

# Open Source Configuration of Bioinformatics Infrastructure

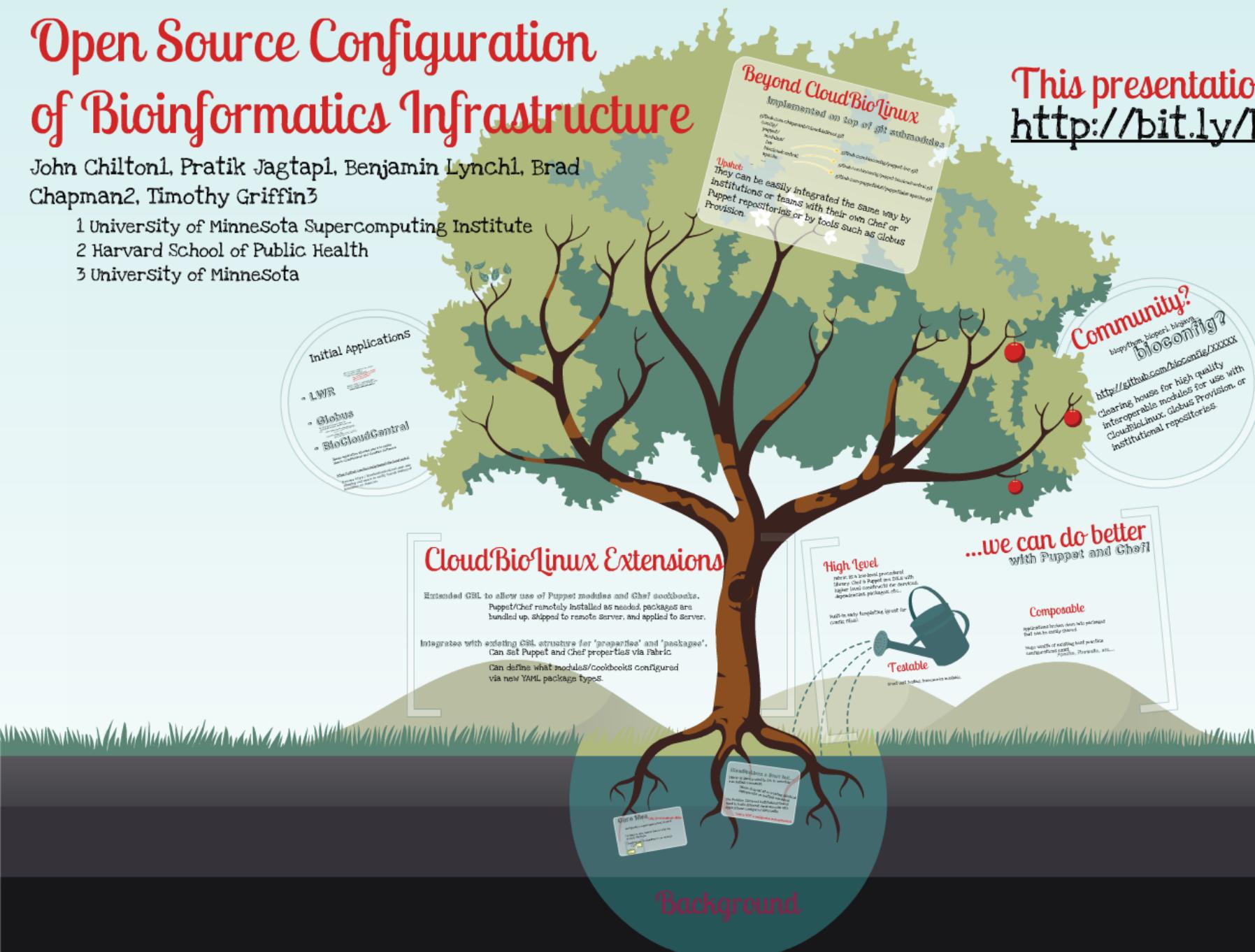
John Chilton<sup>1</sup>, Pratik Jagtap<sup>1</sup>, Benjamin Lynch<sup>1</sup>, Brad Chapman<sup>2</sup>, Timothy Griffin<sup>3</sup>

<sup>1</sup> University of Minnesota Supercomputing Institute

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This presentation:  
<http://bit.ly/bosc2013>



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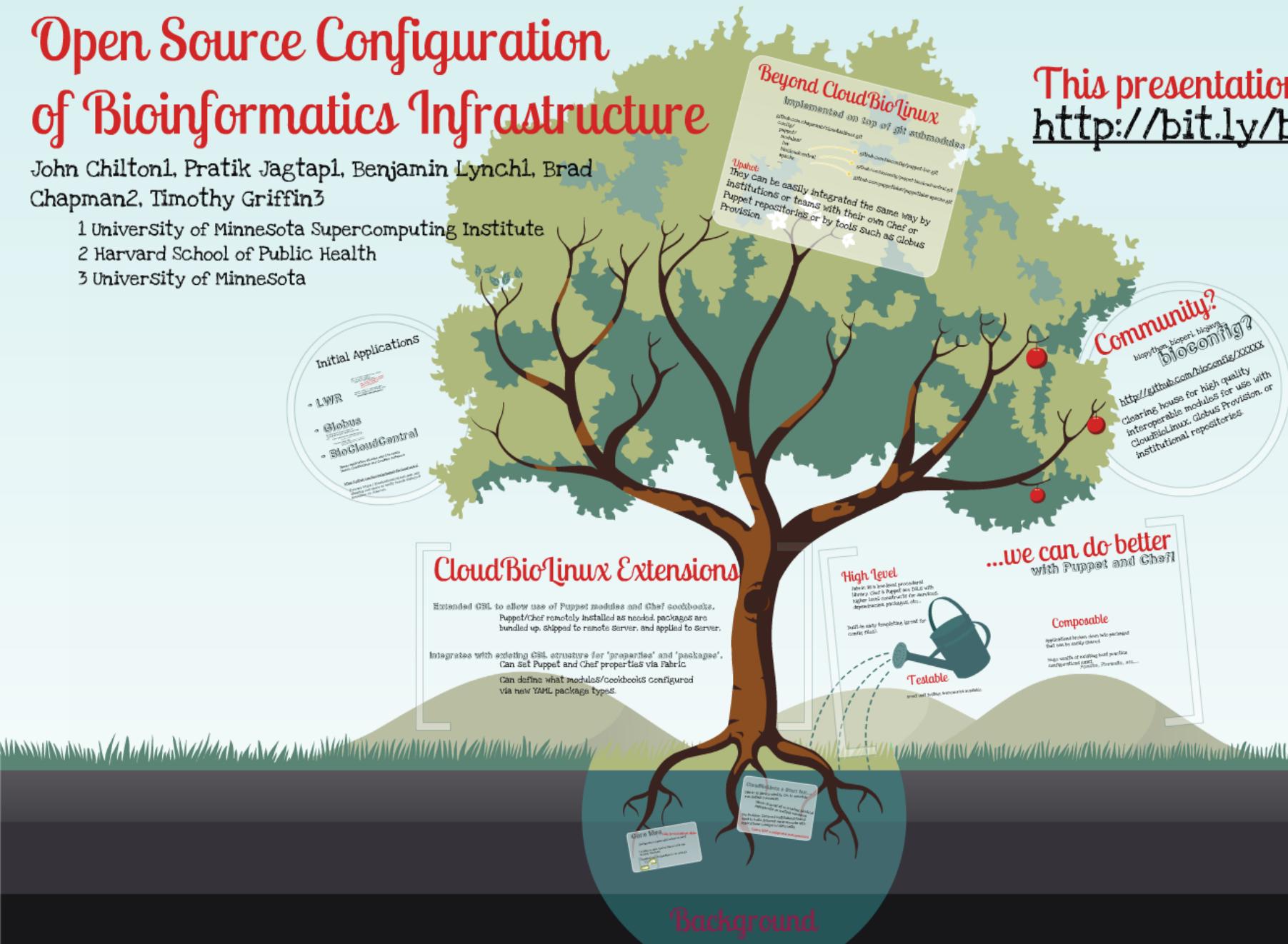
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# Background

## Core Idea

[bit.ly/prodcloudman-slides](http://bit.ly/prodcloudman-slides)

Configuring complex applications is hard!  
Building on open Source frameworks can  
Simplify this task.

CloudBioLinux (& CloudMan) is an example.



## CloudBioLinux a Start but...

Fabric is library used by CBL to remotely run install commands.

Fabric is great at recreating identical deployments on multiple machines.

The Problem: Different institutions/teams want to build different environments with applications configured differently.

Fabric is NOT a configuration management tool.

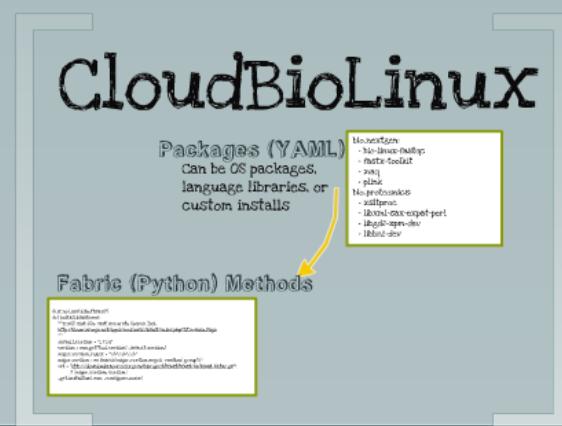
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# CloudBioLinux

## Packages (YAML)

Can be OS packages,  
language libraries, or  
custom installs

```
bio_nextgen:  
- bio-linux-fastqc  
- fastx-toolkit  
- maq  
- plink  
bio_proteomics:  
- xsltproc  
- libxml-Sax-expat-perl  
- libgd2-xpm-dev  
- libbz2-dev
```

## Fabric (Python) Methods

```
@.if.not.installed("bfast")  
def installbfast(env):  
    """BFAST: Blat-like Fast Accurate Search Tool.  
    http://Sourceforge.net/apps/mediawiki/bfast/index.php?title=Main_Page  
    """  
    default.version = "0.7.0a"  
    version = env.get("tool.version", default.version)  
    major.version.regex = "\d+\.\d+\.\d+."  
    major.version = re.search(major.version.regex, version).group(0)  
    url = "http://downloads.sourceforge.net/project/bfast/bfast/%s/bfast-%s.targz"\br/>        % (major.version, version)  
    .get.install(url, env, .configure.make)
```

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        % (major_version, version)
    _get_install(url, env, _configure_make)
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# CloudBioLinux a Start but...

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Fabric is great at recreating identical deployments on multiple machines.

The Problem: Different institutions/teams want to build different environments with applications configured differently.

Fabric is NOT a configuration management tool.

## High Level

Fabric is a low-level procedural library. Chef & Puppet are DSLs with higher level constructs for services, dependencies, packages, etc...

Built-in easy templating (great for config files).



## Testable

Great unit testing frameworks available.

# ...we can do better with Puppet and Chef!

## Composable

Applications broken down into packages that can be easily shared.

Huge wealth of existing best practice configurations exist.  
Apache, Firewalls, etc...

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# CloudBioLinux Extensions

Extended CBL to allow use of Puppet modules and Chef cookbooks.

Puppet/Chef remotely installed as needed, packages are bundled up, Shipped to remote Server, and applied to Server,

Integrates with existing CBL structure for 'properties' and 'packages'.

Can Set Puppet and Chef properties via Fabric

Can define what modules/cookbooks configured via new YAML package types.



# Initial Applications

- **LWR**

LWR is a tool to stage and run Galaxy jobs on remote servers.

<https://lwr.readthedocs.org/>

Here to get this tightly integrated into CloudMan instances by default, potentially a path forward for cloud bursting Galaxy instances.

Puppet module for configuring LWR has been integrated into CloudBioLinux.

<https://github.com/bioconfig/puppet-lwr>

- **Globus**

The Globus Toolkit provides utilities for federated data transfer, identity management, etc...

<https://github.com/bioconfig/chef-globus>

Part of the Globus Toolkit chef recipes.

<http://bitly/cbl-gridfs>

Instructions for doing stuff like transferring data into CBL instances created with Globus.

- **BioCloudCentral**

Django application allowing users to easily launch CloudBioLinux and CloudMan instances

<https://github.com/bioconfig/puppet-biocloudcentral>

Powers <https://biocloudcentral.msi.umn.edu> allowing end users to easily launch Galaxy-P instances on Amazon.



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# Globus

The Globus Toolkit provides utilities for federated data transfer, identity management, etc...

<https://github.com/bioConfig/chef-globus>  
Fork of the Globus Provision Chef recipes.

<http://bit.ly/cbl-gridftp>  
Instructions for using GridFTP to transfer data into CBL instance created with Globus.

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# Beyond CloudBioLinux

Implemented on top of git submodules

github.com:chapmanb/cloudbiolinux.git  
config/  
puppet/  
modules/  
lwr  
biocloudcentral  
apache  
....

github.com:bioconfig/puppet-lwr.git  
github.com:bioconfig/puppet-biocloudcentral.git  
github.com:puppetlabs/puppetlabs-apache.git

## Upshot:

They can be easily integrated the same way by institutions or teams with their own Chef or Puppet repositories or by tools such as Globus Provision.

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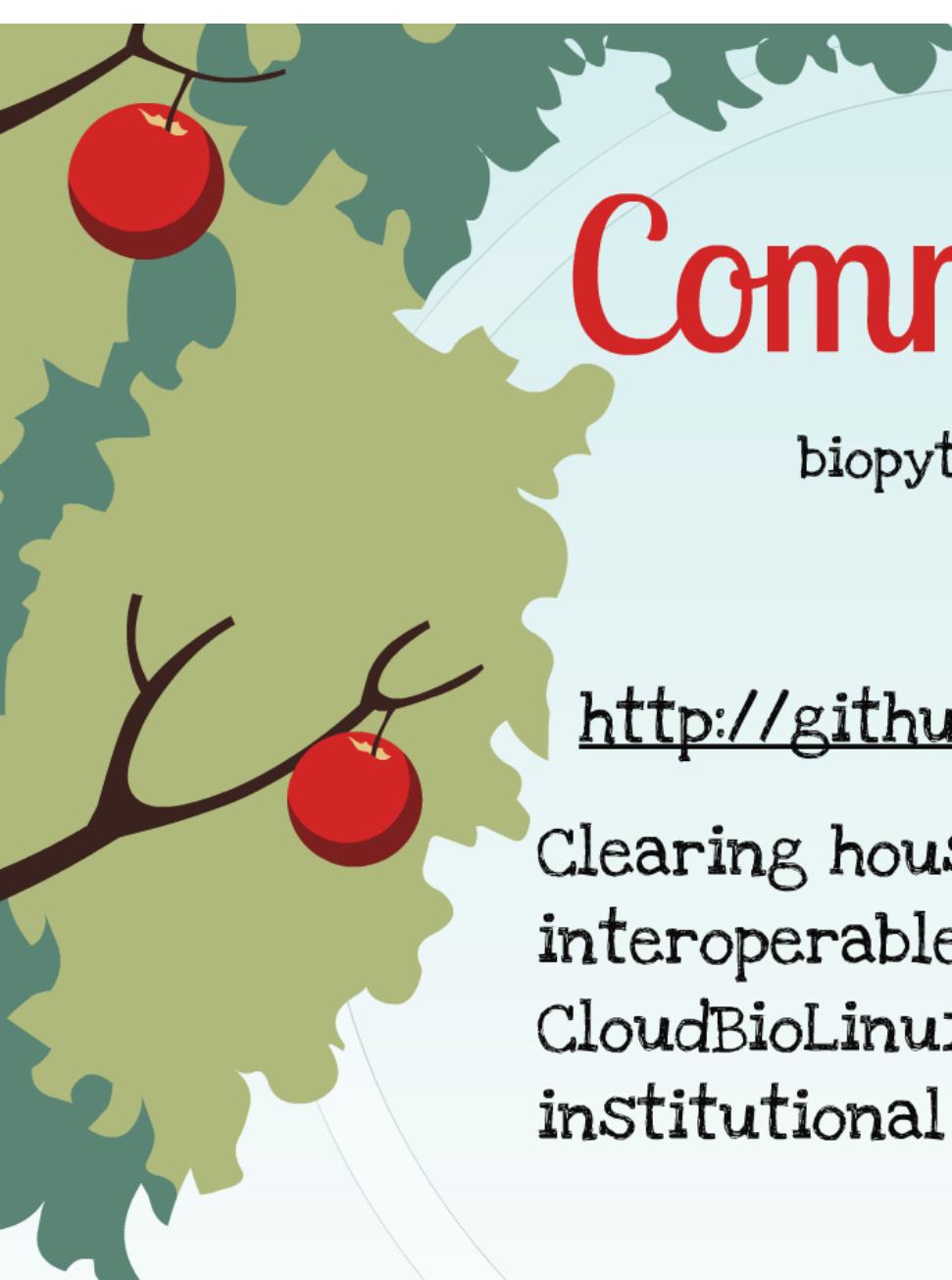
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# Community?

biopython, bioperl, biojava...

**bioconfig?**

<http://github.com/bioConfig/XXXXX>

Clearing house for high quality  
interoperable modules for use with  
CloudBioLinux, Globus Provision, or  
institutional repositories.