
jbiot Documentation

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This is the documentation of **jbiot**.

This jbiot python packages designed for bioinformatics develop toolkits

1.1 Installation

use pip to install:

```
pip install jbiot
```

or use git to clone latest code:

```
git clone git@123.57.226.13:/expan/DevRepos/jbiot.git
```

with jbiot install on your computer, the following script can be used:

```
- lsub
- csub
- smartFqs.py
- jbio.start/stop/send
- docker2sing.py
- startup
- md2html.py
- always
- filterTable.py
- render.py
```

1.2 Contents

1.2.1 Usage

lsub

use lsub to subject jobs ,type lsub -h to check the detail usage:

```
lsub -h

Usage:
  lsub <cmdfile> [--with-docker|--with-singularity][--dry][-e <email>][-w <wexin_
↪name>][-n <job_nam>]

Options:
  -h --help                print this screen
  --dry                    all done but run script
  --with-docker            prefer to use docker when run cmd
  --with-singularity       prefer to user singularity when run cmd
  -e,--email=<email>      email of you want to remind of
  -w,--wechat=<name>      wechat name you want to send to
  -n,--name=<job_name>    the name of this task.
```

csub

use csub to subject jobs to cluster, type csub -h to check detail usage

Note: documents will updated in time. ...

1.2.2 Developers

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1.2.3 jbiot

jbiot package

Subpackages

jbiot.jbio package

Submodules

jbiot.jbio.jmail module

jbiot.jbio.sysinfo module

Module contents

jbiot.render package

Submodules

jbiot.render.add_html module

jbiot.render.add_pdf module

jbiot.render.add_png module

jbiot.render.add_pngs module

jbiot.render.add_svg module

jbiot.render.add_text module

jbiot.render.add_tsv module

jbiot.render.add_xls module

jbiot.render.render module

jbiot.render.svg module

Module contents

jbiot.startup package

Submodules

jbiot.startup.arrange module

jbiot.startup.bin module

jbiot.startup.conf module

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- [search](#)