
Lambda tips Documentation

Release 0.1

carushi

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1.1 carushi

- Computational biologist
- [Google sites](#)
- [Github](#)

Bioinformatics

2.1 How much?

2.1.1

		(Gb)		(run)
Illumina	MiniSeq	7.5	\$50,000	–
–	MiSeq	15	\$100,000	~10,0000
–	NextSeq	120	\$250,000	–
–	Hiseq	1500	\$740,000	–
–	HiSeq X	1800 (2)	\$1,000,000	\$1000 / hs genome 30x ?

Reference

- <http://jp.illumina.com/systems/sequencing.html>
- http://jp.illumina.com/content/dam/illumina-marketing/apac/japan/documents/pdf/2014_illumina_introducing_nextseq.pdf
- <http://nextgenseek.com/2012/08/comparing-price-and-tech-specs-of-illumina-miseq-ion-torrent-pgm-454-gs-junior-and-pacbio-rs/>
- <http://www.captodayonline.com/productguides/instruments/next-generation-sequencing-instrument-november-2015/illumina-miseq-sequencing-november-2015.html>

				(run)
Pacbio	RS II	–	\$750,000	\$25,000 / hs genome 30x
–	Sequel	–	\$350,000	\$10,000 / hs genome 30x

Reference

- <http://nextgenseek.com/2015/10/pacbio-announces-a-new-sequencer-pacbio-sequel/>

16.06.04

2.2 Differential gene expression analyses

2.2.1 edgeR

2.2.2 Cuffdiff

2.2.3 DEseq2

2.3 Go enrichment

How to use readthedocs

3.1 Creat a new sphinx project

- Reference: <http://rcmdnk.github.io/blog/2016/05/01/computer-brew-file-github/>

```
mkdir test
cd test
sphinx-quickstart ## answer or type <enter>
```

MathJaxenabled conf.py

- .gitignore

```
echo docs/_build/* > .gitignore
```

sphinx-quickstartbuildsource_build

- githubpush

```
git add -A
git commit -m'<comment>'
git push origin <branch>
```

- localhtml

```
make html
```

_buildhtmlreadthedocssphinx rds template

3.2 Use readthedocs template

- <https://github.com/readthedocs/template>

3.3 github

- Admin -> Repository URLdocument

3.4 build

- Admin -> Advanced Settingsdocs/conf.py
- <http://stackoverflow.com/questions/32729978/read-the-docs-build-failing-without-errors>

MySQL

4.1 How to start mysql server and input source

brewmysql.serverMySQL

sql stop

```
mysql.server start
mysql -u root
mysql> SET PASSWORD FOR root@localhost=PASSWORD('hoge')
mysql> exit
mysql -u root -h localhost -p #password
mysql.server stop
```

4.1.1 Test set

Employdbfull set <https://launchpad.net/test-db/+download>

```
mysql> use db #
mysql> source file
```

Mysqlstorage_engine

```
-- set storage_engine = InnoDB error
```

stop

```
DROP DATABASE IF EXISTS dbname;
```

<http://www.liquidweb.com/kb/delete-a-mysql-database-on-linux-via-command-line/>

4.2 Manage database

4.2.1

```
SELECT * FROM tablename WHERE LIMIT start,end
```

[https://technet.microsoft.com/en-us/library/bb264565\(v=sql.90\).aspx](https://technet.microsoft.com/en-us/library/bb264565(v=sql.90).aspx)

4.2.2 PyMySQL

<https://donjajo.com/using-pymysql-as-mysql-driver-for-python3/#.V33kSZN972I>

4.2.3 GUIMySQL

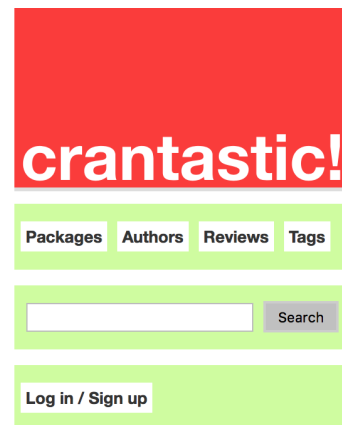
macOSSequel Pro tables



5.1 Packages

copulaR * GOFcopula * copulaGOF * copula * VineCopula

Search

1. [copula](#) ★ ★ ★
Classes (S4) of commonly used elliptical, Archimedean, extreme value and some more **copula** families. Methods for density, distribution, random number generation, bivariate depen...
2. [vines](#)
Implementation of the vine graphical model for building high-dimensional probability distributions as a factorization of bivariate **copulas** and marginal density functions. This p...
3. [nacopula](#)
An R package for working with nested Archimedean **copulas**. Specifically, providing procedures for computing function values and cube volumes, characteristics such as Kendall's ta...
4. [Depela](#)
Implement semiparametric estimation of **copula** model, and deal with structural break problems in **copula** modelling.
5. [SpatialExtremes](#)
Tools for the statistical modelling of spatial extremes using max-stable processes, **copula** or Bayesian hierarchical models.
6. [fCopulae](#)
Environment for teaching "Financial Engineering and Computational Finance".
7. [faac](#)



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5.1.1 copula

```
copulaGOFcopula :: install.package("copula")
```

Indices and tables

- `genindex`
- `modindex`
- `search`