

Why we develop and deploy using Guix and why you should too—an experience report from GeneNetwork

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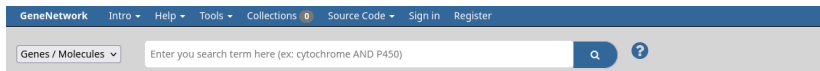
Documentation

Online manuals, handbooks, fact sheets and FAQs



News

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- one of the oldest (since 1994) bioinformatics platforms on the web
- developed at the University of Tennessee Health Science Center
- small team of around 10 programmers
- largely a Python code base (43k lines) with a bit of Rust and increasingly Guile scattered over several git repositories
- lots of legacy code (from very old Python 2) that needs migration and maintenance
- no cloud machines; we host everything on our own machines

We use Guix

for everything!

- for packages
- for development environments
- for continuous integration
- for continuous deployment of a test development instance
- for production deployment (WIP)
- for HPC clusters

How do we use Guix?

Packages

- bioinformatics requires many domain specific packages
- we maintain our packages in our own `guix-bioinformatics` channel
- we contribute upstream when more widely useful
- gives us a lot of freedom to quickly add or fix packages
- gives us the flexibility to do nasty hacks like disabling tests

How do we use Guix?

Development environments

- `guix shell` with `manifest.scm` and `guix.scm` for developer environments
- all team members have the exact same development environment
- team can use `guix describe` to communicate the exact environment
- team can reproduce bugs easily
- we pin a specific commit of Guix upstream to ease keeping up

How do we use Guix?

Pin a specific commit of Guix upstream

- pin a specific commit of Guix upstream in `.guix-channel` of the `guix-bioinformatics` channel
- prevents upstream changes from breaking our code without warning

```
(channel
 (dependencies
  (channel
   (name guix)
   (url "https://git.savannah.gnu.org/git/guix.git")
   (commit "330b94e8bd88baf903d2bc11bf96e23b119e0fe5")
   ...))
 ...))
```

guix system containers

What are they?

```
(operating-system
  (host-name "genenetwork-development")
  (timezone "UTC")
  (locale "en_US.utf8")
  (services
    (cons*
      (service laminar-service-type
        (laminar-configuration
          (title "GeneNetwork_CI")
          (bind-http "localhost:9089")))
      (service cgit-service-type
        (cgit-configuration
          (server-name "git.genenetwork.org")
          (repository-directory "/home/git/public")))
      ...)))
```


How do we use Guix?

guix system containers

- our servers run Debian with Guix as a foreign package manager
- this is hardly an impediment—we can still run `guix system containers`

```
$ guix system container -N ...  
/gnu/store/...-container  
# ln -sf /gnu/store/...-container  
/usr/local/bin/my-guix-container  
# ln -sf /usr/local/bin/my-guix-container  
/var/guix/gcroots  
# systemctl start my-guix-container.service  
# systemctl enable my-guix-container.service
```

How do we use Guix?

guix system containers

```
my-guix-container.service
```

```
[Unit]
```

```
Description = Run my guix container
```

```
[Service]
```

```
ExecStart = /usr/local/bin/my-guix-container
```

```
[Install]
```

```
WantedBy = multi-user.target
```

How do we use Guix?

guix system containers

<https://git.genenetwork.org/gn-machines/>

git index : gn-machines

Guix configuration for genenetwork machines

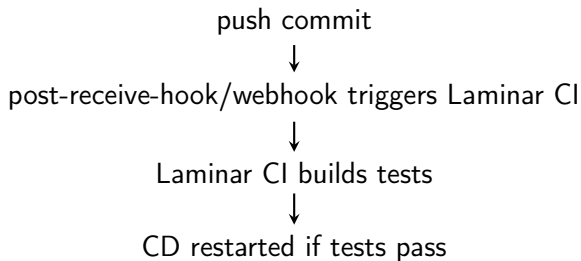
about summary refs log **tree** commit diff

path: root/genenetwork-development.scm

```
1075 (operating-system
1076   (host-name "qenenetwork-development")
1077   (timezone "UTC")
1078   (locale "en_US.utf8")
1079   (bootloader (bootloader-configuration
1080     (bootloader grub-bootloader)
1081     (targets (list "/dev/sdX"))))
1082   (file-systems %base-file-systems)
1083   (users %base-user-accounts)
1084   (packages %base-packages)
1085   (sudoers-file
1086     (mixed-text-file "sudoers"
1087       "@include " %sudoers-specification
1088       ;; Permit the laminar user to restart genenetwork2
1089       ;; and qenenetwork3.
1090       "\nlaminar ALL = NOPASSWD: "
1091       (file-append shepherd "/bin/herd") " restart qenenetwork2, "
1092       (file-append shepherd "/bin/herd") " start qenenetwork3, "
1093       (file-append shepherd "/bin/herd") " stop qenenetwork3, "
1094       (file-append shepherd "/bin/herd") " restart qenenetwork3, "
1095       (file-append shepherd "/bin/herd") " start qn-auth, "
1096       (file-append shepherd "/bin/herd") " stop qn-auth, "
1097       (file-append shepherd "/bin/herd") " restart qn-auth\n"
1098       ;; Permit the acme user to restart nginx.
```

How do we use Guix?

guix system containers

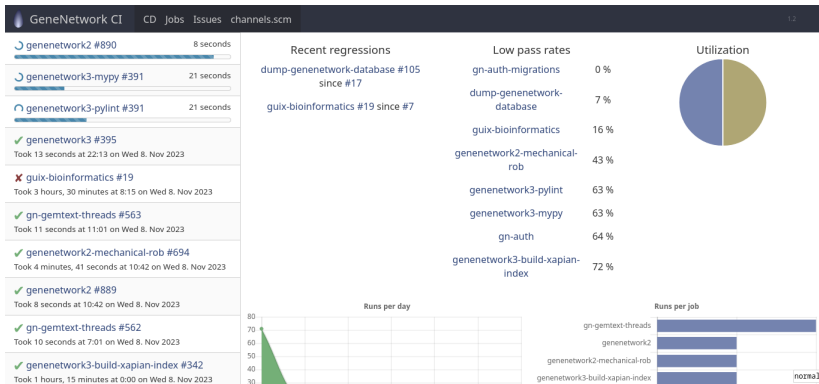


- Our git repos themselves are single-package Guix channels ¹
- CI just pulls the channel and builds the package
- This is trivial to replicate even outside the CI on a developer machine

¹<https://guix.gnu.org/blog/2023/>

How do we use Guix?

Continuous integration



How do we use Guix?

Continuous deployment

GeneNetwork CI CD Jobs Issues channels.scm

✓ genenetwork3 #395



Reason Webhook
Queued for 0 seconds
Started 22:13 on Wed 8. Nov 2023
Completed 22:13 on Wed 8. Nov 2023
Duration 13 seconds

```
[laminar] Executing cfg/jobs/genenetwork3.run
Building /gnu/store/qmm7nmi487gwz00c6kwlv3c8rjwj6k84-genenetwork3

1 successes, 0 failures
=====
[laminar] Executing cfg/jobs/genenetwork3.after
Service genenetwork3 has been started.
Service genenetwork2 has been started.
genenetwork2:#890
```

How do we use Guix?

Production deployment

- Public SPARQL endpoint using a virtuoso Guix service at <https://sparql.genenetwork.org/sparql>
- We deploy legacy `genenetwork1` in a Guix container using packages from the `guix-past` channel
- Complete Guix service for all of GeneNetwork is work in progress
- Guix on our HPC cluster—improves reproducibility and helps users install packages easily

How do we use Guix?

SPARQL

Virtuoso SPARQL instance at
<https://sparql.genenetwork.org/sparql>

The screenshot shows the Virtuoso SPARQL Query Editor interface. At the top, there is a navigation bar with "SPARQL Query Editor", "About", and "Tables" (with a dropdown arrow). On the right side of the navigation bar is a "Permalink" link. Below the navigation bar, there are "Extensions" (cxml, save to dav, sponge) and "User: SPARQL". The main area contains a "Default Data Set Name (Graph IRI)" input field, which is currently empty. Below that is a "Query Text" area with a text area containing the query: `SELECT * WHERE {?s ?p ?o}`. At the bottom, there is a "Results Format" dropdown menu set to "HTML". Below the dropdown are two buttons: "Execute Query" (in blue) and "Reset". At the very bottom, there is an "Execution timeout" input field set to "0" milliseconds, with a unit selector set to "milliseconds".

How do we use Guix?

Documentation

Ad-hoc documentation at <https://issues.genenetwork.org>

► Hint

[113 All](#) [35 open issues](#) [26 closed issues](#) [52 documents](#) [0 commits](#)

Guix system containers and how we use them

DOCUMENT created on Mar 31 2023 by Arun Isaac, last updated 6 weeks ago by Pjotr Prins

...use **Guix system containers**. Note that **Guix system containers** are different from **guix shell containers** (and the older **guix environment containers**). **guix shell containers** are meant for interactive use...

CI/ CD for genetwork projects

DOCUMENT created on Oct 12 2022 by Munyoki Kilyungi, last updated on Jul 13 2023 by Pjotr Prins

Normally, **Guix VMs** and **containers** created by ``guix system`` can only access the store read-only. Since **containers** don't have write access to the store, you cannot ``guix build`` from within a **container**...

Running postgres in a Guix container

DOCUMENT created on Jan 17 2023 by Pjotr Prins

...**container** in the background you may want to use `screen` and/or `tmux`.

To have the postgres client outside the **container** install it with

...

```
~/opt/guix-pull/etc/profile  
guix package -i postgresql@14.4...
```

Next Steps

DOCUMENT created on Sep 09 2021 by jgart, last updated on Mar 14 2022 by Frederick Muriuki Muriithi

How do we use Guix?

Links

- <https://issues.genenetwork.org>
- <https://guix-forge.systemreboot.net>
- <https://git.genenetwork.org/guix-bioinformatics>
- <https://git.genenetwork.org/gn-machines>

