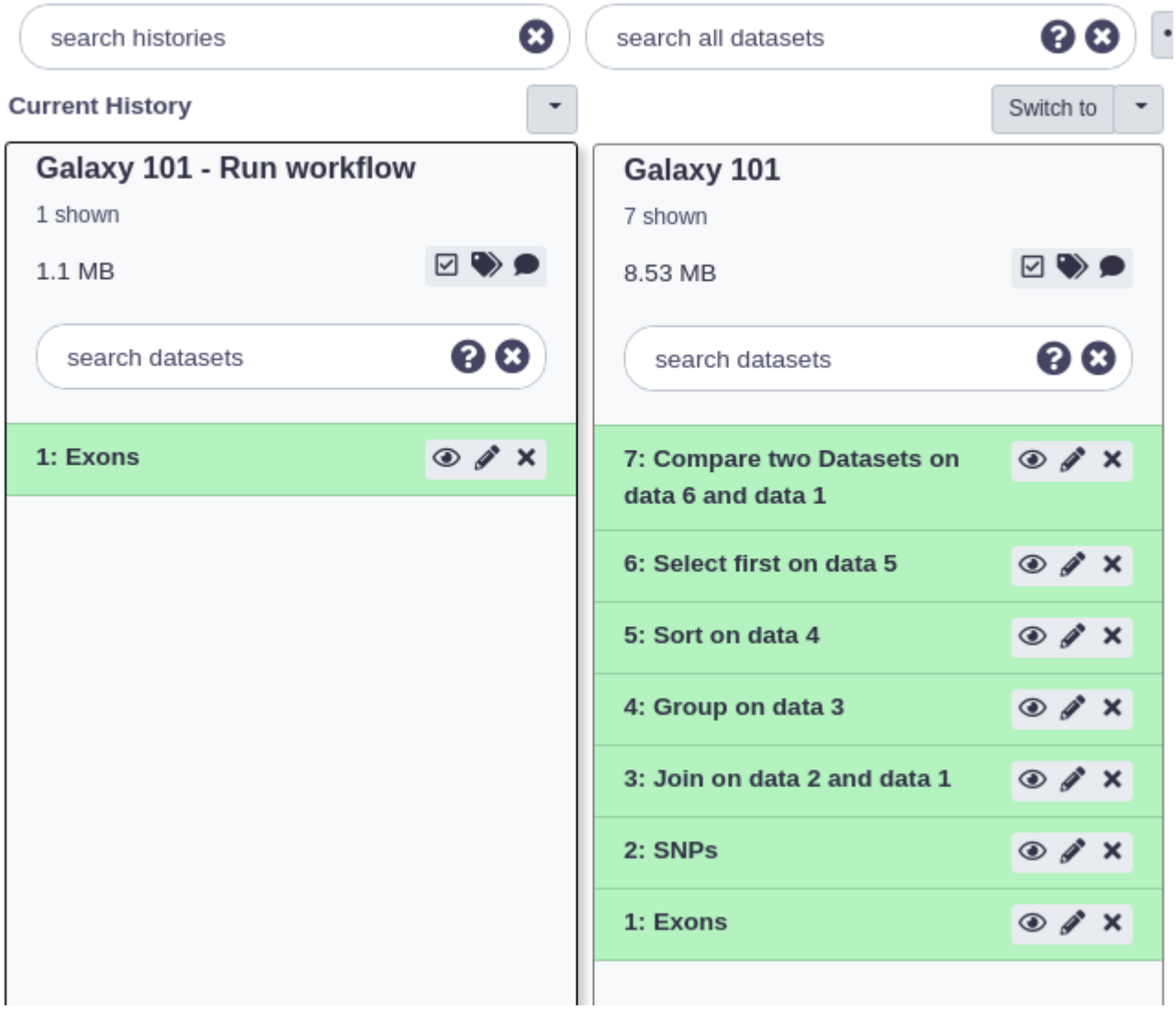
+ Create | Import

Name	Tags	Updated	Sharing	Bookmarked
Find exons with the highest number of SNPs		a few seconds ago		

Name	Tags	Updated	Sharing	Bookmarked
Find exons with the highest number of features		6 minutes ago		

- Edit
- Copy
- Download
- Rename
- Share
- View
- Delete


Compare two Datasets
Compare
against
out_file1
Exons
output
Select first
File to select
outfile
Join
Join
with
output (interval)
Sort
Sort Query
outfile
SNPs
output
Group
Select data
out_file1 (tabular)


search histories
search all datasets
Current History
Switch to
Galaxy 101 - Run workflow
1 shown
1.1 MB
search datasets
1: Exons
Galaxy 101
7 shown
8.53 MB
search datasets
7: Compare two Datasets on data 6 and data 1
6: Select first on data 5
5: Sort on data 4
4: Group on data 3
3: Join on data 2 and data 1
2: SNPs
1: Exons

Share your work

To share a history, click on the galaxy- **gear icon** in the history panel and select **Share or Publish**. On this page you can do 3 things:

Make History Accessible via Link. This generates a link that you can give out to others. Anybody with this link will be able to view your history.

Make History Accessible and Publish. This will not only create a link, but will also publish your history. This means your history will be listed under Shared Data → Histories in the top menu.

Share with a user. This will share the history only with specific users on the Galaxy instance.

Share your work

Share your work

python™

R

PyPi

Bioconductor
OPEN SOURCE SOFTWARE FOR BIOINFORMATICS

Python PyPi

Search projects

Help Sponsors Log in Register

isoelectric 1.0

```
pip install isoelectric
```

Latest version

Released: Sep 11, 2019

IPC (Isoelectric Point Calculator) - prediction of isoelectric point of proteins and peptides

Navigation

Project description

Release history

Project description

IPC is a program (available also as web service at isoelectric.org) for the accurate estimation of protein and peptide isoelectric point (pI) using Henderson-Hasselbach equation and pKa sets.

isoelectric 1.0

```
pip install isoelectric
```

Latest version

Released: Sep 11, 2019

Meta

License: Public Domain

Author: Lukasz Pawel Kozlowski

protein, peptide, isoelectric point, pI, biochemistry, proteomics

Requires: Python >=3.0

Maintainers

lukaskoz

Classifiers

License

- Public Domain

Operating System

- OS Independent

INSTALLATION:

wget http://isoelectric.org/ipc.zip; unzip ipc.zip; # sudo apt-get install unzip (if not present) cd ipc; sudo python setup.py install

USAGE:

python ipc.py <fasta_file> <pKa set> <output_file> <plot_file>

ipc <fasta_file> <pKa set> <output_file> <plot_file> (if installed into system using setup.py)

```
<fasta_file>    protein sequence(s) in fasta format, see ./examples
<pKa set>       one from pKa sets which will be used to calculate pI, default 'ALL' (report pI
                valid options are:
                        'ALL', 'IPC_protein', 'IPC_peptide',
                        'Bjellqvist', 'Dawson', 'Grimsley',
                        'Toseland', 'EMBOSS', 'Kozlowski',
                        'DTASelect', 'Wikipedia', 'Rodwell',
                        'Patrickios', 'Sillero', 'Thurlkill',
                        'Solomon', 'Nozaki_Tanford',
```

Python PyPi

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isoelectric 1.0

```
pip install isoelectric
```

Latest version

Released: Sep 11, 2019

Meta

License: Public Domain

Author: Lukasz Pawel Kozlowski

protein, peptide, isoelectric point, pI, biochemistry, proteomics

Requires: Python >=3.0

Maintainers

lukaskoz

Classifiers

License

- Public Domain

Operating System

- OS Independent

INSTALLATION:

wget http://isoelectric.org/ipc.zip; unzip ipc.zip; # sudo apt-get install unzip (if not present) cd ipc; sudo python setup.py install

USAGE:

python ipc.py <fasta_file> <pKa set> <output_file> <plot_file>

ipc <fasta_file> <pKa set> <output_file> <plot_file> (if installed into system using setup.py)

```
<fasta_file>    protein sequence(s) in fasta format, see ./examples
<pKa set>       one from pKa sets which will be used to calculate pI, default 'ALL' (report pI
                valid options are:
                        'ALL', 'IPC_protein', 'IPC_peptide',
                        'Bjellqvist', 'Dawson', 'Grimsley',
                        'Toseland', 'EMBOSS', 'Kozlowski',
                        'DTASelect', 'Wikipedia', 'Rodwell',
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```

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This changes affects maintainers of packages.

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1. biocblog post
2. branch renaming FAQ

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The development version of *Bioconductor* is version 3.14; it works with *R* version 4.1.0. More recent 'devel' versions of *R* (if available) will be supported during the next *Bioconductor* release cycle.

Install the latest release of R, then get the latest version of *Bioconductor* by starting R and entering the commands

```
if (!requireNamespace("BiocManager", quietly = TRUE))
    install.packages("BiocManager")
BiocManager::install(version = "3.13")
```

It may be possible to change the *Bioconductor* version of an existing installation; see the 'Changing version' section of the BiocManager vignette.

The current release of *Bioconductor* is version 3.17; it works with *R* version 4.3.0. Users of older R and *Bioconductor* must update their installation to take advantage of new features and to access packages that have been added to *Bioconductor* since the last release.

The development version of *Bioconductor* is version 3.18; it works with *R* version 4.3.0. More recent 'devel' versions of *R* (if available) will be supported during the next *Bioconductor* release cycle.

Install the latest release of R, then get the latest version of *Bioconductor* by starting R and entering the commands

```
if (!require("BiocManager", quietly = TRUE))
    install.packages("BiocManager")
BiocManager::install(version = "3.17")
```

It may be possible to change the *Bioconductor* version of an existing installation; see the 'Changing version' section of the BiocManager vignette.

Details, including instructions to install additional packages and to update, find, and troubleshoot are provided below. A devel version of *Bioconductor* is available. There are good reasons for using `BiocManager::install()` for managing *Bioconductor* resources.

Install specific packages, e.g., "GenomicFeatures" and "AnnotationDbi", with

```
BiocManager::install(c("GenomicFeatures", "AnnotationDbi"))
```

The `install()` function (in the BiocManager package) has arguments that change its default behavior; type `?install` for further help.

https://www.bioconductor.org/install/

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phyloseq

platforms all | rank 73 / 2042 | support 3 / 4 | in Bioc 9 years
build ok | updated before release | dependencies 75

DOI: 10.18129/B9.bioc.phyloseq

Handling and analysis of high-throughput microbiome census data

Bioconductor version: Release (3.13)

phyloseq provides a set of classes and tools to facilitate the import, storage, analysis, and graphical display of microbiome census data.

Author: Paul J. McMurdie <joey711 at gmail.com>, Susan Holmes <susan at stat.stanford.edu>, with contributions from Gregory Jordan and Scott Chamberlain

Maintainer: Paul J. McMurdie <joey711 at gmail.com>

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```
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```

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https://www.bioconductor.org/packages/devel/bioc/manuals/idpr/

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Package ‘idpr’

May 21, 2021

Type Package

Title Profiling and Analyzing Intrinsically Disordered Proteins in R

Version 1.3.0

Date 2020-09-14

Description ‘idpr’ aims to integrate tools for the computational analysis of intrinsically disordered proteins (IDPs) within R. This package is used to identify known characteristics of IDPs for a sequence of interest with easily reported and dynamic results. Additionally, this package includes tools for IDP-based sequence analysis to be used in conjunction with other R packages.

BugReports https://github.com/wmm27/idpr/issues

License LGPL-3

Encoding UTF-8

LazyData true

biocViews StructuralPrediction, Proteomics, CellBiology

RoxygenNote 7.1.1

Depends R (>= 4.0.0)

Imports ggplot2 (>= 3.3.0), magrittr (>= 1.5), dplyr (>= 0.8.5), plyr (>= 1.8.6), jsonlite (>= 1.6.1), rlang (>= 0.4.6), Biostrings (>= 2.56.0), methods (>= 4.0.0)

Suggests knitr, rmarkdown, msa, ape, testthat, seqinr

VignetteBuilder knitr

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VignetteBuilder knitr

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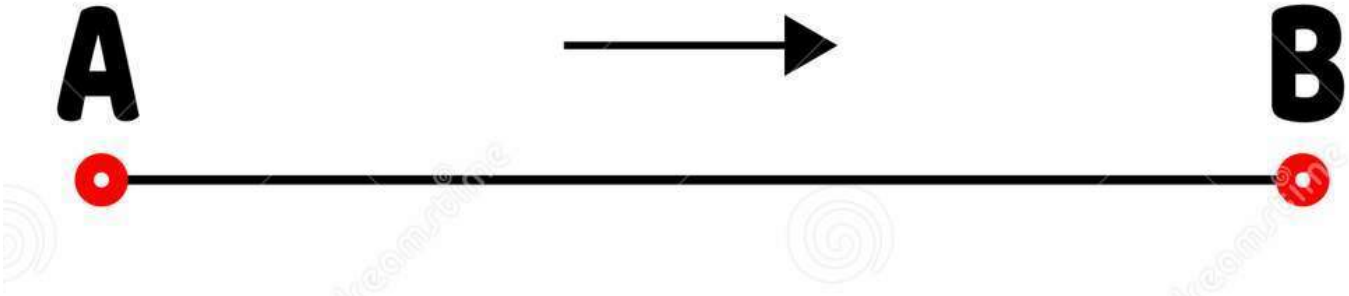
Problem to solve

Problem to solve



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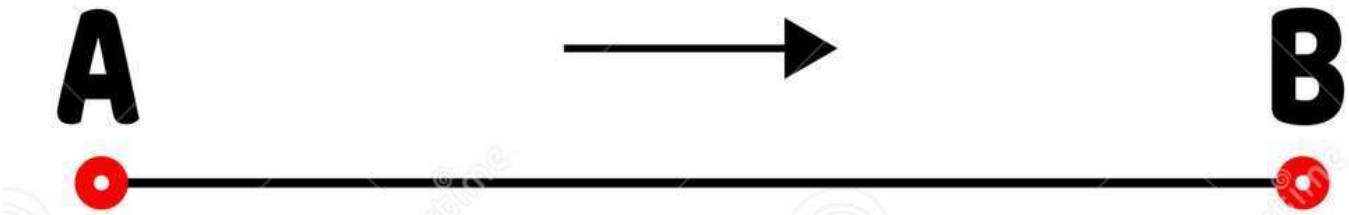

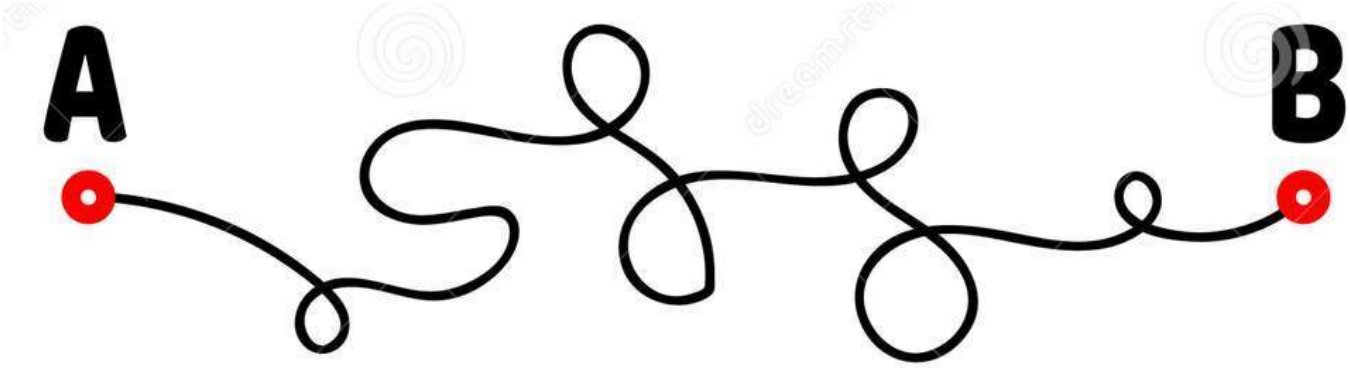

Problem to solve

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NIH National Institutes of Health

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Problem to solve

Grant assessment takes (at least) 6 months

(the bigger project, more parties involved, the longer)

Problem to solve

Grant assessment takes (at least) 6 months

(the bigger project, more parties involved, the longer)

Success rate is ~20%

(even if you have very good track record)

Problem to solve

The research
(1-2 years, if you are lucky)

Problem to solve

The research
(1-2 years, if you are lucky)

Problem to solve

Presenting results

Problem to solve

Presenting results

(6-12 months, if you are lucky)

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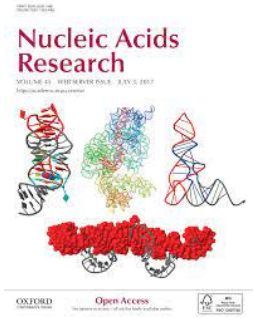

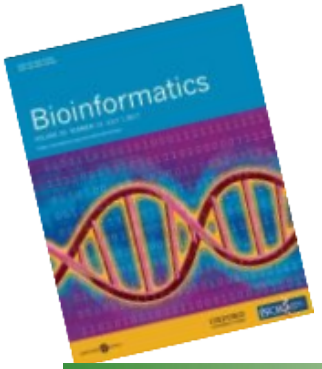

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Lukasz P. Kozlowski

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Ariel Erijman, Lukasz Kozlowski, Salma Sohrabi-Jahromi, James Fishburn, Linda Warfield, Jacob Schreiber, William S. Noble, Johannes Söding, Steven Hahn

bioRxiv 2019.12.11.872986; doi: https://doi.org/10.1101/2019.12.11.872986

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A high-throughput screen for transcription activation domains reveals their sequence characteristics and permits reliable prediction by deep learning

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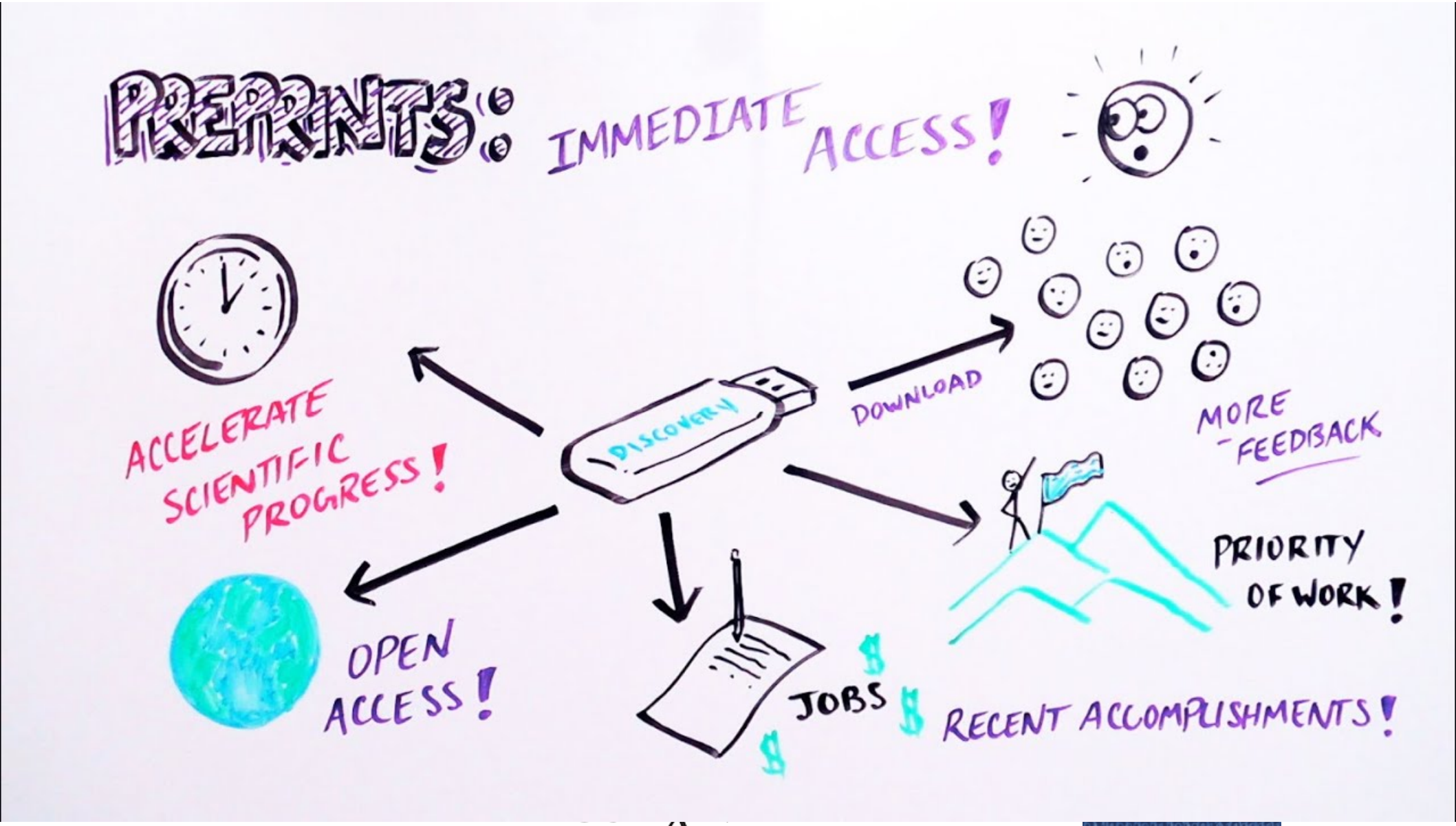
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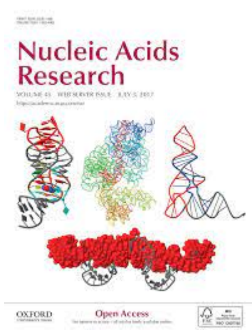

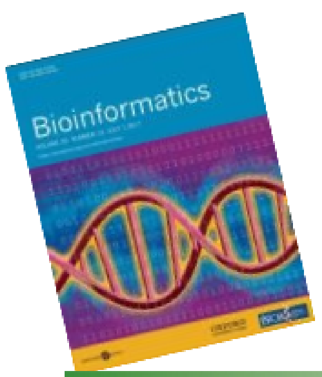

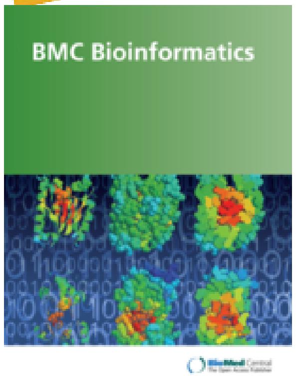

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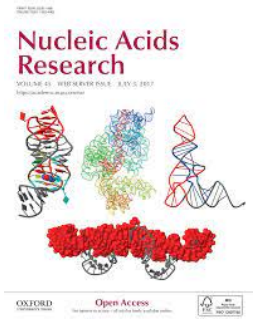

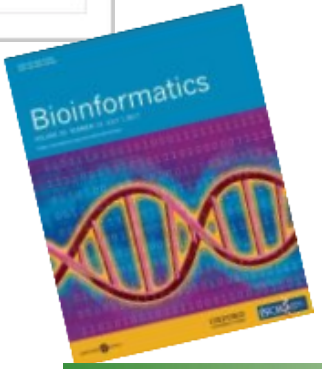

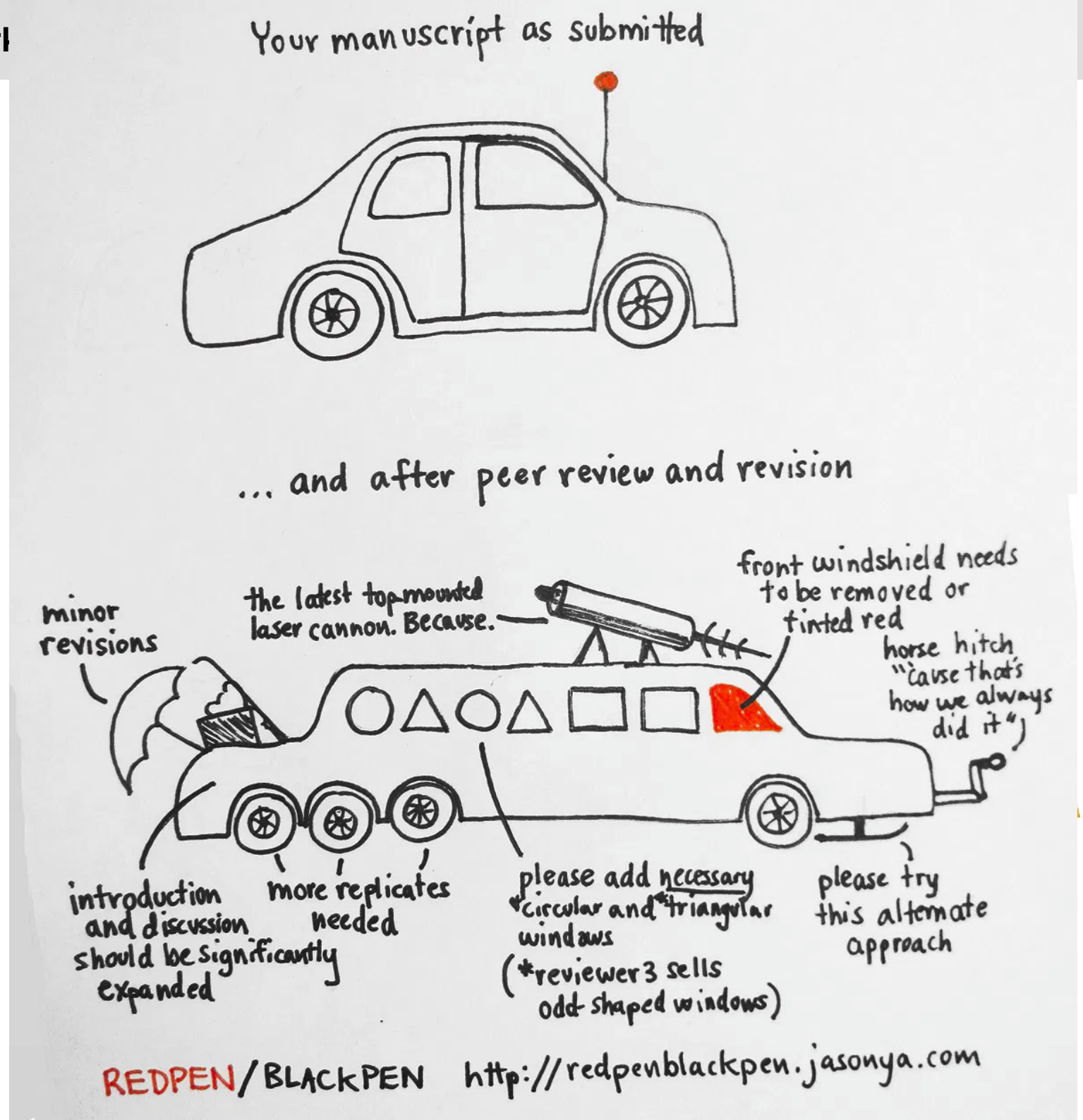
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Problem to solve

Idea & Grant (6-12 months) → **Research (1-3 years)** → **Publishing (6-12 months)**

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Problem to solve

Idea & Grant
(6-12 months)

Research
(1-3 years)

GitHub

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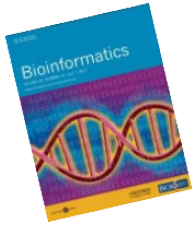

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(6-12 months)

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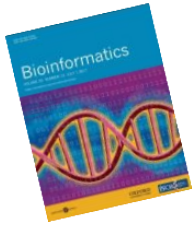

Publishing
(6-12 months)

Post Production
(at least 3-5 years)

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(6-12 months)

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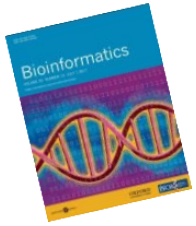

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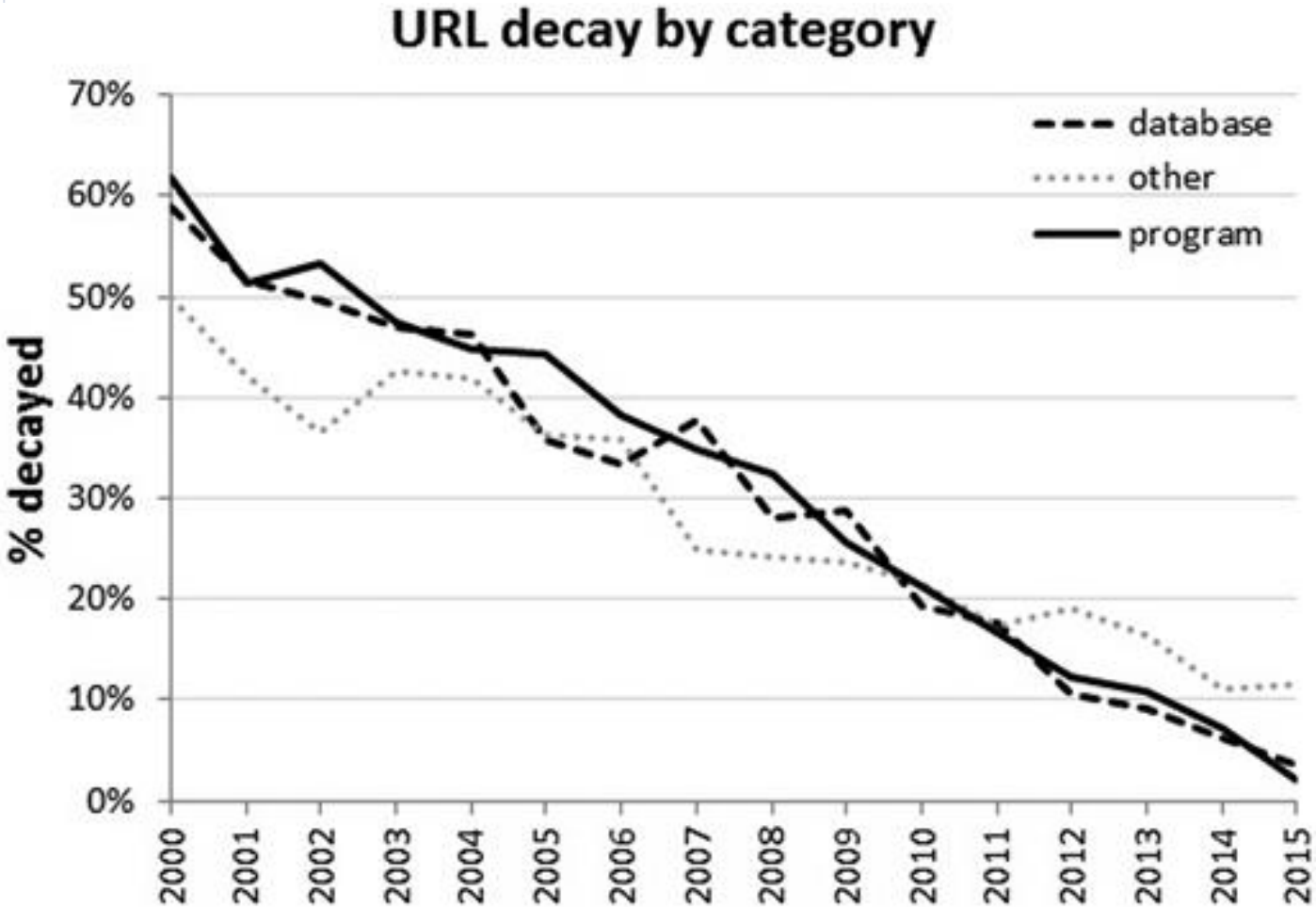

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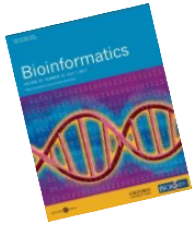
(1-3 years)

bioRχiv



Publishing
(6-12 months)

Post Production (at least 3-5 years)

Projects

Projects presentation will be done during last week on the lecture (10.06.25)

Formal requirements:

- the project has the github repository

- the project has the documentation

- license, data, scripts, test/examples are provided

Additionally, the project will be described by the leader of the Group (or few members) in short presentation (up to 20 min, plus 5-10 min for discussions).

The format: pdf/ppt and/or if possible interactive presentation of the project in the browser

Projects presentation will be done during last week on the lecture (10.06.25)

Presentation should include:

- the introduction of the project (problem to be solved)

- the objectives (what you wanted to achieve)

- the results (what you achieved)

- the conclusions & possible directions for the future (what the software can do and what can be improved if more people would join)

Projects presentation will be done during last week on the lcture (10.06.25)

Presentation should include:

- the introduction of the project (problem to be solved)

- the objectives (what you wanted to achieve)

- the results (what you achieved)

- the conclusions & possible directions for the future (what the software can do and what can be improved if more people would join)

The project and presentations should be finished up to 09.06.
(please upload the presentation to the github of your repository up to 09.06)

Thank you for your time
and
See you at the next lecture

Any other
questions & comments

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