Galaxy Project Update:
New Release Process
Data Managers

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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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- 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://GetGalaxy.org)

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
The Galaxy Team

http://wiki.galaxyproject.org/GalaxyTeam