

# openbiox | 生物信息学创新协作小组

Inventing, Optimizing, Sharing

**openbiox community**

**2019-04-20**

## 主讲人自我介绍



Jianfeng, Doctoral candidate

- High-throughput sequencing (HTS) data analysis (e.g. leukemia and lymphoma)
- Development of web-based tool and knowledge base (KB)

# 主讲人自我介绍



Set your status

**Jianfeng**  
Miachol

Developer Program Member  
★ PRO

Doctoral candidate of Shanghai Jiaotong University and Shanghai Institute of Hematology.

@openbiox  
Shanghai, China

Overview    Repositories 63    Stars 309    Followers 95    Following 53    Gists 4

Pinned / Top repositories

**config**  
Implements the JSON, INI, YAML and TOML parser, for R setting and writing of configuration file.  
R ★ 29 ⚡ 6

**openbiox/Bioinformatics-Resources**  
A curated list of resources for learning bioinformatics.  
★ 78 ⚡ 31

**JhuangLab/annovarR**  
annovarR: a variant annotation and visualization system based on R and Shiny framework  
R ★ 16 ⚡ 6

**JhuangLab/ngstk**  
A toolkit developed by JhuangLab members to facilitate the analysis of next-generation sequencing (NGS) data.  
R ★ 11 ⚡ 2

**ngsjs/ngsjs**  
A set of command line tools, NGS data analysis workflows [WDL, Nextflow, Snakemake, and Bpipe], and R shiny plugins/R markdown document for exploring next-generation sequencing data  
JavaScript ★ 7

**ngsjs/bioshiny**  
A project to develop the R Shiny applications, which is the subproject of ngsjs.  
JavaScript ★ 2

384 contributions in the last year

Contribution settings ▾

2019

2018

2017

2016

Learn how we count contributions.

Less    More



# 主讲人自我介绍

## feedly.com conflict with worldbrain

ACKNOWLEDGED

2

When enabling the worldbrain chrome extension, the feedly.com could not to switch the RSS content.

version: 0.15.5

OS: Windows 10 Insider Preview 18362.1 (19h1\_release)

conflict site: feedly.com

[feedly] initial context ready 4533b8b4-55db-432c-acce-a72148f8dbc8 standard  
(index):1 Failed to execute 'postMessage' on 'DOMWindow': The target origin provided ('https://js.stripe.com') does not match the recipient window's origin ('https://feedly.com').  
en @ (index):1  
feed%2Fhttps%3A%2F%2Futils.ncbi.nlm.nih.gov%2Fentrez%2Futils%2Fers.cgi%3Frss\_guid%3D1NKSH3 UhXTzTtdDpdws8INLHynnOGENlnttNYWFOPYX4tfMnF:1 Unchecked runtime.lastError: The message port closed before a response was received.

bug



Jianfeng

Posted 21 days ago · Updated 4 days ago



Follow

1 reply

Votes

Newest

Oldest

Oliver Sauter · 4 days ago

0

Thanks for the note, we are already aware of the problem but have not been able to address it yet.

r-lib / pkgdown

Code Issues Pull requests Releases More

Watch ⌂ Unstar 406 Fork ⌂

## Incompatible between DT datatable and pkgdown.js #655

Closed in 6fe20ba Miachol opened this issue on May 6, 2018 · 2 comments



Miachol on May 6, 2018 · edited by hadley ·

When I used `DT datatable` in the page, it raised `pkgdown.js` error.

### Error message

```
caught TypeError: $(...).stick_in_parent is not a function
at HTMLDocument.<anonymous> (pkgdown.js:2)
at j (jquery-3.1.0.min.js:2)
at k (jquery-3.1.0.min.js:2)
```

Assignees  
No one assigned

Labels  
`bug`  
`rd-translation`

Projects  
None yet

Preprint File available Feedback requested

Research

Citations

Recomm.

Reads

## nf-core : Community curated bioinformatics pipelines

April 2019

DOI: 10.1101/610741

License · CC BY-NC 4.0

Project: `nf-core`

Philip Ewels · Alexander Peltzer · Sven Fillinger · Show all 9 authors · Sven Nahnsen

Overview Stats Comments Citations References (11) Related research (10+)



Alexander Peltzer requested your feedback on this article · 2 days ago

Add feedback

# 开场故事之一

时间：2017 年 1 月

地点：上海市黄浦区某实验室办公室



The screenshot shows the CRAN package submission interface. On the left, there's a large R logo and links for 'CRAN', 'Mirrors', and 'What's new?'. The main area is titled 'Submit package to CRAN' and is divided into three steps: 'Step 1 (Upload)', 'Step 2 (Submission)', and 'Step 3 (Confirmation)'. Under Step 1, fields for 'Your name\*' and 'Your email\*' are filled with placeholder text. A 'Package\*' field has a file chosen from 'Choose File'. To the right, a large text overlay reads 'Submitting configr package .....'. Below this, there's an email interface showing the recipient as '李剑峰-上海交通大学' and the sender as 'Dirk Eddelbuettel'. A portrait photo of Dirk Eddelbuettel is on the right.

Hi,

Thanks for the configr package -- looks useful. I happen to like TOML configurations a lot, and we made the RcppTOML more general by supporting Windows too. Maybe you want to add it as a fourth option?

Cheers, Dirk

--

<http://dirk.eddelbuettel.com> | @eddelbuettel | [edd@debian.org](mailto:edd@debian.org)

# 开场故事之一



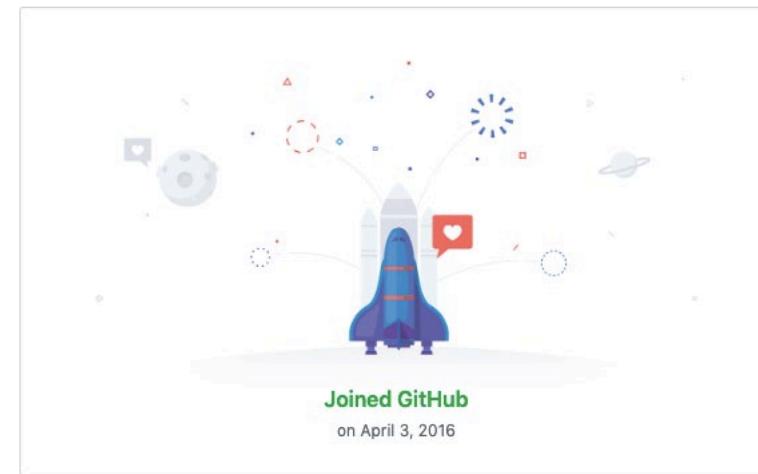
## Contribution activity

May - December 2016

Miachol had no activity during this period.

April 2016

Joined GitHub

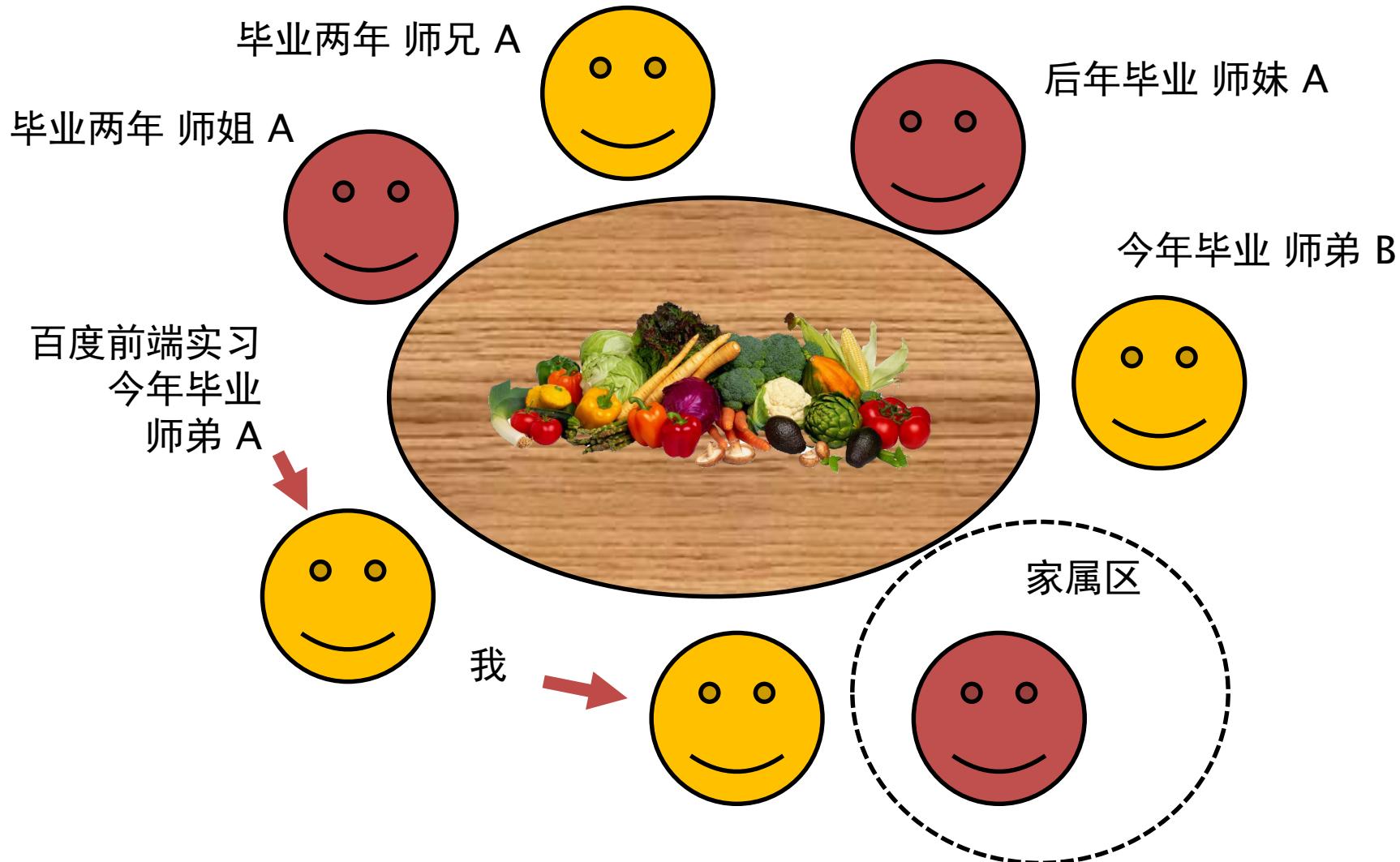


剧终

## 开场故事之二

时间：2019 年 1 月 19 日 18: 00 – 20: 00

地点：上海市黄浦区\*\*光中心\*\*绿色时尚餐厅 C13 桌



## openbiox 简介



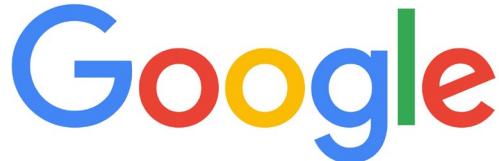
openbiox 成立于 2019 年 3 月，是一个社区驱动建立的生物信息学创新协作组，由来自全世界范围内的知名高校、科研院所的在读中国籍本科生、硕士生、博士生，以及博士后、工作人员所构成。

截止 2019 年 4 月，openbiox 成员共计 69 人，完成至少 11 支项目团队的组建，并发起了 10 余项生物信息学创新实践项目，项目资金超过一万三千余元，网页/计算服务器若干。

**Inventing, Optimizing, Sharing**

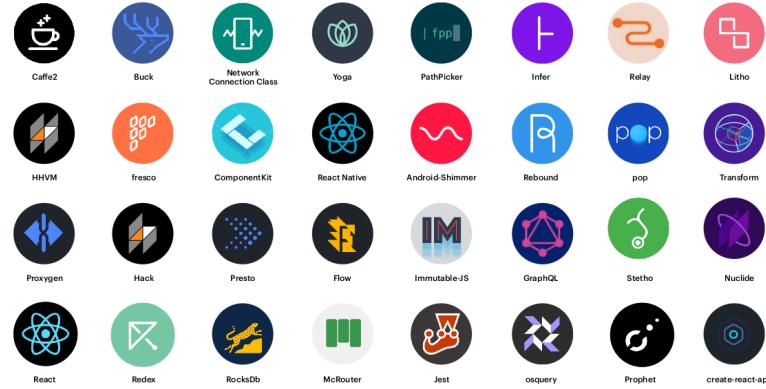
# openbiox 简介

## 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 人员

## 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*

Many experts believe that  
by 2050 machines will have

Law & Contracts



Customer Service



Sales



manual dexterity, and..

Personal Assistants



Investing



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

## openbiox 简介

### openbiox 时间线



# openbiox 简介

## openbiox GitHub 仓库

 **openbiox**

A community-driven bioinformatics innovation collaboration group in China.

📍 China 📩 committee@openbiox.org Verified

Repositories 13  People 62   Teams 11   Projects 10   Settings

Pinned repositories Customize pinned repositories

 [openbiox](#) ≡

Source code of openbiox homepage (under development status).

● Vue ⭐ 4 ⚡ 1

 [openbiox-wiki](#) ≡

Let's get started!

● HTML ⭐ 12 ⚡ 10

 [Cookbook-for-R-Chinese](#) ≡

Cookbook for R 中文翻译

● TeX ⭐ 22 ⚡ 12

 [Bioinformatics-Resources](#) ≡

A curated list of resources for learning bioinformatics.

★ 78 ⚡ 31

 [XenaShiny](#) ≡

A Shiny App for UCSC Xena  
<https://xenabrowser.net/datapages/>

● JavaScript ⭐ 6 ⚡ 2

 [openbiox-disease-kb](#) ≡

Interactive knowledge-base and cloud application for better interpretation of human disease

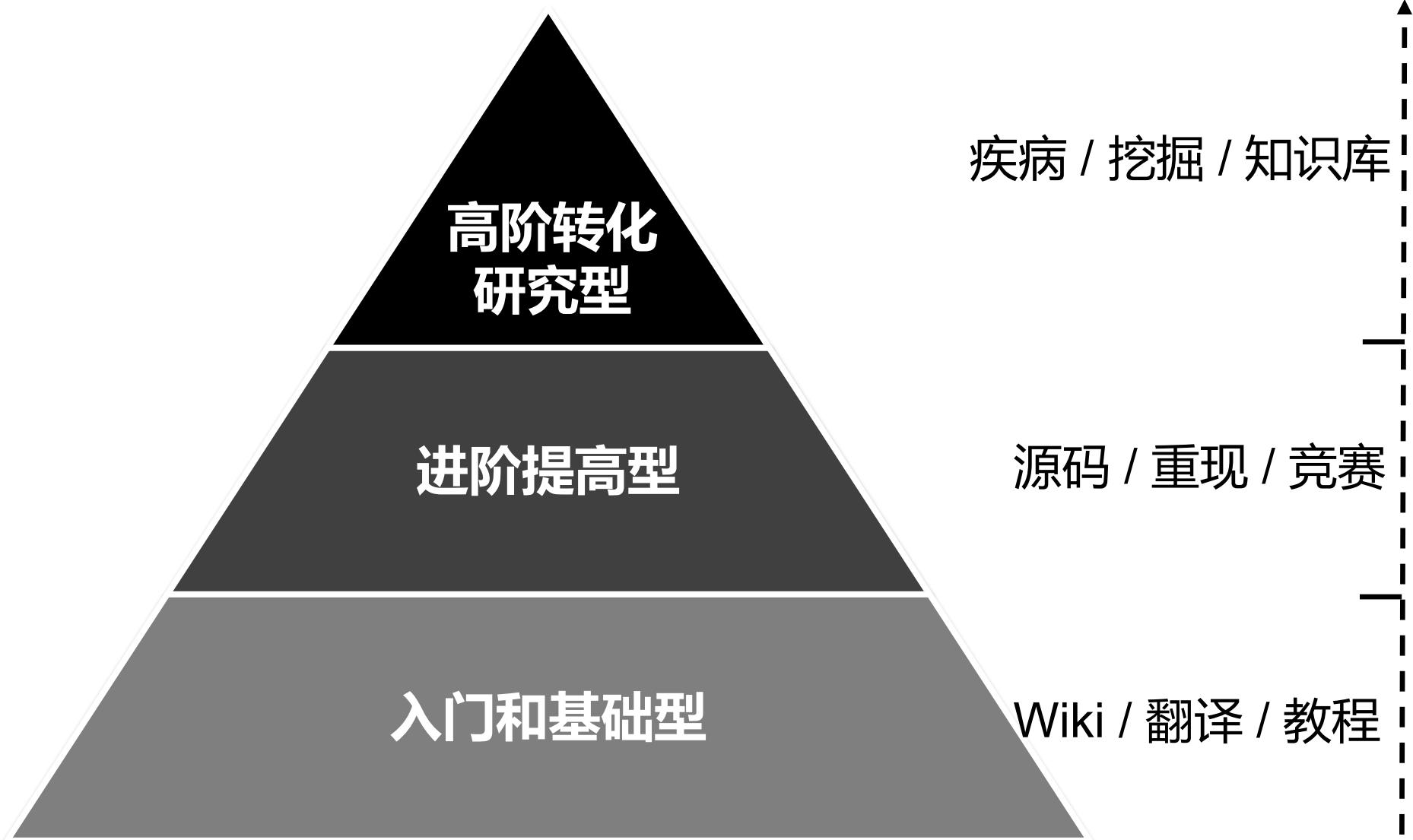
★ 2 ⚡ 1

# openbiox 简介

## openbiox 项目团队

<input type="checkbox"/> Select all		Visibility ▾	Members ▾
<input type="checkbox"/>	ak47		7 members 0 teams
<input type="checkbox"/>	Cookbook4r cookbook for r翻译小队		6 members 0 teams
<input type="checkbox"/>	dnaChat Wechat group! Welcome.		6 members 0 teams
<input type="checkbox"/>	EncodeChallenge Team for the Encode Imputation Challenge		9 members 0 teams
<input type="checkbox"/>	metapip Team for developing clinical pathogens detection pipeline		9 members 0 teams
<input type="checkbox"/>	playcloud		15 members 0 teams
<input type="checkbox"/>	single cell geek team works on scRNA-seq OnlineFlow project		10 members 0 teams
<input type="checkbox"/>	tcgatoolkit collect bioinformatics tools in TCGA publications and make tutorial for them		9 members 0 teams
<input type="checkbox"/>	TranslationGroup Openbiox 翻译小组		8 members 0 teams
<input type="checkbox"/>	wiki-x Maintain the core knowledge base of openbiox.		8 members 0 teams
<input type="checkbox"/>	xenashiny Xena Shiny应用开发小队		6 members 0 teams

## 拟开展创新实践项目类型



# openbiox 简介

## 实践项目实例之一

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

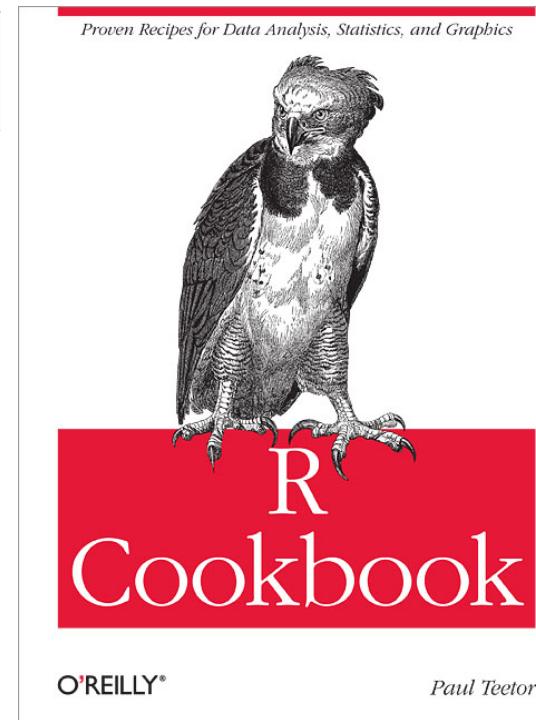
Branch: master Create new file Find File Clone or download

fei0810 and ShixiangWang 02-numbers 校对 (#19) ... Latest commit 0d71162 a day ago

File	Commit Message	Time
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



## 实践项目实例之一

Cookbook for R 中文版

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

≡ Q A ☰

Twitter Facebook Open

**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



# openbiox 简介

## 实践项目实例之二

The screenshot displays the openbiox project management interface, showing a grid of tasks across different categories:

- No Status 10**: Medstudio v0.1.0开发任务 (迭代计划)  
2019/04/13  
文件上传及管理模块, 用户管理模块  
临床指标在线计算模块, 计算模块  
文档相关  
生物信息学工具分析组件库 (基因突变)  
搜索模块, 下载模块 (开放数据)  
0.00%  
v0.1.0
- 计划 7**: 整理临床需要为病人提供的指标计算服务及其公式  
临床  
Hailuan Zeng  
v0.1.0
- 开发中 7**: 用户组及权限管理  
用户  
Jiafeng Li  
v0.1.0
- 待测试 0**: + New
- 已完成 11**: 右上角用户头像及点击后进入更新用户信息界面  
用户  
Jiafeng Li  
v0.1.0
- + New**: 新增、删除、更新用户资料  
用户  
Jiafeng Li  
v0.1.0
- 文件上传及管理模块**: 文件  
2019/01/15  
Jiafeng Li  
文件上传 (前台、后台接收文件部分)  
文件管理 (创建目录、复制、移动、...)  
50.00%  
v0.1.0
- 用户管理模块**: 用户  
2019/01/15  
Jiafeng Li  
右上角用户头像及点击后进入更新用...  
新增、删除、更新用户资料  
用户组及权限管理
- 计算任务的 History 工作区**: 计算  
v0.1.0
- 转录组数据可视化**: 生信组件  
v0.1.0
- 基因突变数据可视化**: 生信组件  
v0.1.0
- 三维基因组可视化**: 生信组件  
v0.1.0
- 组件中 Class 的统一和缩减**: 其他  
v0.1.0
- 使用教程及技术文档**: 文档  
Jiafeng Li, Liang Wu  
v0.1.0
- API 文档**: 文档  
Jiafeng Li  
v0.1.0
- 任务提交弹出框的 UI 设计**: 计算  
Liang Wu  
v0.1.0
- 文件上传 (前台、后台接收文件部分)**: 文件  
Jiafeng Li  
v0.1.0
- CiVIC数据库基因搜索功能**: 搜索  
Jiafeng Li  
v0.1.0
- Oncotar数据库基因搜索功能**: 搜索  
Jiafeng Li  
v0.1.0

MedStudio

# openbiox 简介

## 实践项目实例之二

The screenshots illustrate the MedStudio platform, a medical data analysis cloud platform.

**Search Interface:** Shows search tools for Genes, Disease, Drugs, and Datasets. It includes sections for "Search Gene via Oncotator Gene API" and "Search Gene via CIViC Gene API".

**Login Page:** A "Login MedStudio" form with fields for Username and Password, and buttons for LOGIN and CLEAR.

**Dashboard:** Displays real-time system monitoring metrics. Key data points include:

- Usage of CPU: 14.14%
- Usage of memory: 1.79 GB / 1.95 GB
- Network status: Download: 0 B/s | Upload: 0 B/s
- Usage of disk: 10.03 GB / 39.25 GB
- Read Speed of disk: 0 B/s
- Write Speed of disk: 1.02 MB/s

**Running Environment of Host System:** A detailed view of the host system's components. Key sections include:

- system:** Manufacturer: Alibaba Cloud, Model: Alibaba Cloud ECS, Version: pc-i440fx-2.1, Serial: -, UUID: -, SKU: -.
- bios:** Vendor: SeaBIOS, Version: rel-1.7.5-0-ge5148bc-20140602\_164612-nillson.home.kraxel.org, Release Date: 2014-04-01, Revision: -.
- baseboard:** Manufacturer: -, Model: -, Version: -, Serial: -, Asset Tag: -.
- chassis:** Manufacturer: Alibaba Cloud, Model: -, Type: Other, Version: pc-i440fx-2.1, Serial: -, Asset Tag: -, SKU: -.

MedStudio

# openbiox 简介

## 实践项目实例之二

### Upload Files

Filename	Size	Progress	Speed	Status	Action
yjsjbx.pdf	105.84 KB	<div style="width: 20%;">20%</div>		0%	<span>暂停</span> <span>继续</span> <span>删除</span>
Wu-2018-Water content, not stiffness, dominate.pdf	1.43 MB	<div style="width: 40%;">40%</div>		0%	<span>暂停</span> <span>继续</span> <span>删除</span>
s41467-018-06300-3.pdf	4.47 MB	<div style="width: 30%;">30%</div>		0%	<span>暂停</span> <span>继续</span> <span>删除</span>
Mangul-2018.pdf	3.38 MB	<div style="width: 20%;">20%</div>		0%	<span>暂停</span> <span>继续</span> <span>删除</span>
10.1038@s41587-019-0074-6.pdf	1.38 MB	<div style="width: 10%;">10%</div>		0%	<span>暂停</span> <span>继续</span> <span>删除</span>

Rows per page: 5 1-5 of 5

上一页 下一页 重置 刷新 取消

### Upload Files

Filename	Size	Progress	Speed	Status	Action
yjsjbx.pdf	105.84 KB	<div style="width: 20%;">20%</div>		96.00 KB	success <span>暂停</span> <span>继续</span> <span>删除</span>
Wu-2018-Water content, not stiffness, dominate.pdf	1.43 MB	<div style="width: 40%;">40%</div>		320.00 KB	success <span>暂停</span> <span>继续</span> <span>删除</span>
s41467-018-06300-3.pdf	4.47 MB	<div style="width: 30%;">30%</div>		272.00 KB	success <span>暂停</span> <span>继续</span> <span>删除</span>
Mangul-2018.pdf	3.38 MB	<div style="width: 20%;">20%</div>		32.00 KB	success <span>暂停</span> <span>继续</span> <span>删除</span>
10.1038@s41587-019-0074-6.pdf	1.38 MB	<div style="width: 10%;">10%</div>		32.00 KB	success <span>暂停</span> <span>继续</span> <span>删除</span>

Rows per page: 5 1-5 of 5

上一页 下一页 重置 刷新 取消

### Management of Files

Files	Modified Date	Detail Info
projects	2019-01-17	<span>详细信息</span>
upload	2019-04-17	<span>21.46 MB</span> <span>详细信息</span>
1547648443087-ngstk_0.2.3.tar.gz	2019-01-16	<span>1.04 MB</span> <span>详细信息</span>
1547690363557-ngstk_0.2.3.tar.gz	2019-01-17	<span>1.04 MB</span> <span>详细信息</span>
1548666128929-SunloginClient.exe	2019-01-28	<span>3.74 MB</span> <span>详细信息</span>
1548666459939-访问素材CNN.url	2019-01-28	<span>186 B</span> <span>详细信息</span>
1548666460034-说明read me.txt	2019-01-28	<span>394 B</span> <span>详细信息</span>
1548666460519-素材cnn-sccnm.com_201504180926.jpg	2019-01-28	<span>184.28 KB</span> <span>详细信息</span>
1548666463224-素材cnn-sccnm.com_201504180926.eps	2019-01-28	<span>4.71 MB</span> <span>详细信息</span>
1555498079826-yjsjbx.pdf	2019-04-17	<span>105.84 KB</span> <span>详细信息</span>
1555498096415-Wu-2018-Water content, not stiffness, dominate.pdf	2019-04-17	<span>1.43 MB</span> <span>详细信息</span>
1555498101450-10.1038@s41587-019-0074-6.pdf	2019-04-17	<span>1.38 MB</span> <span>详细信息</span>
1555498103982-Mangul-2018.pdf	2019-04-17	<span>3.38 MB</span> <span>详细信息</span>
1555498111943-s41467-018-06300-3.pdf	2019-04-17	<span>4.47 MB</span> <span>详细信息</span>

添加 分享 下载 删除

### File info

File or Directory Name:	Original Name:	File or Directory ID:	Modified Date	Detail Info
1555498103982-Mangul-2018.pdf	Mangul-2018.pdf	287	2019-01-17	<span>详细信息</span>
<b>Mimetype</b>			2019-04-17	<span>21.46 MB</span> <span>详细信息</span>
application/pdf			2019-01-16	<span>1.04 MB</span> <span>详细信息</span>
<b>Type:</b>	<b>Size:</b>	<b>Created Date:</b>	2019-01-17	<span>1.04 MB</span> <span>详细信息</span>
File	3.38 MB	2019-04-17 18:48:23	2019-01-28	<span>3.74 MB</span> <span>详细信息</span>
<b>Modified Date:</b>			2019-01-17	<span>186 B</span> <span>详细信息</span>
2019-04-17 18:48:23			2019-01-28	<span>394 B</span> <span>详细信息</span>
<b>Path:</b>			2019-01-28	<span>184.28 KB</span> <span>详细信息</span>
/home/zhl/.minio/userdata/62cd780-0db6-11e9-855b-bb4c4b386613/upload/1555498103982-Mangul-2018.pdf			2019-01-28	<span>4.71 MB</span> <span>详细信息</span>
<b>Description:</b>			2019-04-17	<span>105.84 KB</span> <span>详细信息</span>
n/a			2019-04-17	<span>1.43 MB</span> <span>详细信息</span>
<b>User UUID:</b>	<b>Shared?</b>		2019-04-17	<span>1.38 MB</span> <span>详细信息</span>
62cd780-0db6-11e9-855b-bb4c4b386613	No		2019-04-17	<span>3.38 MB</span> <span>详细信息</span>
<b>MD5</b>			2019-04-17	<span>4.47 MB</span> <span>详细信息</span>
n/a			2019-04-17	<span>18.24 MB</span> <span>详细信息</span>

关闭

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# openbiox 简介

## 实践项目实例之二

The screenshot shows the Tencent Cloud Storage (WeCloud) interface. The left sidebar includes icons for search, recent files, and categories like 全部 (All), 文档 (Documents), 图片 (Images), 视频 (Videos), 音乐 (Music), 照片 (Photos), 笔记 (Notes), 共享组 (Shared Groups), 保险箱 (Safe Box), 分享链接 (Share Links), and 回收站 (Recycle Bin). The main area displays a file list for the project 'openbiox-disease-kb'. The list includes:

名称	上次修改时间	大小
expression	04月13日 15:46	49.65 GB
variants	04月10日 11:51	203.04 GB
metabolism	04月06日 02:39	0 B
image	04月06日 02:39	0 B
.resona	04月04日 20:46	551.68 KB

At the bottom left, it says '已用 486.68 GB / 6.01 TB' and has a '扩容 >' button. At the top right, there are links for '超级会员低至 ¥0.52/天' (Super Member starting at ¥0.52/day), '会员中心' (Member Center), 'openbiox' with a QR code, and 'SVIP'.

已上传数据库及相关资源 ~500 GB，其中绝大部分从未上传至微云平台

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# openbiox 简介

## 实践项目实例之三

BioShiny APP

Search...

bioinstaller spack conda datasets2tools pubmed geoquery maftools

**Input files**

Single sample analysis:

- MAF file (laml\_maf)
- Clinical annotation file (laml\_cln)
- MutSig results (laml\_mutsig)

CNV related analysis:

- Gistic all lesions file (all\_lesions)
- Gistic amp genes file (amp\_genes)
- Gistic del genes file (del\_genes)
- Gistic score file (scores\_gls)

Running maftools task steps, waiting please...

**Output of maftools fields summary**

**Output of maftools sample summary**

**Output of maftools MAF summary**

**Output of maftools oncplots**

**Output of maftools oncplots with copy number data**

**Output of maftools oncplots with advanced**

**Output of maftools transition and transversions**

**Output of maftools Lollipop 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 oncplots**

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 ccommit

[shiny.conda.parameters.toml](#)

initial ccommit

[shiny.config.yaml](#)

update bin files and add web.R

[shiny.datasets2tools.parameters.toml](#)

initial ccommit

[shiny.easy\\_project.parameters.toml](#)

initial ccommit

[shiny.geoquery.parameters.toml](#)

initial ccommit

[shiny.maftools.parameters.toml](#)

initial ccommit

[shiny.pubmed.parameters.toml](#)

initial ccommit

[shiny.spack.parameters.toml](#)

initial ccommit

## Plugin-based R Shiny application

# openbiox 简介

## 每周一问



...'s 每周一问

Today 10:22

**问题描述（生活、学习、工作中遇到的问题和疑惑均可）：** 长期的炎症反应会增加某些癌症的患病风险。炎症反应的产生被认为是转录调控网络机制所控制。是否有研究或者数据库系统地收集和分析过人体各个组织在有炎症状态下的形态学，基因组，转录组，蛋白质组及其对应的免疫反应程度？

**标签（如生物信息学，统计学；逗号分隔）：** 生物学，炎症反应

琪琪

...'s 每周一问

04.14 19:15

**问题描述（生活、学习、工作中遇到的问题和疑惑均可）：** 临床预测模型文章质量的高低是不是取决于该模型的可推广性？又或者是所能解决的临床问题比较重要？

**标签（如生物信息学，统计学；逗号分隔）：** 临床预测模型

Read

# openbiox 简介

## 每周一问



达's 每周一问

04.14 10:22

问题描述（生活、学习、工作中遇到的问题和疑惑均可）：目前现有的单细胞的分离方法是可信的吗？单细胞测序在干细胞研究中有什么决定性的帮助呢？



's 每周一问

04.09 09:32

问题描述（生活、学习、工作中遇到的问题和疑惑均可）：多尺度复杂化学系统模型曾获得2013年诺贝尔化学奖，其模拟的系统尺度从原子尺度 $10^{-9}m$ 到宏观尺度 $10^{-2}m$ ，考虑的因素包括量子力学和经典力学，但取得了非常成功的效果。我想知道类似方法是否存在与生物系统模拟，（尺度从生物分子到细胞层面），或者存在相关研究？有了解的同学可以介绍下，谢谢！

标签（如生物信息学，统计学；逗号分隔）：数学模型，计算机模拟，生物系统

## 总结

**The heart of \* is its community.**

“The heart of *nf-core* is its community.”

Philip Ewels, Alexander Peltzer, et al. nf-core : Community curated bioinformatics pipelines. 2019. doi: 10.1101/610741

## openbiox 简介

### 现场纳新通道



**申请方式：**扫描左侧二维码回答 openbiox 每周一问部分题目，合并简历发送至  
[committee@openbiox.org](mailto:committee@openbiox.org)

**招收名额：** <= 10人

**截止日期：** 4月 30 日

# openbiox | 生物信息学创新协作小组

Inventing, Optimizing, Sharing

**openbiox community**

**2019-04-20**