



Georgia Advanced Computing Resource Center (GACRC) University of Georgia

<http://www.gacrc.uga.edu/>

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Overview

- Current status of software on zcluster (Sapelo)
- Application databases
- Installing by users
- Common problems/mistakes
- Troubleshoot
- Getting help from GACRC



Practice Script !

- Work at Interactive Node

```
cp -r /db/iprac .
```

```
cd iprac
```

```
less note.sh
```



Installed Software

- GACRC Wiki Software page (zcluster, sapelo, version)
<https://wiki.gacrc.uga.edu/wiki/Software>
- Cluster onsite
 - Zcluster: *ls /usr/local/*
 - Sapelo: *ls /usr/local/apps*
 - Organized by package name
- Perl Python R packages



Application databases

- GACRC Wiki Software page (zcluster, sapelo, version)
https://wiki.gacrc.uga.edu/wiki/Bioinformatics_Databases
- Cluster onsite

```
ls /db/
```

```
ls /db/ncbiblast
```



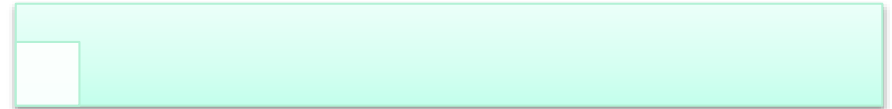
Obtain code – binary or source

Binary



- linux64
- Easy install
- May not compatible
- Slow performance

Source Code



- Need to compile
- Higher chance to be compatible
- Fast computing

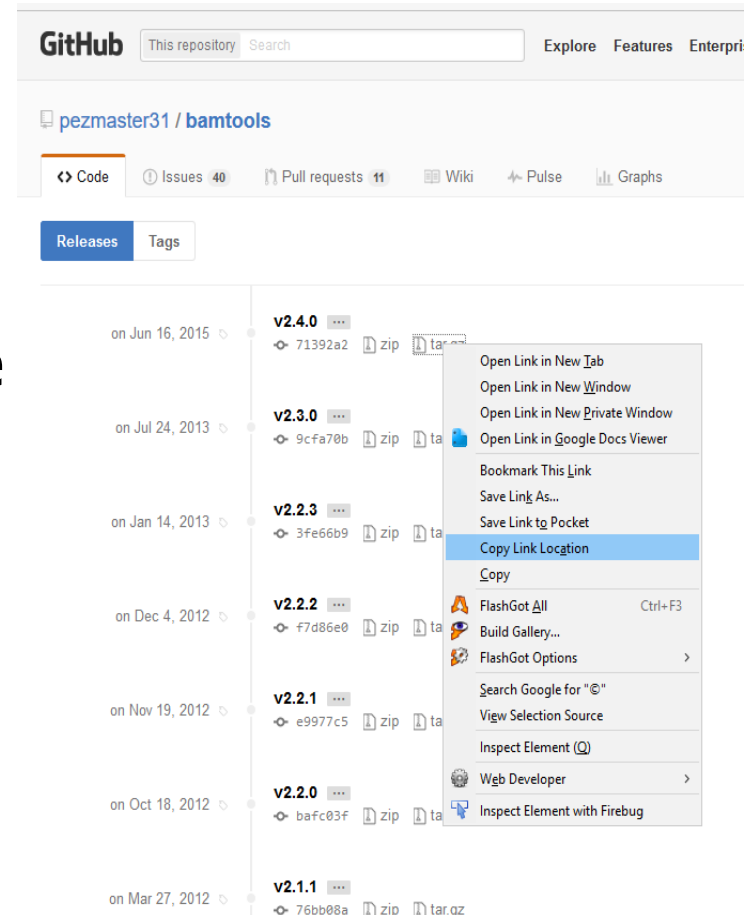


Obtain code – get link

- Go to software website
- Getting major stable releases
- Getting tar.gz if available
- Getting source code if available

```
wget http://...
```

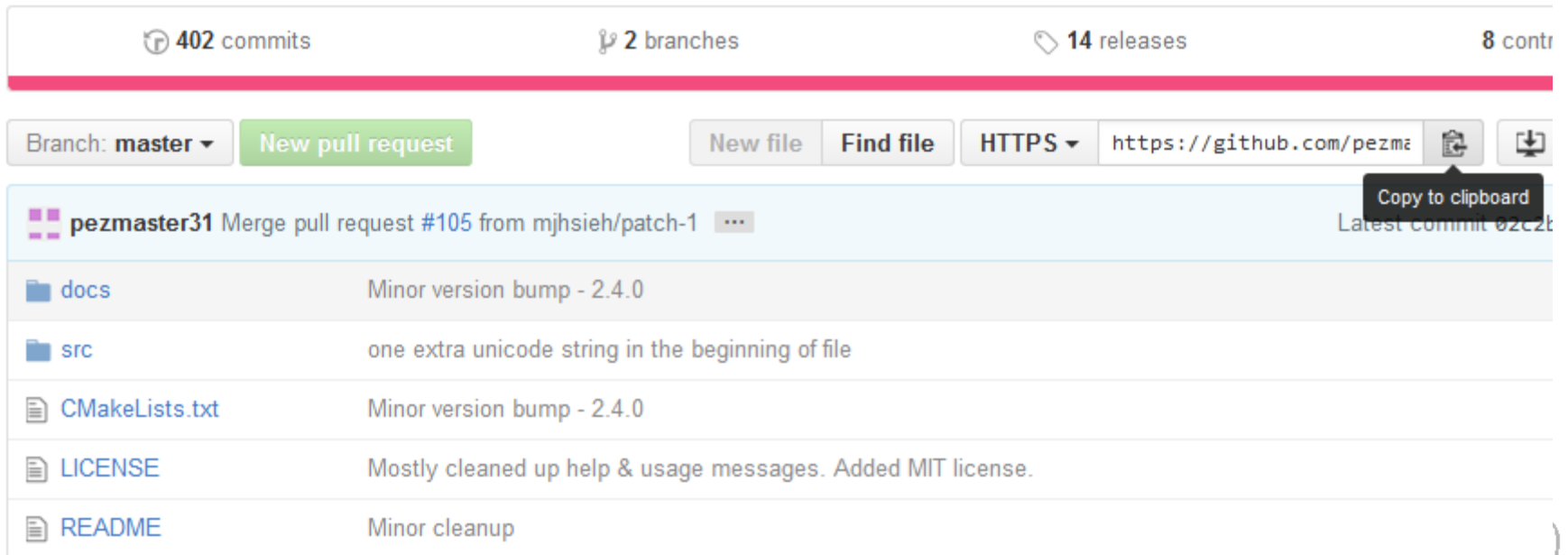
```
curl -OL http://...
```



The screenshot shows the GitHub interface for the repository 'pezmaster31 / bamtools'. The 'Releases' tab is active, displaying a list of releases from v2.1.1 to v2.4.0. A context menu is open over the 'v2.2.3' release, with the 'Copy Link Location' option highlighted. The menu also includes options like 'Open Link in New Tab', 'Bookmark This Link', and 'Inspect Element'.

Release	Date	Assets
v2.4.0	on Jun 16, 2015	71392a2 zip tar.gz
v2.3.0	on Jul 24, 2013	9cfa70b zip tar.gz
v2.2.3	on Jan 14, 2013	3fe66b9 zip tar.gz
v2.2.2	on Dec 4, 2012	f7d86e0 zip tar.gz
v2.2.1	on Nov 19, 2012	e9977c5 zip tar.gz
v2.2.0	on Oct 18, 2012	bafc03f zip tar.gz
v2.1.1	on Mar 27, 2012	76bb08a zip tar.gz

Obtain code – get link (git)



The screenshot shows a GitHub repository page for 'pezmaster31'. At the top, it displays '402 commits', '2 branches', '14 releases', and '8 contributors'. Below this, there are buttons for 'New pull request', 'New file', 'Find file', and an HTTPS link 'https://github.com/pezma'. A file tree is visible with the following items:

File/Folder	Description
docs	Minor version bump - 2.4.0
src	one extra unicode string in the beginning of file
CMakeLists.txt	Minor version bump - 2.4.0
LICENSE	Mostly cleaned up help & usage messages. Added MIT license.
README	Minor cleanup

```
git clone --recursive https://...
```

For bitbucket or google code

```
hg clone https://bitbucket.org/...
```



Decompress code package

- `gtar zxvf bamtools-1.0.2.tar.gz`
- `bunzip2 file.bz2`
- `unzip 10201_clusterware_linux32.zip`
- `tar xvf pygobject-3.19.2.tar`



Read manual

- Document on site:
 - README
 - INSTALL
 - doc/
- Document at website



Dependencies

- Check manual to meet requirement of Dependencies/ prerequisites



Compile and install

- `./configure`
- `make clean`
- `make`
- `make install`



Compile and install advanced

- `./configure -help`

```
./configure
```

```
--prefix=/home/rccstaff/yhuang/apps/hmmer-3.1b2
```

```
>&1| tee yh.config.log
```

- `make 2>&1 | tee yh.make.log`

- `make install 2>&1 | tee yh.install.log`



Validating Installation

- Run test
- Run help

```
/home/rccstaff/yhuang/apps/hmmer-3.1b2/bin/hmmbuild -h
```



Perl and modules

- Perl version (v5.14.1)
- Test if perl lib *File::Basename* is installed

```
perl -MFile::Basename -e 'print "Hello World\n"'
```

- Add custom perl lib to PERL5LIB path:

```
PERL5LIB=${PERL5LIB}:/usr/local/vcftools/  
latest/lib/perl5/site_perl
```



Install Perl Apps

- Script language, no need to compile



Python and Libraries

- Version

- `python2.7`

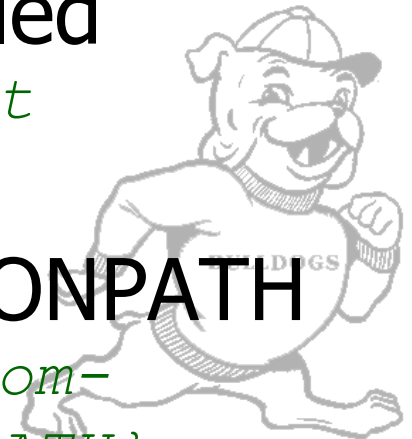
- `python (python2.4)`

- Test if python lib biom is installed

```
python2.7 -c 'import biom; print  
biom.__file__'
```

- Add custom python lib to PYTHONPATH

```
export PYTHONPATH=/usr/local/biom-  
format/1.1.2/lib/biom:${PYTHONPATH}
```



Install Python Apps

- `python2.7 setup.py build >&1 | tee yh.build.log`
- `python2.7 setup.py install --prefix=/home/rccstaff/yhuang/apps/cutadapt-1.9.1 >&1 | tee yh.install.log`
- **Validating**
`python2.7 /home/rccstaff/yhuang/apps/cutadapt-1.9.1/bin/cutadapt --help`



R and packages

- Default Version *3.0.3*
- Test if package "phangorn" is installed
require("phangorn")



Install R Package

- add package "phangorn" to user own lib
*install.packages("phangorn",
repos="http://cran.r-project.org")*



java

- Default Version 1.7.0_01

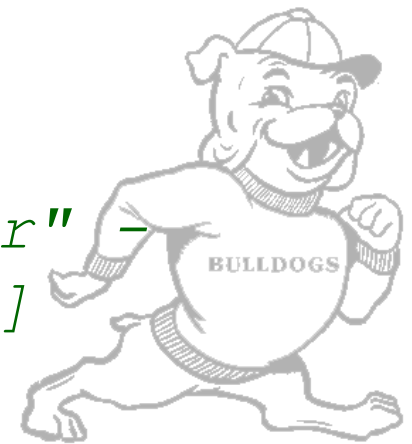
```
java -version
```

- To use v1.8

```
/usr/local/java/jdk1.8.0_05/bin/java -  
version
```

- To add classpath

```
java -classpath  
"/usr/local/bmge/latest/BMGE.jar" -  
Xms512m -Xmx1536m BMGE [options]
```



Support

- Submit ticket at [GACRC support](#) with detail of your command, dir of sample data, error message
- Submit requests with link of website, name and version of software

