从零入门科研数据可视化云平台

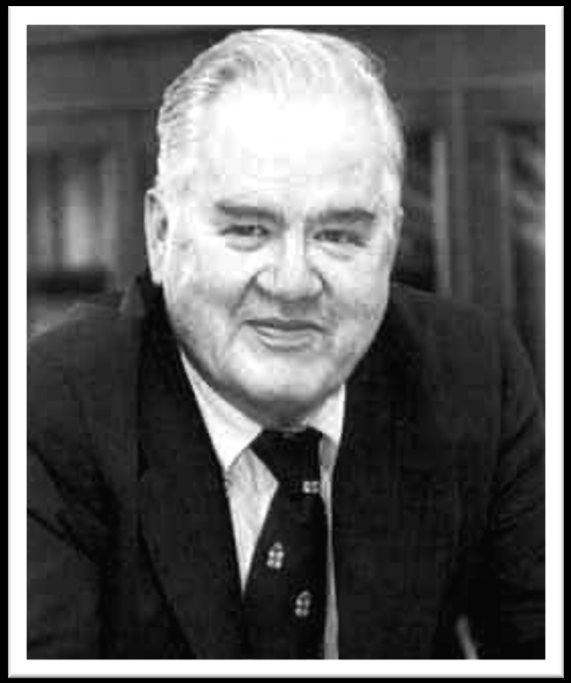
openbiox & Hiplot Team

2020-12-26

Hiplot Team

Shanghai 200025, CHINA

HIPLOT



John Tukey

(1915-2000)

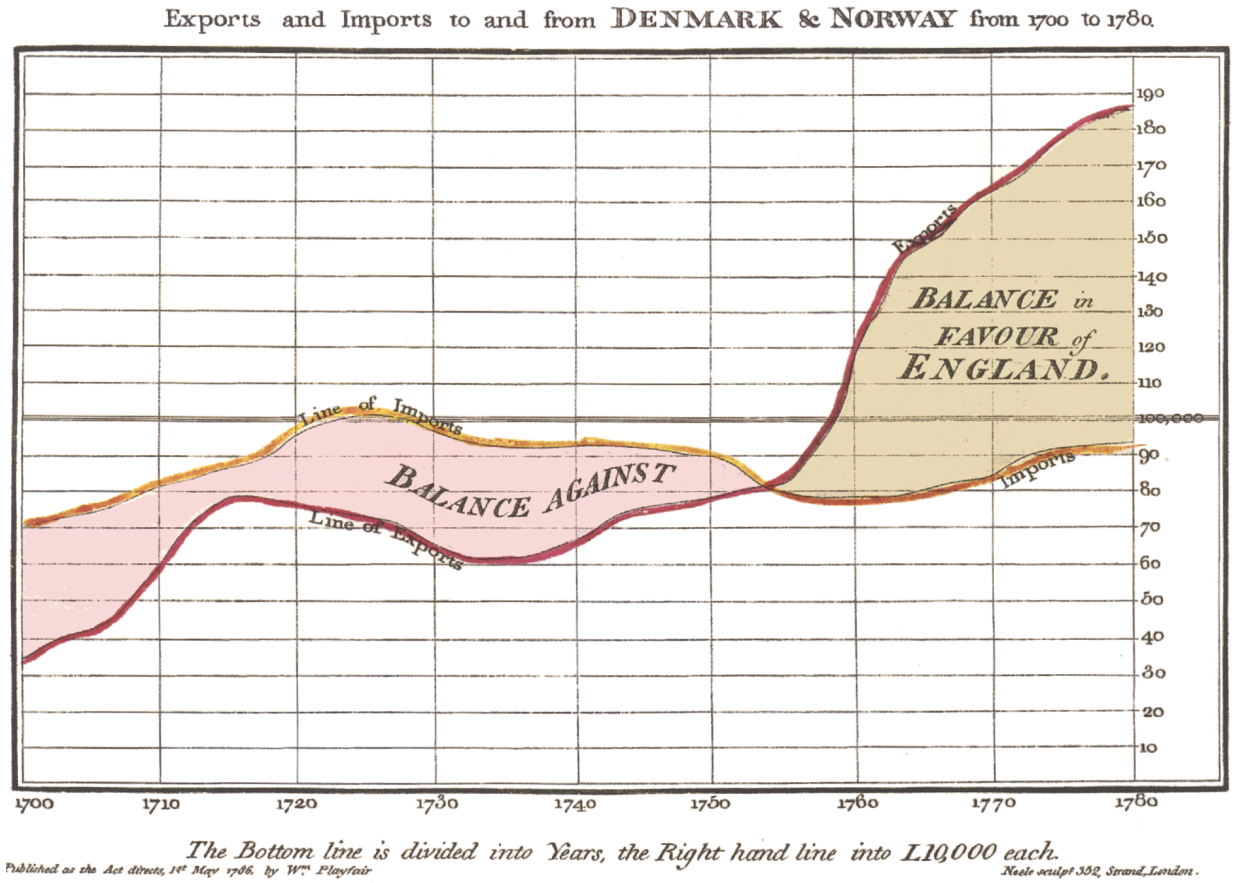
The greatest value of a picture is when it forces us to notice what we never expected to see.

图形的最大价值就是使我们注意到我们从来没有料到过的信息

目录

- 科研绘图实例
- Hiplot 可视化平台简介
- Hiplot 可视化平台操作演示

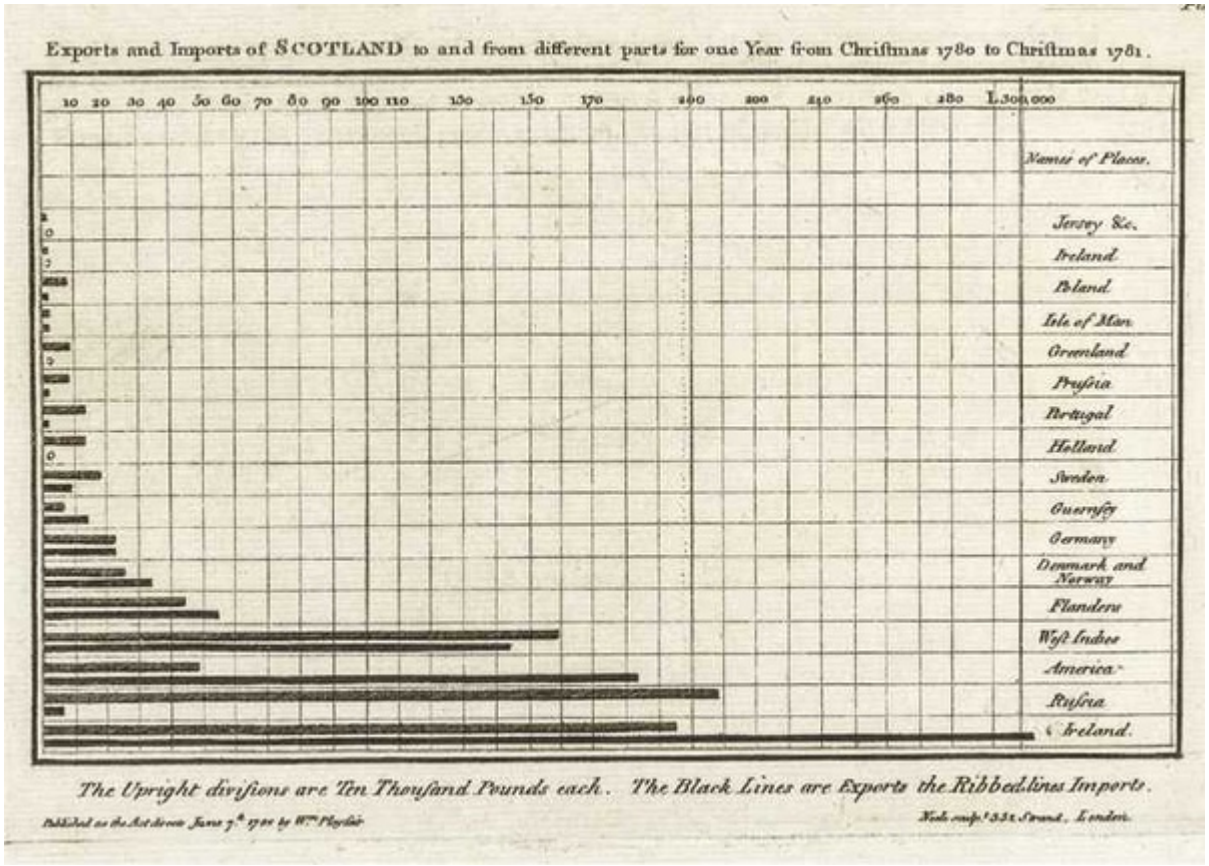
科研绘图实例 | 历史



威廉•普莱费尔（William Playfair，1786) 绘制的线图

英格兰进出口时序数据

https://hiplot.com.cn/books-static/msg-book/history.html#section

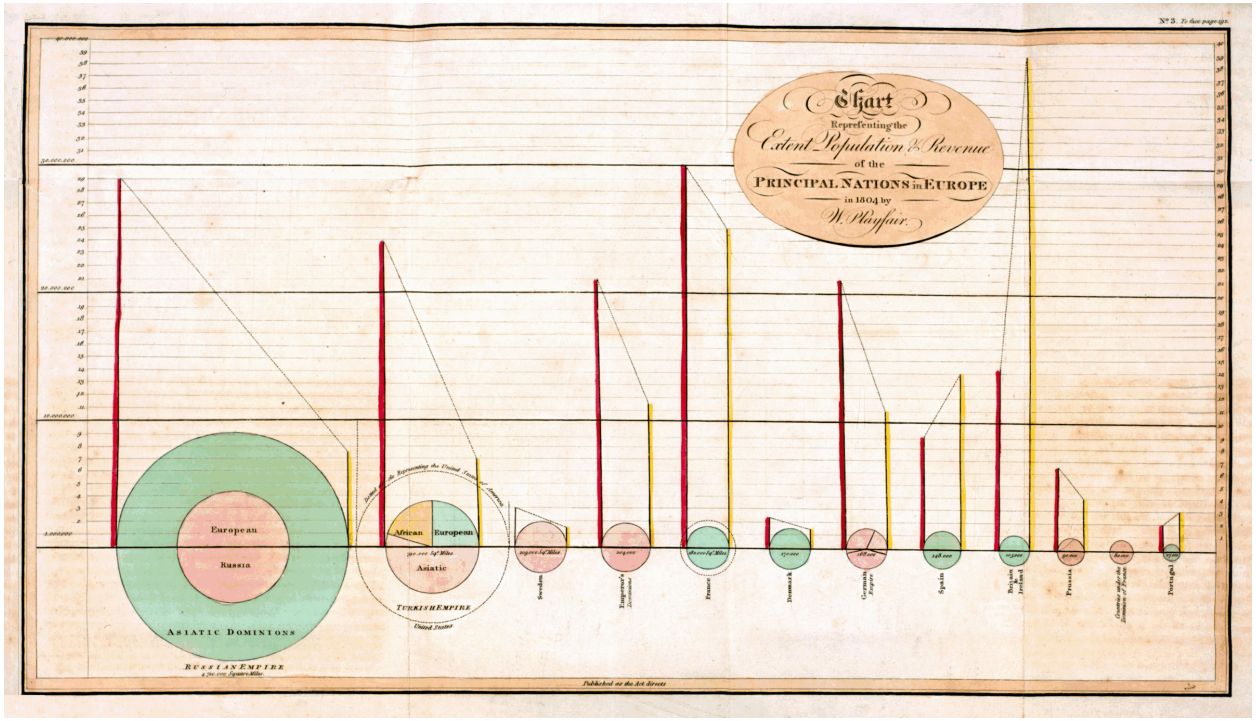


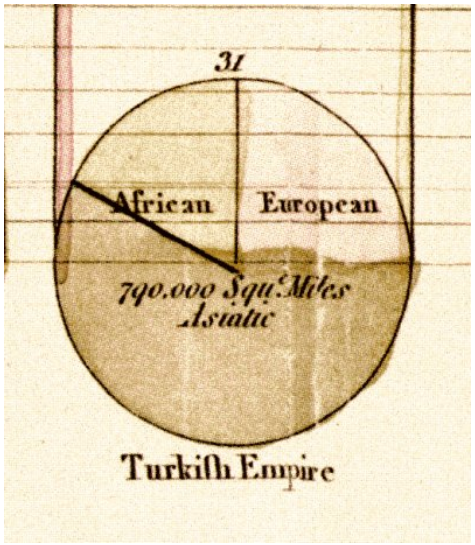
威廉•普莱费尔（William Playfair，1786) 绘制的条形图

苏格兰的贸易伙伴

https://hiplot.com.cn/books-static/msg-book/history.html#section

科研绘图实例 | 历史



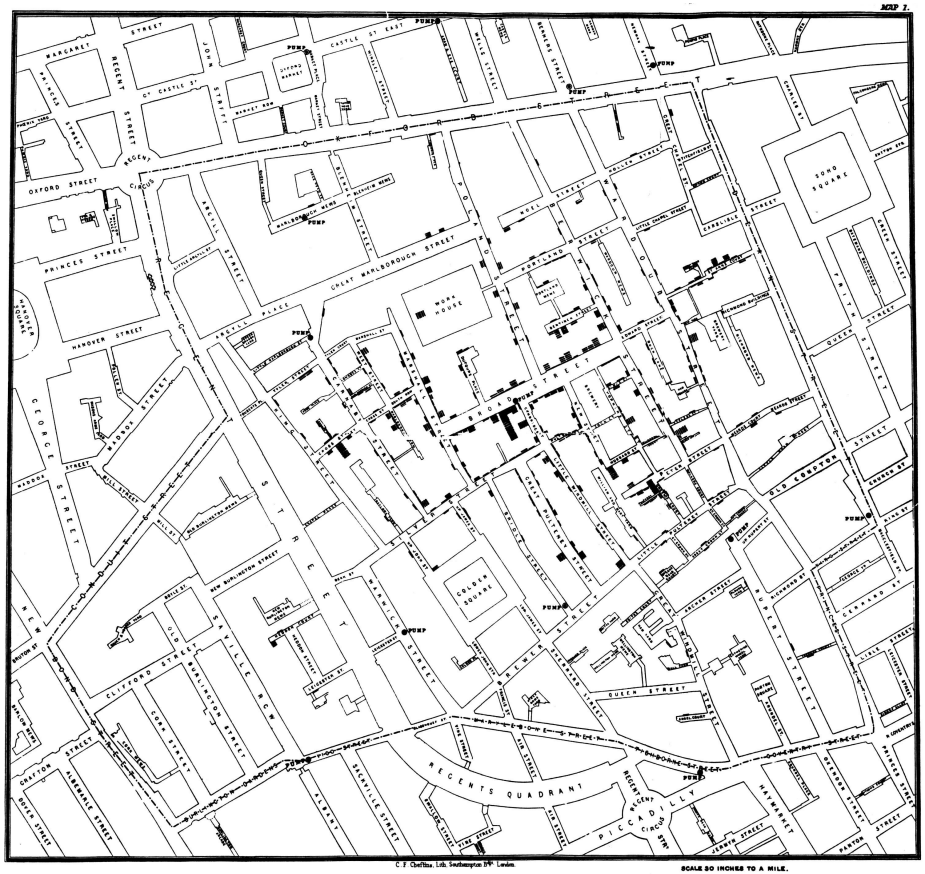


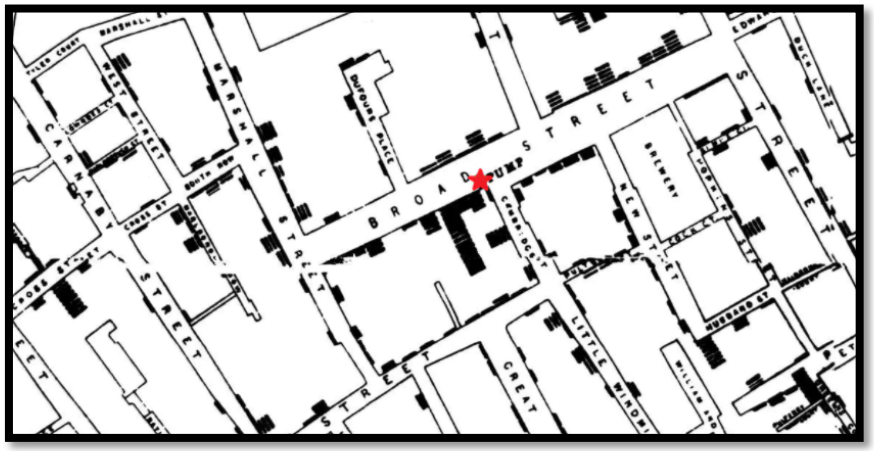
威廉·普莱费尔 （William Playfair，1801) 绘制的饼图

法国大革命前后一些欧洲国家的统计数据

https://hiplot.com.cn/books-static/msg-book/history.html#section

科研绘图实例 | 历史





1854 年英国 Broad 大街大规模爆发霍乱

约翰·斯诺（John Snow）绘制

https://hiplot.com.cn/books-static/msg-book/history.html#section

结构化与非结构化

https://tecky.io/en/blog/

结构化与非结构化

Normal Arial 10

	A	B	C	D	E	F	G
1	species	island	culmen_length	culmen_depth_	flipper_length_	body_mass_g	sex
2	Adelie	Torgersen	39.1	18.7	181	3750	MALE
3	Adelie	Torgersen	39.5	17.4	186	3800	FEMALE
4	Adelie	Torgersen	40.3	18	195	3250	FEMALE
5	Adelie	Torgersen	NA	NA	NA	NA	NA
6	Adelie	Torgersen	36.7	19.3	193	3450	FEMALE
7	Adelie	Torgersen	39.3	20.6	190	3650	MALE
8	Adelie	Torgersen	38.9	17.8	181	3625	FEMALE
9	Adelie	Torgersen	39.2	19.6	195	4675	MALE
10	Adelie	Torgersen	34.1	18.1	193	3475	NA
11	Adelie	Torgersen	42	20.2	190	4250	NA
12	Adelie	Torgersen	37.8	17.1	186	3300	NA
13	Adelie	Torgersen	37.8	17.3	180	3700	NA
14	Adelie	Torgersen	41.1	17.6	182	3200	FEMALE
15	Adelie	Torgersen	38.6	21.2	191	3800	MALE
16	Adelie	Torgersen	34.6	21.1	198	4400	MALE
17	Adelie	Torgersen	36.6	17.8	185	3700	FEMALE

Sheet1

结构化与非结构化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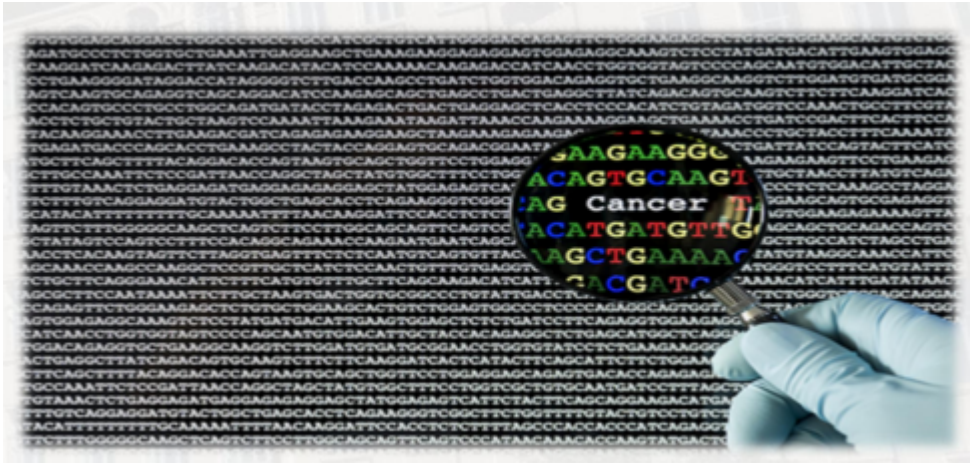
结构化与非结构化


非結構化數據
10011
00111
11010




卫星图像
自然场景
运动场景
自动驾驶
医学影像
文字文本


人脸
虹膜
指纹
掌纹
语音信号
视频信号

科研绘图实例

常见可视化图形

→ 数据的分布规律

→ 数据变量间的关联规律

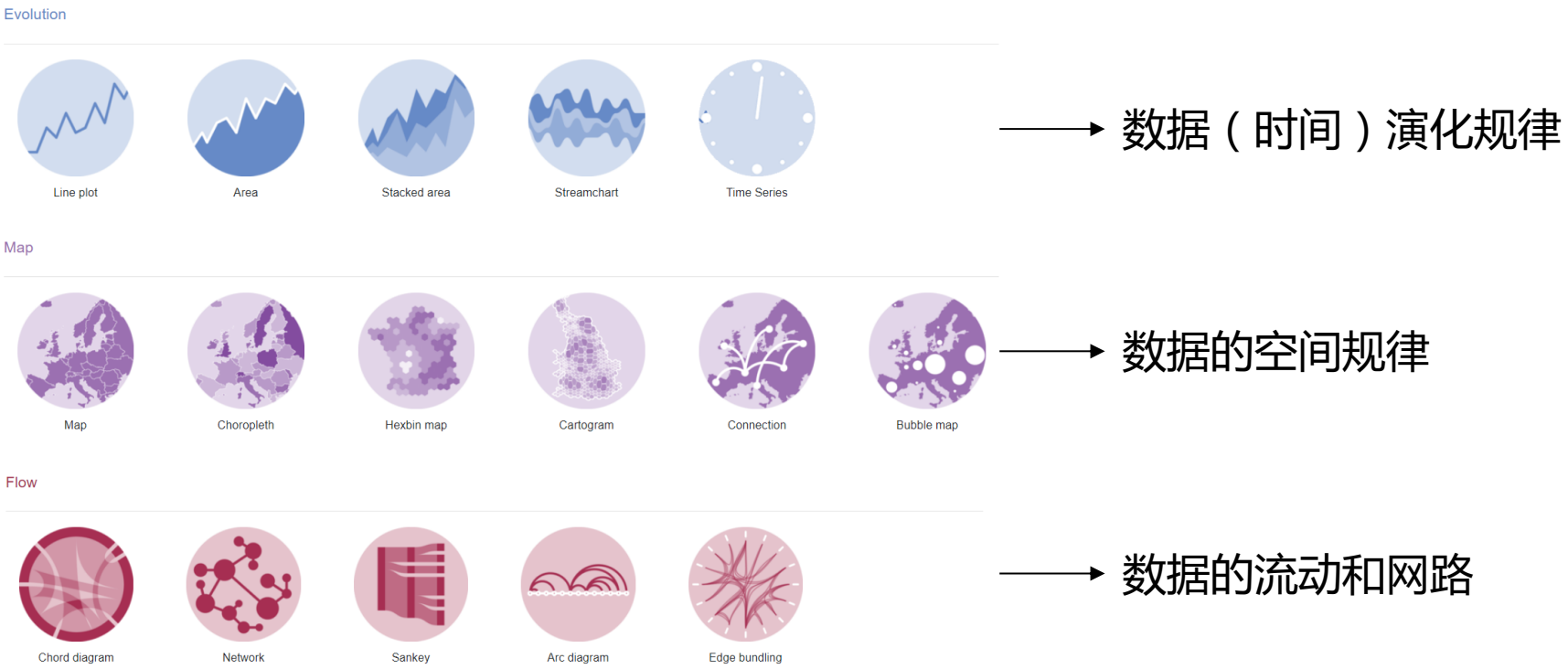
→ 数据的数值高低

→ 数据的归类及其占比

https://hiplot.com.cn/books-static/r-graph-gallery/

科研绘图实例

常见可视化图形



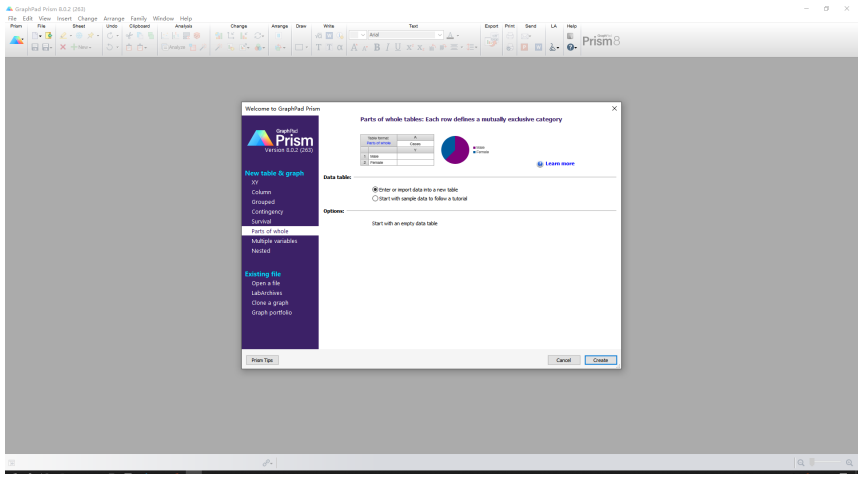
→ 数据（时间）演化规律

→ 数据的空间规律

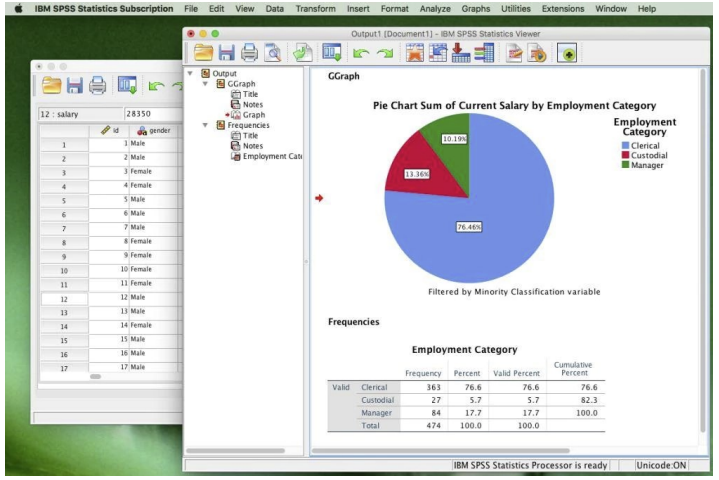
→ 数据的流动和网路

https://hiplot.com.cn/books-static/r-graph-gallery/

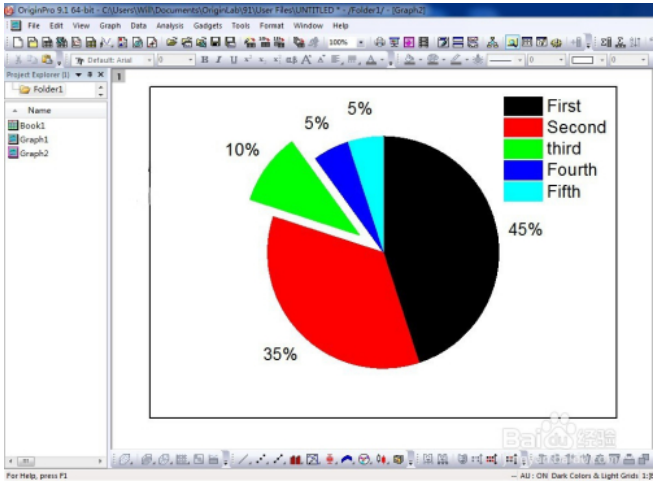
科研绘图实例 | 常用绘图工具



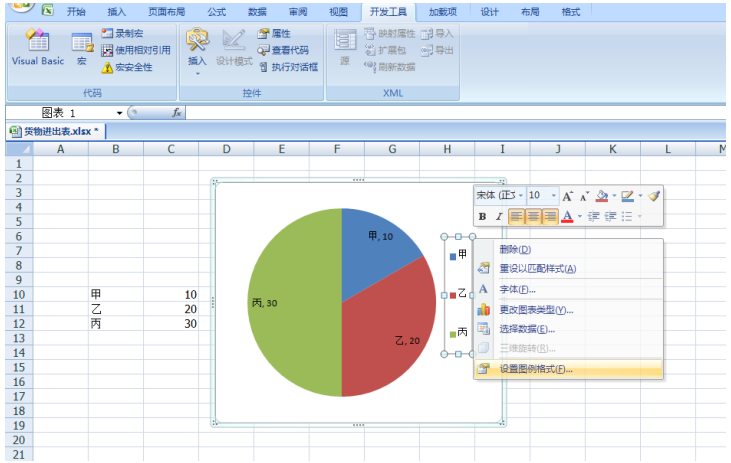
Graphpad



SPSS

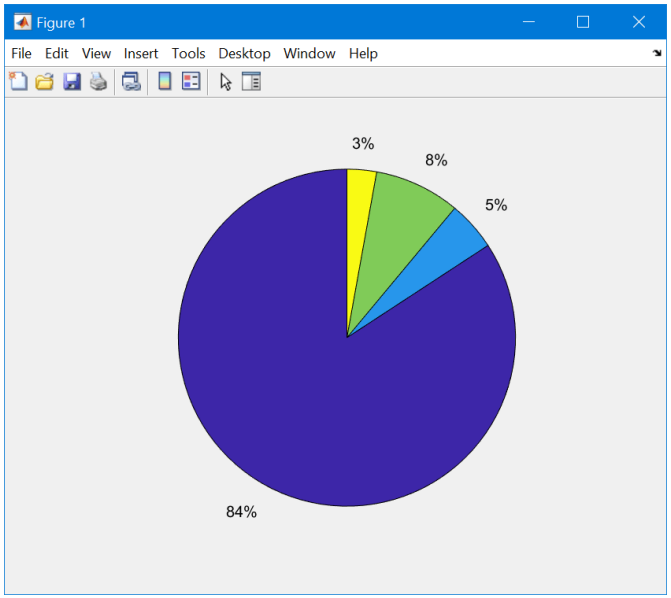


Origin

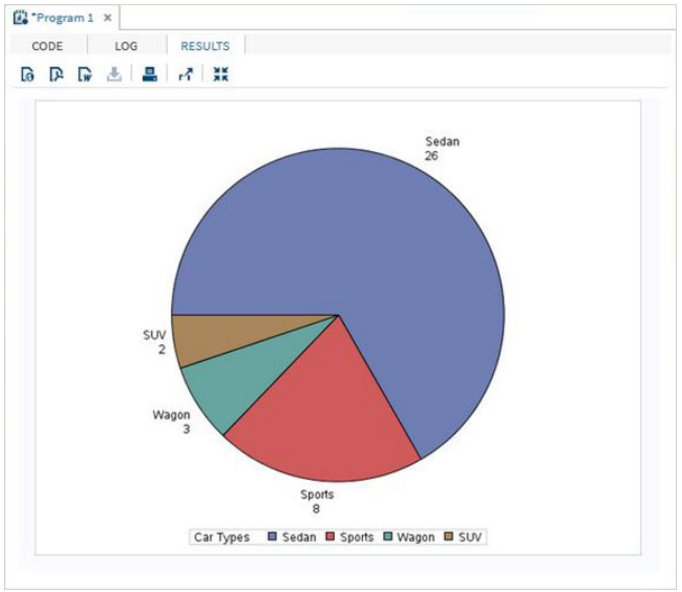


Excel

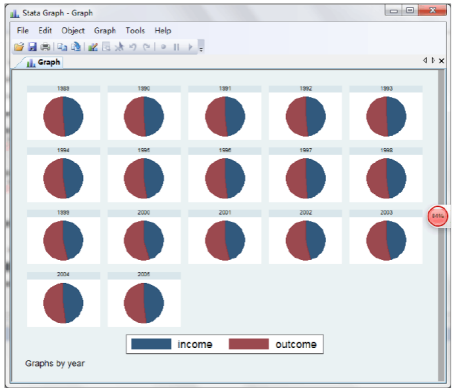
科研绘图实例 | 常用绘图工具



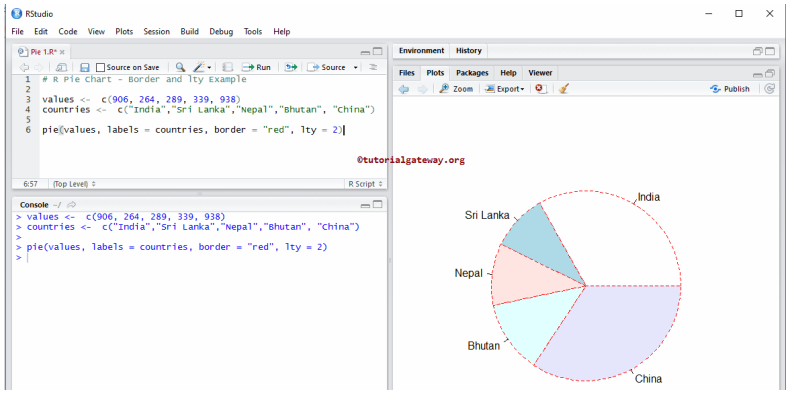
MATLAB



SAS

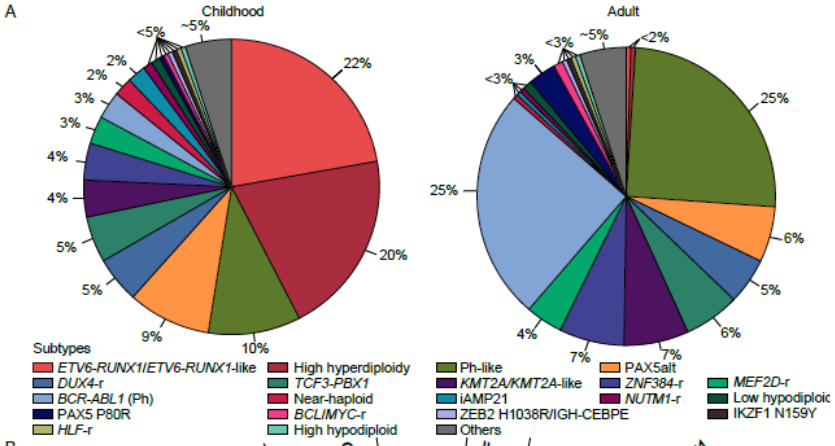


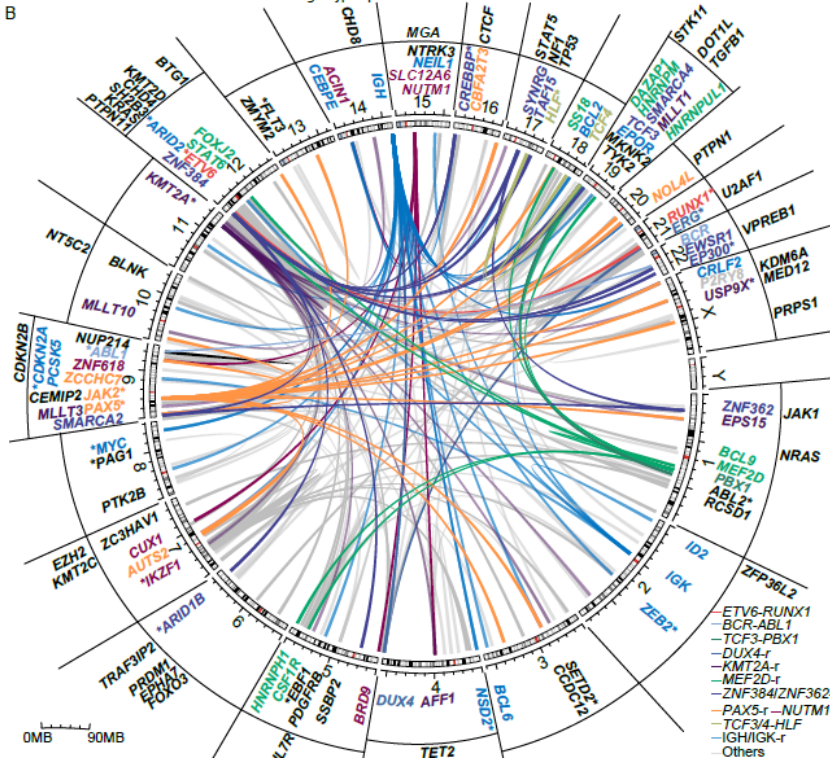
Stata

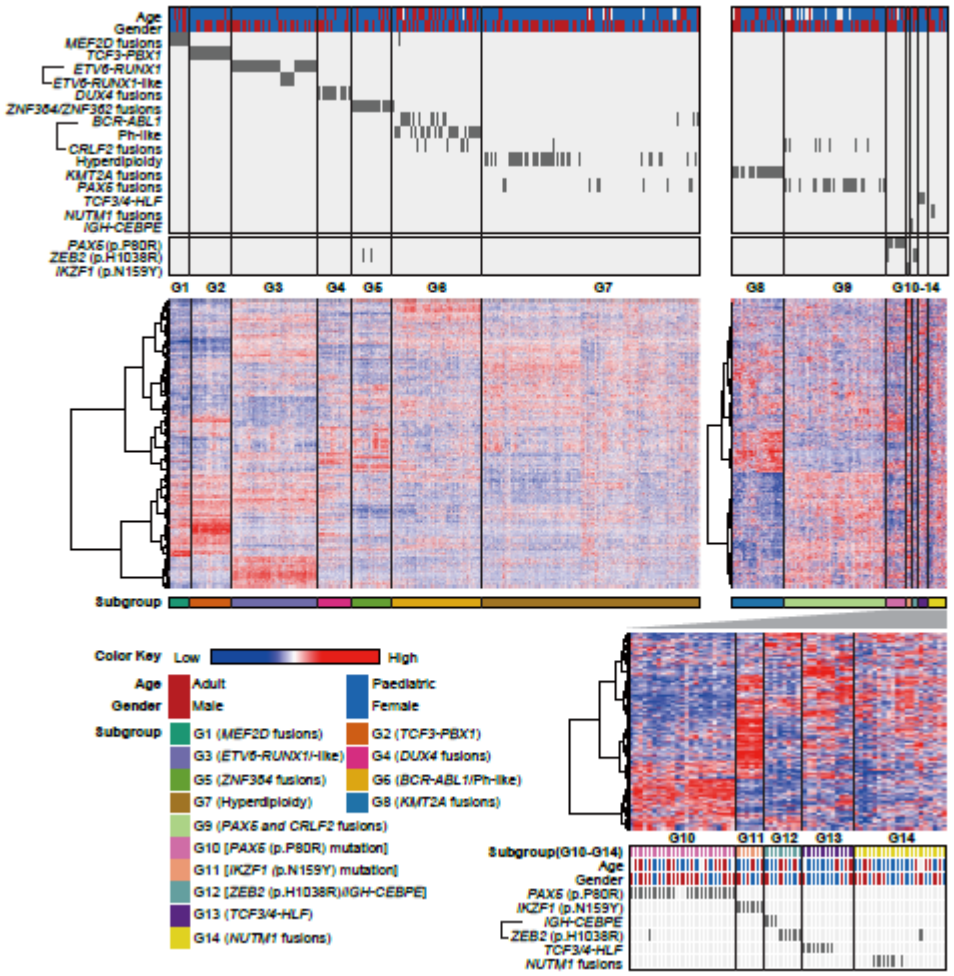


R

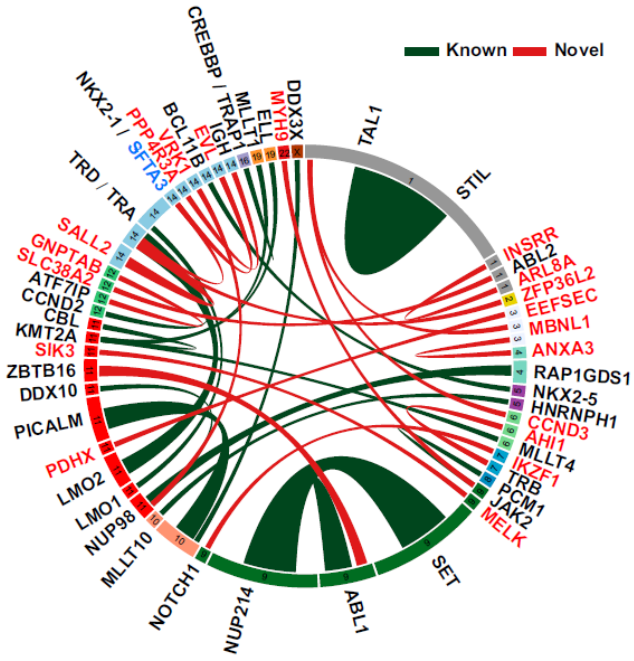
科研绘图实例 | 那些年画过的图





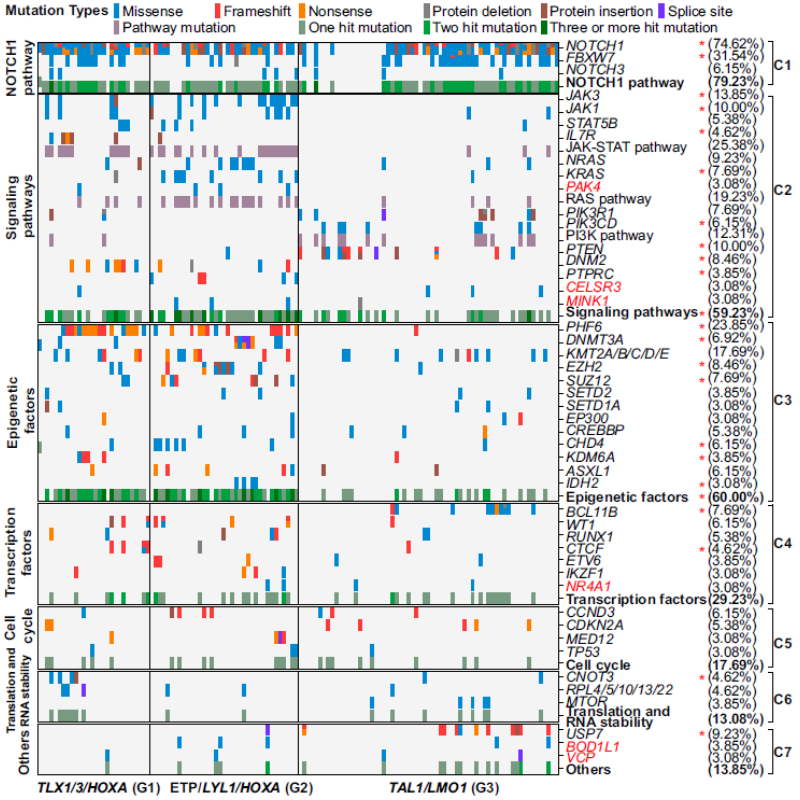


科研绘图实例 | 那些年画过的图

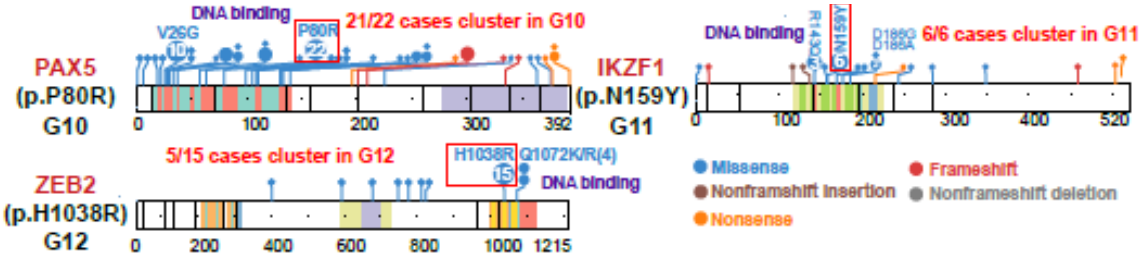


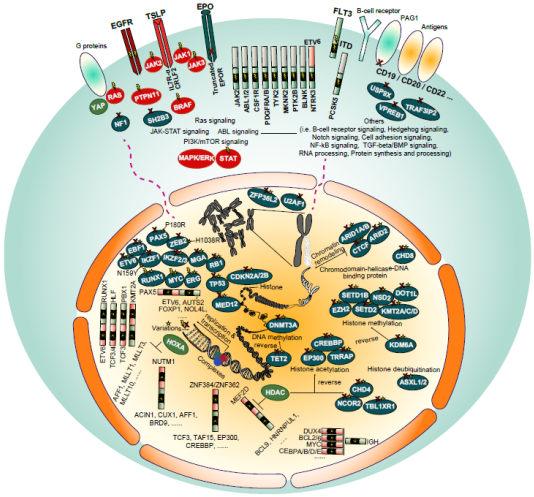
Known Fusions	
STIL-TAL1	*DDX3X-MLLT10*
NUP214-ABL1	*HNRNPH1-MLLT10*
* *SET-NUP214*	*PICALM-MLLT10*
NUP98-DDX10	*NKX2-5-BCL11B*
NUP98-RAP1GDS1	*PCM1-JAK2*
KMT2A-CBL	*CREBBP-TRAP1*
KMT2A-ELL	*LMO1-TRA*
KMT2A-MLLT1	*LMO2-TRA*
KMT2A-MLLT4	*CCND2-TRA*

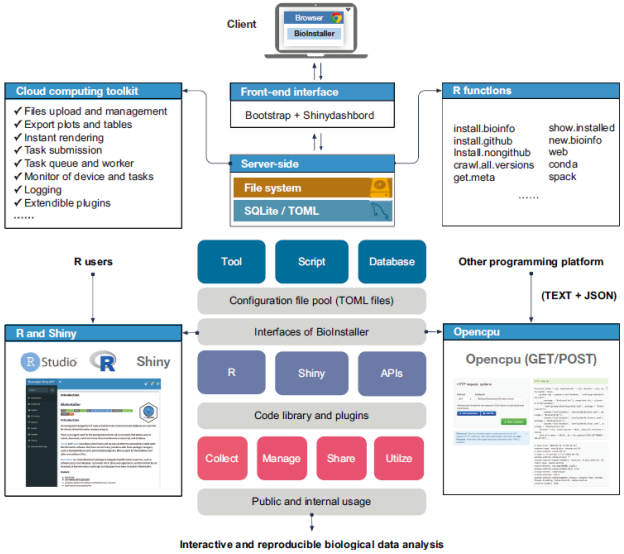
Novel Fusions		
Type1	**Type2**	
* *SLC38A2-ABL2*	* *CCND3-STIL*	
* *GNPTAB-ATF7IP*	*EVL-NKX2-1*	
* *ARL8A-INSRR*	* *EVL-SFTA3*	
MELK-SIK3	**Type3**	
MBNL1-TAL1	* *ZFP36L2-TRA*	
ZBTB16-ABL1	*TRB-AHI1*	
MYH9-JAK2	*TRA-SALL2*	
EEFSEC-PDHX	*TRD-NKX2-1*	
MBNL1-ANXA3		
NUP98-VRK1	**Type4**	
IKZF1-NOTCH1	*PPP4R3A-IGH*	

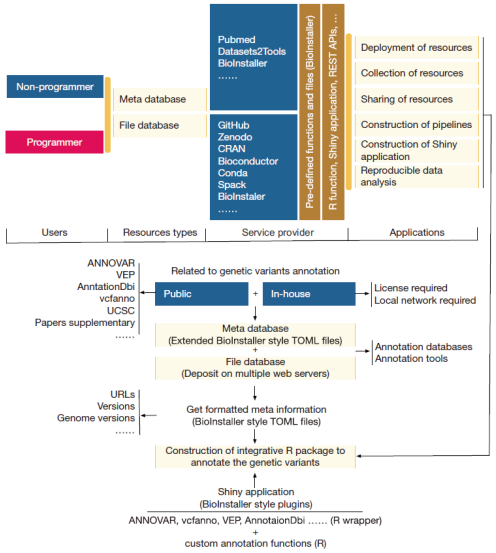


科研绘图实例 | 那些年画过的图









Major points for reproducible NGS data analysis projects

Meta information	Regular directory structure and filenames	Unified pipelines/ workflows
Analysis environment	Logging and History	Interactive results and document report

.....

Meta information
(For all involved resources and computations.)

/path/{project}/{...}/meta.[json | yaml | toml]

[SQLite | Mongodb | PostgreSQL | MySQL | ...]

[xlsx for communication with collaborator]

Regular directory structure and filenames

doc/ data/ analysis/ test/ download/ {.../}

{...}/[wgs | wes | rnaseq | chipseq | atacseq | ...]

{time stamp}_{taskid}_{sampleid}{...}

Unified pipelines/workflows

[Snakemake | WDL | Nextflow | Bpipe | ...]

Using fixed software parameters in the same project based on configuration files or command line scripts.

Using pipelines/workflows with code quality control and assessment of performance.

Analysis environment

docker npm devtools BioInstaller CONDA Spack

.....

Logging and history

Recording the executed tasks, commands and scripts with the date, system status, user id, etc. (Log files with unique index)

Using version control tools for codes and analysis. Keeping backup copies of result. (with data analysis environment)

Interactive results and document report

Studio Shiny Opencpu

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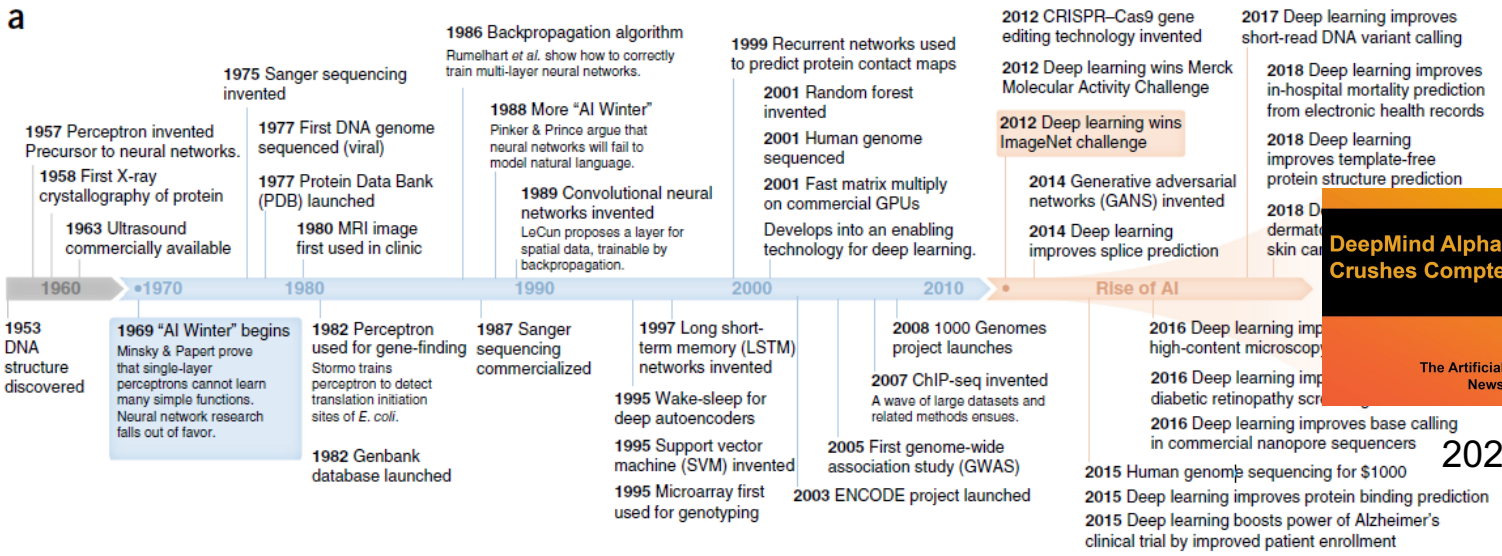
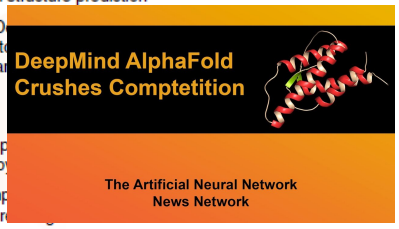
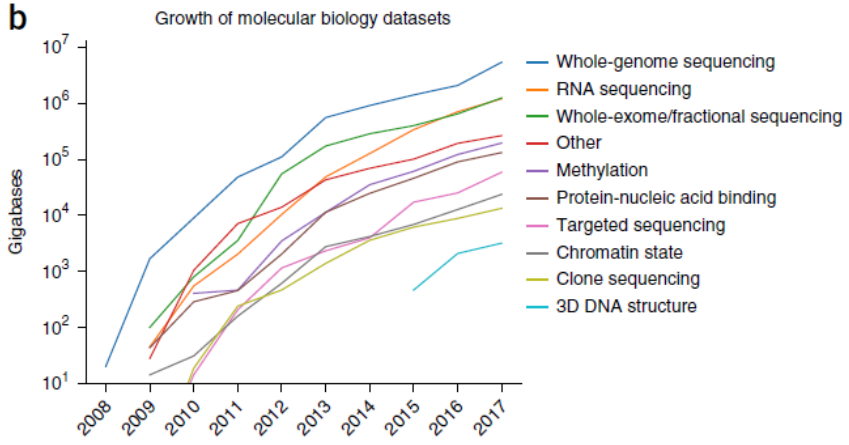
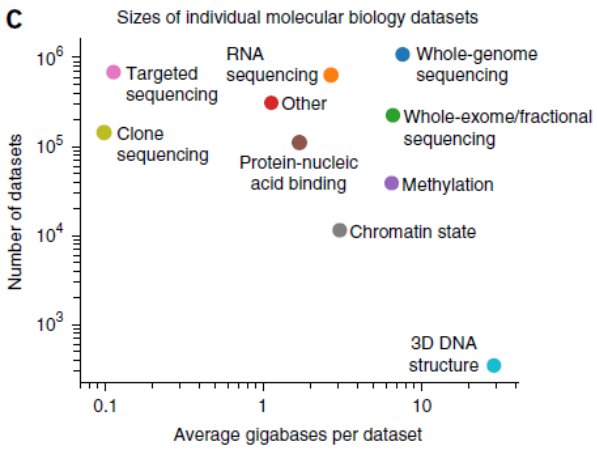
Hiplot 可视化平台简介 | 背景





2020 Alphafold2



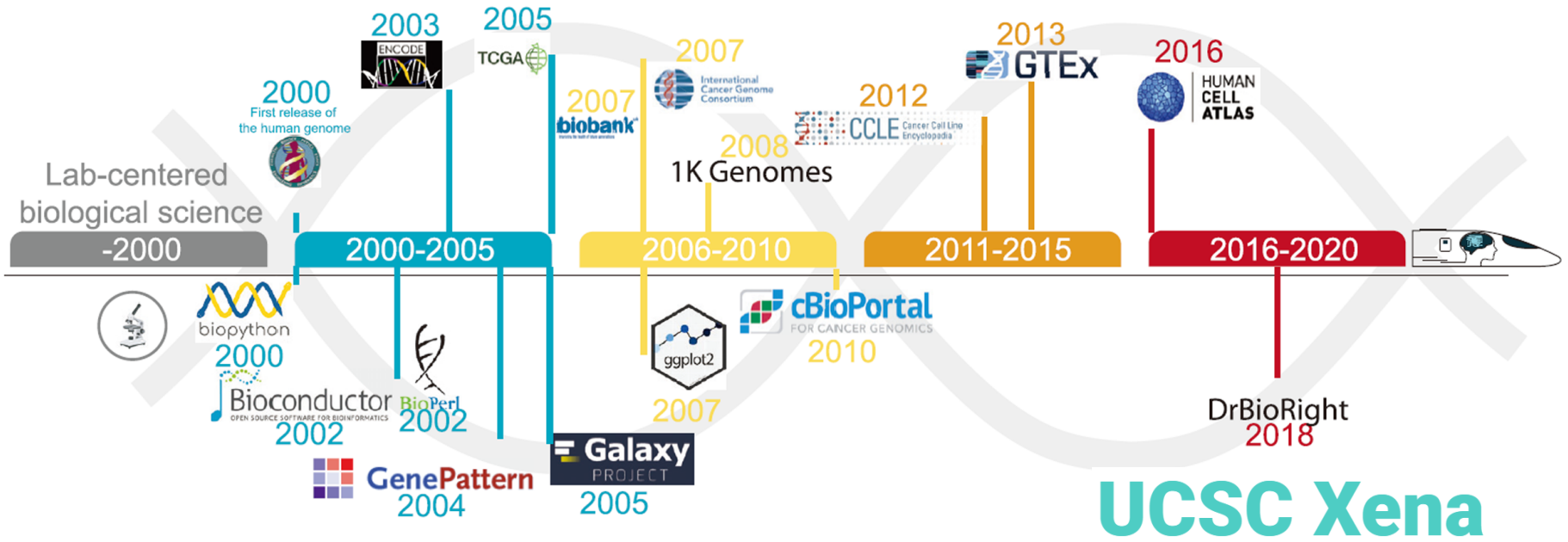


由技术和数据驱动的生物医学研究迎来发展黄金时期

Wainberg M, Nat Biotechnol 2018

HIPLOT

Hiplot 可视化平台简介 | 背景

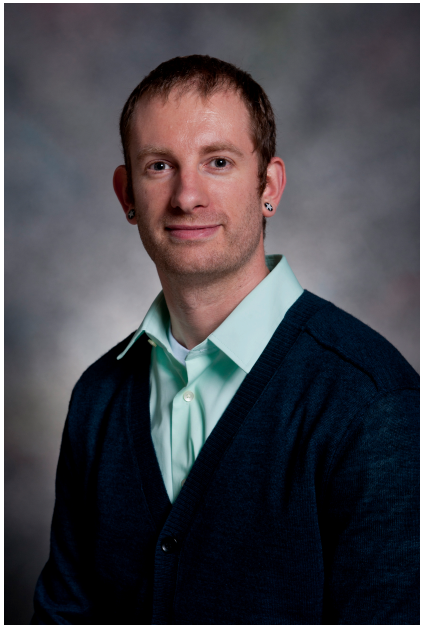


过去 20 年期间，组学数据相关的知名数据分析平台和工具

Li, J. Cancer Cell. 2020

HIPLOT

Hiplot 可视化平台简介 | 背景



Pinned

tidyverse/ggplot2
An implementation of the Grammar of Graphics in R
R 4.7k 1.7k

tidyverse/dplyr
dplyr: A grammar of data manipulation
R 3.6k 1.3k

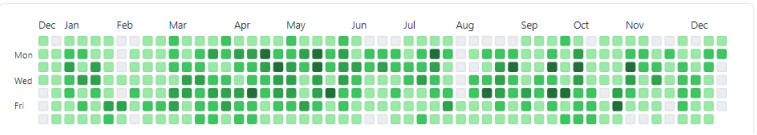
tidyverse/tidyverse
Easily install and load packages from the tidyverse
R 977 207

r4ds
R for data science: a book
R 2.7k 3.3k

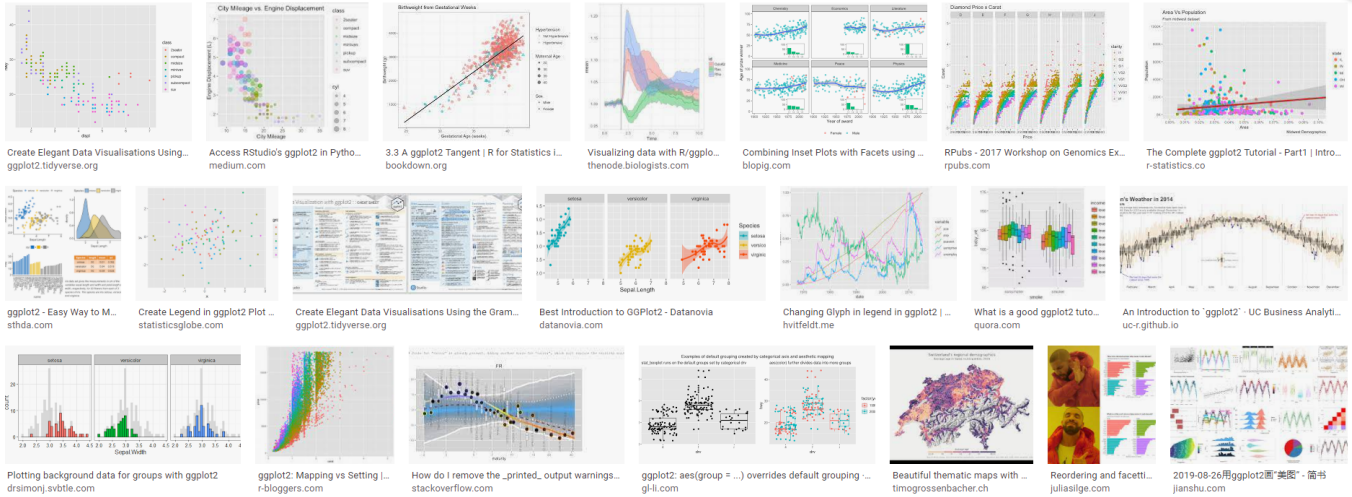
r-lib/devtools
Tools to make an R developer's life easier
R 2k 709

adv-r
Advanced R: a book
TeX 1.8k 1.6k

4,446 contributions in the last year



2020
2019
2018
2017



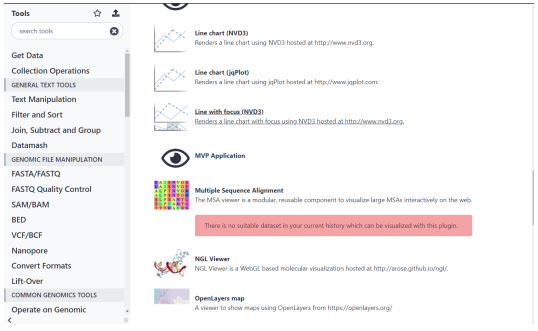
Create Elegant Data Visualisations Using... ggplot2.tidyverse.org
Access RStudio's ggplot2 in Pytho... medium.com
3.3 A ggplot2 Tangent | R for Statistics i... bookdown.org
Visualizing data with R/ggplo... thenode.biologists.com
Combining Inset Plots with Facets using ... blopig.com
RPubs - 2017 Workshop on Genomics Ex... rpubs.com
The Complete ggplot2 Tutorial - Part1 | Intro... r-statistics.co
ggplot2 - Easy Way to M... sthda.com
Create Legend in ggplot2 Plot ... statisticsglobe.com
Create Elegant Data Visualisations Using the Gram... ggplot2.tidyverse.org
Best Introduction to GGPlot2 - Datanovia datanovia.com
Changing Glyph in legend in ggplot2 | ... hvitfeldt.me
What is a good ggplot2 tuto... quora.com
An Introduction to `ggplot2` · UC Business Analyti... uc-r.github.io
Plotting background data for groups with ggplot2 drsimonj.svbtle.com
ggplot2: Mapping vs Setting |... r-bloggers.com
How do I remove the _printed_ output warnings... stackoverflow.com
ggplot2: aes(group = ...) overrides default grouping ·... gl-li.com
Beautiful thematic maps with ... timogrossenbacher.ch
Reordering and facetti... juliasilge.com
2019-08-26用ggplot2画"美图" - 简书 jianshu.com

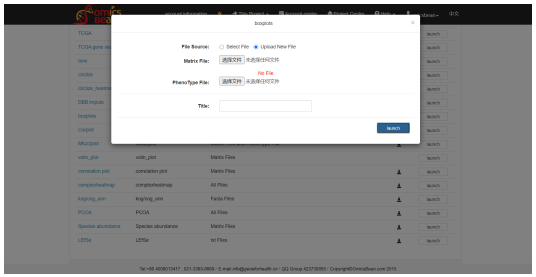
Hadley Wickham

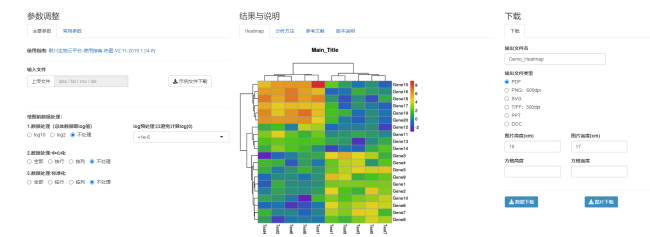
HIPLOT

Hiplot 可视化平台简介 | 背景

动机和目标







我们希望构建一个更优秀、更全面的工具

（重新定义科研数据可视化云工具）

界面简洁、上手简单、即开即用、无广告、不收费

功能丰富、易扩展

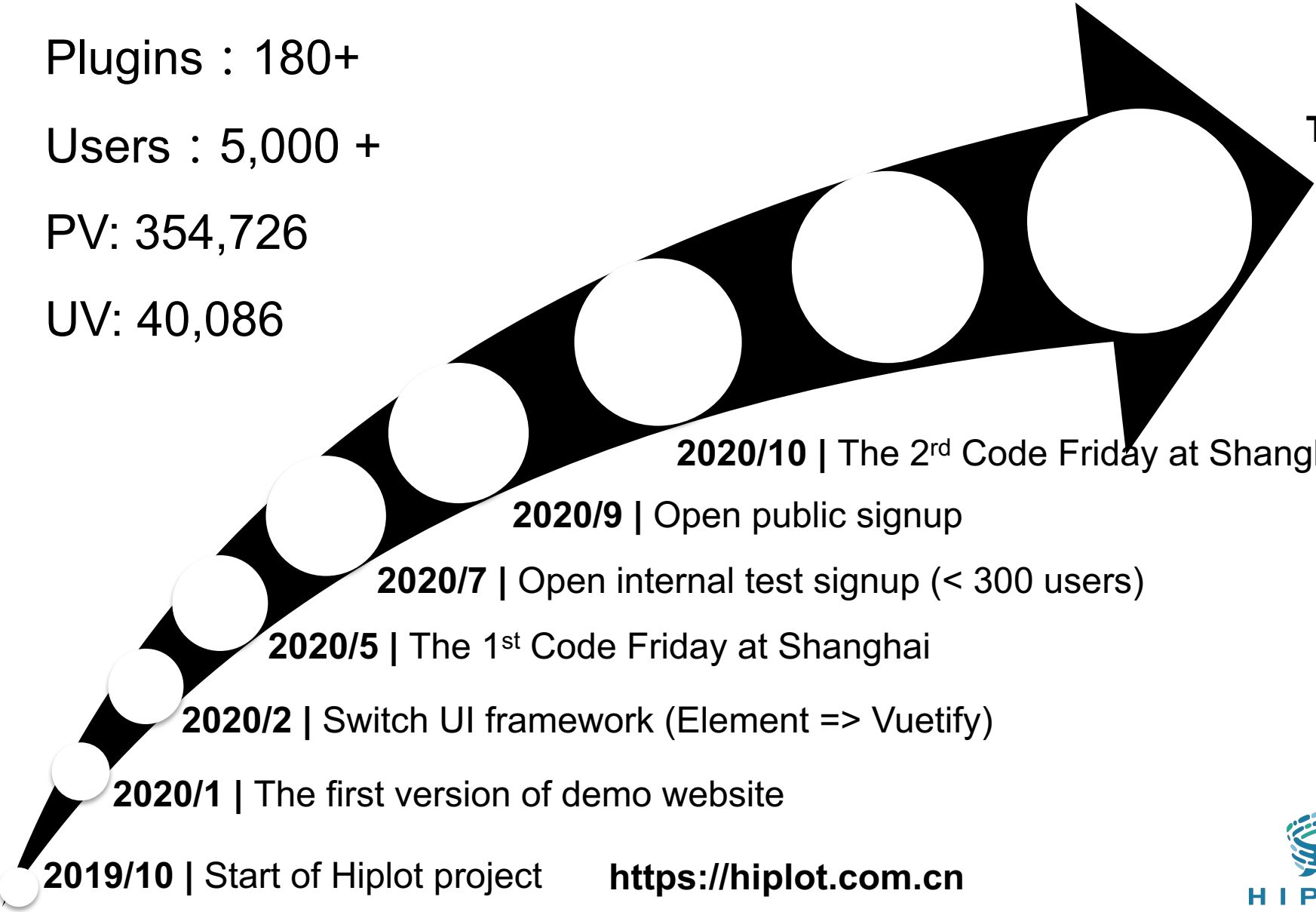
Hiplot 可视化平台简介 | 发展历程

Plugins：180+

Users：5,000 +

PV: 354,726

UV: 40,086



Today

2020/10 | The 2rd Code Friday at Shanghai

2020/9 | Open public signup

2020/7 | Open internal test signup (< 300 users)

2020/5 | The 1st Code Friday at Shanghai

2020/2 | Switch UI framework (Element => Vuetify)

2020/1 | The first version of demo website

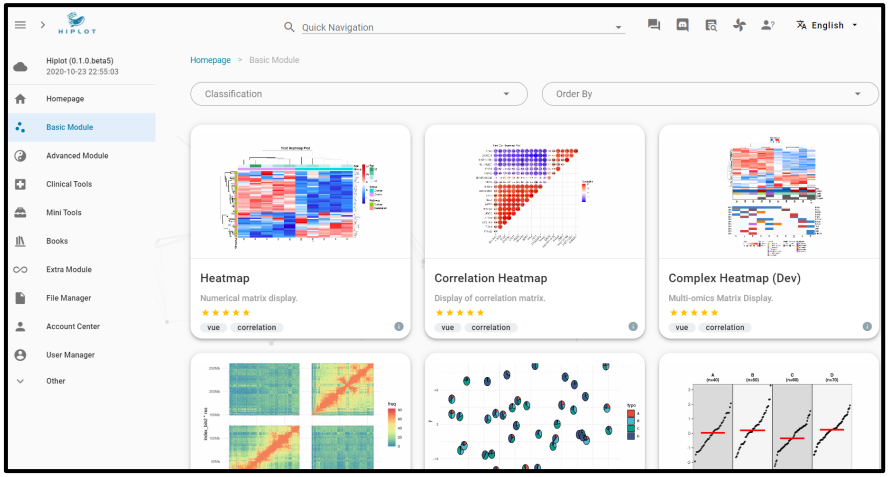
2019/10 | Start of Hiplot project

https://hiplot.com.cn

HIPLOT

Hiplot 可视化平台简介 | 主要模块

Web Interface



CLI

```
ljf@head1 ~ hctl
Command-line client to draw plots of [Hiplot](https://hiplot.com.cn) website. More se

Usage:
  hctl [flags]
  hctl [command]

Available Commands:
  config      Initializing a config.json file of hiplot application.
  help        Help about any command
  login       Login Hiplot Website.
  plot        Plot functions of Hiplot Website.

Flags:
  -h, --help              help for hctl
      --log-dir string    log dir. (default "/cluster/home/ljf/_log")
  -o, --out-dir string    output dir. (default "/cluster/home/ljf")
      --save-log          Save log to file.
  -k, --task-id string    task ID (default is random). (default "d4f728c2-1d33-4559-bb
      --verbose int       verbose level (0:no output, 1: basic level, 2: with env info
  -v, --version           version for hctl

Use "hctl [command] --help" for more information about a command.
```

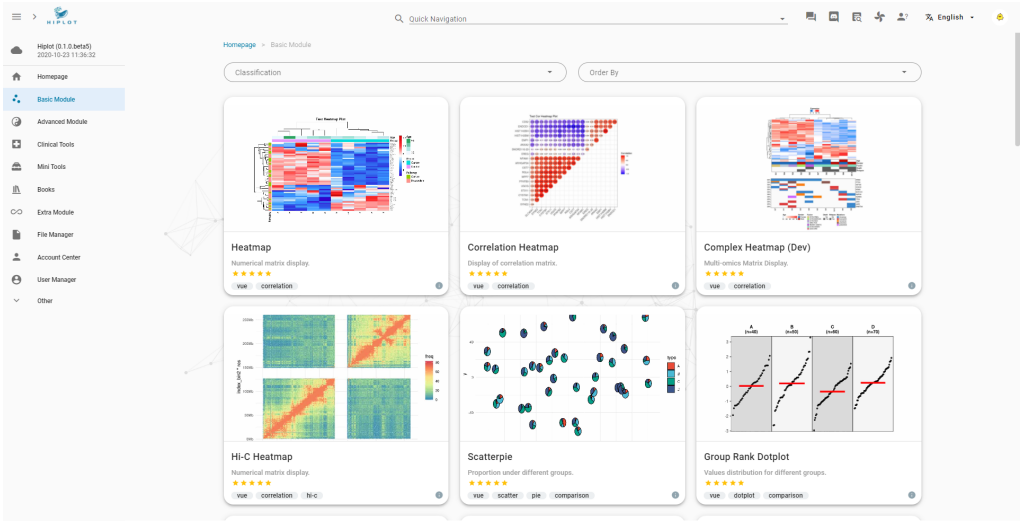
Basic, Advanced, Mini-tools, and Clinical-tools Modules

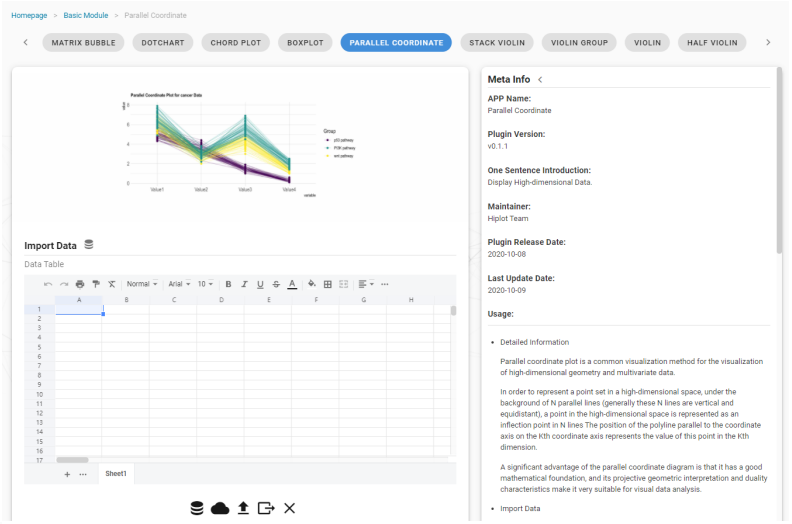
File Manager	Task Manager	User Manager	Setting
Extra Module	Q&A	Feedback	Mirrors

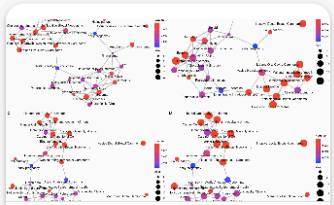
Components of Hiplot

HIPLOT

Hiplot 可视化平台简介 | 网页接口



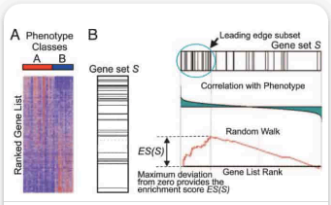




GO/KEGG Analysis

GO/KEGG analysis by clusterProfiler.

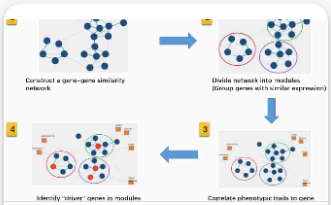
vue expression



Broad GSEA

Gene Set Enrichment Analysis.

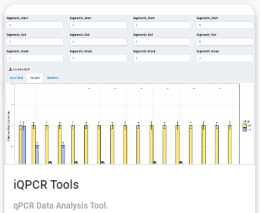
vue expression



WGCNA

Co-expression network analysis.

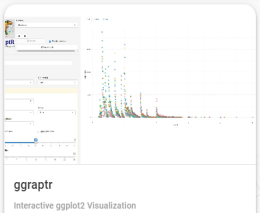
vue expression



iQPCR Tools

qPCR Data Analysis Tool.

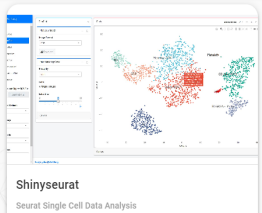
shiny qpcr



ggraptr

Interactive ggplot2 Visualization

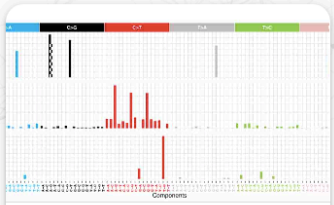
shiny ggplot2



Shinyseurat

Seurat Single Cell Data Analysis

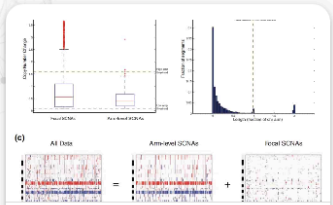
shiny single cell



Sigflow

Mutation Signature Analysis.

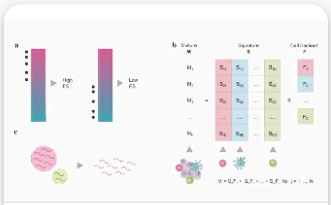
vue mutation



GISTIC2

Copy Number Data Analysis.

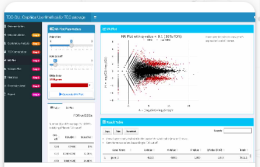
vue mutation CNV



Immunedeconv

Immunoinfiltration analysis.

vue expression immune



TCC-GUI

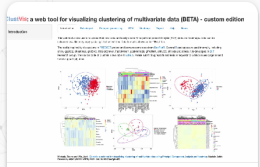
Transcriptome Analysis Tool

shiny expression

START

Transcriptome Analysis Tool

shiny expression



ClustVis

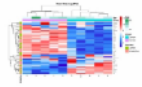
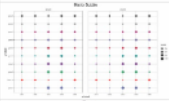
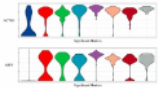
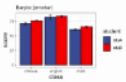
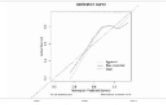
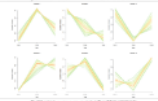
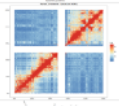
PCA & Cluster

shiny pca cluster

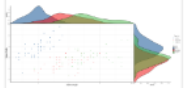
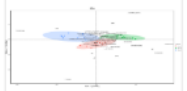
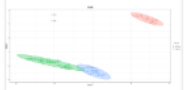
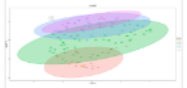
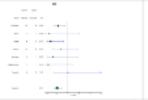
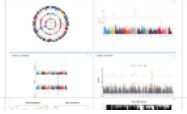
Screenshot of Hiplot

HIPLOT

Hiplot 可视化平台简介 | 网页接口

	A	B	C	D	E	F	G	H
1	**Tool Name**	**Tags**	**Module**	**Description**	**Input**	**Output & Interpretation**	**App Address**	**Thumbnail**
2	Heatmap	Correlation	Basic	An intuitive and visual method for analyzing the distribution of data	Numeric matrix (i,e. FPKM and TPM)	Represent the levels of input data (i.e gene expression); conduct unsupervised clustering finding potential patterns	https://hiplot.com.cn/basic/heatmap	
3	Matrix Bubble	Gene Expression	Basic	The color matrix bubble is used to visualize the expression matrix data of multiple genes (rows) in various cells (columns).	<1st-col>: (String) cell sample name as X axis, <2nd-col>: (String) gene name as the Y axis, <3rd-col>: (Numeric) Gene expression, [4th-col]: (String) groups.	Color matrix bubble diagram of genes expression level in multiple cells.	https://hiplot.com.cn/basic/matrix-bubble	
4	Chord Plot	Interaction	Basic	The complex interaction is visualized in the form of chord graph.	Data frame or matrix of interaction of genes with pathways or gene ontologys.	Chord graph of genes with KEGG pathways or GO terms.	https://hiplot.com.cn/basic/chord	
5	Violin Group	Comparison	Basic	Violin and box plot of grouped data with T-test.	Data frame. <1st-col>: (Numeric) value data, <2nd-col>: (String) 1st-rank groups, <3rd-col>: (String) 2nd-rank groups.	Visualizing all data that meets this need and structure.	https://hiplot.com.cn/basic/violin-group	
6	Stack Violin	Gene Expression	Basic	The expression of key genes in each cluster in single-cell transcriptomic (Single Cell RNA-Seq)analysis.	Gene expression matrix. Gene expression matrix in all cells and groups in single cell transcriptome analysis (Single Cell RNA-Seq).	Stacked violin diagram of key genes (Y axis) and cell clusters (X axis). Genes expression value are presented by violins.	https://hiplot.com.cn/basic/stack-violin	
7	Barplot (Errorbar)	Comparison	Basic	Bar plot with error-lines and groups.	Data frame. <1st-col>: (Numeric) values as Y-axis. < 2nd-col>: (Numeric or String) classes as X-axis. <3rd-col>: (String) groups as colors and legend.	Bar plot with error-lines and groups. The color and width of error-lines can be regulated by web components.	https://hiplot.com.cn/basic/barplot-errorbar	
8	Calibration Curve	Model	Basic	The calibration curve is used to evaluate the consistency / calibration, i.e. the difference between the predicted value and the real value	Data frame of multi columns data (Numeric allow NA). i.e the survival data (status with 0 and 1).	Calibration curve visualization of LM or COX model.	https://hiplot.com.cn/basic/calibration-curve	
9	Gene Cluster Trend	Gene Expression Clustering	Basic	Visualization and soft clustering of time series gene expression data based on Mfuzz R package.	Gene expression matrix. A data frame of multi-column data with the first column contains unique gene IDs and the rest of the columns cantains time series gene expression data.	Multi-line charts displaying different gene expression trends based on soft clustering.	https://hiplot.com.cn/basic/gene-trend	
10	Gene Density	Density	Basic	The gene density plot is used to calculate gene density across every chromosome and visualize their distribution on the chromosome.	Two files containing the chromosome length and gene positions on the chromosome. Each file contains three columns, the first with the chromosome name, the second and third with the start and end position of every gene or chromosome.	Gene density distribution across every chromosome.	https://hiplot.com.cn/basic/gene-density	
11	HiC Heatmap	Correlation	Basic	The HiC heatmap is used to display the interaction frequency matrix of HiC data with selected resolution.	Numeric matrix. A data frame containing three columns, the first with the bin1 index, the second with the bin2 index and the third with the frequency value.	Heatmap displaying the frequency intensity between two different bin sites across every chromosome.	https://hiplot.com.cn/basic/hic-heatmap	

Hiplot 可视化平台简介 | 网页接口

	Tool Name	Tags	Module	Description	Input	Output & Interpretation	App Address	Thumbnail
18	Genome Circos	Genomics	Advance	The information contained in genome is displayed in the form of circle in the whole genome map.	Multiple files include chrome data as outermost ring, heatmap data, histogram data, scatter data, ribbon data, link data, etc.	Genome multiple circles ring from outermost to innermost ring to display genome information.	https://hiplot.com.cn/advance/genome-circos	
19	Gene ID Convert	Gene	Advance	According to the information records of genes in a variety of databases, the ID of multiple genes is converted into the ID of one or more databases.	One column contains the gene ID.	A data frame contains multi-columns gene ids corresponding databases.	https://hiplot.com.cn/advance/genome-circos	
20	miRNA Gene Prediction	MiRNA	Advance	Simultaneously search multiple miRNA databases to predict the target genes of miRNA.	The name of one or more miRNAs. File or input in area of text is supported.	A data frame contains miRNA and target genes with detail information from differential miRNA databases.	https://hiplot.com.cn/advance/mirna-prediction	
21	Point Density	Combination	Advance	Integrate scatter plot and density plot together to visualize complex grouped data.	Data frame. <1st-col>: (Numeric) X-axis data. <2nd-col>: (Numeric) Y-axis data. <3rd-col>: (String) groups name.	A diagram of integrating scatter and density plots.	https://hiplot.com.cn/advance/point-density	
22	RDA Visual	Dimension Reduction	Advance	Redundancy analysis (RDA) is a sort method combining regression analysis with principal component analysis, and it is also an extension of multiple response regression analysis.	Three tables needed. <1st-table>: (Data frame) species data. <2nd-table>: (Data frame) environment data. <3rd-table>: (Data frame) simple with group data.	Diagram. Dimension reduction thinking solves the problem of correlation between species and environmental factors and visualizes the results.	https://hiplot.com.cn/advance/rda-visual	
23	Echarts	Animation	Advance	The data interface of echarts.js is integrated into R language and the data and visualization process are controlled by web components.	Data frame for different applications.	Diagrams of bar plot, line plot, scatter plot, etc.	https://hiplot.com.cn/advance/echarts	
24	T-SNE Ellipse	Dimension Reduction	Advance	T-SNE: t-distributed Stochastic Neighbor Embedding.	Data frame. <1st-col>: (String) record id as point label. <mid-cols>: (Numeric) middle cols with numeric value <end-col>: (String) groups name.	Diagram with points, arrows, 95%CI ellipses after t-SNE dimension reduction.	https://hiplot.com.cn/advance/tsne-ellipse	
25	UMAP Ellipse	Dimension Reduction	Advance	Uniform Manifold Approximation and Projection for Dimension Reduction	Data frame. <1st-col>: (String) record id as point label. <mid-cols>: (Numeric) middle cols with numeric value <end-col>: (String) groups name.	Diagram with points, arrows, 95%CI ellipses after UMAP dimension reduction.	https://hiplot.com.cn/advance/umap-ellipse	
26	Forestplot	Survival Analysis	Advance	In addition to meta-analysis, forest mapping is also widely used in observational studies and clinical trials, such as risk analysis / survival analysis.	Two tables needed. <1st-table>: <1st-col>: (Numeric) mean data. <2nd-col>: (Numeric) lower data. <3rd-col>: (Numeric) upper data. <2nd-table>: (String or Numeric) text table.	Diagram of forest plot.	https://hiplot.com.cn/advance/forestplot	
27	CM Plot	Genetic Variation	Advance	A high-quality drawing tool designed for Manhattan plot of genomic analysis.	Data frame. <1st-col>: (String) SNP ID. <2nd-col>: (Numeric) chromsome ID. <3rd-col>: (Numeric) position. <4th-col>~<nth-col>: (Numeric)	Diagrams with circular_manhattan, rectangular_manhattan, multracks_manhattan, multraits_manhattan, snp_density, qqplot, multracks_qqplot and multraits_qqplot.	https://hiplot.com.cn/advance/cmplot	

Hiplot 可视化平台简介 | 命令行程序

```
Command-line client to draw plots of [Hiplot](https://hiplot.com.cn) website. More see here https://github.com/hiplot.

Usage:
  hctl [flags]
  hctl [command]

Available Commands:
  config      Initializing a config.json file of hiplot application.
  help        Help about any command
  login       Login Hiplot Website.
  plot        Plot functions of Hiplot Website.

Flags:
  -h, --help              help for hctl
      --log-dir string    log dir. (default "/home/cfd/code-friday/part2/se07/_log")
  -o, --out-dir string    output dir. (default "/home/cfd/code-friday/part2/se07")
      --save-log          Save log to file.
  -k, --task-id string    task ID (default is random). (default "001667f9-c2d2-43a9-8952-4f93e60b0cbc")
      --verbose int       verbose level (0:no output, 1: basic level, 2: with env info) (default 1)
  -v, --version           version for hctl

Use "hctl [command] --help" for more information about a command.
```

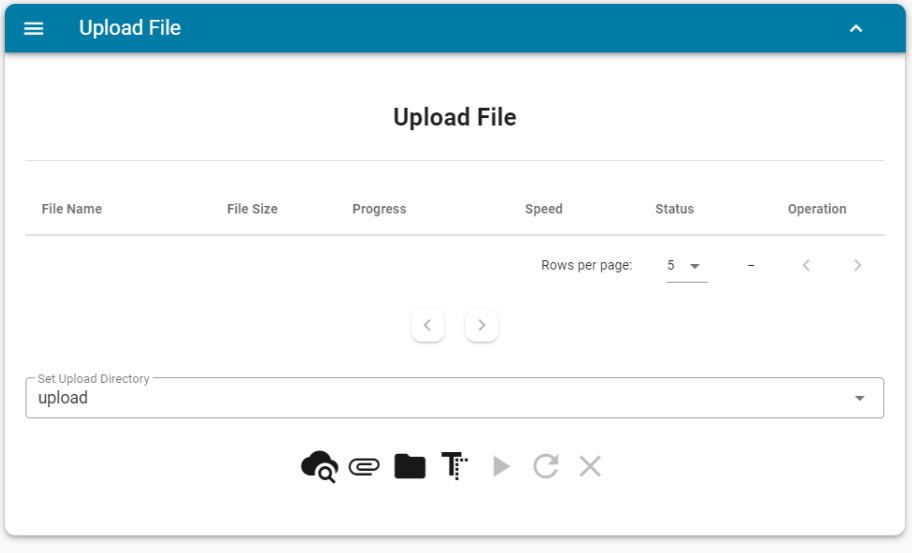
```
# https://hiplot.com.cn/docs/download/#hctl

hctl plot -c _demo/heatmap/config2.json -t heatmap -o /tmp/hiplot-pure-remote-data-mode

hctl config basic/heatmap
```

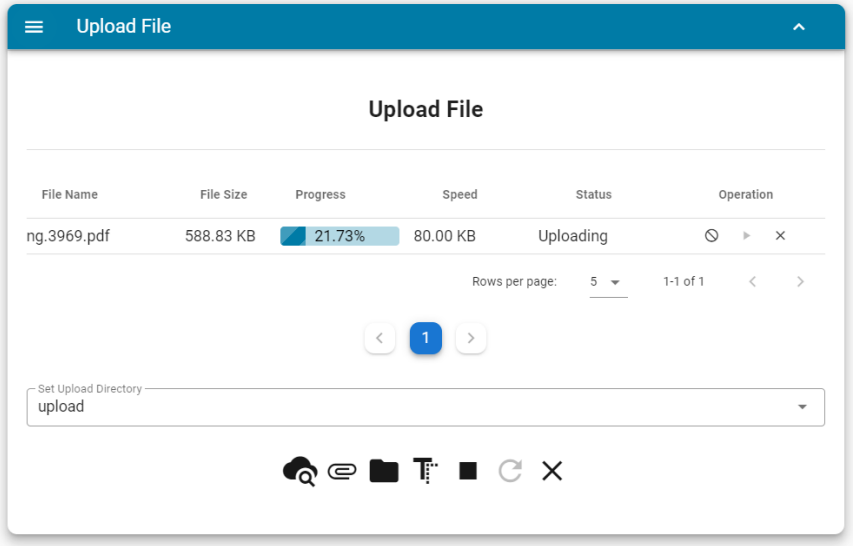
这是我在世界范围内看到的最好的生信产品。

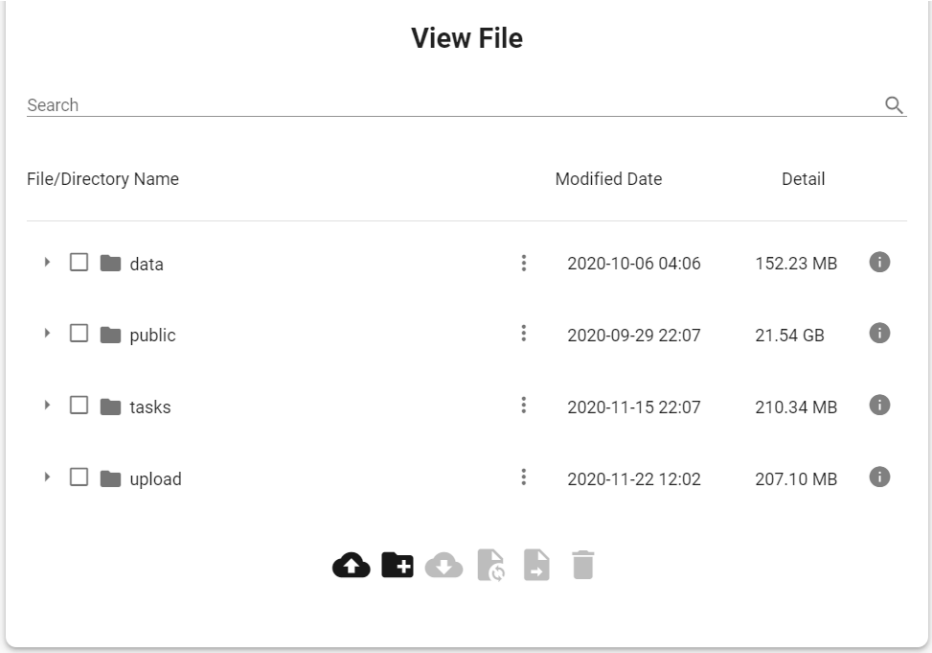
木烁 (知乎用户)

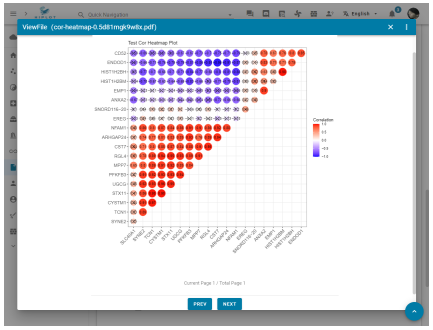
在我个人看来这个平台的意义不亚于 ggplot 的发布（ggplot 也是大神的博士论文，基本上重新定义了 R 绘图的方式）。

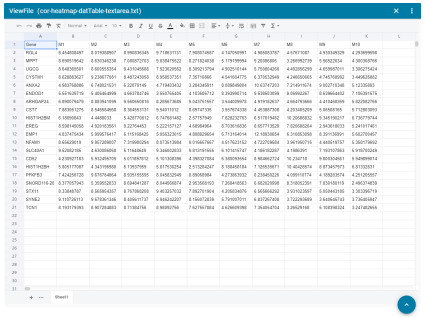
Hiplot 可视化平台简介 | 数据的导入和导出

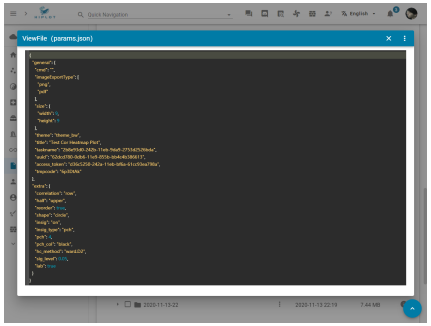








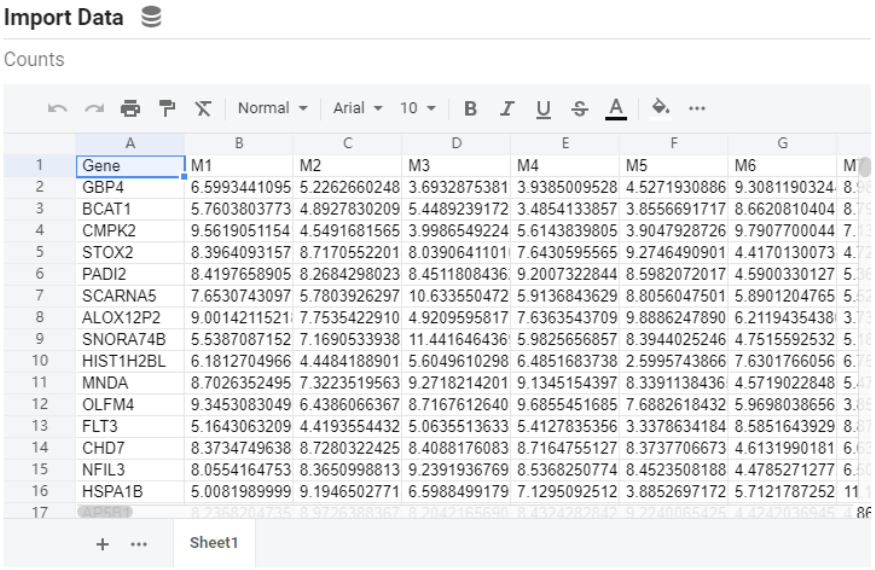




文件管理模块

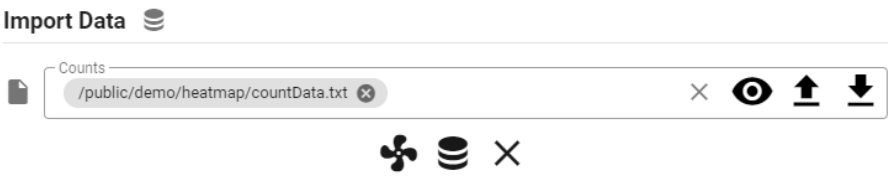
HIPLOT

Hiplot 可视化平台简介 | 数据的导入和导出



	A	B	C	D	E	F	G
1	Gene	M1	M2	M3	M4	M5	M6
2	GBP4	6.5993441095	5.2262660248	3.6932875381	3.9385009528	4.5271930886	9.3081190324
3	BCAT1	5.7603803773	4.8927830209	5.4489239172	3.4854133857	3.8556691717	8.6620810404
4	CMPK2	9.5619051154	4.5491681565	3.9986549224	5.6143839805	3.9047928726	9.7907700044
5	STOX2	8.3964093157	8.7170552201	8.0390641101	7.6430595565	9.2746490901	4.4170130073
6	PADI2	8.4197658905	8.2684298023	8.4511808436	9.2007322844	8.5982072017	4.5900330127
7	SCARNA5	7.6530743097	5.7803926297	10.633550472	5.9136843629	8.8056047501	5.8901204765
8	ALOX12P2	9.0014211521	7.7535422910	4.9209595817	7.6363543709	9.8886247890	6.2119435438
9	SNORA74B	5.5387087152	7.1690533938	11.441646436	5.9825656857	8.3944025246	4.7515592532
10	HIST1H2BL	6.1812704966	4.4484188901	5.6049610298	6.4851683738	2.5995743866	7.6301766056
11	MNDA	8.7026352495	7.3223519563	9.2718214201	9.1345154397	8.3391138436	4.5719022848
12	OLFM4	9.3453083049	6.4386066367	8.7167612640	9.6855451685	7.6882618432	5.9698038656
13	FLT3	5.1643063209	4.4193554432	5.0635513633	5.4127835356	3.3378634184	8.5851643929
14	CHD7	8.3734749638	8.7280322425	8.4088176083	8.7164755127	8.3737706673	4.6131990181
15	NFIL3	8.0554164753	8.3650998813	9.2391936769	8.5368250774	8.4523508188	4.4785271277
16	HSPA1B	5.0081989999	9.1946502771	6.5988499179	7.1295092512	3.8852697172	5.7121787252

表格模式

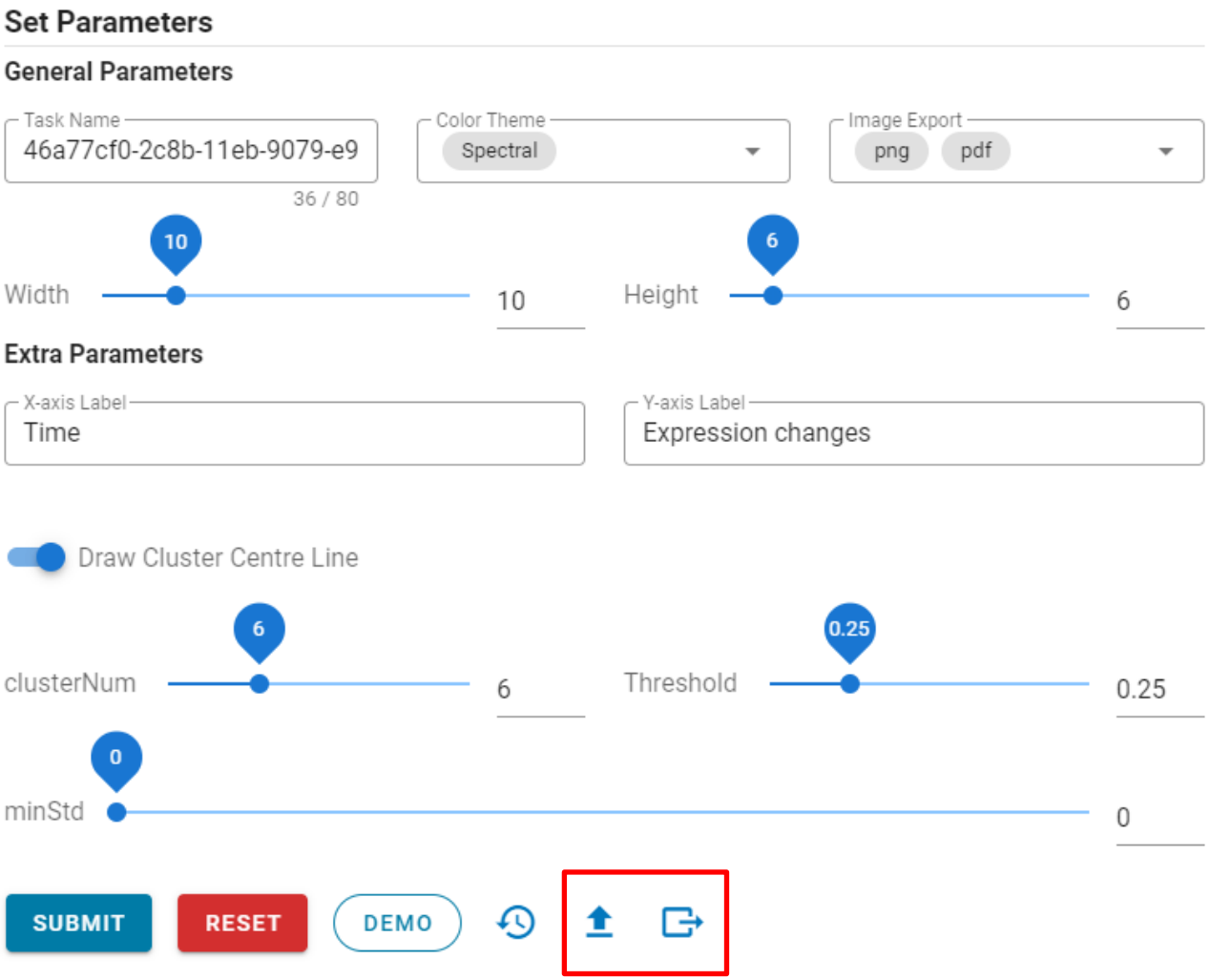


文件选择模式

在绘图插件内导入和导出数据

HIPLOT

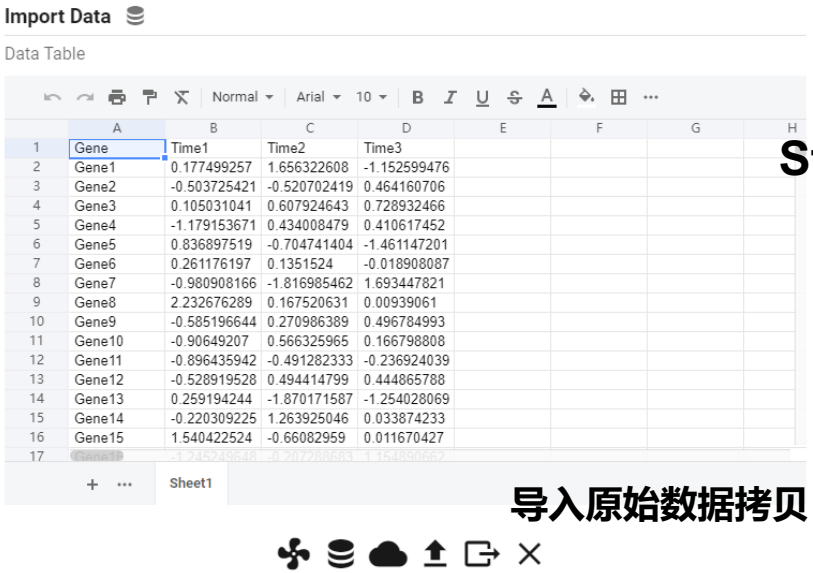
Hiplot 可视化平台简介



绘图参数的导入和导出

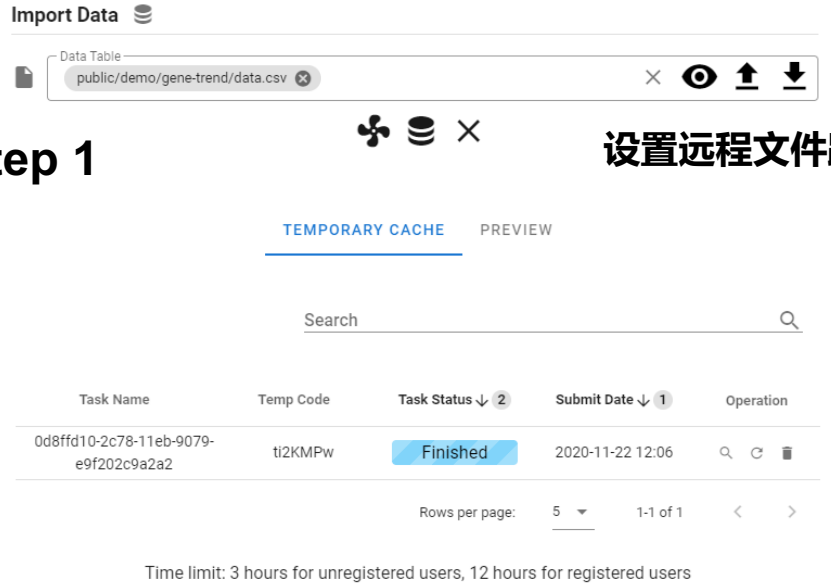
HIPLOT

Hiplot 可视化平台简介



导入原始数据拷贝

Step 1

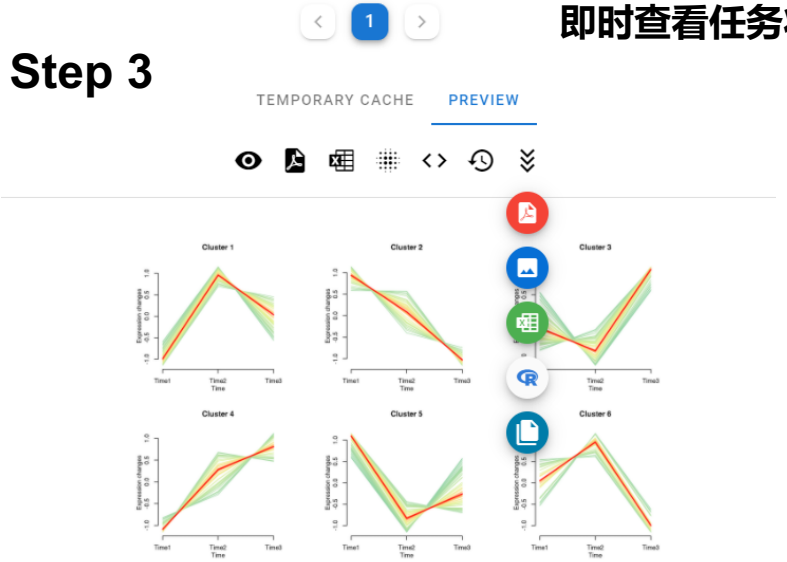


设置远程文件路径

Step 2

设置参数

Step 3

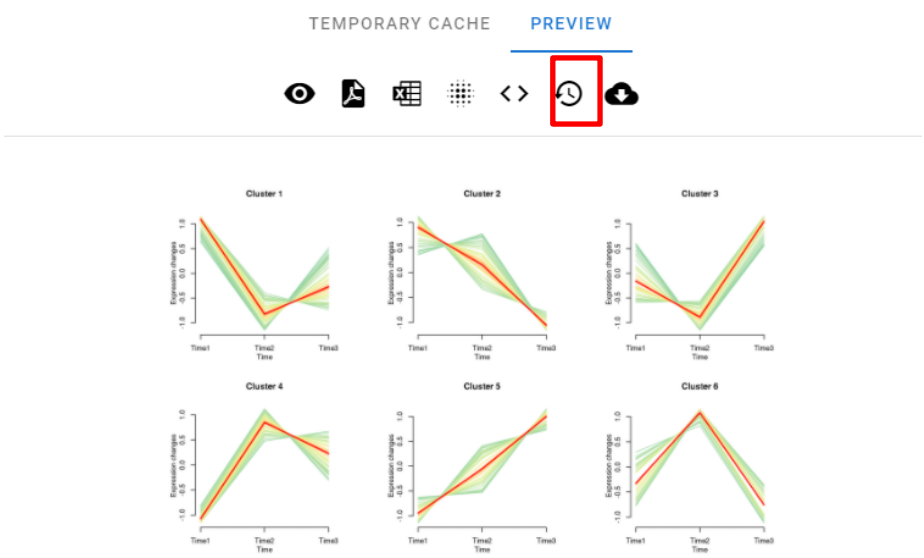


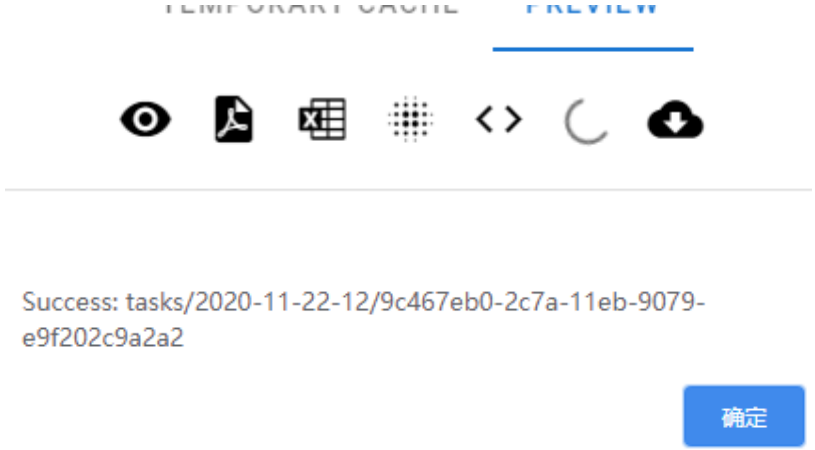
即时查看任务状态

结果预览和下载

提交绘图任务

Hiplot 可视化平台简介

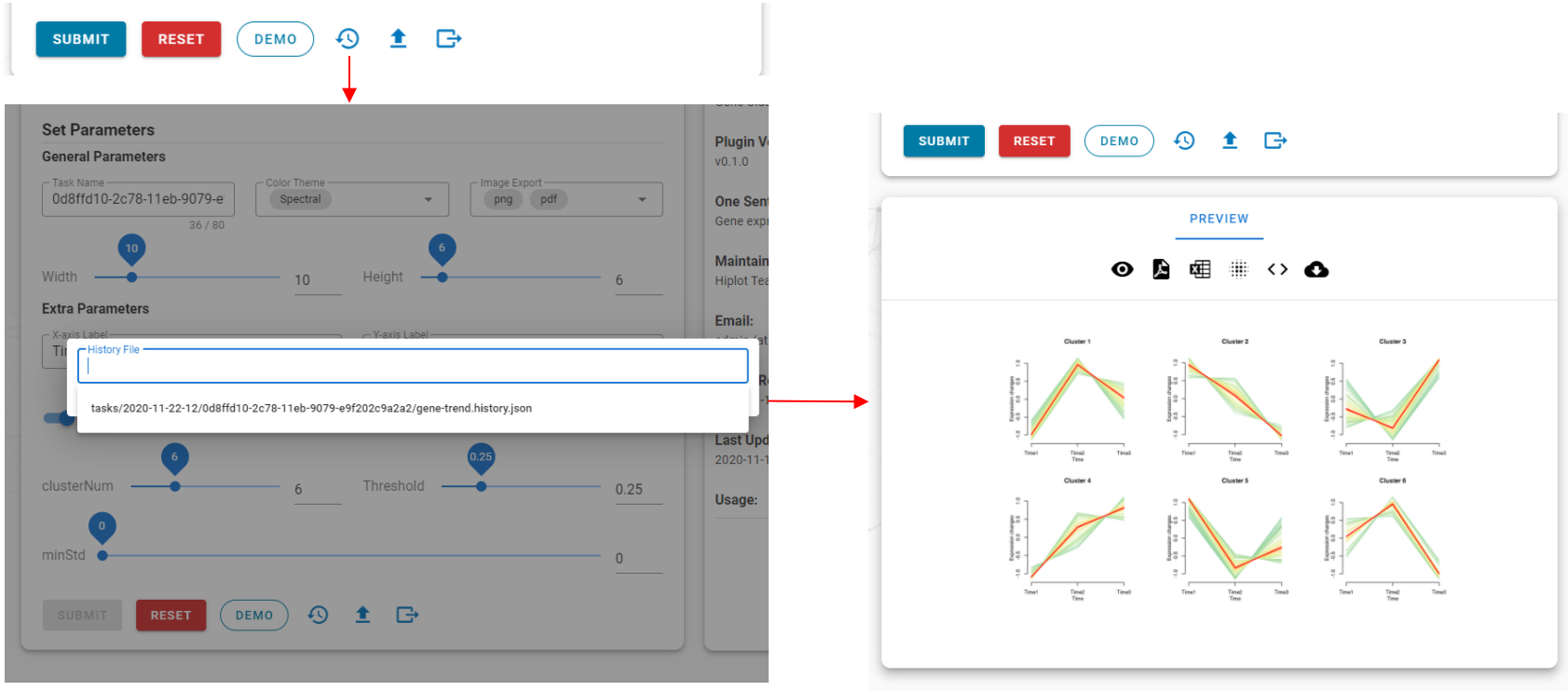




同步任务至云端文件库

HIPLOT

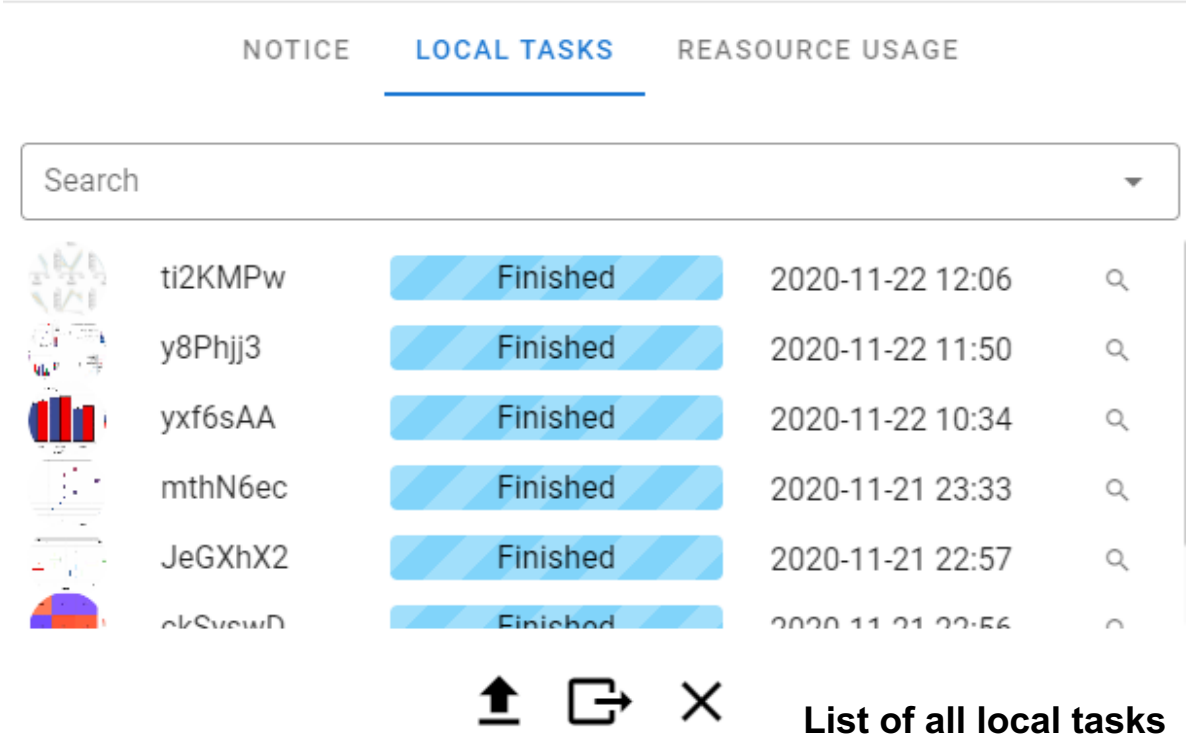
Hiplot 可视化平台简介



从云端加载绘图任务结果

HIPLOT

Hiplot 可视化平台简介



List of all local tasks

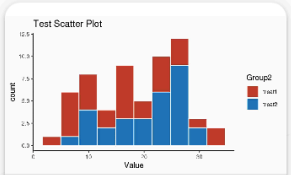
Exported tasks info

导出和导入临时任务记录

HIPLOT

实践是检验真理的唯一标准 - 毛泽东选集

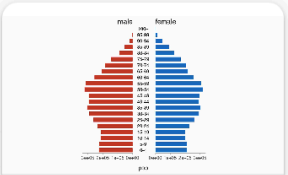
Hiplot 可视化平台操作演示 | 基础模块



Histogram

Display data distribution.

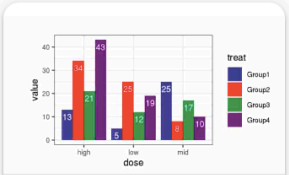
vue distribution



Pyramid Chart

Display data values.

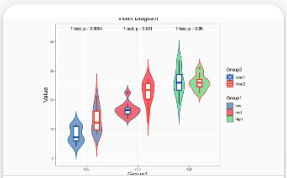
vue distribution



Barplot

Display data values.

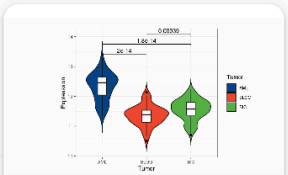
vue distribution



Violin Group

Display the data distribution.

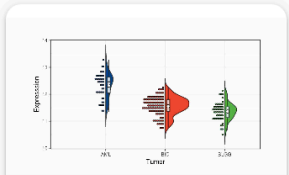
vue distribution



Violin

Display the data distribution.

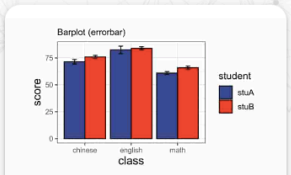
vue distribution



Half Violin

Display the data distribution.

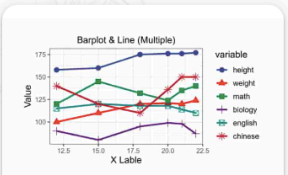
vue distribution



Barplot (errorbar)

Display data values.

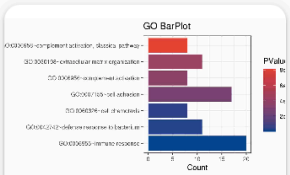
vue distribution



Multiple Barplot&Line

Display data values.

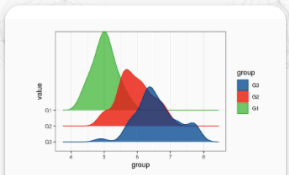
vue distribution correlation



Barplot Gradient

Display data values.

vue distribution



Ridge

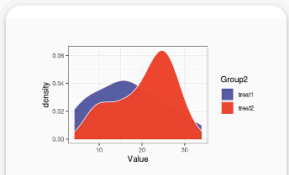
Display the data distribution.

vue distribution

Dist Plot

Display the data distribution.

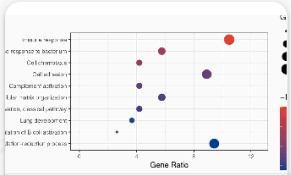
vue distribution



Density

Display data distribution.

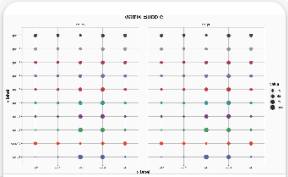
vue distribution



Bubble

Display the variables.

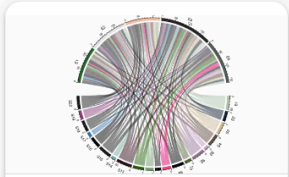
vue correlation



Matrix Bubble

Display matrix bubble.

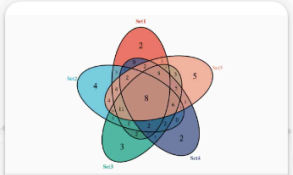
vue correlation



Chord Plot

Corelation Visualization.

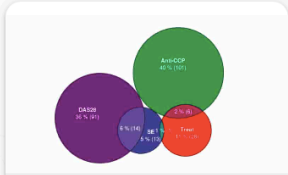
vue correlation



Venn

Data sets cross-relationships.

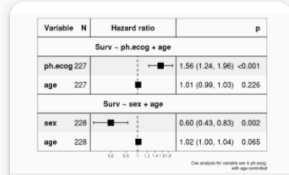
vue part-of-a-whole



Eulerr Plot

Display the data ratio.

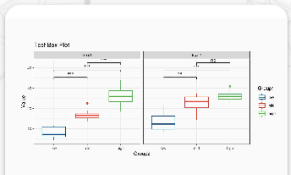
vue part-of-a-whole



Cox Models Forest

Used for survival data analysis.

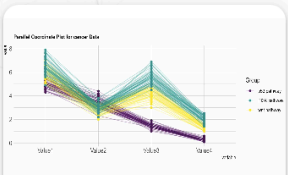
vue model survival



Boxplot

Display differences between groups.

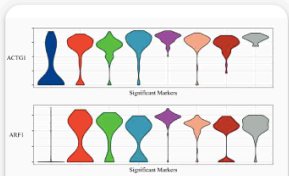
vue distribution



Parallel Coordinate

Display High-dimensional Data.

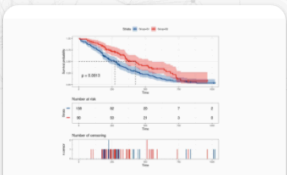
vue distribution



Stack Violin

Display the data distribution.

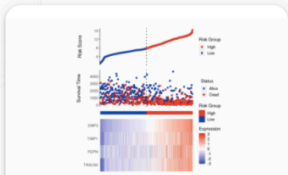
vue distribution



Survival Analysis

Used for survival data display.

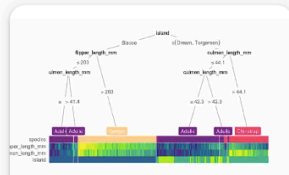
vue model survival



Risk Factor Analysis

Survival Data Analysis.

vue survival model

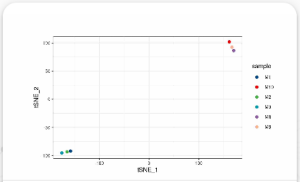


Treeheatr

Decision tree visualizations.

vue model

Hiplot 可视化平台操作演示 | 基础模块

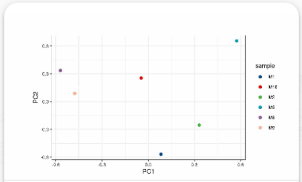


tSNE

Dimension reduction methods.

★★★★★

vue correlation

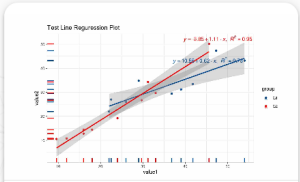


PCA

Dimension reduction methods

★★★★★

vue correlation

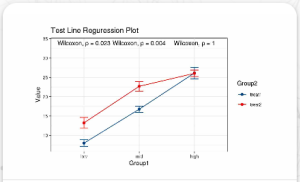


Line Regression

Display the variables.

★★★★★

vue correlation

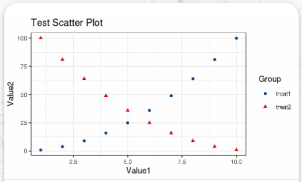


Line Regression (errorbar)

Display the variables.

★★★★★

vue correlation

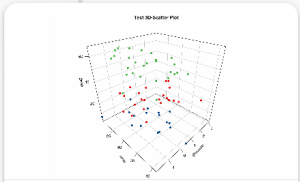


Scatter

Display the variables.

★★★★★

vue correlation

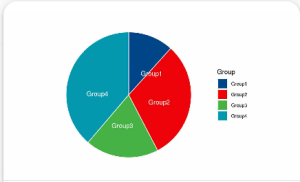


3D Scatter

Display the variables.

★★★★★

vue correlation

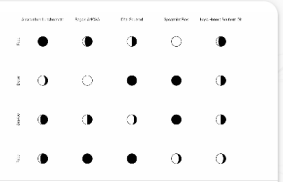


Pie

Display the data ratio.

★★★★★

vue part-of-a-whole

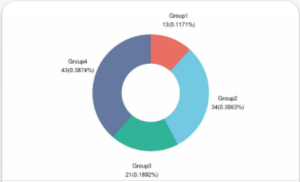


Moon charts

Display the data ratio.

★★★★★

vue part-of-a-whole

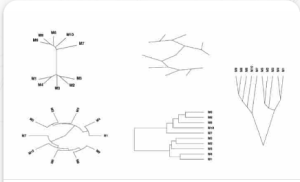


Donut

Display the data ratio.

★★★★★

vue part-of-a-whole

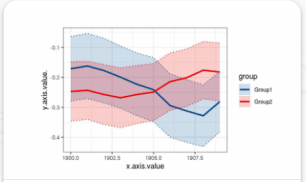


Dendrogram

Clustering method.

★★★★☆

vue correlation

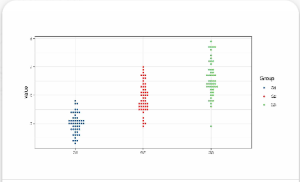


Ribbon

Display data hierarchy.

★★★★☆

vue correlation

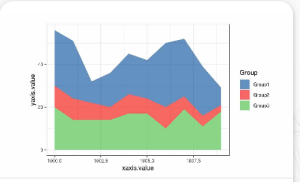


Beeswarm

Display the data distribution.

★★★★☆

vue distribution

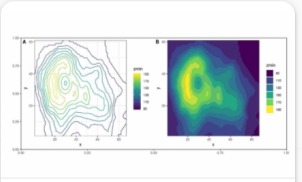


Area

Display the data distribution.

★★★★☆

vue distribution

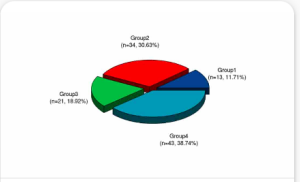


Contour (Matrix)

Display the altitude.

★★★★☆

vue distribution

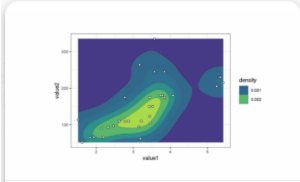


3D Pie

Display the data ratio.

★★★★☆

vue part-of-a-whole

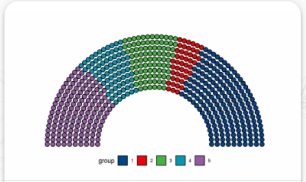


Contour (XY)

Display the altitude.

★★★★☆

vue distribution

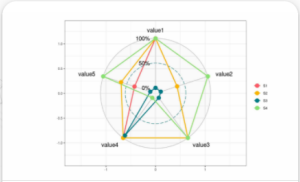


Parliament

Display the data ratio.

★★★★☆

vue part-of-a-whole

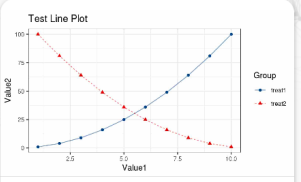


Radar

Display the variables.

★★★★☆

vue ranking

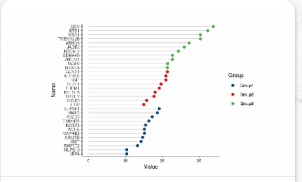


Line

Display the variables.

★★★★☆

vue correlation

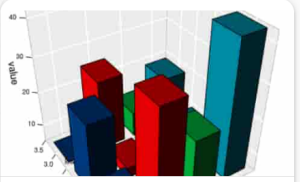


Dotchart

Common way to show digital dramas.

★★★★☆

vue correlation



3D Barplot

Display data values.

★★★★☆

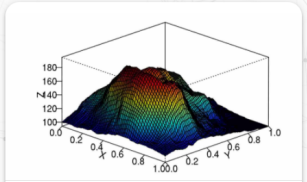
vue distribution

Simplified Correlation Heatmap

Simplified Variables Correlation Heatmap.

★★★☆☆

correlation heatmap

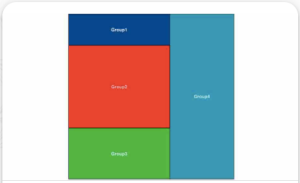


Perspective

Display multidimensional data.

★★★☆☆

vue distribution



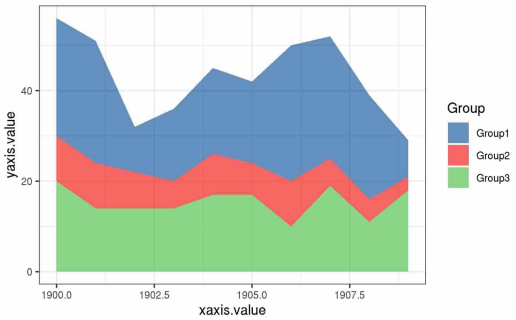
Treemap

Display the data ratio.

★★★☆☆

vue part-of-a-whole

Hiplot 可视化平台操作演示 | 基础模块



Import Data

Data Table

Normal | Arial | 10

	A	B	C	D	E	F	G	H
1	group	xaxis.value	yaxis.value					
2	Group1	1900	26					
3	Group1	1901	27					
4	Group1	1902	10					
5	Group1	1903	16					
6	Group1	1904	19					
7	Group1	1905	18					
8	Group1	1906	30					
9	Group1	1907	27					
10	Group1	1908	23					
11	Group1	1909	8					
12	Group2	1900	10					
13	Group2	1901	10					
14	Group2	1902	8					
15	Group2	1903	6					
16	Group2	1904	9					
17	Group2	1905	7					

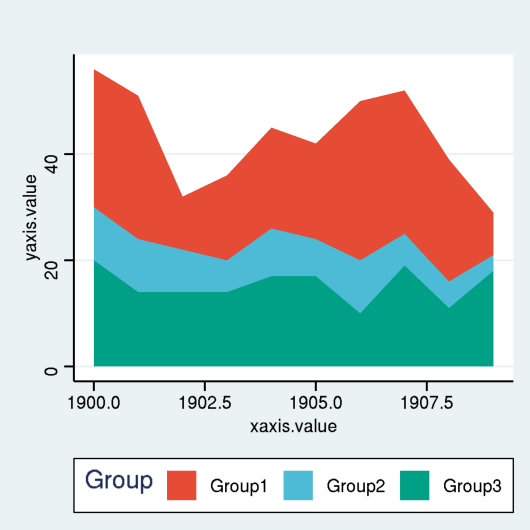
Sheet1

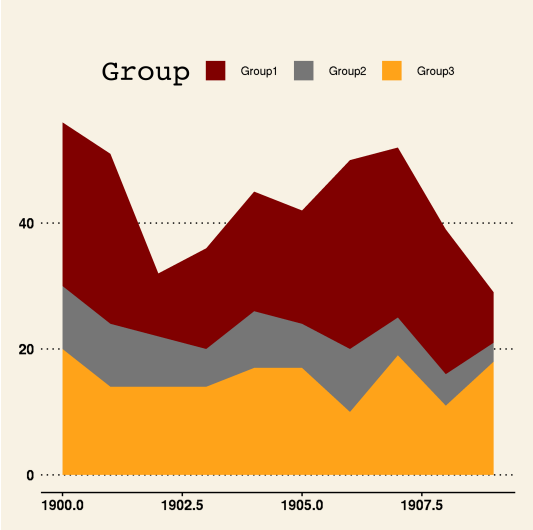
Area input and output

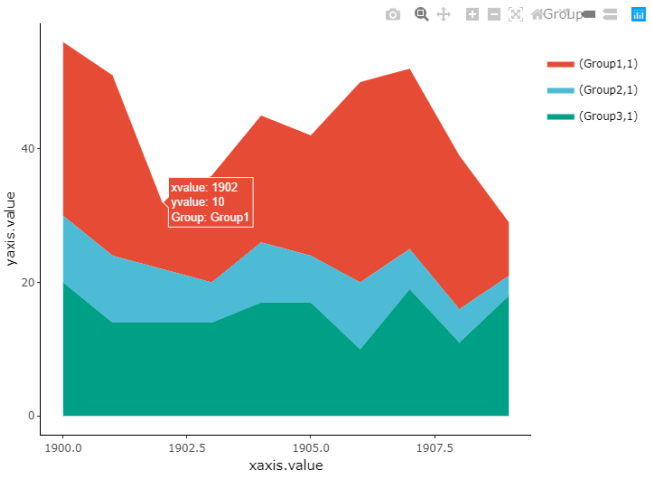
https://hiplot.com.cn/basic/area

HIPLOT

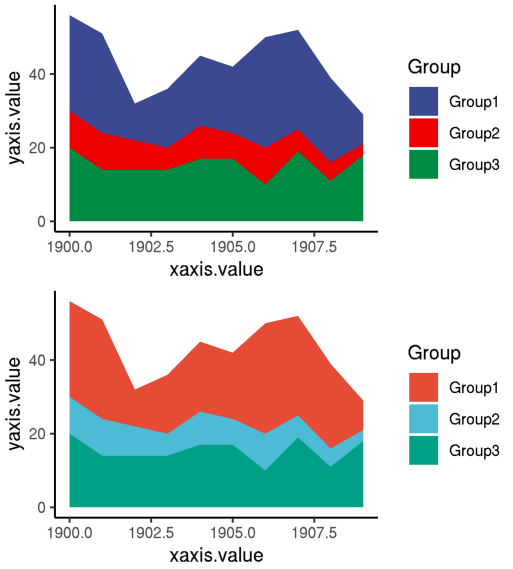
Hiplot 可视化平台操作演示 | 基础模块

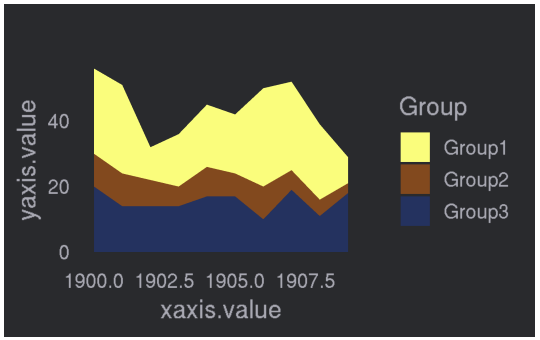


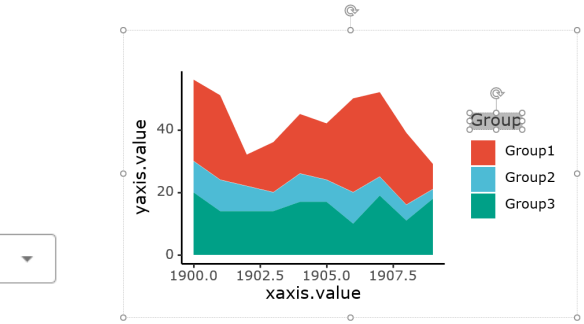




Plotly





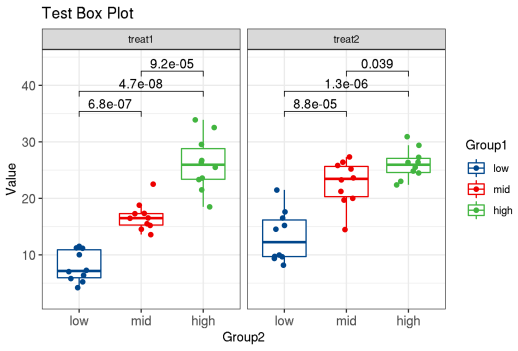


PPT edit

Area output style

HIPLOT

Hiplot 可视化平台操作演示 | 基础模块



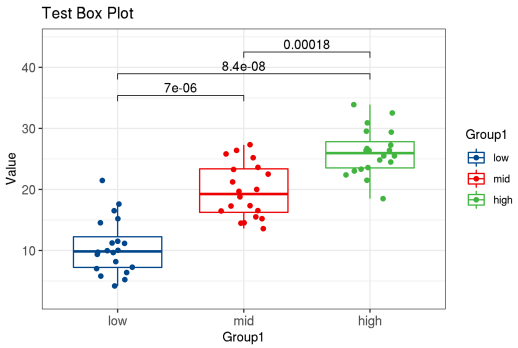
Import Data

Data Table

Normal Arial 10

	A	B	C
1	Value	Group1	Group2
2	4.2	low	treat1
3	11.5	low	treat1
4	7.3	low	treat1
5	5.8	low	treat1
6	6.4	low	treat1
7	10	low	treat1
8	11.2	low	treat1
9	11.2	low	treat1
10	5.2	low	treat1
11	7	low	treat1
12	16.5	mid	treat1
13	16.5	mid	treat1
14	15.2	mid	treat1
15	17.3	mid	treat1
16	22.5	mid	treat1

Sheet1



Import Data

Data Table

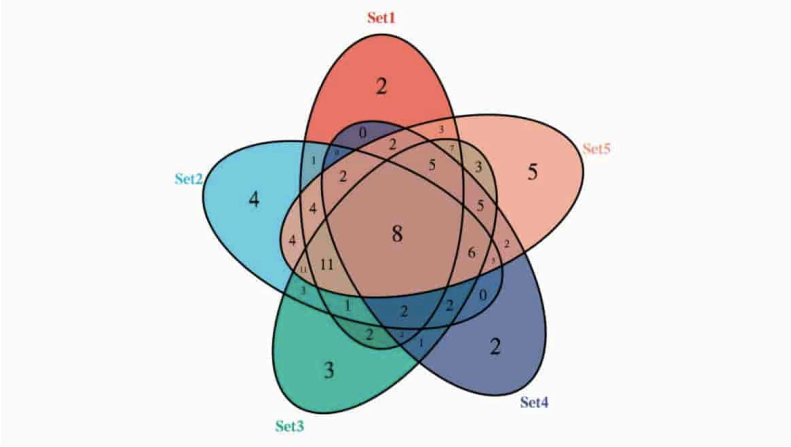
Normal Arial 10

	A	B	C
1	Value	Group1	
2	4.2	low	
3	11.5	low	
4	7.3	low	
5	5.8	low	
6	6.4	low	
7	10	low	
8	11.2	low	
9	11.2	low	
10	5.2	low	
11	7	low	
12	16.5	mid	
13	16.5	mid	
14	15.2	mid	
15	17.3	mid	
16	22.5	mid	

Sheet1

Boxplot input and output https://hiplot.com.cn/basic/boxplot

Hiplot 可视化平台操作演示 | 基础模块

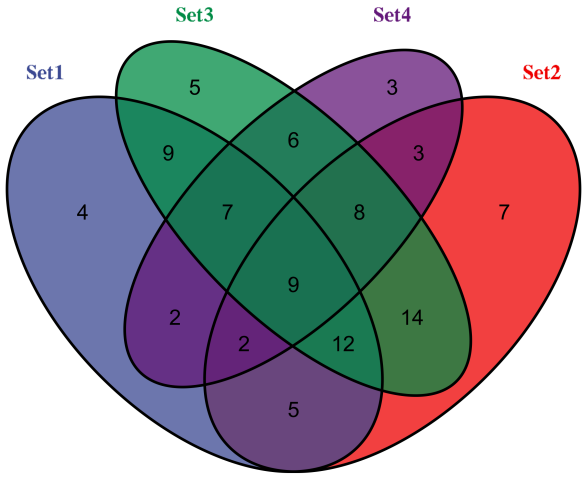


Import Data

Data Table

	A	B	C	D	E
1	Set1	Set2	Set3	Set4	Set5
2	ISG15	HES5	DVL1	MATP6P1	FAM132A
3	TTLL10	AURKAIP1	ARHGEF16	MIR551A	AGRN
4	HES4	LINC00982	OR4F16	C1orf222	WBP1LP6
5	OR4G4P	FAM87B	SKI	MIR200B	KLHL17
6	MND2P28	SKI	WASH7P	LINC00115	FAM41C
7	FAM87B	GABRD	MEGF6	ATAD3B	PANK4
8	MIR200B	OR4G11P	LINC00115	PANK4	CDK11A
9	PLCH2	CALML6	MMP23B	MORN1	AURKAIP1
10	MXRA8	C1orf86	ATAD3C	TPRG1L	SDF4
11	PEX10	ATAD3B	PRDM16	B3GALT6	MND1P23
12	TNFRSF4	HES4	OR4F29	LINC00982	FAM213B
13	CICP27	ANKRD65	TMEM52	OR4F16	SAMD11
14	CCDC27	OR4F5	VWA1	C1orf86	ATAD3B
15	WBP1LP6	CCNL2	GNB1	DDX11L1	SSU72
16	SCNN1D	TNFRSF18	FAM41C	AURKAIP1	SKI

Sheet1



Import Data

Data Table

	A	B	C	D	E	F
1	Set1	Set2	Set3	Set4		
2	ISG15	HES5	DVL1	MATP6P1		
3	TTLL10	AURKAIP1	ARHGEF16	MIR551A		
4	HES4	LINC00982	OR4F16	C1orf222		
5	OR4G4P	FAM87B	SKI	MIR200B		
6	MND2P28	SKI	WASH7P	LINC00115		
7	FAM87B	GABRD	MEGF6	ATAD3B		
8	MIR200B	OR4G11P	LINC00115	PANK4		
9	PLCH2	CALML6	MMP23B	MORN1		
10	MXRA8	C1orf86	ATAD3C	TPRG1L		
11	PEX10	ATAD3B	PRDM16	B3GALT6		
12	TNFRSF4	HES4	OR4F29	LINC00982		
13	CICP27	ANKRD65	TMEM52	OR4F16		
14	CCDC27	OR4F5	VWA1	C1orf86		
15	WBP1LP6	CCNL2	GNB1	DDX11L1		
16	SCNN1D	TNFRSF18	FAM41C	AURKAIP1		

Sheet1

Venn input and output (up to 5 sets)

https://hiplot.com.cn/basic/venn

Hiplot 可视化平台操作演示 | 基础模块

Counts

Gene	M1	M2	M3	M4	M5	M6	M7
GBP4	6.5993441095	5.2262660248	3.6932875381	3.9385009528	4.5271930886	9.3081190324	8.9878
BCAT1	5.7603803773	4.8927830209	5.4489239172	3.4854133857	3.8556691717	8.6620810404	8.7933
CMPK2	9.5619051154	4.5491681565	3.9986549224	5.6143839805	3.9047928726	9.7907700044	7.1331
STOX2	8.3964093157	8.7170552201	8.0390641101	7.6430595565	9.2746490901	4.4170130073	4.7252
PADI2	8.4197658905	8.2684298023	8.4511808436	9.2007322844	8.5982072017	4.5900330127	5.3682
SCARNA5	7.6530743097	5.7803926297	10.633550472	5.9136843629	8.8056047501	5.8901204765	5.5279
ALOX12P2	9.0014211521	7.7535422910	4.9209595817	7.6363543709	9.8886247890	6.2119435438	3.7320
SNORA74B	5.5387087152	7.1690533938	11.441646436	5.9825656857	8.3944025246	4.7515592532	5.1812
HIST1H2BL	6.1812704966	4.4484188901	5.6049610298	6.4851683738	2.5995743866	7.6301766056	6.7582
MNDA	8.7026352495	7.3223519563	9.2718214201	9.1345154397	8.3391138436	4.5719022848	5.4783
OLFM4	9.3453083049	6.4386066367	8.7167612640	9.6855451685	7.6882618432	5.9698038656	3.8563
FLT3	5.1643063209	4.4193554432	5.0635513633	5.4127835356	3.3378634184	8.5851643929	8.8763
CHD7	8.3734749638	8.7280322425	8.4088176083	8.7164755127	8.3737066673	4.6131990181	6.6362
NFIL3	8.0554164753	8.3650998813	9.2391936769	8.5368250774	8.4523508188	4.4785271277	6.5062
HSPA1B	5.0081989999	9.1946502771	6.5988499179	7.1295092512	3.8852697172	5.7121787252	11.133

Sheet1

GeneInfo

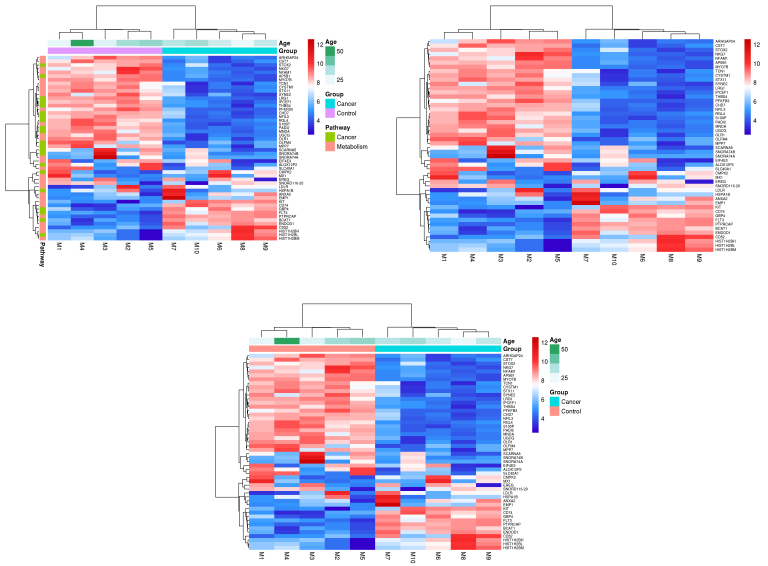
Gene	Pathway
GBP4	Cancer
BCAT1	Cancer
CMPK2	Cancer
STOX2	Cancer
PADI2	Cancer
SCARNA5	Cancer
ALOX12P2	Cancer
SNORA74B	Cancer
HIST1H2BL	Cancer
MNDA	Cancer
OLFM4	Cancer
FLT3	Cancer
CHD7	Cancer
NFIL3	Cancer
HSPA1B	Cancer

Sheet1

SampleInfo

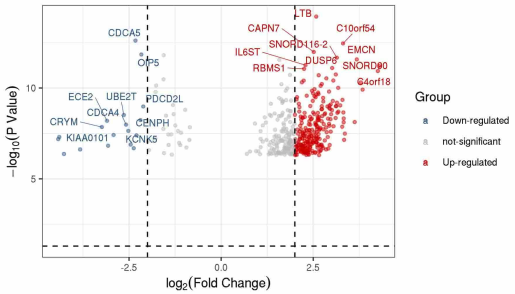
Sample	Group	Age
M1	Control	23
M2	Control	34
M3	Control	25
M4	Control	52
M5	Control	36
M6	Cancer	28
M7	Cancer	31
M8	Cancer	22
M9	Cancer	29
M10	Cancer	34

Sheet1



Heatmap input and output https://hiplot.com.cn/basic/heatmap

Hiplot 可视化平台操作演示 | 基础模块



Import Data

Data Table

Normal | Arial | 10

	A	B	C	D	E	F	G	H
1	Symbol	logFC	P.Value					
2	LTB	2.580830574	1.17E-14					
3	CDCA5	-2.326302376	2.46E-13					
4	C10orf54	3.307901298	3.53E-13					
5	CAPN7	2.514235402	1.04E-12					
6	OIP5	-2.16662036	1.43E-12					
7	SNORD116-2	3.139661776	2.15E-12					
8	PKIG	-1.560503944	1.58E-12					
9	EMCN	3.681695861	2.68E-12					
10	B2M	1.578095238	2.82E-12					
11	IL6ST	2.287862908	5.51E-12					
12	SNORD90	4.285534102	6.12E-12					
13	DUSP6	3.01388868	7.90E-12					
14	RBMS1	2.251183421	8.82E-12					
15	C4orf18	4.252879583	1.17E-11					
16	SKAP1	3.112284552	1.80E-11					
17	CD48	1.8697202	1.89E-11					

Sheet1

Symbol: Symbol

P.Value: P.Value

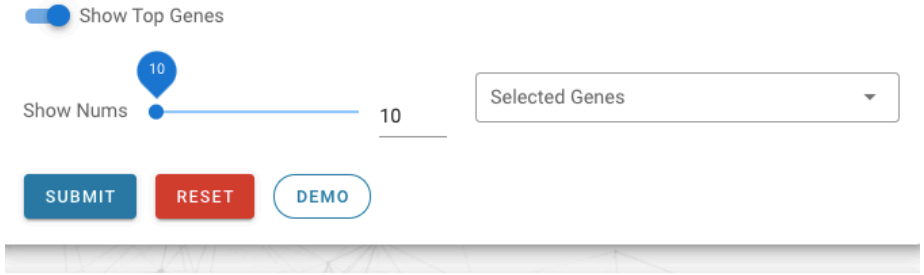
logFC: logFC

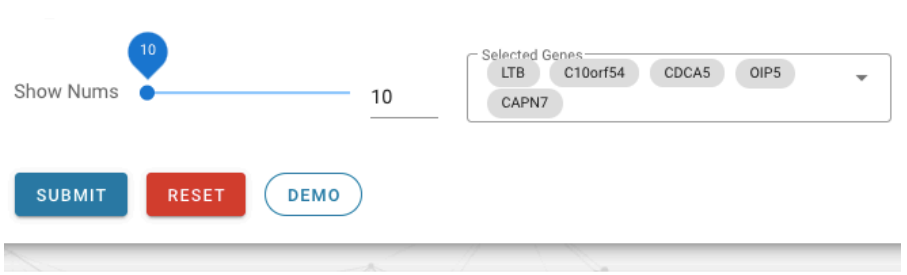
Volcano input data

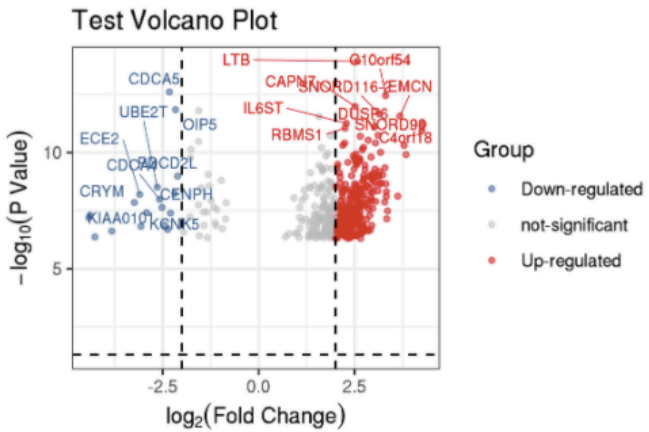
https://hiplot.com.cn/basic/volcano

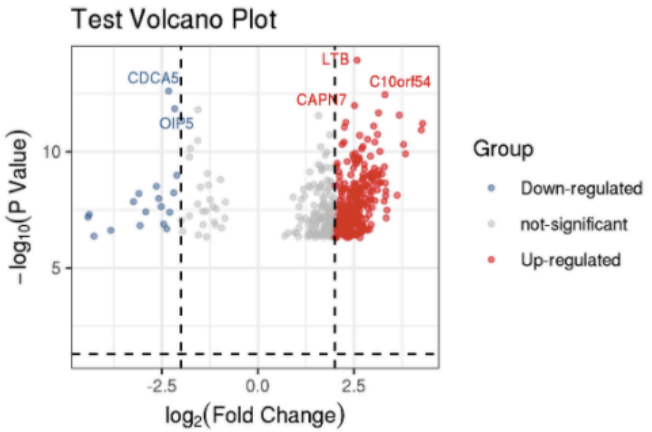
HIPLOT

Hiplot 可视化平台操作演示 | 基础模块







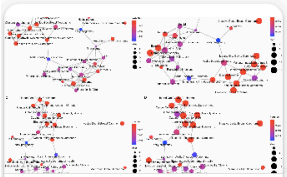


Assign the text label in volcano plot

https://hiplot.com.cn/basic/volcano

HIPLOT

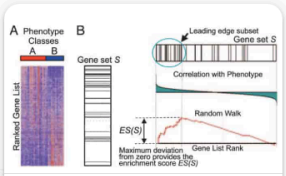
Hiplot 可视化平台操作演示 | 进阶模块



GO/KEGG Analysis

GO/KEGG analysis by clusterProfiler.

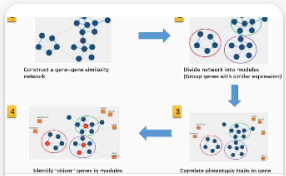
vue expression



Broad GSEA

Gene Set Enrichment Analysis.

vue expression



WGCNA

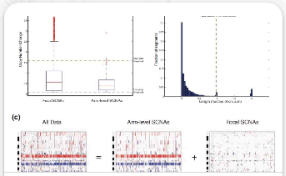
Co-expression network analysis.

vue expression

Sigflow

Mutation Signature Analysis.

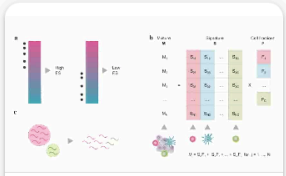
vue mutation



GISTIC2

Copy Number Data Analysis.

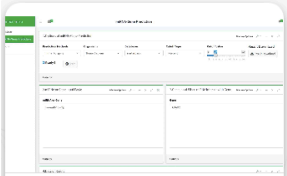
vue mutation CNV



Immunedeconv

Immunoinfiltration analysis.

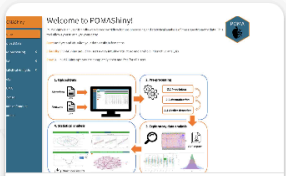
vue expression immune



miRNA-Gene Prediction

miRNA Functional Analysis.

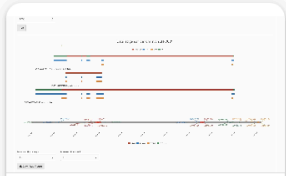
shiny miRNA gene



POMA Shiny

Mass Spectrometry Data Analysis.

shiny mass spectrometry



SMART

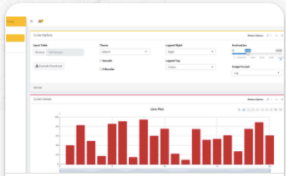
Methylation Analysis Resource Tool.

shiny methylation clinical TCGA

Raincloud Shiny

Interactive Raincloud Visulization

shiny raincloud



Echarts Shiny

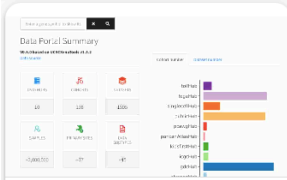
Interactive Javascript Visulization

shiny echarts

t-SNE Ellipse Shiny

Interactive t-SNE Visulization

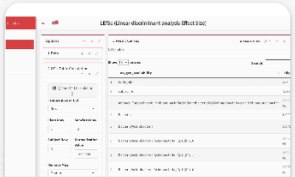
shiny tsne



UCSCXenaShiny

UCSCXena Hub Shiny App.

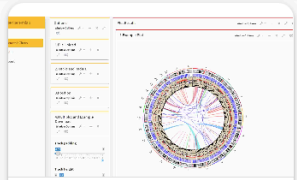
shiny expression mutation TCGA



LEfSe

Metagenomic Data Analysis Application.

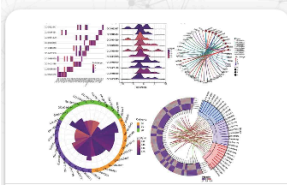
shiny microbiome



Genome Circos

Genome Circos Plot.

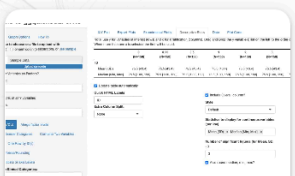
shiny genome circos



EnrichVisBox Shiny

Visualization of Enrichment Analysis

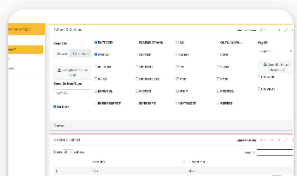
shiny enrichment GO



ggquickeda

Quick Exploration of Data

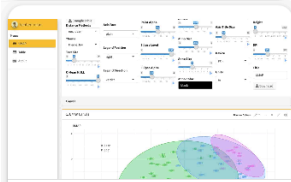
shiny summary exploration



Gene ID Convertor

Format Convertor.

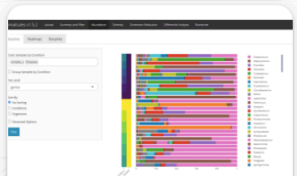
shiny gene



UMAP Ellipse Shiny

Interactive UMAP Visulization

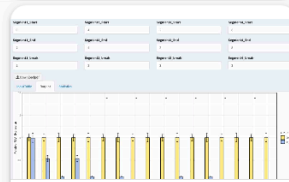
shiny umap



Animalcules

Interactive Microbiome Analysis

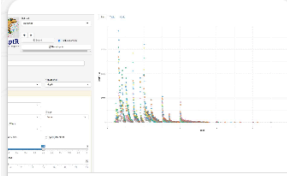
shiny microbiome



iQPCR Tools

qPCR Data Analysis Tool.

shiny qpcr



ggraptr

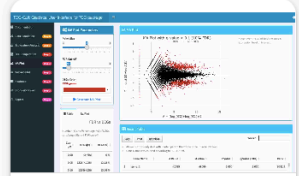
Interactive ggplot2 Visualization

shiny ggplot2

Shinyseurat

Seurat Single Cell Data Analysis

shiny single cell



TCC-GUI

Transcriptome Analysis Tool

shiny expression

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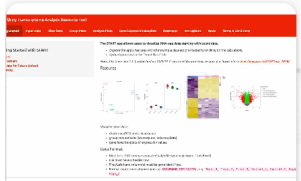
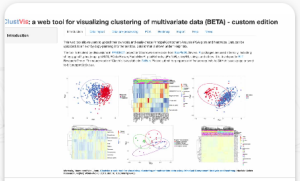


START

Transcriptome Analysis Tool

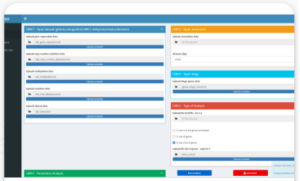
shiny expression



ClustVis

PCA & Cluster

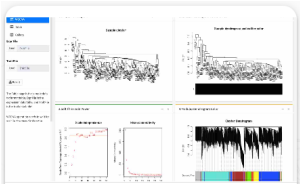
shiny pca cluster



Gmiec Shiny

Integrate Multi-omics Data

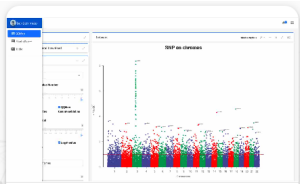
shiny multi-omics drug



WGCNA Shiny

Co-expression network analysis.

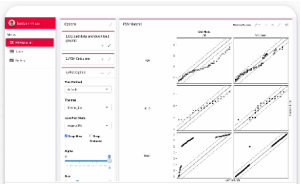
shiny expression



Manhattan Shiny

Manhattan Plots.

shiny genome gwas



Propensity Score Matching Shiny

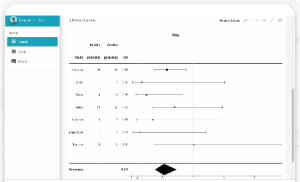
Propensity Score Matching (MatchIt and cabalt).

shiny statistics

gggenes

Gene Visualization

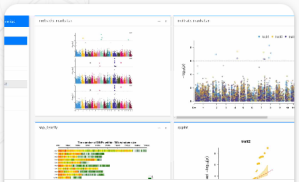
shiny genome



Forestplot

Forest Visualization

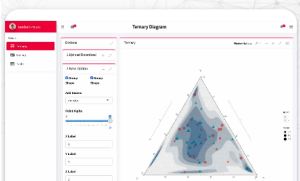
shiny forest



CMplot

GWAS Visualization

shiny genome



Ternary Diagram

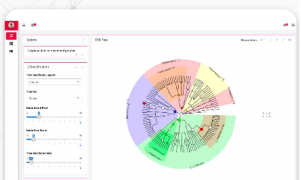
Describe the Three Variables.

shiny ternary correlation

MSA Shiny

Multiple sequence alignment.

shiny seq



OTU-Tree Shiny

Amplicon/Metagenome OTU abundance.

shiny metagenome

Chromosome Shiny

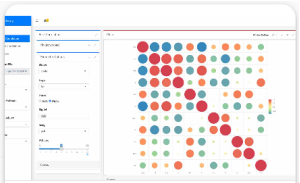
Chromosome Visualization.

shiny genome

Community Shiny

Community Network Analysis.

shiny expression



Shiny ggcorrplot2

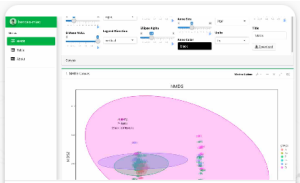
Correlation Heatmap Shiny.

shiny correlation

Standardized Mean Differences

Visualization of Statistical Parameters

shiny statistics



NMDS Ellipse

Non-metric Multidimensional Scaling Visualization

shiny general

Multi Ribbon

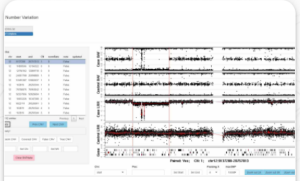
Multi-ribbon Shiny

shiny general

Network Shiny

Network Plot.

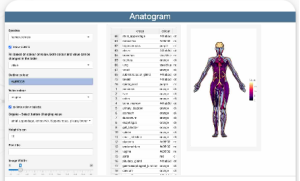
shiny expression



Shiny CNV

Visualization of CNV

shiny mutation



Anatogram Shiny

Anatogram.

shiny medcine

PCoA Ellipse Shiny

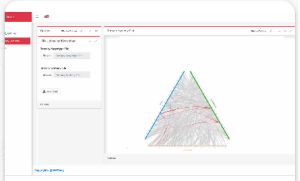
Interactive PCoA analysis.

shiny general

PCA Ellipse Shiny

Interactive PCA analysis.

shiny general



Synteny Viewer

Ternary Synteny Plot.

shiny general

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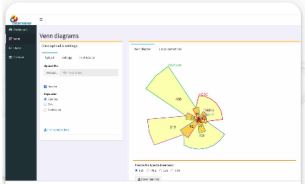
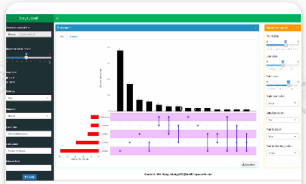


Shiny Intervene

Data sets cross-relationships.

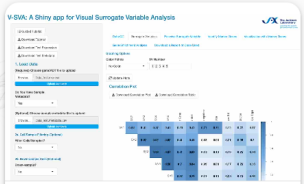
shiny general



Shiny UpSetR

Data sets cross-relationships.

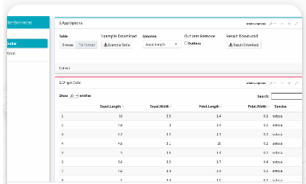
shiny general



V-SVA Shiny

Visual Surrogate Variable Analysis.

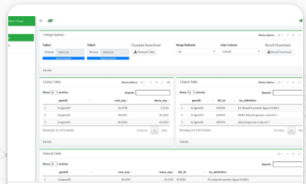
shiny qc



Outlier Process

Table Operation

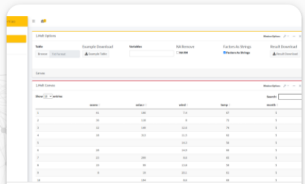
shiny table



Merge Table

Table Operation

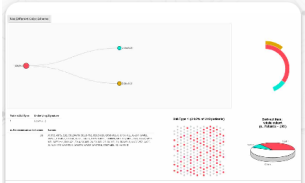
shiny table



Melt Table

Table Operation

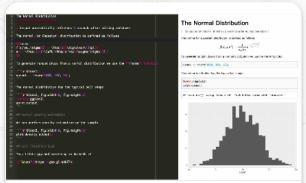
shiny table



Cellector Shiny

Selection of Cancer Cell Line.

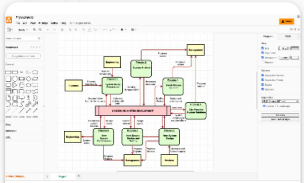
shiny cell-line



Rmarkdown Preview

Real time preview the R markdown.

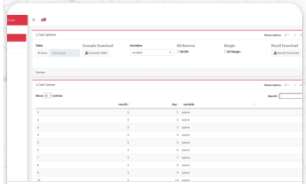
shiny general



Drawio Flow

Open souce drawio.

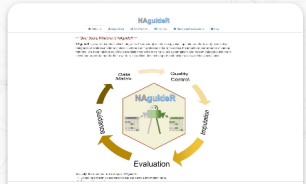
js flow



Cast Table

Table Operation

shiny table



NAguideR

Table Operation

shiny table

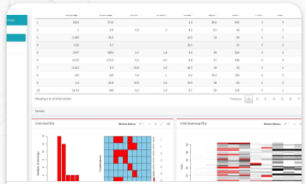
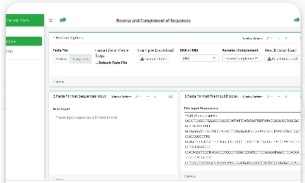


Table NA Process

Table Operation

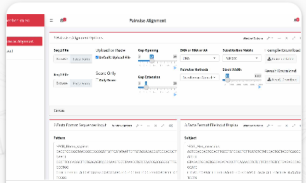
shiny table



Reverse & Complement

Sequence Operation

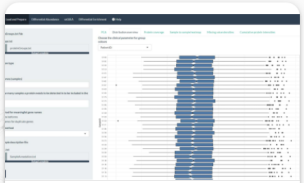
shiny seq



Pairwise Alignment

Sequence Operation

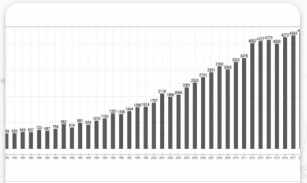
shiny seq



Eatomics

Proteomics Data Visualization

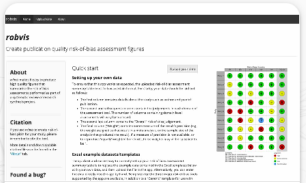
shiny protein proteomics



Tinyscholar

Google Scholar Author Citations

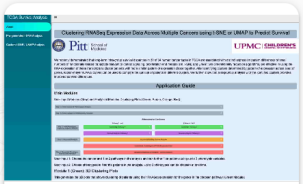
vue google



Robvis Shiny

Risk-of-bias assessment.

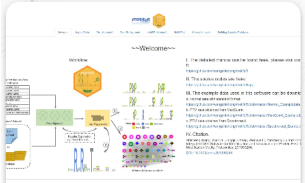
shiny qc



TCGA t-SNE/UMAP Survival Analysis

TCGA Survival Data Analysis.

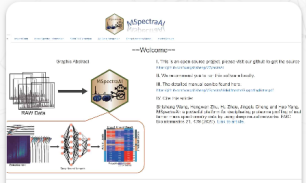
shiny TCGA expression



MotifeR Shiny

Protein Post-Translational Modification

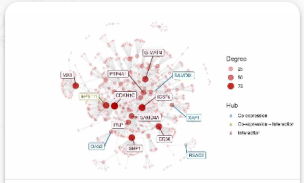
shiny protein



MSpectraAI Shiny

Proteomics Data Visualization

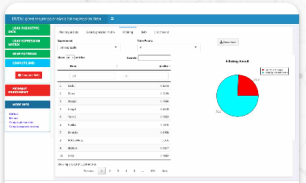
shiny protein



CEMitool

Co-expression modules analysis.

vue expression geneset



BMDx Shiny

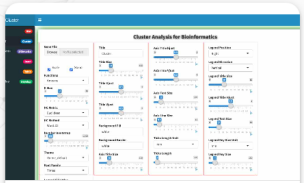
Dose response analysis (expression).

shiny expression

DscoreApp

Computation of the Implicit Association Test.

shiny statistics



Cluster Shiny

Interactive cluster analysis.

shiny expression

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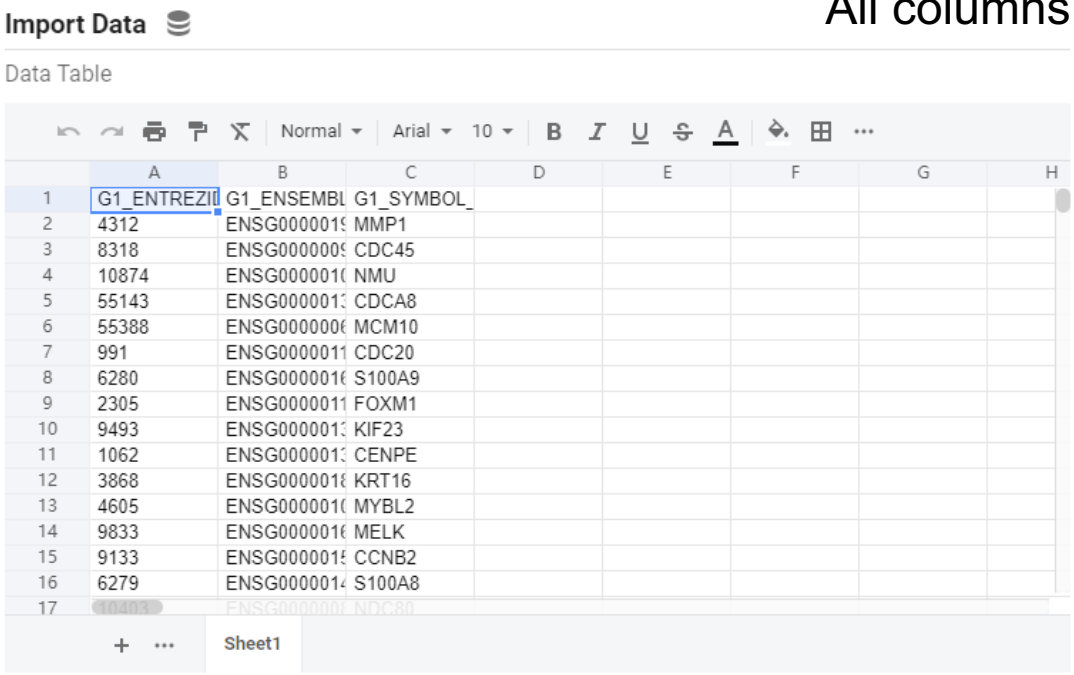
All columns will be included in the analysis



	A	B	C
1	G1_ENTREZI	G1_ENSEMBL	G1_SYMBOL_
2	4312	ENSG0000019	MMP1
3	8318	ENSG0000009	CDC45
4	10874	ENSG0000010	NMU
5	55143	ENSG0000013	CDCA8
6	55388	ENSG0000006	MCM10
7	991	ENSG0000011	CDC20
8	6280	ENSG0000016	S100A9
9	2305	ENSG0000011	FOXM1
10	9493	ENSG0000013	KIF23
11	1062	ENSG0000013	CENPE
12	3868	ENSG0000018	KRT16
13	4605	ENSG0000010	MYBL2
14	9833	ENSG0000016	MELK
15	9133	ENSG0000015	CCNB2
16	6279	ENSG0000014	S100A8
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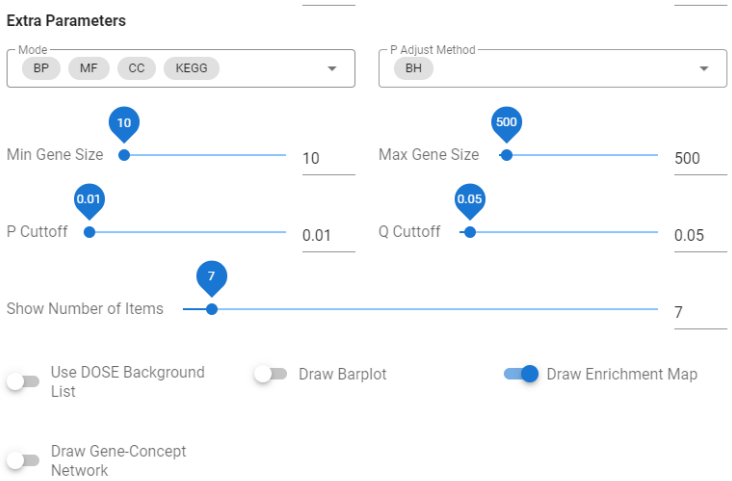

GO/KEGG Analysis Input

https://hiplot.com.cn/advance/clusterprofiler-go-kegg

HIPLOT

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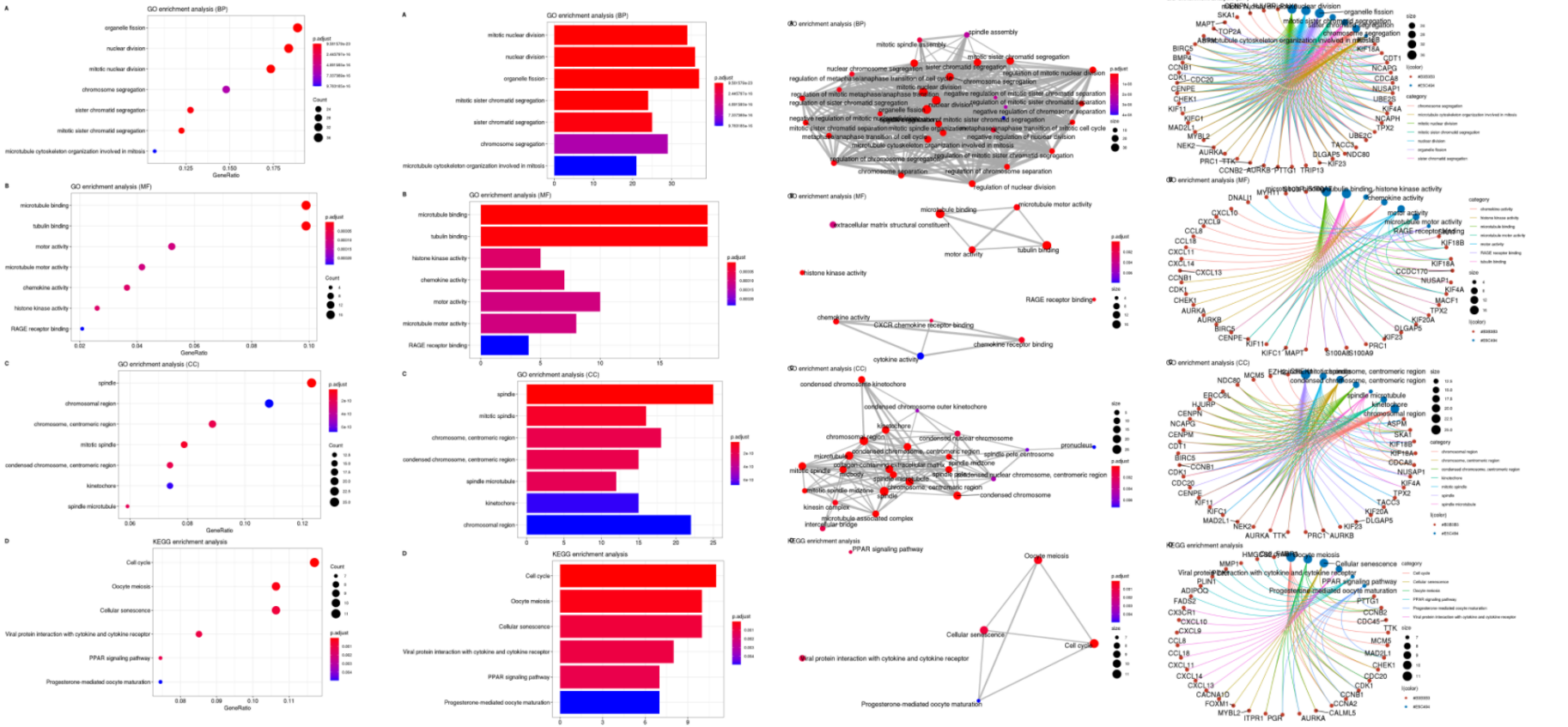

GO/KEGG Analysis Output

https://hiplot.com.cn/advance/clusterprofiler-go-kegg

HIPLOT

Hiplot 可视化平台操作演示 | 进阶模块

public/demo/gsea/P53.txt

NAME	DESCRIPTION	786-0	BT-549	CCRF-CEM	COLO 205	EKVX	HCC-2998	HCT-15	HOP-62	HOP-92	HS 578T	HT29	K-562	KM12	M14	MDA-MB-231/A	MDA-MB-435	NCI-H
TACC2	na	46.05	82.17	16.87	98.6	141.02	114.32	134.34	44.95	73.96	74.29	130.04	24.04	197.63	33.82	72.22	53.78	64.19
C14orf132	na	108.34	59.04	25.61	33.11	42.53	9.12	9.36	310.96	101.74	241.05	15.52	19.46	5.05	32.39	18.11	18.4	122.9
AGER	na	42.2	25.75	76.01	40.41	32.17	48.28	58.27	42.4	49.68	58.18	59.93	36.98	45.58	32.58	48.13	45.04	47.23
32385_at	na	7.43	13.94	8.55	21.13	15.09	19.05	16.47	7.6	10.88	9.36	14.91	14.37	15.96	13.75	6.21	11.21	23.3
RBM17	na	11.4	3.0	3.16	2.34	4.43	1.56	6.04	6.16	1.41	7.1	2.05	2.85	1.43	4.92	5.45	2.6	3.05
DYT1	na	148.09	317.17	316.66	147.23	125.78	261.39	268.41	212.51	142.51	163.06	252.58	183.74	174.92	156.65	241.41	177.62	145.9
CORO1A	na	8.62	9.12	1572.53	5.91	5.31	11.98	128.77	7.51	7.04	6.01	5.67	15.35	8.05	6.29	6.22	7.94	9.81
WT1	na	206.74	136.71	141.34	129.09	138.01	138.16	130.14	123.8	131.91	142.58	94.59	148.7	127.9	115.71	113.4	157.55	140.1
SYCP2	na	7.94	35.68	7.8	1.97	7.75	4.73	7.23	5.72	2.02	1.16	25.92	15.13	4.79	17.41	9.4	3.68	20.36
SULF1	na	10.45	8.5	4.05	4.77	2.35	3.72	3.34	809.88	2.58	1211.69	2.77	5.62	4.85	4.93	4.93	6.06	4.06
C19orf21	na	6.22	5.16	3.95	37.56	110.36	208.29	251.67	4.43	3.34	4.87	126.02	4.73	171.15	3.88	4.17	3.65	4.05
PHYH	na	209.99	253.07	90.36	61.83	360.49	145.01	130.16	165.5	343.02	121.41	125.69	68.44	252.22	236.32	147.41	159.43	193.8
31336_at	na	3.35	5.28	2.98	4.82	4.36	1.45	5.57	4.38	3.57	4.43	1.62	3.23	6.47	8.43	6.78	9.15	4.71
TOP2B	na	349.1	462.16	1348.41	274.07	730.39	350.95	635.21	644.7	516.55	553.51	258.29	600.56	604.43	540.68	462.45	288.08	494.4
ATP9A	na	126.28	197.49	117.66	380.3	354.14	84.19	243.24	235.76	252.57	219.15	1130.06	4.92	191.27	105.05	50.89	71.97	285.6
TGFBR1	na	11.73	13.13	16.2	12.97	9.55	8.3	20.65	17.05	19.68	18.75	13.34	16.27	9.35	25.7	9.79	16.0	14.65
IRF7	na	98.46	246.49	52.48	70.54	33.35	198.34	155.66	144.43	56.44	17.4	967.34	42.65	54.76	111.66	74.16	44.61	95.72
ZNF189	na	24.28	56.32	45.09	44.11	36.9	37.76	65.64	36.62	24.88	30.68	38.62	25.76	47.39	33.97	34.34	32.48	43.85
VTI1B	na	184.52	85.33	123.2	128.74	167.21	135.93	165.11	182.51	245.75	88.73	116.11	121.28	112.04	82.78	131.74	94.24	185.5
32413_at	na	32.17	23.72	14.51	14.68	22.96	18.22	6.37	19.93	8.14	16.0	11.38	12.38	16.73	22.59	18.53	14.54	19.81
RPS6KB1	na	74.05	33.55	52.15	50.15	81.86	96.03	86.38	90.16	69.21	34.65	45.23	46.43	66.0	46.23	61.02	41.25	111.0
KCNB1	na	5.55	13.95	7.29	4.92	12.74	8.6	3.66	4.17	36.61	7.02	7.31	6.2	5.81	8.12	6.14	4.59	111.2
RAPGEF4	na	7.44	4.51	4.38	4.38	2.75	4.87	3.62	3.27	1.09	1.67	4.03	0.88	5.65	6.01	7.86	5.03	3.16
ALDH9A1	na	168.62	224.42	318.53	291.52	258.23	266.74	535.4	314.31	227.49	315.75	155.98	215.25	524.49	430.31	355.17	456.22	263.1
39520_at	na	86.48	76.1	52.11	63.33	77.98	74.89	73.68	102.35	78.91	84.45	70.91	47.47	67.45	61.88	77.16	76.17	70.43
TGM1	na	20.18	12.0	13.36	6.64	10.52	6.57	11.5	9.83	6.35	12.43	12.12	15.81	9.04	8.37	13.84	13.38	17.02
DDX18	na	82.2	69.63	186.94	109.83	114.81	127.14	103.26	99.43	134.82	95.5	102.81	152.11	146.47	130.47	79.95	186.04	147.8
HSU79275	na	84.33	66.8	93.74	113.44	133.74	114.09	95.67	98.26	113.66	54.4	74.25	70.87	72.26	109.16	83.56	87.95	100.9
OR2F2	na	23.91	26.29	17.09	14.98	14.09	17.71	16.09	15.77	15.36	22.5	13.68	14.46	15.94	19.33	19.34	39.29	17.7
PPP6R2	na	37.67	76.64	102.88	59.58	65.62	75.45	94.97	104.82	43.16	63.64	51.3	74.11	113.46	63.95	45.57	52.75	66.64

Sheet1

```
50 2 1
#MUT WT
MUT MUT MUT MUT MUT MUT MUT MUT MUT MUT MUT MUT MUT MUT MUT MUT MUT MUT MUT MUT MUT MUT MUT MUT MUT MUT MUT MUT MUT MUT MUT MUT MUT MUT
WT WT WT WT WT WT WT WT WT WT WT WT WT WT WT WT WT WT
```

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KEGG_GLYCOLYSIS_GLUCONEOGENESIS http://www.gsea-msigdb.org/gsea/msigdb/cards/KEGG_GLYCOLYSIS_GLUCONEOGENESIS ACSS2 GCK PGK2 PGK1
PDHB PDHA1 PDHA2 PGM2 TPI1 ACSS1 FBP1 ADH1B HK2 ADH1C HK1 HK3 ADH4 PGAM2 ADH5 PGAM1 ADH1A ALDOC ALDH7A1 LDHAL6B
PKLR LDHAL6A ENO1 PKM PFKP BPGM PCK2 PCK1 ALDH1B1 ALDH2 ALDH3A1 AKR1A1 FBP2 PFKM PFKL LDHC GAPDH ENO3 ENO2
PGAM4 ADH7 ADH6 LDHB ALDH1A3 ALDH3B1 ALDH3B2 ALDH9A1 ALDH3A2 GALM ALDOA DLD DLAT ALDOB G6PC2 LDHA G6PC PGM1 GPI
KEGG_CITRATE_CYCLE_TCA_CYCLE http://www.gsea-msigdb.org/gsea/msigdb/cards/KEGG_CITRATE_CYCLE_TCA_CYCLE IDH3B DLST PCK2 CS PDHB PCK1
PDHA1 PDHA2 SUCLG2P2 FH SDHD OGDH SDHB IDH3A SDHC IDH2 IDH1 ACO1 ACLY MDH2 DLD MDH1 DLAT OGDHL PC SDHA
SUCLG1 SUCLA2 SUCLG2 IDH3G ACO2
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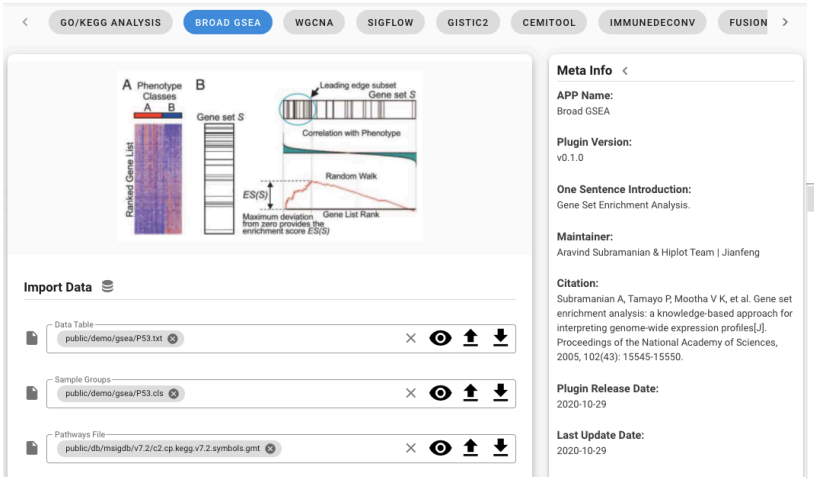
GSEA analysis input

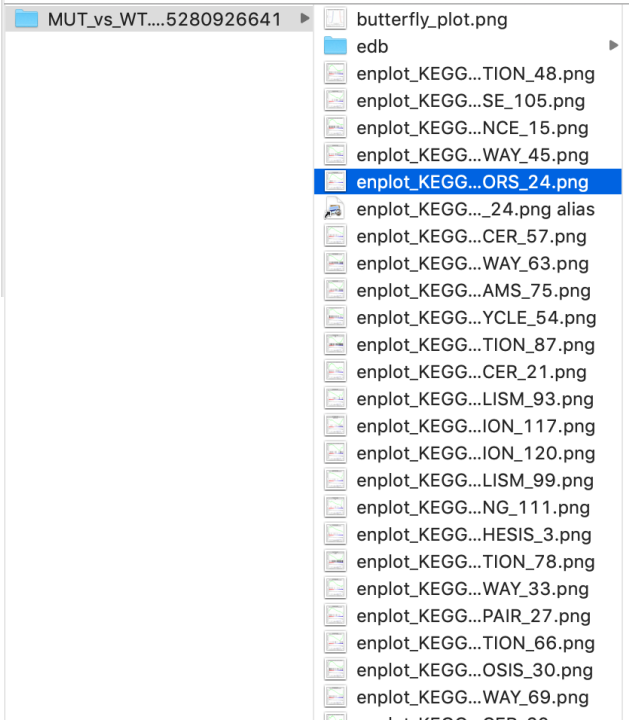
https://hiplot.com.cn/advance/gsea

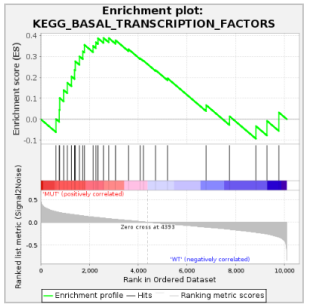
HIPLOT

Hiplot 可视化平台操作演示 | 进阶模块



You can choose multiple gene sets





enplot_KEGG_BASAL_TRANSCRIPTION_FACTORS_24.png
PNG image - 31 KB

Tags	Add Tags...
Created	Yesterday, 11:22 PM
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Content created	2020/11/13
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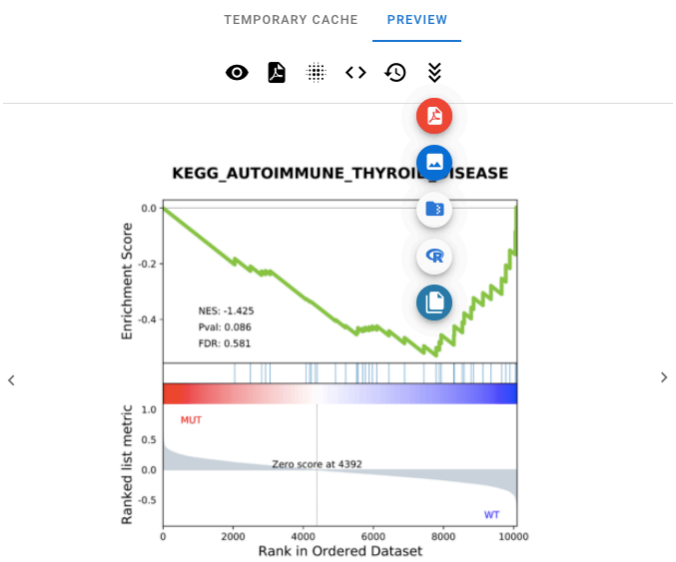
Color space	RGB

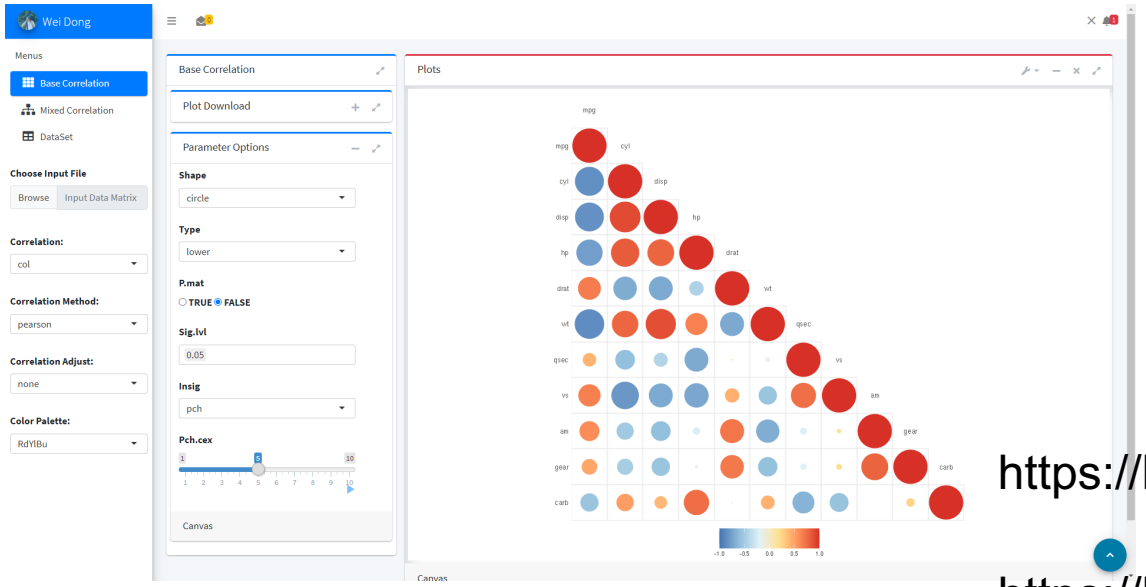


GSEA analysis output

https://hiplot.com.cn/advance/gsea

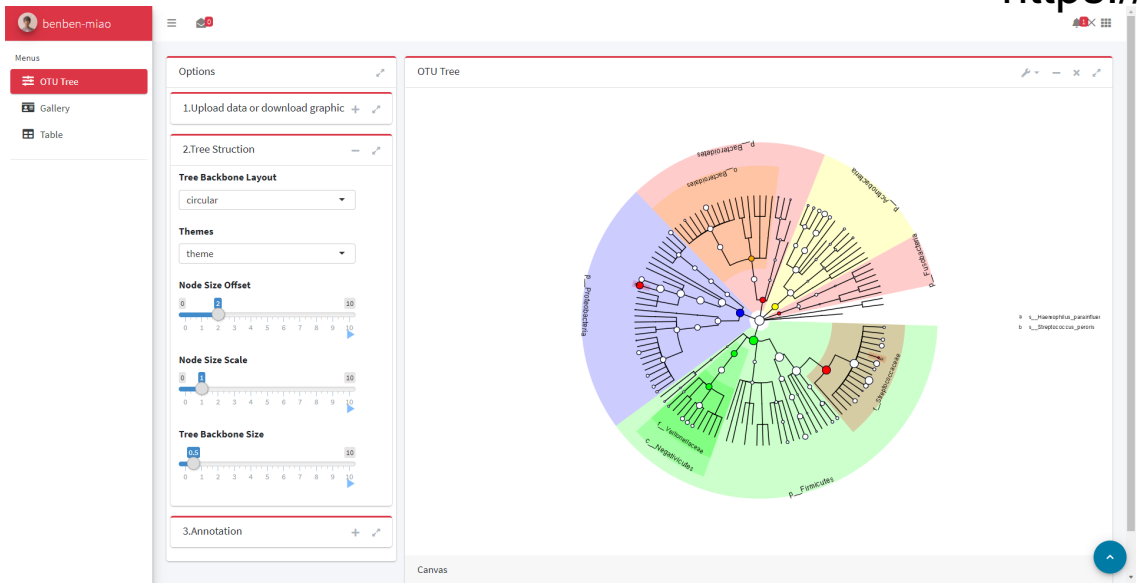
HIPLOT

Hiplot 可视化平台操作演示 | 进阶模块

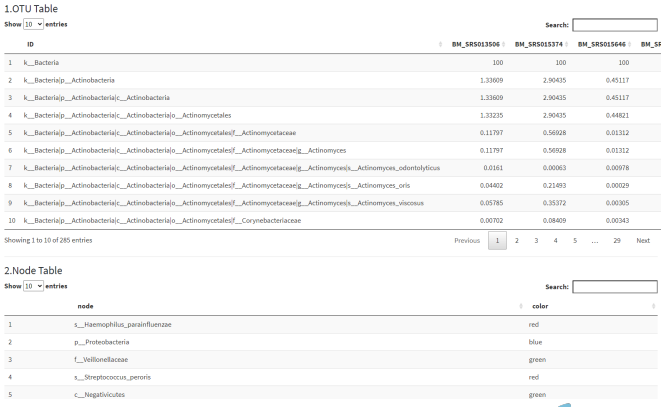


	mpg	cyl	disp	hp	drat
Mazda RX4	21	6	160	110	3.9
Mazda RX4 Wag	21	6	160	110	3.9
Datsun 710	22.8	4	108	93	3.85
Hornet 4 Drive	21.4	6	258	110	3.08
Hornet Sportabout	18.7	8	360	175	3.15
Valiant	18.1	6	225	105	2.76
Duster 360	14.3	8	360	245	3.21
Merc 240D	24.4	4	146.7	62	3.69
Merc 230	22.8	4	140.8	95	3.92
Merc 280	19.2	6	167.6	123	3.92

https://hiplot.com.cn/advance/ggcorrplot2



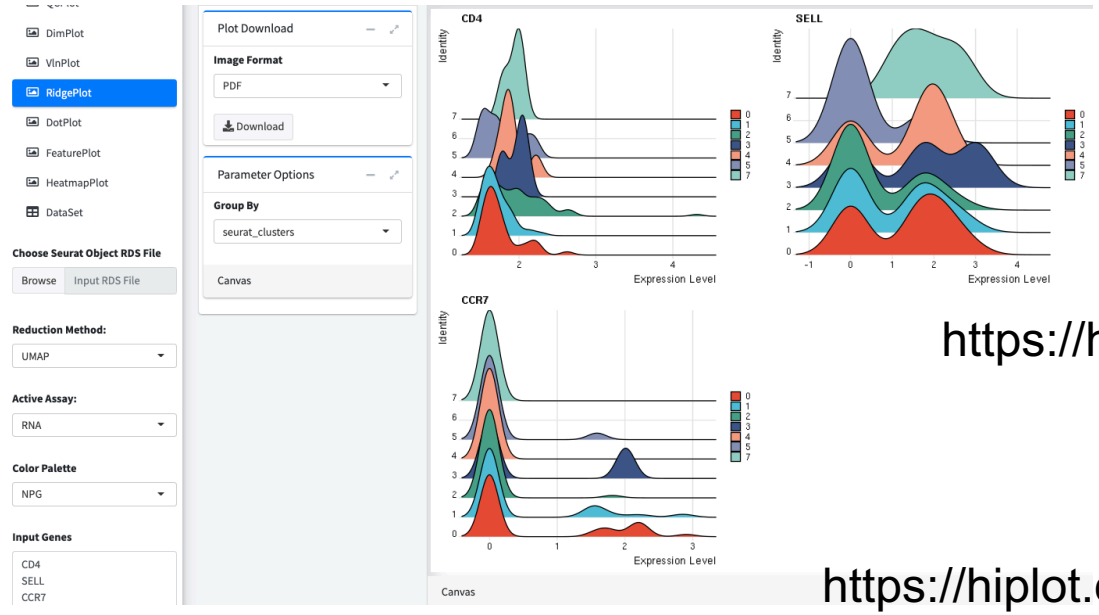
https://hiplot.com.cn/advance/otu-tree



Interactive Shiny Applications

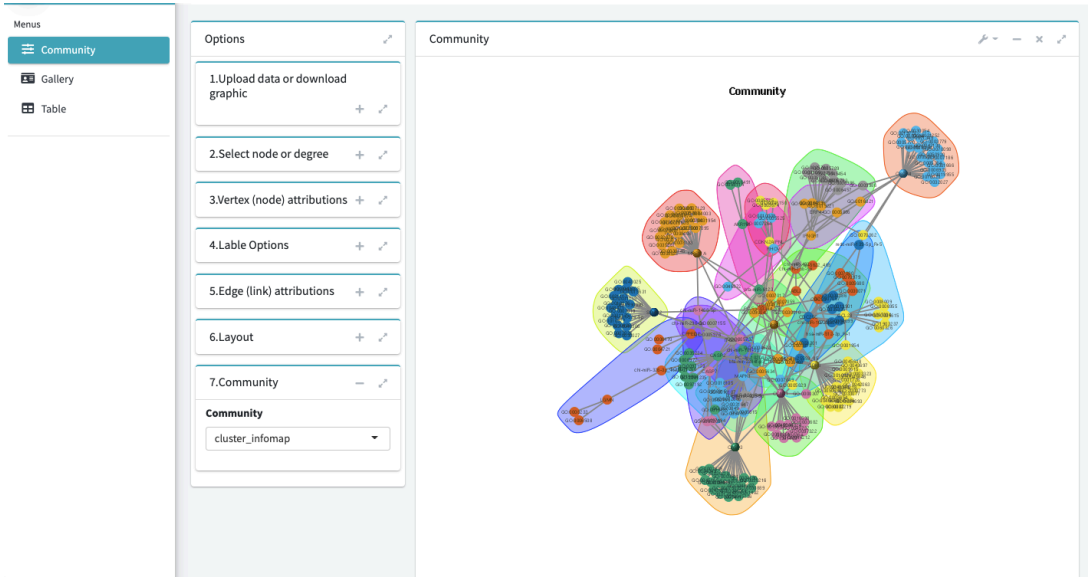
HIPLOT

Hiplot 可视化平台操作演示 | 进阶模块



Input RDS object of Seurat

https://hiplot.com.cn/advance/shinyseurat



https://hiplot.com.cn/advance/community-shiny

Show 10 entries

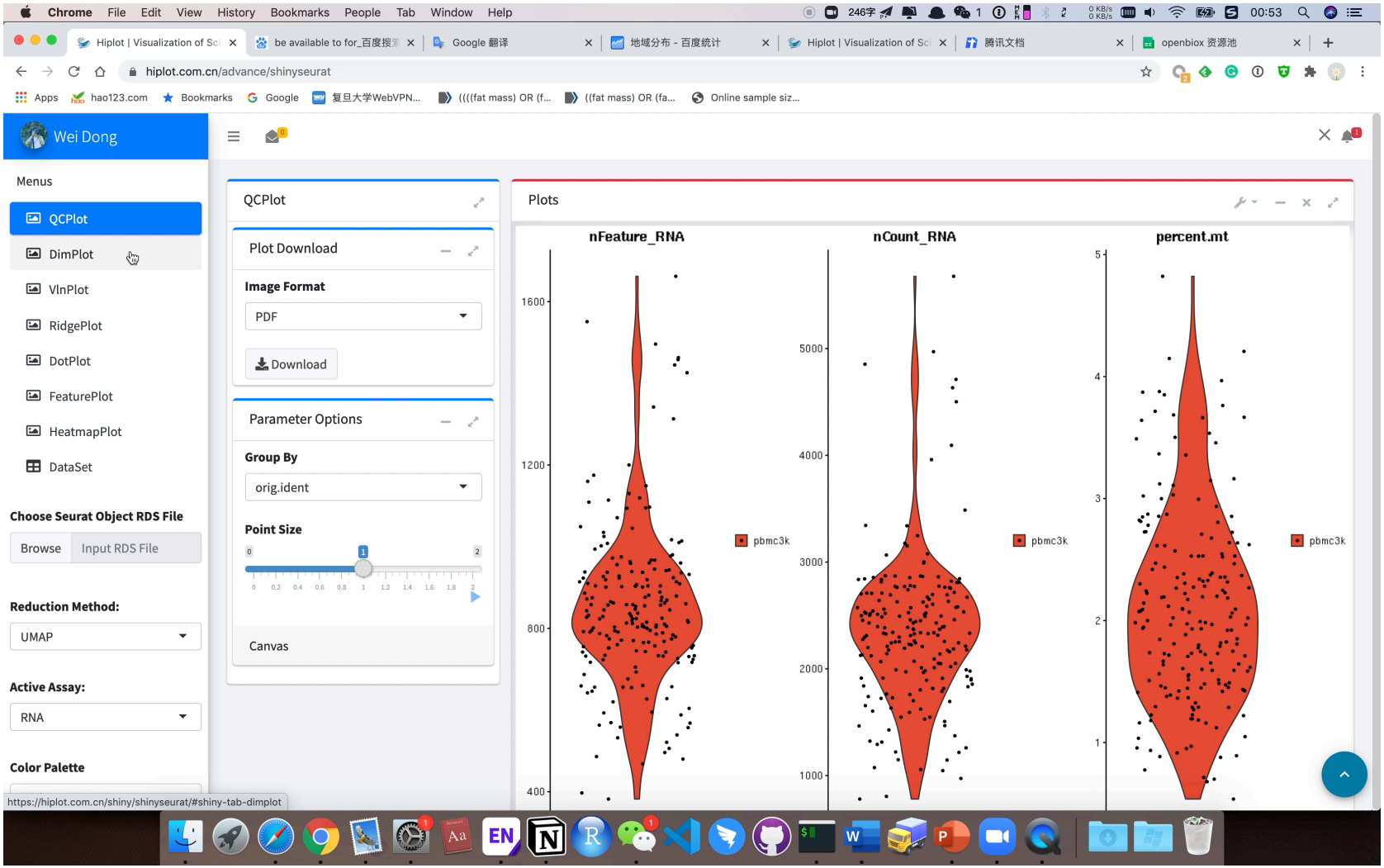
	node1	node2
1	ABL2	PC-3p-5622_465
2	ABL2	PC-5p-33384_55
3	ABL2	chi-miR-107-3p
4	ABL2	chi-miR-15b-5p
5	CASP2	PC-3p-10204_250
6	CASP2	bta-miR-6123
7	CASP2	bta-mir-2284f-p3_1ss6CA
8	CASP2	chi-miR-326-3p_1ss21CT
9	CASP2	PC-5p-33384_55
10	CASP3	bta-miR-30d_R-4

Showing 1 to 10 of 284 entries

Interactive Shiny Applications

HIPLOT

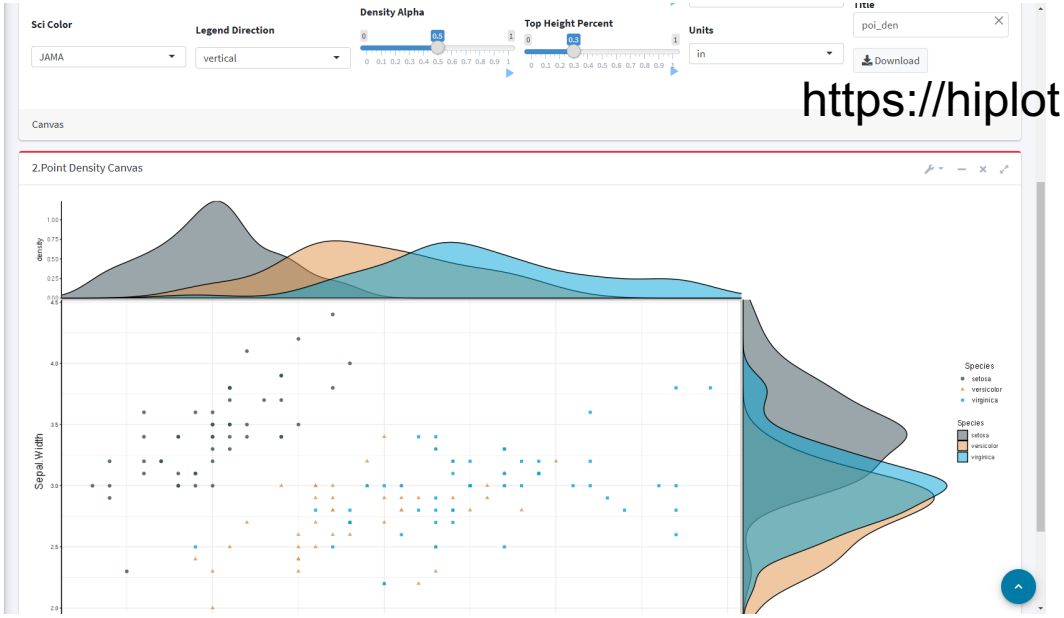
Hiplot 可视化平台操作演示 | 进阶模块



Shinyseurat Application

HIPLOT

Hiplot 可视化平台操作演示 | 进阶模块



https://hiplot.com.cn/advance/point-density

Sepal.Length	Sepal.Width	Species
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4.9	3	setosa
4.7	3.2	setosa
4.6	3.1	setosa
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5.4	3.9	setosa
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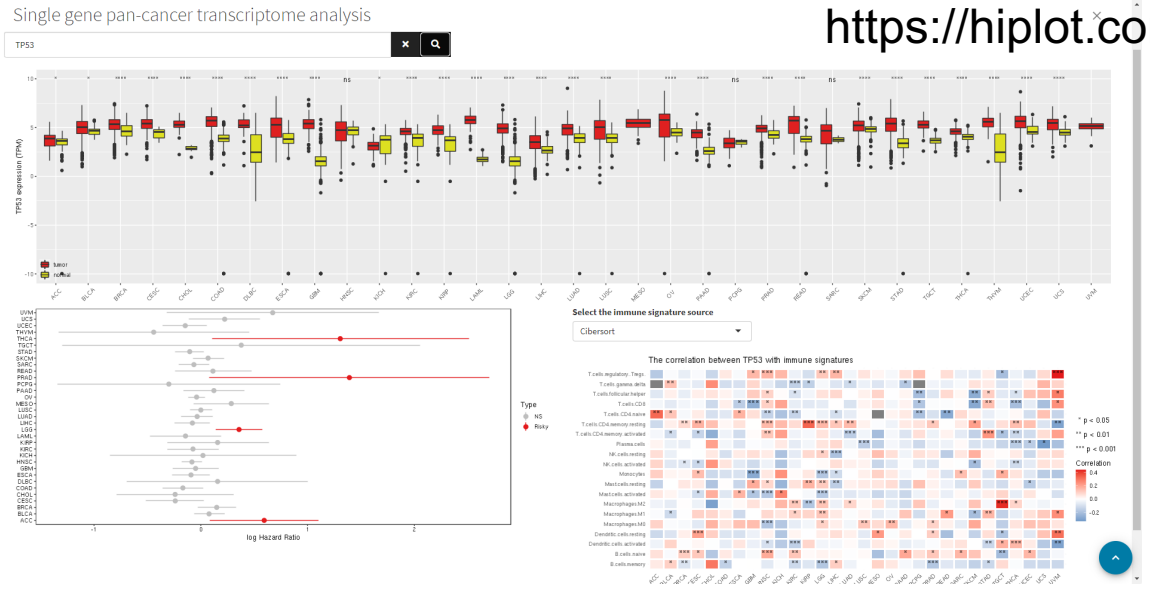
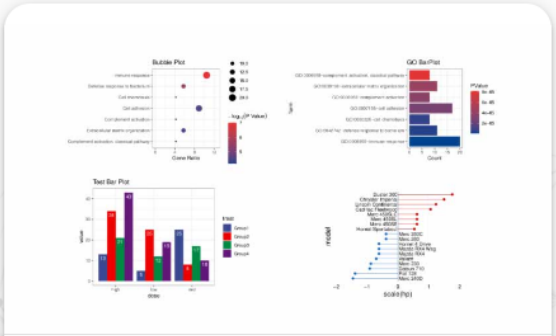


https://hiplot.com.cn/advance/ucsc-xena-shiny

Interactive Shiny Applications

HIPLOT

Hiplot 可视化平台操作演示 | 小工具箱

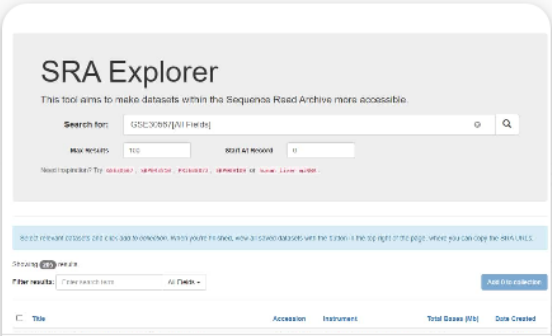


PDF Collage Maker

Hiplot PDF Collage Maker.

★★★★★

vue pdf merge

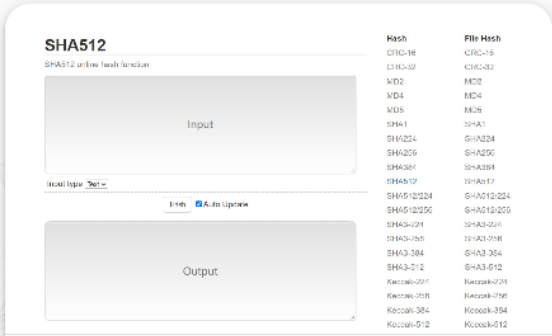


SRA Explorer

Download SRA Data.

★★★★★

sra



Online Encode & Decode

String Encode & Decode.

★★★★★

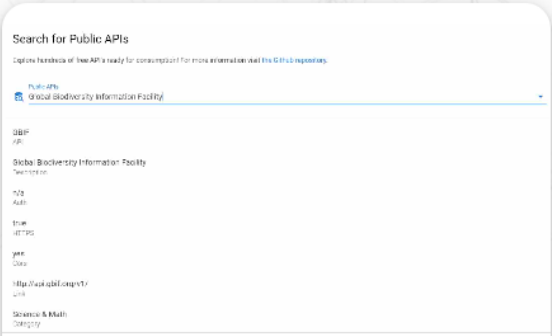
encode decode

Clipboard to Markdown

Generating Markdown.

★★★½☆

markdown



Public APIs

Explore Public APIs.

★★★☆☆

api

HTML to Markdown Converter

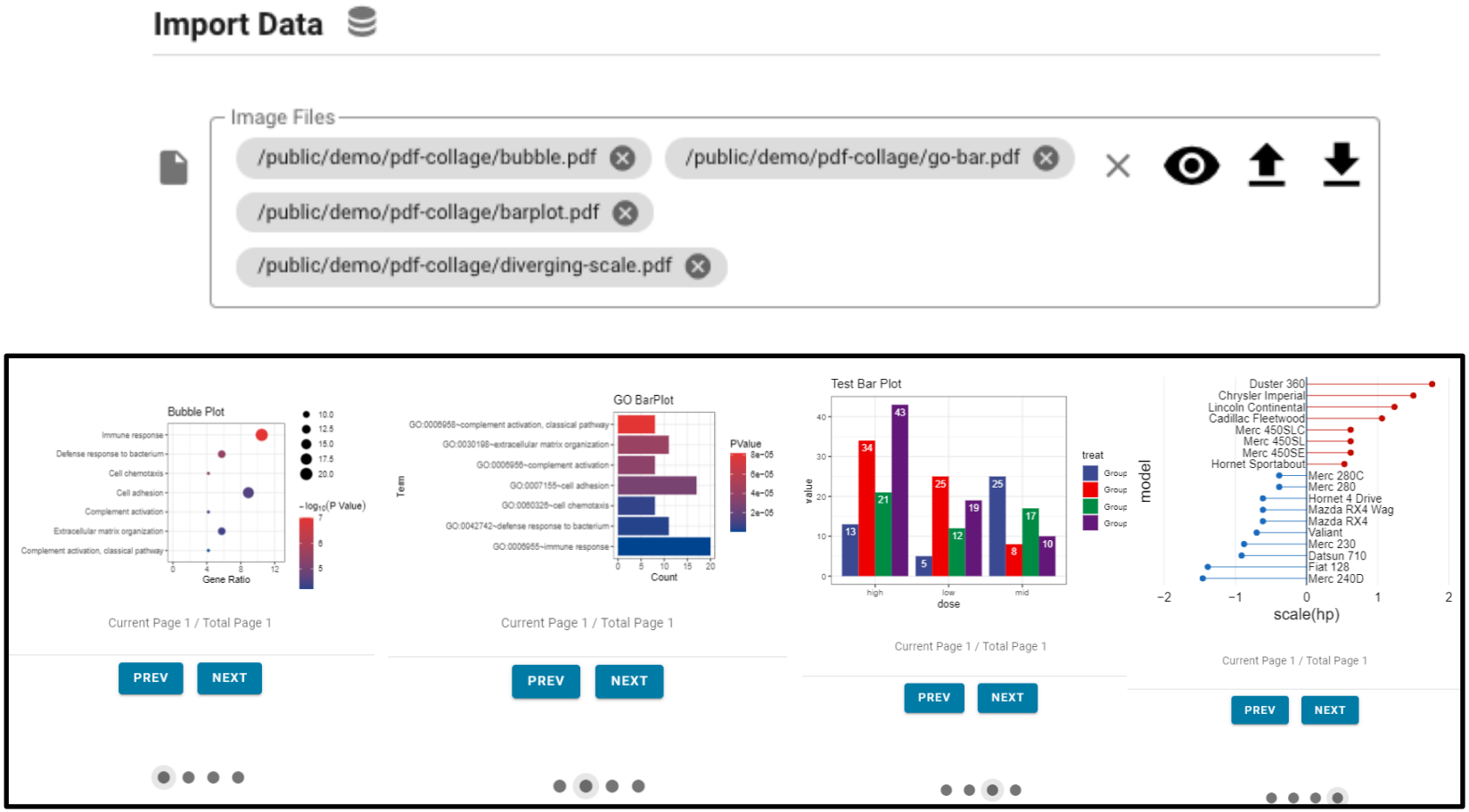
Convert HTML and Markdown.

★★★☆☆

markdown

Under development

Hiplot 可视化平台操作演示 | 小工具箱

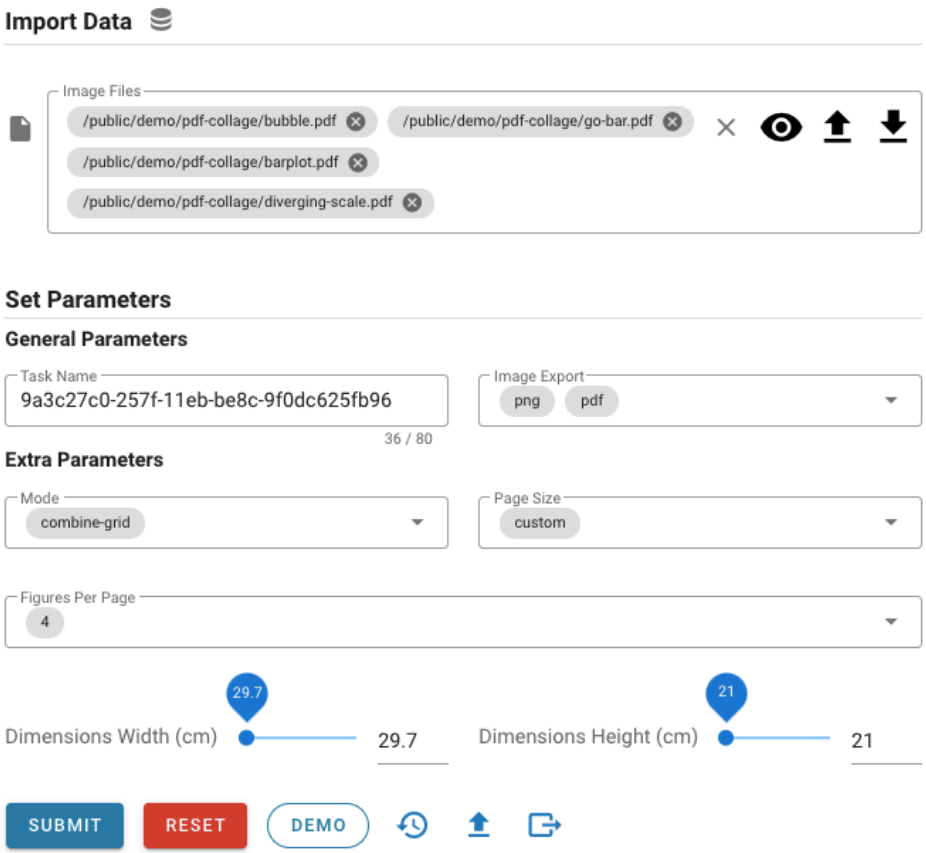


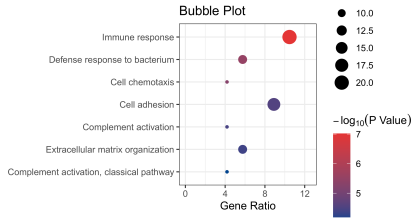
Preview PDF-Collage input files

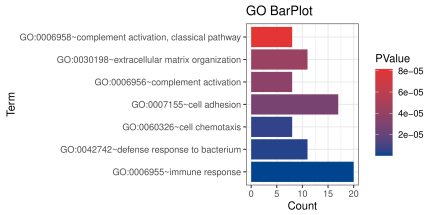
https://hiplot.com.cn/mini-tools/pdf-collage

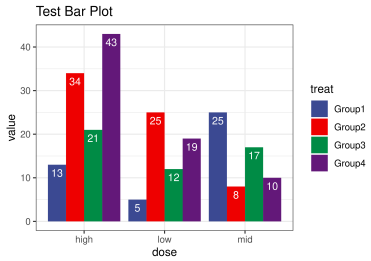
HIPLOT

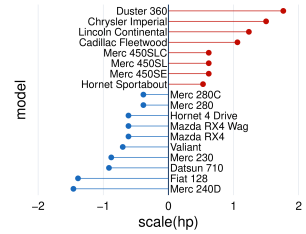
Hiplot 可视化平台操作演示 | 小工具箱









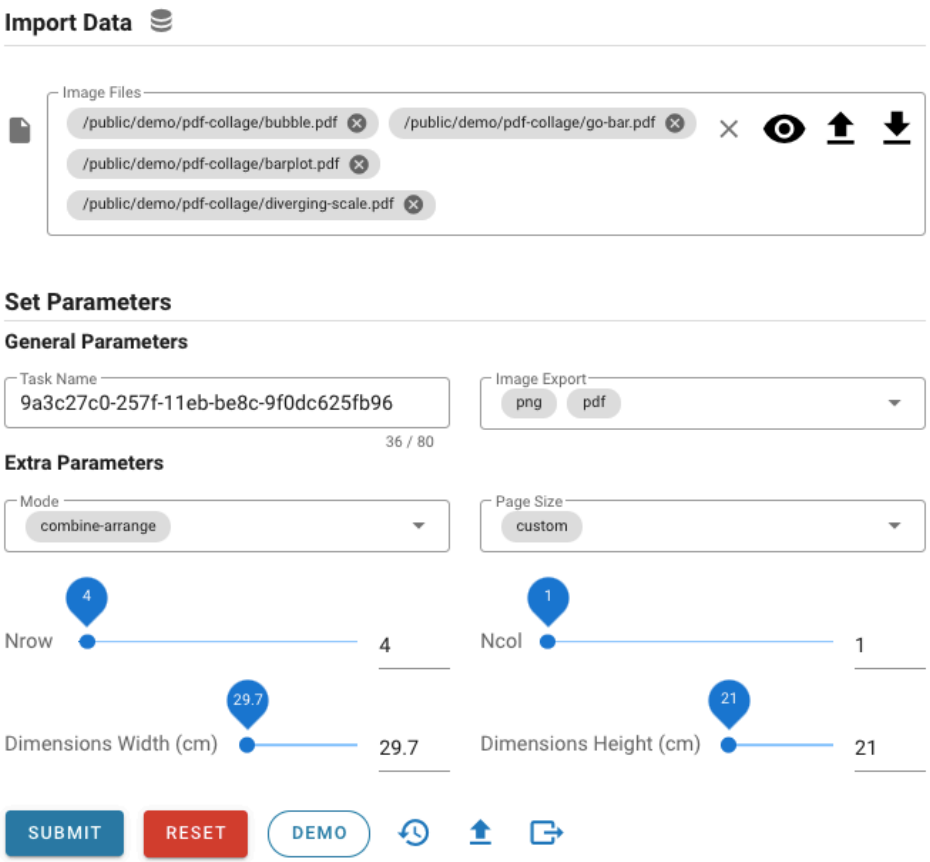


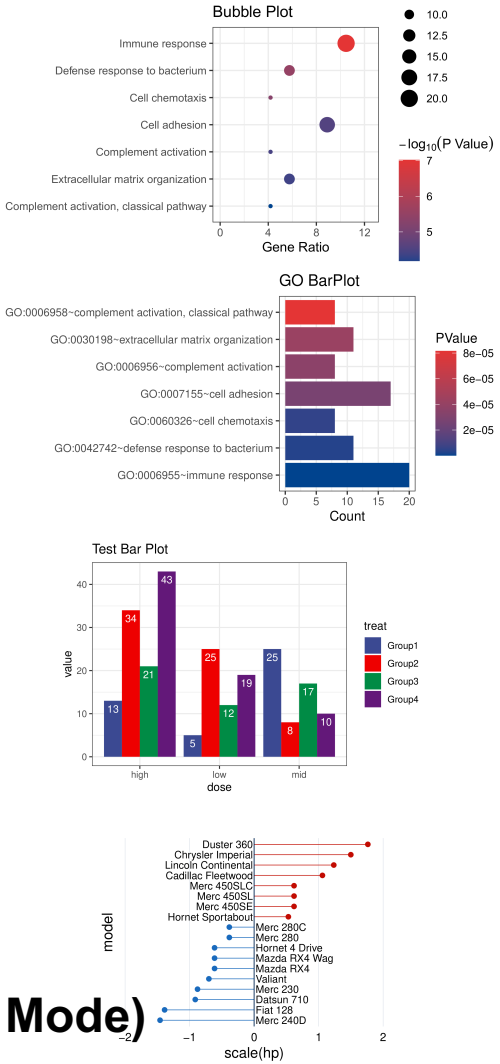
Merge Images (Grid Mode)

https://hiplot.com.cn/mini-tools/pdf-collage

HIPLOT

Hiplot 可视化平台操作演示 | 小工具箱



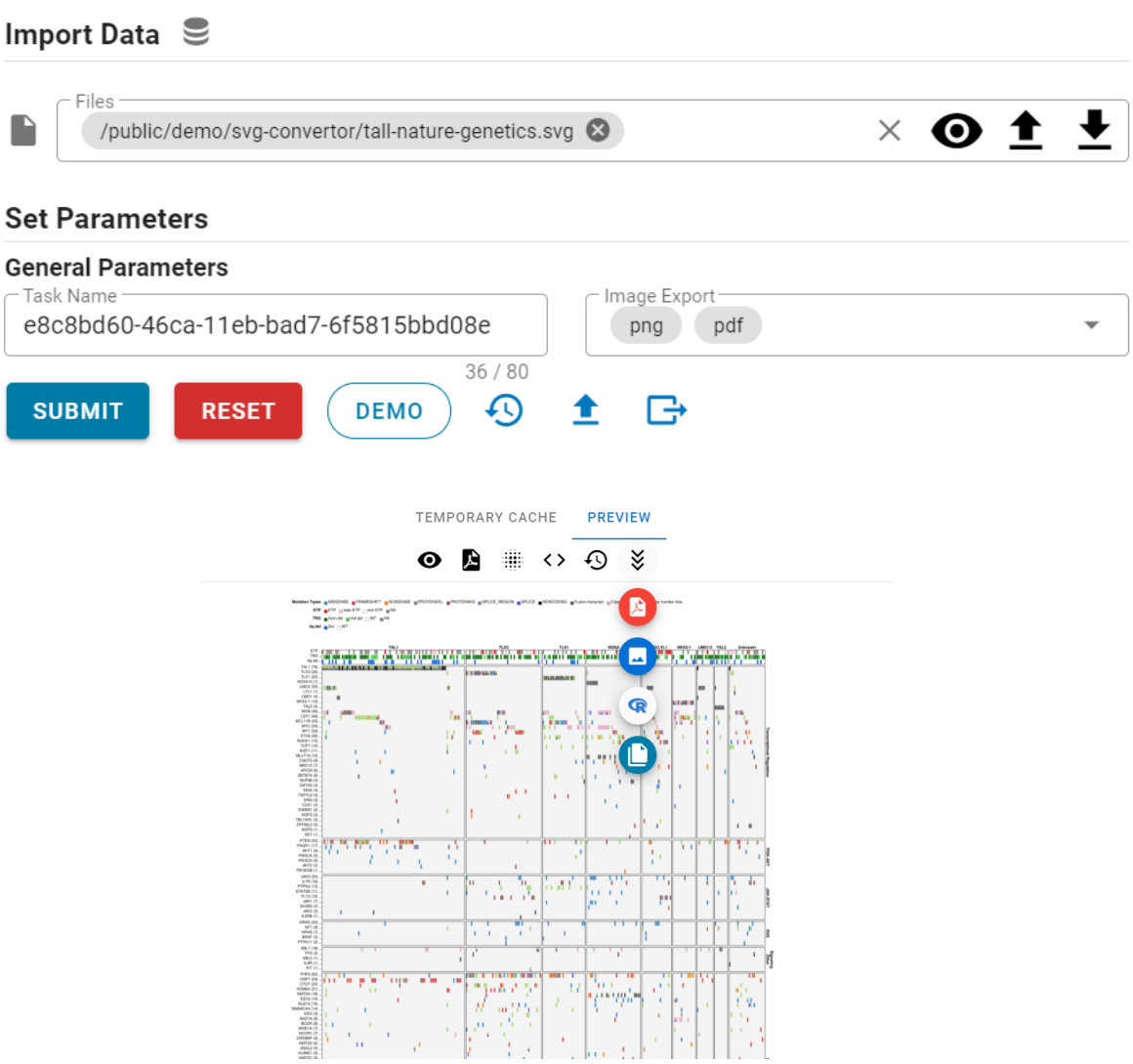


Merge Images (Arrange Mode)

https://hiplot.com.cn/mini-tools/pdf-collage

HIPLOT

Hiplot 可视化平台操作演示 | 小工具箱



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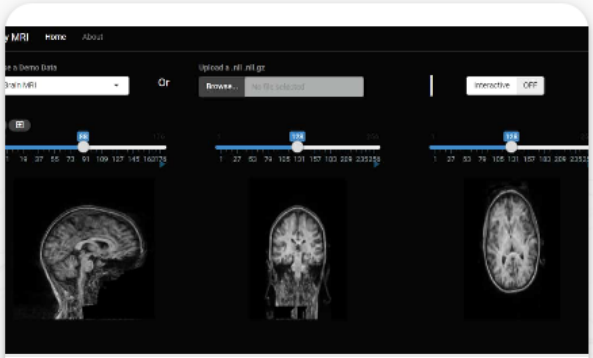
HIPLOT

Hiplot 可视化平台操作演示 | 临床工具

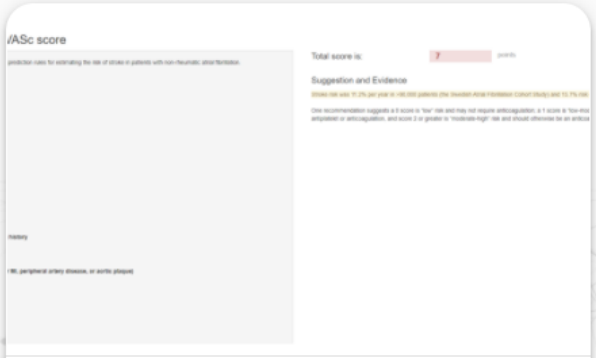


ShinyMRI

Visualize 3D/4D Medical Imaging Data.

★★★★★

shiny clinical mri

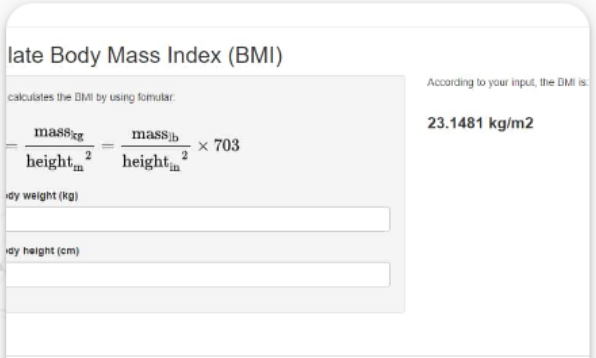


The CHA2DS2-VASc score

Estimating the risk of stroke in patients.

★★★★½

shiny clinical

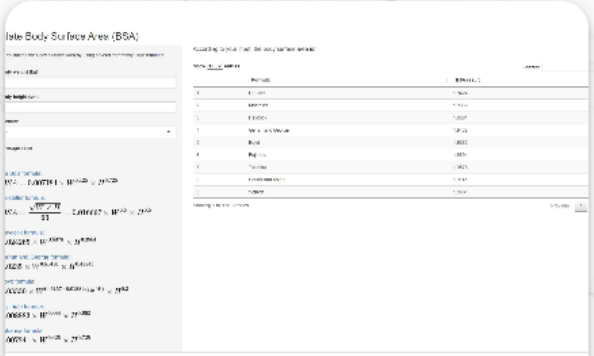


Body Mass Index (BMI)

Clinical Calculations Project.

★★★★☆

shiny clinical

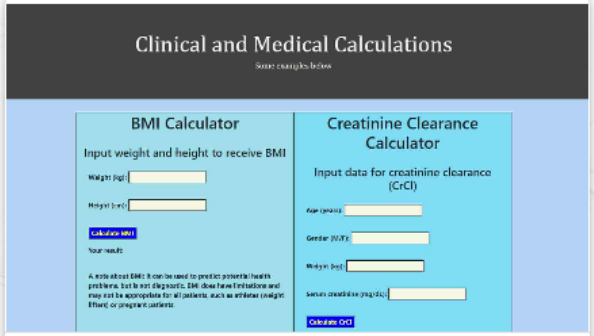


Body Surface Area (BSA)

Clinical Calculations Project.

★★★★☆

shiny clinical

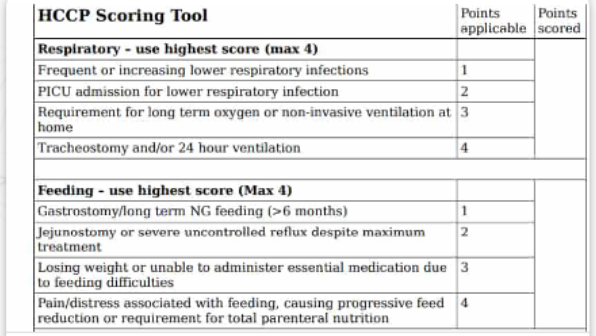


BMI & CrCl

Clinical Calculations Project.

★★★½☆

clinical



HCCP Scoring Tool	Points applicable	Points scored
Respiratory - use highest score (max 4)		
Frequent or increasing lower respiratory infections	1	
PICU admission for lower respiratory infection	2	
Requirement for long term oxygen or non-invasive ventilation at home	3	
Tracheostomy and/or 24 hour ventilation	4	
Feeding - use highest score (Max 4)		
Gastrostomy/long term NG feeding (>6 months)	1	
Jejunostomy or severe uncontrolled reflux despite maximum treatment	2	
Losing weight or unable to administer essential medication due to feeding difficulties	3	
Pain/distress associated with feeding, causing progressive feed reduction or requirement for total parenteral nutrition	4	

HCCP Score

The Health Complexity in Community Paediatrics.

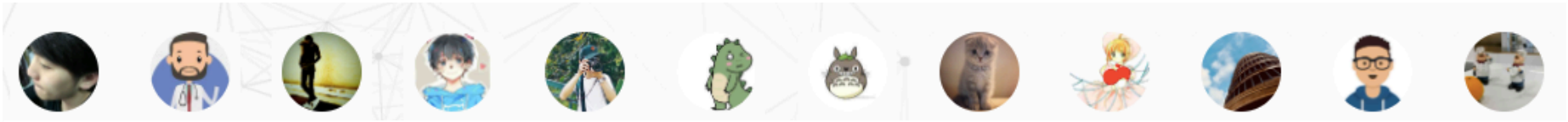
★★★½☆

clinical

Under development

致谢

- Cancer Researchers & clinicians
- Postgraduates
- Bioinformatics Community
- Scientific We Media



HIPLOT

用户交流社群

Hiplot可视化平台用户群-3

该二维码7天内(12月28日前)有效，重新进入将更新

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从零入门科研数据可视化云平台

openbiox & Hiplot Team

2020-12-26

Hiplot Team

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HIPLOT