

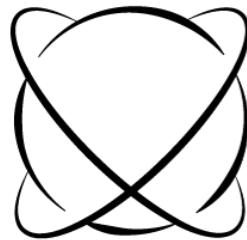
openbiox | Code Friday

Inventing, Optimizing, Sharing

openbiox community

2020-05-29

openbiox 社区简介



openbiox

openbiox 成立于 2019 年 3 月，是一个社区驱动建立的生物信息学创新协作组，由来自全世界范围内的知名高校、科研院所的在读中国籍本科生、硕士生、博士生、博士后、以及工作人员所构成。

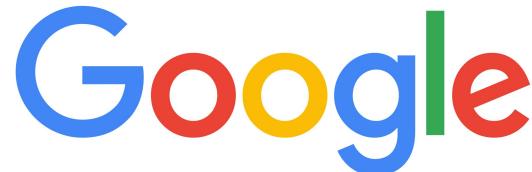
目前，openbiox 社区成员共计 75 人，拥有项目经费万余元，网页服务器和计算服务器若干，并已贡献 10 余项开源项目

Inventing, Optimizing, Sharing

纳新 | 发送简历和申请信至 committee@openbiox.org

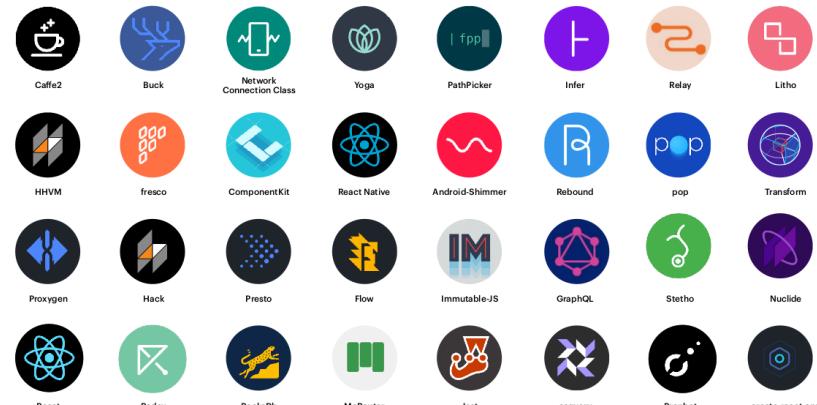
openbiox 简介

openbiox 起源



2005 年 – 至今

平台和资金的提供者



开源组织

面向对象：针对学生。只有学生身份才能申请参加（包括本科、硕士、博士）

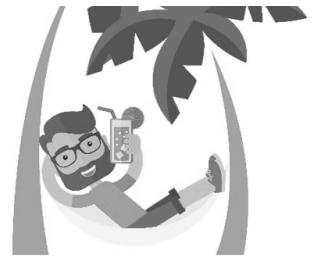
根据 GSoC 2017 的数据，在注册的 20651 个学生里面有 4764 个提交了申请，最后被接受的学生有 1318 个。从参加学生的国家来看，印度 569，美国 126，德国 55，斯里兰卡 54，俄罗斯 54，中国大陆 49 人。

openbiox 简介

openbiox 起源

Artificial Intelligence Startups

Augmenting knowledge work using AI



25% of all job-based tasks
will be automated by 2019
- Forrester Research

Law & Contracts
ROSS K

Customer Service
FinGenius

Sales
AVISO
CONVERSICA

Personal Assistants
x.ai

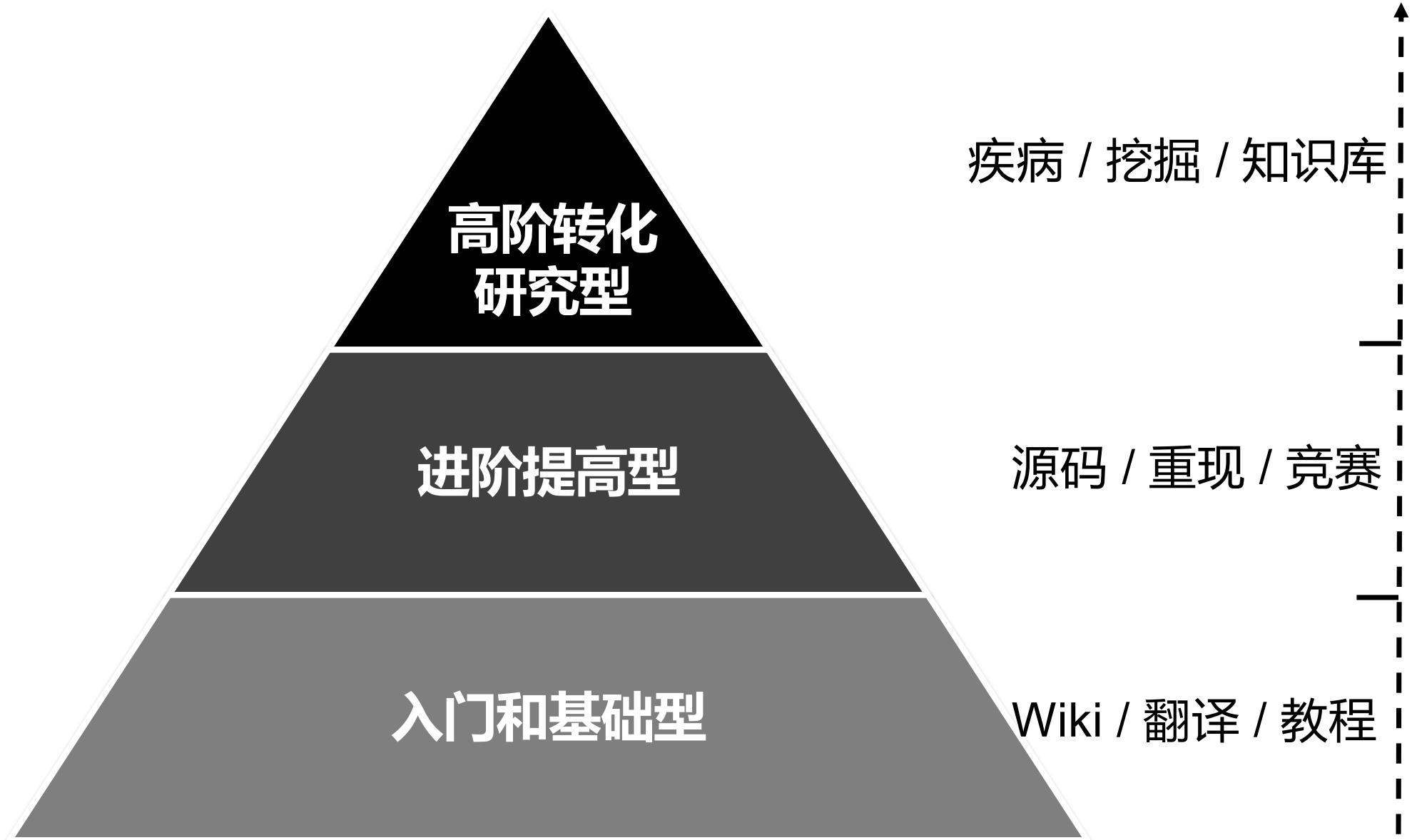
...al dexterity, and...

在 openbiox 出来之前，我认识的很多做生信的人大都处在一个一盘散沙的状态，很多人“半路出家”，凭借自己的爱好，坚持在这个领域内深耕。

—— 临床医生 / 生物信息学工程师 Jack Wang

大多生物、医学背景的人的计算机基础比较薄弱。建立一个社群，有稳定输出，也能帮助其他有需要的人，再构建一个完整的生物信息圈子，是非常有意义的一件事。—— 生物信息学应届博士生 *洋

社区项目类型



openbiox 简介

社区项目实例之一

openbiox / Cookbook-for-R-Chinese ✓

Code Issues 2 Pull requests 0 Projects 0 Wiki More ▾ Settings

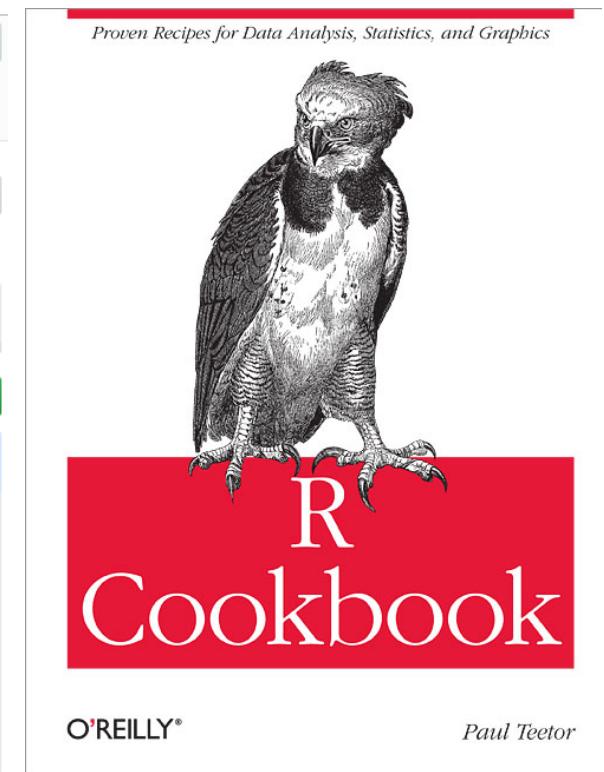
Cookbook for R 中文翻译 <https://openbiox.github.io/Cookbook-f...> Edit

r cookbooks notebook Manage topics

113 commits 1 branch 0 releases 1 environment 6 contributors Apache-2.0 990 KB

Branch: master ▾ Create new file Find File Clone or download ▾

	fei0810 and ShixiangWang	02-numbers 校对 (#19)	...
	book	02-numbers 校对 (#19)	a day ago
	cookbook	👉 IMPROVE: 整合chapter9	4 days ago
	docs	DOC: update website	3 days ago
	.gitignore	📦 NEW: 使用bookdown, 初步渲染gitbook网站	3 days ago 38 Bytes
	LICENSE	Create LICENSE	a month ago 11.09 KB
	README.md	DOC: update website	3 days ago 1.08 KB



《Cookbook for R》 书籍翻译

openbiox 简介

社区项目实例之一

Cookbook for R 中文版

≡ ⌂ A ☰

欢迎

作者简介

1 基础

2 数字

3 字符串

4 公式

5 数据的导入与导出

6 操作数据

7 统计分析

8 图形

9 脚本与函数

10 工具

附录

A 资料推荐

参考文献

本书由 bookdown 强力驱动

Cookbook for R 中文版

Winston Chang (著)

王诗翔 等 (译)

2019-04-14

欢迎

这是“Cookbook for R 中文版”的网站。这本书以直观明了的问题/需求和方案为基本内容向读者介绍R的基础和如何解决常见的分析问题：读者将会学习安装和使用三方包、操作基础的数据类型，学习数据的导入、操作和可视化，学习统计分析和编写脚本，以及其他工具。这本书是R问题方案参考手册，建议读者配合系统的R语言读物使用，如《R for Data Science》。

这个网站是（永久）免费的，它以[署名-非商业使用-禁止演绎](#)CC许可协议发布。如果你想要该书的实体版本，请期待它的出版。

非常感谢以下成员的参与，如果不是他们，这本中文书再过两年也不会跟大家见面。

- 陈颖珊
- 梁其云
- 王慧美
- 熊逸
- 杨芮
- 张浩浩
- 赵飞



王诗翔
于 上海科技大学

社区项目实例之二

Purpose:

- Provide some of bioinformatics learning resources for
- Provide a profiling of bioinformatics

Field:

- Next generation sequencing (NGS)
- Bioinformatics Data Analysis

▼ Table of content

Table of content

- Resources
 - General
 - Journal
 - Sequencing Technology
 - Tools
 - Books&Tutorial
 - Paper

- Skills

- Organization

- Institute

- People

- Blog

- Contributors

Virus and Microbial Related

- [viral-ngs](#)
- [qap](#)
- [ROP](#): discovering the source of all RNA-seq reads, including those originating from repeat sequences, recombinant B and T cell receptors, and microbial communities
- [ViFi](#): pipeline for identifying viral integration and fusion mRNA reads from NGS data
- [hgtid](#): an efficient and sensitive workflow to detect human-viral insertion sites using next-generation sequencing data
- [MicroPro](#): a software to perform profiling of both known and unknown microbial organisms for metagenomic dataset.
- [FEAST](#): a scalable algorithm for quantifying the origins of complex microbial communities.
- [mcorr](#): inferring bacterial recombination rates from large-scale sequencing datasets.
- [VirusFinder2](#): a new software tool for characterizing intra-host viruses through next generation sequencing (NGS) data.
- [VirusSeq](#): a algorithmic tool for detecting known viruses and their integration sites using next-generation sequencing of human cancer tissue.
- [BatVI](#): a fast and sensitive method to determine viral integrations.

Paper

Basic of High-throughput sequencing technology

- Hadfield, J. & Retief, J. A profusion of confusion in NGS methods naming. *Nat Methods* 15, 7-8 (2018): <http://enseqlopedia.com/enseqlopedia/>,
- Schuster S C. Next-generation sequencing transforms today's biology[J]. *Nature methods*, 2008, 5(1): 16-18.
- Ozsolak F, Milos P M. RNA sequencing: advances, challenges and opportunities.[J]. *Nature Reviews Genetics*, 2011, 12(2):87-98.
- Stark R, Grzelak M, Hadfield J. RNA sequencing: the teenage years[J]. *Nature Reviews Genetics*, 2019, 20(11): 631-656
- Ansorge W J. Next-generation DNA sequencing techniques[J]. *New biotechnology*, 2009, 25(4): 195-203.
- Heather J M, Chain B. The sequence of sequencers: The history of sequencing DNA[J]. *Genomics*, 2016, 107(1): 1-8.
- Schneider G F, Dekker C. DNA sequencing with nanopores[J]. *Nature biotechnology*, 2012, 30(4): 326.
- Restrepo-Pérez L, Joo C, Dekker C. Paving the way to single-molecule protein sequencing[J]. *Nature nanotechnology*, 2018, 13(9): 786-796.

openbiox 简介

社区项目实例之三

Lightweight downloader for bioinformatics data, databases and files (under development). It will provides a simple and parallelized method to access various bioinformatics resources. More see here <https://github.com/openanno/bget>.

Usage:

```
bget [flags]  
bget [command]
```

Available Commands:

api	Query bioinformatics website APIs.
doi	Can be used to access files via DOI.
help	Help about any command
i	Can be used to access URLs via a key string.
seq	Can be used to access sequence data via unique id (dbGAP and EGA) or manifest files (TCGA).
url	Can be used to access URLs via Golang http, wget, curl, axel and git, and rsync.

Flags:

--clean	remove _download and _log in current dir.
-h, --help	help for bget
--log-dir string	log dir. (default "/Users/apple/Downloads/_log")
--save-log	Save log to file.
-k, --task-id string	task ID (default is random). (default "gb9av65knktesc8")
--verbose int	verbose level (0:no output, 1: basic level, 2: with env info) (default 1)
-v, --version	version for bget

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

bget | 文献原文及附录文件下载

openbiox 简介

社区项目实例之三

```
/tmp/bget> cat cmd.sh
echo "bget doi testing....."
echo "bget doi 10.1126/science.aax5345 -f --suppl -t 3"
bget doi 10.1126/science.aax5345 -f --suppl -t 3

echo "\n"
echo "bget doi 10.1016/j.cell.2019.08.054 --suppl -f -t 3"
bget doi 10.1016/j.cell.2019.08.054 --suppl -f -t 3

echo "\n"
echo "bget doi 10.1038/s41586-019-1617-1 --suppl -t 3 -f"
bget doi 10.1038/s41586-019-1617-1 --suppl -t 3 -f
/tmp/bget> sh cmd.sh
bget doi testing.....  
bget doi 10.1126/science.aax5345 -f --suppl -t 3
[2019-10-14 22:17:48] [INFO] Visiting https://doi.org/10.1126/science.aax5345
[2019-10-14 22:17:56] [INFO] Visiting https://science.sciencemag.org/content/sci/early/2019/10/02/science.aax5345/tab-figures-data
```

openbiox 简介

社区项目实例之四

```
A simple command line tool to extract information from text and json files. More see here https://github.com/openbiox/bioextr.
```

Usage:
bioextr [filename] [flags]

Examples:
extract from pubmed abstract
bget api ncbi -q "Galectins control MTOR and AMPK in response to lysosomal damage to induce autophagy OR MTOR-independent autophagy induced by interrupted endoplasmic reticulum-mitochondrial Ca2+ communication: a dead end in cancer cells. OR The PARK10 gene USP24 is a negative regulator of autophagy and ULK1 protein stability OR Coordinate regulation of autophagy and the ubiquitin proteasome system by MTOR." | biocctl cvrt --xml2json pubmed - | bioextr --mode pubmed -w 'MTOR,AMPK,autophagy' --call-cor
-
extract from sra json
bget api ncbi -d 'sra' -q PRJNA527714 | biocctl cvrt --xml2json sra - | bioextr --mode sra --call-cor -w "Chromatin,mouse" -

Flags:
--call-cor Wheather to calculate the corelated keywords, and return the sentence contains >=2 keywords.
--clean remove log dir.
-h, --help help for bioextr
-w, --keywords string Keywords to extracted from abstract. (default "algorithm, tool, model, pipeline, method, database, workflow, dataset, bioinformatics, sequencing, http, github.com, gitlab.com, bitbucket.org")
--log-dir string log dir. (default "/Users/apple/Downloads/_log")
--mode string mode to extract information (pubmed, sra).
-o, --out string out specifies destination of the returned data (default to stdout or current woring directory).
-s, --save-log save log to file.
-k, --task-id string task ID (default is random). (default "oc3qjtq6rmg4tqa")
-t, --thread int thread to process. (default 1)
--verbose int verbose level(0:no output, 1: basic level, 2: with env info (default 1)
--version version for bioextr

openbiox 简介

社区项目实例之四

```
(base) ~/Downloads ➔ bget api ncbi -q "database or method or algorithm" --size 200 -m 200 | bioctl cvrt --xml2json pubmed - | bioextr --mode pubmed --call-cor - | json2csv - -o dat.csv
[2020-05-29 11:34:02] [INFO] Available retrieve 9150759 records.
[2020-05-29 11:34:02] [INFO] Will retrieve 200 records, from 1 to 200.
[2020-05-29 11:34:02] [INFO] Attempting to retrieve 200 records: 1-200 with 5 retries.
[2020-05-29 11:34:09] [INFO] Retrieved records with 1 retries... writing out.
```

1	Pmid	Doi	Title	Abs	Journal	Issue	Volume	Date	Issn	Author	Affiliation	Correlati	URLs	Keywords
6	32460443	10.1111/tbed.13650	[Evaluation of the diet basec African swine fever (ASF) is	Vopr Pitan		2	89	2020/5/27	0042-8833	["Melina Fisi ["Friedrich-L"]]				["method"]
8	32460439	10.1111/edt.12575	[Evaluation of the diet basec In an edentulous mandible n	Vopr Pitan		2	89	2020/5/27	0042-8833	["Stefan Krei ["NumBioLai"]]				["model"]
14	32460429	10.1002/ncp.10496	[Evaluation of the diet basec Lipid injectable emulsions (Il	Vopr Pitan		2	89	2020/5/27	0042-8833	["Jay M Mirt ["The Ameri"]]				["method"]
18	32460419	10.1002/cssc.202001006	[Evaluation of the diet basec High capacity metal oxide co	Vopr Pitan		2	89	2020/5/27	0042-8833	["Bishnu P Ti ["University"]]				["method"]
22	32460407	10.1002/chem.202001766	[Evaluation of the diet basec A non-oxidant and metal-free	Vopr Pitan		2	89	2020/5/27	0042-8833	["Xinxin Lin", "Nanjing Te"]				["method"]
28	32460397	10.1002/bmc.4908	[Evaluation of the diet based In this study, a simplified, se	Vopr Pitan		2	89	2020/5/27	0042-8833	["Chun Peng" ["College of"]]				["method"]
35	32460377	10.1002/bmc.4907	[Evaluation of the diet basec Creatinine is an important di	Vopr Pitan		2	89	2020/5/27	0042-8833	["Juraj Piestr ["Departmer"]]				["tool", "method"]
36	32460374	10.1111/jdv.16677	[Evaluation of the diet basec Hidradenitis suppurativa (HS)	Vopr Pitan		2	89	2020/5/27	0042-8833	["Tien V Ngu ["Bellevue D"]]				["database", "tool"]
45	32460330	10.1093/heapol/czaa040	[Evaluation of the diet basec When seeking to ensure fina	Vopr Pitan		2	89	2020/5/27	0042-8833	["Ulla K Griffi ["Health Sec"]]				["method"]
46	32460329	10.1093/eurpub/ckaa072	[Evaluation of the diet basec Low SEP, especially in childh	Vopr Pitan		2	89	2020/5/27	0042-8833	["Gary K K Ch ["The Jockey"]]				["model"]
63	32460303	10.12659/MSM.924934	[Evaluation of the diet basec BACKGROUND Rhinitis is the	Vopr Pitan		2	89	2020/5/27	0042-8833	["Zhanfeng Y ["Departmer ("dataset+database": "MA"]]				["dataset", "database"]
64	32460302	10.1159/000508544	[Evaluation of the diet basec As the coronavirus disease 2	Vopr Pitan		2	89	2020/5/27	0042-8833	["Abhilash Ki ["Division of"]]				["method"]
71	32460293	10.1159/000508960	[Evaluation of the diet basec The most reliable and easily	Vopr Pitan		2	89	2020/5/27	0042-8833	["Valeri Vele [""]"]				["method"]
75	32460289	10.1159/000506812	[Evaluation of the diet basec The International Pain Assoc	Vopr Pitan		2	89	2020/5/27	0042-8833	["Anna A Tyr ["A.V. Zhirm"]]				["method"]
77	32460284	10.2166/wst.2020.164	[Evaluation of the diet basec A nitrogen-doped reduced gr	Vopr Pitan		2	89	//	0042-8833	["Jing Bai", "School of A"]				["method"]
78	32460282	10.2166/wst.2020.162	[Evaluation of the diet basec In recent years, industrial co	Vopr Pitan		2	89	//	0042-8833	["Zhiqiang D ["Center for"]]				["method"]
79	32460281	10.2166/wst.2020.161	[Evaluation of the diet basec MgFe-layered double hydrox	Vopr Pitan		2	89	//	0042-8833	["Qian Wang ["School of M"]]				["method"]
80	32460277	10.2166/wst.2020.149	[Evaluation of the diet basec Biofouling is unwanted accu	Vopr Pitan		2	89	//	0042-8833	["S Ahmed", "Departmer"]				["method"]
81	32460273	10.2166/wst.2020.152	[Evaluation of the diet basec Mass production of nanomat	Vopr Pitan		2	89	//	0042-8833	["Qijie Liu", "School of C"]				["method", "model"]
82	32460267	10.1088/1361-648X/ab96ef	[Evaluation of the diet basec The chiral spin textures of a	Vopr Pitan		2	89	2020/5/27	0042-8833	["Zhaoen Li ["Departmer"]]				["method"]
83	32460264	10.1088/1361-6528/ab96e8	[Evaluation of the diet basec A facile strategy was introdu	Vopr Pitan		2	89	2020/5/27	0042-8833	["Neha Rani ["Physics, De"]]				["method"]
84	32460262	10.1088/1361-6528/ab96e5	[Evaluation of the diet basec Composites of nanostructure	Vopr Pitan		2	89	2020/5/27	0042-8833	["Nelson Nav ["Departame"]]				["method"]
85	32460261	10.1088/1361-6560/ab9702	[Evaluation of the diet basec For each institute, the select	Vopr Pitan		2	89	2020/5/27	0042-8833	["Felicia Fibi ["Departmer"]]				["dataset", "model"]
86	32460258	10.1088/1361-6528/ab96e2	[Evaluation of the diet basec Herein, porous CuO spindle-l	Vopr Pitan		2	89	2020/5/27	0042-8833	["Shupei Sun ["Sichuan Ur"]]				["method"]
87	32460254	10.1088/1361-6560/ab9703	[Evaluation of the diet basec Treating multiple brain meta	Vopr Pitan		2	89	2020/5/27	0042-8833	["Jordan M S ["Radiation z"]]				["method", "model"]
88	32460252	10.1088/1361-6560/ab9706	[Evaluation of the diet basec This paper presents a generi	Vopr Pitan		2	89	2020/5/27	0042-8833	["Jianfeng Zl ["University ("model+method": "Bothn"]]				["model", "method"]
89	32460250	10.1088/1361-6560/ab9704	[Evaluation of the diet basec Grating-based X-ray phase-c	Vopr Pitan		2	89	2020/5/27	0042-8833	["Eva-Maria ["Physics, Te"]]				["method"]
90	32460247	10.1088/1361-6528/ab96e6	[Evaluation of the diet basec We demonstrate graphene c	Vopr Pitan		2	89	2020/5/27	0042-8833	["Annalisa D ["Departmer"]]				["method"]
94	32460235	10.1530/EJE-20-0030	[Evaluation of the diet basec Objective Liquid chromatogr	Vopr Pitan		2	89	2020/5/1	0042-8833	["Charlotte N ["C Fries, Me"]]				["method"]
98	32460227	10.1016/j.ejogrb.2020.04.021	[Evaluation of the diet basec Bilateral CIA temporary clam	Vopr Pitan		2	89	2020/4/21	0042-8833	["Seyhun Suc ["Gaziantep"]]				["method"]
99	32460223	10.1016/j.forsciint.2020.110302	[Evaluation of the diet basec With the continuous innovati	Vopr Pitan		2	89	2020/5/19	0042-8833	["Chen-Jun N ["East China"]]				["method", "model"]

bioextr | 简单的文本关联分析和信息提取

openbiox 简介

社区项目实例之四

1	doi	Filename	Keywords	Correlation
114	10.1007/s1 data/fulltext/10.1007/s11886-020-01291-4/s11886-020-01291-4.pdf plain		"ACE", "ACE2", "ADH", "CG", "DS", "GH", "JAMA", "["ACE+ACE2"]": "ACE initially inhibits ACE leading to decreased angiotensin I levels, causing a possible negative feedback loop that ultimately upregulates more ACE2 receptor	
116	10.1007/s data/fulltext/10.1007/s00134-020-06026-1/s00134-020-06026-1.pdf plain		"ACE2", "AS", "DSC", "Ge", "JAMA", "SARS", "TMPI ("ACE2+SARS")": "Therefore, the coexpression of ACE2 and TMPRSSs is a key determinant for the entry of SARS-CoV-2 into host cells, and improves host conditions for coronavir	
117	10.1007/s1 data/fulltext/10.1007/s10654-020-00628-1/s10654-020-00628-1.pdf plain		"ACE", "ACE2", "ADAM17", "AR", "ET", "SARS", "SE ("ACE2+ADAM17+SARS)": "Tumor necrosis factor-alpha convertase (ADAM17) mediates regulated ectodomain shedding of the severe-acute respiratory syndrome-coronavirus	
119	10.1007/s1 data/fulltext/10.1007/s12015-020-09976-7/s12015-020-09976-7.pdf plain		"ACE", "ACE2", "AC5", "CAN", "CD143", "CD147", "["ACE+CD147"]": "Moreover, progenitor/stem cells can be extensively recruited in pulmonary fibrosis of COVID-19 patients and possibly suffer direct invasion via CD147 or AC	
129	10.1002/r data/fulltext/10.1002/rmv.2107/rmv.2107.pdf plain		"[14(1), 1441]", "AC", "ACE2", "AK", "AP-1", "BT", "["ACE2+SARS"]": "Airborne SARS-CoV-2 leads to infection of ACE2 expressing target cells such as alveolar type 2 cells or other unknown target cells.", "Structural basis for the rec	
139	10.1007/s1 data/fulltext/10.1007/s13337-020-00579-x/s13337-020-00579-x.pdf plain		"ACE2", "AP2", "AS", "CD", "CI", "CT", "DS", "IL10", "["AS+CI"]": "Paules CI, Marston HD, Fauci AS."], "LT+QC": "Phan LT, Nguyen TV, Luong QC, et al."], "MCP1+IL10+IL2+IL7+TNFa": "More severe patients have higher plasma levels of	
148	10.1007/s1 data/fulltext/10.1007/s12072-020-10043-z/s12072-020-10043-z.pdf plain		"ACE2", "AK", "AR", "CT", "CYP3A4", "DS", "EI", "HI ("ACE2+SARS)": "Composition and divergence of coronavirus spike proteins and host ACE2 receptors predict potential intermediate hosts of SARS-CoV-2.", "AK+AR+HL": "Chui	
153	10.1007/s1 data/fulltext/10.1007/s15010-020-01401-y/s15010-020-01401-y.pdf plain		"[2F1]", "ACE2", "ACE2+", "ARI", "CI", "CP", "CPAP", "["ACE2+SARS"]": "Expression of elevated levels of pro-inflammatory cytokines in SARS-CoVinfected ACE2+ cells in SARS patients: relation to the acute lung injury and pathogen	
160	10.1007/s data/fulltext/10.1007/s40292-020-00380-3/s40292-020-00380-3.pdf plain		"ACE", "ACE2", "ACE", "AM", "CIR", "FA", "GM", "Ji ("ACE+ACE2)": "Although not directly inhibited by ACE inhibitors, ACE2 is affected by chronic treatment with this class of drugs, which leads to an increase in ACE2 expression	
163	10.1007/s data/fulltext/10.1007/s42399-020-00264-6/s42399-020-00264-6.pdf plain		"ACE", "ACE2", "Men", "S2", "SARS", "SN"]": "["ACE+ACE2": "There are some medical conditions, which are being treated by ACE inhibitors and angiotensin II type-I receptor blockers, such as type-1 and type-2 diabetes ar	
167	10.1002/r data/fulltext/10.1002/rmv.2106/rmv.2106.pdf plain		"[6.3]", "623", "AC", "ACE2", "AK", "AM", "AN", "AS ("ACE2+LAMP+NAT+NP+SARS)": "KEYWORDS MERS-CoV, nucleic acid testing, SARS-CoV, SARS-CoV-2 (2019-nCoV), serological testing, specimen collection Abbreviations: +ssRI	
172	10.1007/s1 data/fulltext/10.1007/s12250-020-00207-4/s12250-020-00207-4.pdf plain		"ACE2", "ADAM17", "AK", "ARD", "AS", "BS", "BT", "["ACE2+ARD"]": "In a murine ARD model, loss of ACE2 expression resulted in enhanced vascular permeability, increased lung edema, neutrophil accumulation, and diminished	
173	10.1007/s1 data/fulltext/10.1007/s00204-020-02734-1/s00204-020-02734-1.pdf plain		"ACE", "ACE2", "AST", "GA", "MCP-1", "SARS"]": "["ACE+ACE2": "Patients suffering either from diabetes type 1 or 2, or developing hypertension, often receive blood pressure reducing ACE inhibitors and angiotensin II type I n	
178	10.1007/s1 data/fulltext/10.1007/s12519-020-00354-4/s12519-020-00354-4.pdf plain		"ACE2", "CD16", "CD16", "CD4", "CD4", "["CD16+CD4 + CD56": "TBNK lymphocyte subset analysis revealed decreased percentage of CD16 + CD56 + lymphocytes (4/8) and Th/Ts (1/8), and increased percentage of CD	
180	10.1007/s1 data/fulltext/10.1007/s12098-020-03263-6/s12098-020-03263-6.pdf plain		"ACE2", "ASM", "AST", "BCR", "CD", "CRD", "CS", "["BCR+H1N1+SARS": "In comparison, the BCR of SARS was 2 and 1.3 for pandemic flu H1N1 2009 [2]."], "IL10+IL2+IL7+MCP1+TNFa": "This progression is associated with extre	
194	10.1007/s1 data/fulltext/10.1007/s12250-020-00218-1/s12250-020-00218-1.pdf plain		"[\u0003F3]", "1D", "ACE2", "AM", "B1", "CAS", "C", "["\u0003F3+B1+F2+C+F3+F1P": "A 25 IL reaction system includes 1 9 isothermal amplification buffer, 6 mmol/L MgSO4, 1.4 mmol/L dNTPs, 8 units of WarmStart Bst 3.0 DN	
198	10.1016/j. data/fulltext/10.1016/j.acpm.2020.02.002/pdf1-s2.0-S2352556820300291-ma		"[6.3]", "ACE", "ACE2", "AF", "AM", "AR", "BH", "CD", "["ACE+SARS": "Molecularly, like SARS-CoV, the SARS-CoV-2 virus likely uses ACE-2 as entry receptor, which is highly expressed in the lung and gastrointestinal tract [10-12]."], "1	
211	10.1007/s1 data/fulltext/10.1007/s12250-020-00219-0/s12250-020-00219-0.pdf plain		"AC", "ACE2", "AR", "AS", "BT", "CAS", "CI", "CT", "["AC+GM": "Eurosurveillance 14:19292 Donnelly CA, Ghani AC, Leung GM, Hedley AJ, Fraser C, Riley S, Abu-Raddad LJ, Ho L-M, Thach T-Q, Chau P (2003) Epidemiological dete	
215	10.1002/c1 data/fulltext/10.1002/cbic.202000047/cbic.202000047.pdf plain		"ACE2", "Gen", "Hua", "IRF3", "NF", "Ray", "S1", "S ("ACE2+SARS": "As little is known so far about the virulence of this virus, we shall also discuss the interactions between spike and ACE2 that might challenge the current view t	
228	10.1007/s1 data/fulltext/10.1007/s11427-020-1637-5/s11427-020-1637-5.pdf plain		"ACE2", "CAS", "DPP4", "Ge", "S1", "S2", "SARS", "["ACE2+SARS": "Then according to the crystal structure of SARS-CoV S-protein RBD domain complexed with its receptor ACE2 (PDB code: 2AJF), the 3-D complex structure of I	
235	10.1016/j. data/fulltext/10.1016/j.bbi.2020.03.016/pdf1-s2.0-S0889159120303664-main.j		"ACE2", "ARC", "CD4+", "CSR", "H1N1", "JAMA", "["ARC+SARS": "Brain, Behavior, and Immunity xxx (xxxx) xxx-xxx Contents lists available at ScienceDirect Brain, Behavior, and Immunity journal homepage: www.elsevier.co	
237	10.1016/j. data/fulltext/10.1016/j.acvd.2020.03.009/pdf1-s2.0-S1875213620300802-main		"[6.3]", "ACE2", "AM", "JAMA", "KL", "LMNA", "RG", "["ACE2+TMPRSS2": "SARS-CoV-2 Cell Entry Depends on ACE2 and TMPRSS2 and Is Blocked by a Clinically Proven Protease Inhibitor."], "KL+TC": "[15] Tsui KL, Leung TC, Yam LY,	
251	10.1007/s data/fulltext/10.1007/s40121-020-00295-5/s40121-020-00295-5.pdf plain		"[6.3]", "603", "653", "ACE2", "AS", "CD", "CH", "DS ("6.3+653+SARS+603)": "Infect Dis Ther Table 3 Key findings from the Chinese Center for Disease Control and Prevention report (modified from [24, 25]) Baseline characteristi	
256	10.1016/j. data/fulltext/10.1016/j.antiviral.2020.104759/pdf1-s2.0-S0166354220300929-i		"["673-", "ACE2", "Ge", "SARS", "\u03b1B"]": "["SARS+ACE2": "The angiotensin converting enzyme II (ACE2) is a known cell receptor for SARS in human and bats, and is also used by SARS-CoV-2 (Zhou et al., 2020)."]	
257	10.1007/s data/fulltext/10.1007/s40256-020-00406-0/s40256-020-00406-0.pdf plain		"[693-", "ACE", "ACE2", "AS", "CCS", "GC", "JAMA ("ACE+ACE2)": "The findings from human studies [21-24] have discredited the association of levels of ACE2 with the use of ACE inhibitors and ARBs, although one study [25] dic	
259	10.1016/j. data/fulltext/10.1016/j.antiviral.2020.104742/pdf1-s2.0-S0166354220300528-i		"[ACE2", "AC5", "CD4+", "EVA", "FP", "GBP2", "Ge ("ACE2+SARS": "Isolation and characterization of a bat SARS-like coronavirus that uses the ACE2 receptor."], "CD4+gp160": "Identification of the Paired Basic Convertases Im	
261	10.1007/s data/fulltext/10.1007/s0264-020-00935-2/s0264-020-00935-2.pdf plain		"ACE", "ACE2", "AT1", "EMA", "FH", "GM", "JAMA", "["ACE+ACE2": "In turn, this results in excessive production of angiotensin by ACE, whereas less ACE2 is capable of converting it to angiotensin (1-7), an heptapeptide with vaso	
264	10.1016/j. bbi.2020.03.031/pdf1-s2.0-S0889159120303573-main.j		"[633-", "ACE2", "ACS", "ER", "IL-15", "IL-6", "MOF ("ACE2+ER+TNF": "Ab: antibody; ACE2: angiotensin-converting enzyme 2; CSF: cerebrospinal fluid; ER: endoplasmic reticulum; TNF: tumor necrosis factor."), "ACE2+SARS": "In	
266	10.1016/j. data/fulltext/10.1016/j.ancard.2020.04.001/pdf1-s2.0-S0003392820300561-ma		"[ACE", "ACE2", "AS", "BCRP", "CI", "CP", "CYP2D6 ("ACE+FHMI": "Di Francesco, FHM Heart Groups: patients with COVID19 should continue ACE inhibitors and ARBs."], "ACE2+SARS": "SARScoronavirus modulation of myocardi	
283	10.1016/j. data/fulltext/10.1016/j.aejg.2020.03.002/pdf1-s2.0-S1521661620302394-main.j		"[ACE2", "AST", "AT2", "BH", "BSG", "CP", "CR, "CR ("ACE2+AT2)": "Recent bioinformatics analysis revealed that ACE2 was not only highly expressed in alveolar type II (AT2) cells in the lung, but also in the glandular cells of gast	
284	10.1016/j. data/fulltext/10.1016/j.clim.2020.108410/pdf1-s2.0-S088915912030489X-main.j		"[ACE2", "+KIR+", "ID", "ACE2", "CD28", "CD38", "["ACE2+CD4+": "(B) Normalized mRNA expression values of ACE2 in CD4+T cells isolated from lupus patients compared to healthy controls.", "DNA methylation beta values we	
285	10.1016/j. data/fulltext/10.1016/j.bbi.2020.04.027/pdf1-s2.0-S088915912030489X-main.j		"[ACE2", "CD14+", "CRP", "GM-CSF", "GM-CSF+", "["CD14+GM-CSF": "Aberrant pathogenic GM-CSF+ T cells and inflammatory CD14+CD16+ monocytes in Severe Pulmonary Syndrome Patients of a New Coronavirus."], "H1N	
288	10.1002/r data/fulltext/10.1002/jmv.25888/jmv.25888.pdf plain		"[ACE2", "CRP", "CT", "DC", "GC", "SARS", "SARS", "["ACE2+SARS": "Hamming I, Timens W, Bulthuis ML, Lely AT, Navis G, van Goor H. Tissue distribution of ACE2 protein, the functional receptor for SARS coronavirus.", "Structu	

Sheet 1

+

Ready 523 of 3172 records found

田 圆 四 - 100%

社区项目实例之五

XenaShiny



CRAN 0.4.0 downloads 4667 lifecycle experimental emoji-log build passing build passing codecov 0%

The goal of **UCSCXenaShiny** is to provide a web app for downloading, analyzing and visualizing datasets from [UCSC Xena](#), which is a collection of UCSC-hosted public databases such as TCGA, ICGC, TARGET, GTEx, CCLE, and others. Databases are normalized so they can be combined, linked, filtered, explored and downloaded.

Installation

You can install stable release of **UCSCXenaShiny** from CRAN with:

```
install.packages("UCSCXenaShiny")
```

You can install the development version of **UCSCXenaShiny** from Github with:

```
remotes::install_github("openbiox/XenaShiny")
```

Xena Shiny | UCSC Xena

openbiox 简介

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Xena Shiny Home Repository Modules Pipelines Help Developers

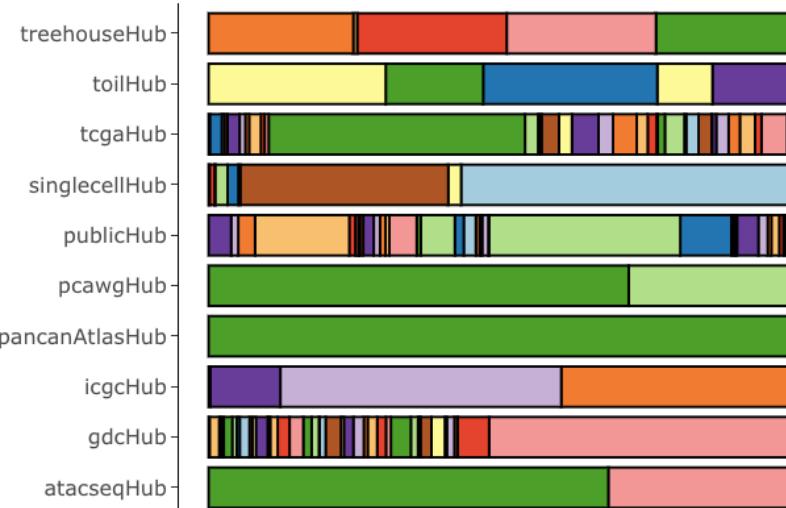
Enter a gene symbol to show its pan-can distribution, e.g. TP

Data Portal Summary

XenaShiny version 0.4.0
Data are controled by UCSC Xena

 DATA HUBS 10	 COHORTS 140	 DATASETS 1646
 SAMPLES 2373387	 PRIMARY SITES 37	 DATA SUBTYPES 45

Sample Distribution Dataset Distribution



A horizontal stacked bar chart titled "Dataset Distribution" showing the proportion of samples across different datasets for ten different hubs. The hubs listed on the y-axis are: treehouseHub, toilHub, tcgaHub, singlecellHub, publicHub, pcawgHub, pancanAtlasHub, icgcHub, gdchub, and atacseqHub. Each bar is composed of multiple colored segments representing different dataset proportions.

treehouseHub
toilHub
tcgaHub
singlecellHub
publicHub
pcawgHub
pancanAtlasHub
icgcHub
gdchub
atacseqHub

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Xena Shiny Home Repository Modules Pipelines Help Developers

Active Data Hub : Show 10 entries Search:

ID	XenaCohorts	Label	URL
1	Breast Cancer Cell Lines (Neve 2006)	Neve Cell Line gene expression	https://ucscpublic.xenahubs.net/download/ucsfNeve_public/ucsfNeveExp_genomicMatrix.gz
2	Breast Cancer Cell Lines (Neve 2006)	Phenotypes	https://ucscpublic.xenahubs.net/download/ucsfNeve_public/ucsfNeve_public_clinicalMatrix.gz

Dataset Hub Cohort Samples Subtype Label

ID	Dataset	Hub	Cohort	Samples	Subtype	Label
1	ucsfNeve_public/ucsfNeveExp_genomicMatrix	publicHub	Breast Cancer Cell Lines (Neve 2006)	51	gene expression	Neve Cell Line gene expression
2	ucsfNeve_public/ucsfNeve_public_clinicalMatrix	publicHub	Breast Cancer Cell Lines (Neve 2006)	57	phenotype	Phenotypes
3	kotliarov2006_public/kotliarov2006_genomicMatrix	publicHub	Glioma (Kotliarov 2006)	194	copy number	Kotliarov Glioma CGH
4	kotliarov2006_public/kotliarov2006_public_clinicalMatrix	publicHub	Glioma	194	phenotype	Phenotypes

Cohort Name : Selected Data: Wait until a table shows... Of note, single dataset file can be downloaded by clicking URL

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社区项目实例之六

BioShiny APP

Search...

bioinstaller spack conda datasets2tools pubmed geoquery **maftools**

Input files

Single sample analysis:

MAF file (laml.maf)
/home/ljf/R/library/3.5/maftools/extdata/tcga_laml.maf.gz

Clinical annotation file (laml_clin)
/home/ljf/R/library/3.5/maftools/extdata/tcgla_laml_annot.tsv

MutSig results (laml_mutsig)
/home/ljf/R/library/3.5/maftools/extdata/LAML_sig_genes.txt.gz

CNV related analysis:

Gistic all lesions file (all_lesions):
/home/ljf/R/library/3.5/maftools/extdata/all_lesions.conf_99.txt

Gistic amp genes file (amp_genes)
/home/ljf/R/library/3.5/maftools/extdata/amp_genes.conf_99.txt

Gistic del genes file (del_genes)
/home/ljf/R/library/3.5/maftools/extdata/del_genes.conf_99.txt

Gistic score file (scores_gistic)
/home/ljf/R/library/3.5/maftools/extdata/scores.gistic

Running maftools task steps, waiting please...

Output of maftools fields summary

Output of maftools sample summary

Output of maftools MAF summary

Output of maftools oncoplots

Output of maftools oncoplots with copy number data

Output of maftools oncoplots with advanced

Output of maftools transition and transversions

Output of maftools Lollipop2 plots for amino acid changes

Output of maftools comparing mutation load

Output of maftools VAF boxplot

Output of maftools somatic interactions

Output of maftools somatic interactions (oncostrip)

Output of maftools oncoplots

Altered in 141 (73.06%) of 193 samples.

R commands for task
oncoplot(maf = laml, top = 10, font\$size = 12)

height (cm) width (cm)

Export Update plot

shiny.bioinstaller.parameters.toml	initial cmmi
shiny.conda.parameters.toml	initial cmmi
shiny.config.yaml	update bin files and add web.R
shiny.datasets2tools.parameters.toml	initial cmmi
shiny.easy_project.parameters.toml	initial cmmi
shiny.geoquery.parameters.toml	initial cmmi
shiny.maftools.parameters.toml	initial cmmi
shiny.pubmed.parameters.toml	initial cmmi
shiny.spack.parameters.toml	initial cmmi

Plugin-based R Shiny application (bioshiny)

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社区项目实例之七

The screenshot displays the Hiplot web application interface. On the left is a sidebar with navigation links:

- Hiplot (0.1.0.beta2) 2020-05-29 14:58:19
- Homepage
- Dashboard
- File Management
- Basic Plot** (selected)
- Omics Plots
- Task Queue
- User Management
- Account Setting
- Extra
- Switch Languages
- Document
- Discord Channel

The main area contains six plot cards:

- Scatter**: Display the variables. (★★★★★)
A scatter plot titled "Test Scatter Plot" showing two groups: "treat1" (blue dots) and "treat2" (red triangles). The x-axis is "Value1" and the y-axis is "Value2".
- 3D Scatter**: Display the variables. (★★★★★)
A 3D scatter plot titled "Test 3D-Scatter Plot" showing data points in three dimensions.
- Bubble**: Display the variables. (★★★★★)
A bubble plot titled "Test Bubble Plot" showing data points with varying sizes and colors. The x-axis is "Gene Ratio" and the y-axis is "-log₁₀(P Value)". A legend indicates bubble sizes from 10.0 to 20.0.
- Dendrogram**: Clustering method. (★★★★★)
A dendrogram plot showing hierarchical clustering results.
- Heatmap**: Numerical matrix display. (★★★★★)
A heatmap plot titled "Test Heatmap Plot" showing a color-coded numerical matrix.
- Corelation Heatmap**: Display of correlation matrix. (★★★★★)
A heatmap plot titled "Test Correlation Heatmap Plot" showing a triangular correlation matrix.

At the bottom, there is a navigation bar with page numbers 1, 2, 3, and arrows, and a blue circular button with an upward arrow icon.

Hiplot

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Inventing, Optimizing, Sharing

openbiox community

2020-05-29