

# Codefest 2012

Brad Chapman

Bioinformatics Open Source Conference, 13 July 2012

- 2 day coding session before BOSC
- 3rd year
- Everyone is welcome

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## Codefest 2012

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OpenBio Codefest 2012 will take place July 11th and 12th, 2012 (the two days before [BOSC 2012](#)) in Los Angeles, California at [Loyola Marymount University](#). This is a great opportunity for open source bioinformatics developers to meet and work collaboratively. We hope to have developers from projects such as [BioPerl](#), [BioJava](#), [Biopython](#), [BioRuby](#), [Galaxy](#) and [EMBOSS](#) in attendance.







[http://open-bio.org/wiki/Codefest\\_2012](http://open-bio.org/wiki/Codefest_2012)

# Bio-Linux packages

- Galaxy packaging
- Moving towards intelligent configuration with available tools + wrappers during install on Bio-Linux
- Packaged Shrimp aligner + Trinity + additional lab software
- Tim Booth, Torsten Seemann, Soon Gweon

https:

[//launchpad.net/~nebc/+archive/galaxy/+packages](https://launchpad.net/~nebc/+archive/galaxy/+packages)

▶  galaxy - 1.bl.20120509-lucid1	(changes file) tbooth	13 hours ago	Published	Lucid	Science	✓
▶  gnx-tools - 0.1+20120305-1	(changes file) soonio	2012-03-23	Published	Lucid	Science	✓
▶  hyphy - 2.1+20111219-6	(changes file) soonio	2012-03-08	Published	Lucid	Science	✓
▶  lastz - 1.02.00-2	(changes file) tbooth	2011-12-20	Published	Lucid	Science	✓
▶  leaps - 2.9-1ubuntu1	(changes file) soonio	2012-02-03	Published	Lucid	Gnu-r	✓
▶  macs - 2.0.9.1-1ubuntu3	(changes file) tbooth	2012-01-05	Published	Lucid	Science	✓

- Easier entry page: pulls existing clusters and pre-fills
- Generalize S3 buckets: 1000 genomes + loads of data
- Eucalyptus
- SQLite deployment for local installations
- Ntino Krampis, Enis Afgan, Dannon Baker

## **BioCloudCentral**

Easily launch [CloudMan](#), [CloudBioLinux](#) and [Galaxy](#) platforms on Cloud Computing resources (including [Amazon Web Services](#)).

<http://biocloudcentral.org>

# 1000 genomes documentation

- Work with 1000 genomes data on public resources
- Full workflow: BioCloudCentral, CloudBioLinux, CloudMan, Galaxy, IGV
- Example of complex workflow that requires full reproducibility
- Long <http://j.mp/PR08wp> and short <http://j.mp/LkZxD1> versions
- Dawei Lin, Michael Heuer, Bertrand Néron, Aaron Pilgrim

# CloudBioLinux packages

- Versions and details for all installed software
- Reproducibility: provide fully reproducible history of versioned software, integrated with GitHub code
- Accessibility: make packages available on nice web page like <http://www.biogems.info/>
- Debian packages, Python libraries, R libraries, custom installed packages
- Hervé Ménager, Brad Chapman