

# Galaxy Project Update:

## New Release Process

### Data Managers

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# The Galaxy Team

<http://wiki.galaxyproject.org/GalaxyTeam>

# Overview

## **New Release Process**

- ✦ Why?
- ✦ When?
- ✦ How?

## **Data Managers**

- ✦ What?
- ✦ Demo

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# New Release Process Goals

- Bug fixes can be rapidly applied directly to *stable* branch
- Higher quality of Tagged releases
- New features can be developed collaboratively over longer periods of time
- Longer testing period for upcoming *stable*

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- ✦ Why?
- ✦ **When?**
- ✦ How?

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- ✦ What?
- ✦ Demo

# When?

- New policy is in effect now
- New *stable* releases will occur approximately every 2 months

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# Changes required for updating

- <http://GetGalaxy.org>
- [http://wiki.galaxyproject.org/DevNewsBriefs/2013\\_02\\_08](http://wiki.galaxyproject.org/DevNewsBriefs/2013_02_08)

We have made some improvements to our `release` process, and because of this, you **must** include the new distribution `release` tag in your `hg update` command to upgrade to this distribution `release`:

```
% hg pull
% hg update release_2013.02.08
```

If you do not include the `release_2013.02.08` tag, your repository will update to the default branch, which includes unstable code. After updating, you can verify that you are on the stable branch with:

```
% hg branch
stable
```

Once you're on the stable branch, `hg pull -u` without a specific revision or branch will cause you to remain on the stable branch.

# Branches

- **default**
  - all new development (features) occurs here
  - always exists
- **stable**
  - Runs on main
  - always exists
  - Updated ~ every 2 months with new features from *default* (via *next-stable*)
  - Bug fixes can be applied directly
- **next-stable**
  - Runs on main, when exists
  - created ~2 weeks before *stable* is updated from *default*, disappears after *stable* is updated
  - Once created, only bug fixes can be applied (no new features)

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# Data Managers

- Allows for the **creation of built-in** (pre-cached) data
  - data tables
  - \*.loc files
- Specialized Galaxy tools that can only be accessed by an admin
- Defined **locally** or installed from **Tool Shed**
- Examples:
  - Fetching Genome (fasta) sequences
  - Building short read mapper indexes for genomes

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# Data Manager Demo

- Fetch the Genome Sequence for sacCer2
  - UCSC as the source
  - uses a locally defined Data Manager
  - all\_fasta table is populated automatically
- Build BWA indexes for sacCer2
  - Install indexing tool from Tool Shed
  - Build indexes
  - bwa\_index table is populated automatically

<http://localhost:8080>





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