

build guix from source [pjotr_notes] ()

To overcome errors with gcrypt

- export GUILE_LOAD_PATH=/home/bonfacem/.guix-profile/share/guile/site/3.0/
- export GUILE_LOAD_COMPILED_PATH=/home/bonfacem/.guix-profile/lib/guile/3.0/site-ccache

guix environment -C guix --ad-hoc bash gcc-toolchain guile-gcrypt guile

Inside the environment

- rm -rf autom4te.cache/ && make clean
- ./bootstrap
- ./configure --localstatedir=/var --sysconfdir=/etc
- make clean && make clean-go
- time make -j 8

Get outside the environment

exit

See what you get after a --dry-run

env GUIX_PACKAGE_PATH=../guix-bioinformatics/ GENENETWORK_FILES=/home/bonface/gnu/data/gn2_data ./pre-inst-env guix package -p ~/opt/genenetwork2 --substitute-urls="http://guix.genenetwork.org https://berlin.guixsd.org https://ci.guix.gnu.org https://mirror.hydra.gnu.org" -i genenetwork2 --dry-run

STEP 1 : DATABASE SETUP - you need to have redis setup - mariadb setup - use test db for this

```
- export the db_webqtl db

- mysql -u username -p database_name < /path/to/file.sql
```

- building gn2

step: clone the guix-bioinformatics repo(contains the guix packages for gn2) clone the guix_past repo

- create maybe ~/opt for your profile then run

See what you get after a --dry-run

- genetwork files setup

mkdir /data/genotype_files/genotype

- copy the bxd geno file cp bxd.Geno /^

```
env GUIX_PACKAGE_PATH="/home/kabui/guix-bioinformatics:/home/kabui/guix-past/modules" GENENETWORK_FILES=/home/kabui/data/genotype_files
./pre-inst-env guix package -p ~/opt/genenetwork2 --substitute-urls="http://guix.genenetwork.org https://berlin.guixsd.org https://ci.guix.gnu.org
https://mirror.hydra.gnu.org" -i genenetwork2 --fallback --dry-run
```

/edits to gn2

/default_settings

modify

SQL_URI = "mysql://gn2:mysql_password@localhost/db_webqtl_s"

SQL_URI = "mysql://kabui:1234@localhost/db_webqtl"

also modify env TMPDIR=~/.tmp WEBSERVER_MODE=DEBUG LOG_LEVEL=DEBUG GENENETWORK_FILES=/export/data/genenetwork/genotype_files/
SQL_URI=mysql://webqtlout.webqtlout@localhost/db_webqtl ./bin/genenetwork2 etc/default_settings.py -gunicorn-dev

to run the unittest

```
env GN2_PROFILE=/home/kabui/opt/python3-genenetwork2 TMPDIR=/home/kabui/tmp SERVER_PORT=5004 WEBSERVER_MODE=DEBUG LOG_LEVEL=DEBUG
GENENETWORK_FILES=/home/kabui/data/genotype_files /home/kabui/project3/genenetwork2/bin/genenetwork2
/home/kabui/project3/genenetwork2/etc/default_settings.py -c -m unittest discover -v
```

to run gn server

```
env GN2_PROFILE=$HOME /opt/python3-genenetwork2 TMPDIR=$HOME/tmp SERVER_PORT=5004 WEBSERVER_MODE=DEBUG LOG_LEVEL=DEBUG
GENENETWORK_FILES=$HOME/data/genotype_files $HOME/project3/genenetwork2/bin/genenetwork2 $HOME/project3/genenetwork2/etc/default_settings.py
```