



compute | calcul  
canada | canada



# Installing software using EasyBuild in your cluster home

Ata Roudgar  
Simon Fraser University  
Compute Canada

## Why do we need to install a software in home?

1. Users who run a software that has some config files and need to be customized
2. Users who needs to upgrade a software
3. Users who need to modify the source code

## Types of installation, globally vs. locally

- Globally
  - software is installed on a path where anyone have access to, e.g., CVMFS (/cvmfs directory)
  - by admins
  - users cannot modify or delete it
  - Installed only once for all users
- In user's home
  - Installed in user's home directory (easybuild -> \$HOME/.local/easybuild directory)
  - by user or admin
  - User can modify or delete files
  - By default, it is accessible only by the user

## Traditional method of installing

- Download the source file
- If software comes with configure file, run `./configure` with proper arguments.
- Use commands like "make" and "make install"
- Most of the time it is a complicated process
- Not always reproducible particularly when compiler or dependencies change version.
- Requires a good knowledge about options that are used to compile the software

**Easybuild a software build framework**

# Easybuild

## Easybuild a software build and installation framework

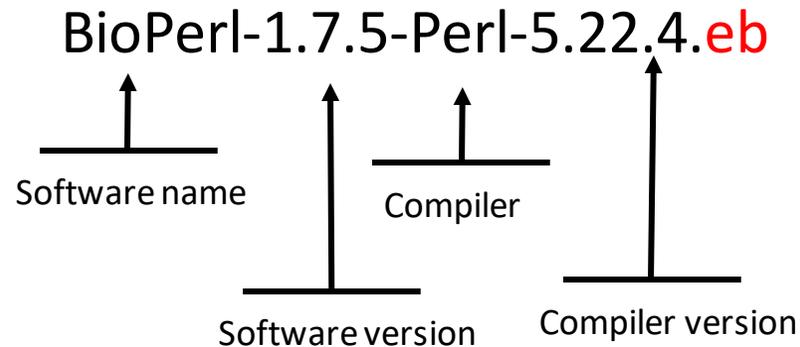
- It is written in Python
- allows for easily reproducing previous builds
- keep the software build recipes simple and human-readable
- **enables sharing with the HPC community**
- supports co-existence of versions/builds via dedicated installation prefix and module files
- retain logs for traceability of the build processes
- It still complicated but complication part is done by admin when install for the first time.

# Easybuild

## Easybuild recipe (easyconfig)

- Easybuild recipe is a text file (in python syntax) to instruct easybuild how to install a software
- Creating a recipe from scratch could be very challenging
- Compute Canada collected huge number of recipes at <https://github.com/ComputeCanada/easybuild-easyconfigs/tree/computecanada-main/easybuild/easyconfigs>
- Upon successful installation a copy of the recipe is copied at <installdir>/easybuild.
- Standard easybuild recipe filename format:

**<software name>-<version>-<compiler>-<compiler version>.eb**



# Easybuild recipe

## Basic concept of easybuild recipe parameters

**name**: The name of the software. `%(name)s` to call its value

**Version**: The version of the software. `%(version)s` to call its value

**Homepage**: The homepage of the software

**Description**: A short description about the software. This description is the same as the one at [https://docs.computecanada.ca/wiki/Available\\_software](https://docs.computecanada.ca/wiki/Available_software)

**source\_urls**: The website where easybuild loo for to download the source file

**Source**: The name of the source file (in zip or tar.gz format)

**Builddependencies**: software dependencies at installation time

**sanity\_check\_paths**: check to see if such executable files exist after installation. Paths are given with respect to the install directory

**moduleclass**: bio, math, chem, phys, geo, vis

```
easyblock = 'ConfigureMake'

name = 'BLAST+'
version = '2.4.0'

homepage = 'http://blast.ncbi.nlm.nih.gov/'
description = """Basic Local Alignment Search Tool, or BLAST, is an
algorithm for comparing primary biological sequence information, such as
the amino-acid sequences of different proteins or the nucleotides of DNA
sequences."""

toolchain = {'name': 'GCC', 'version': '7.3.0'}

source_urls =
['http://ftp.ncbi.nlm.nih.gov/blast/executables/blast+%(version)s/']
sources = ['ncbi-blast-%(version)s+-src.tar.gz']
patches = ['%(name)s-%(version)s_boost_backport.patch']

builddependencies = [
('Boost', '1.54.0'),
('Python', '2.7.14')
]

configopts = " --with-64 --with-bin-release --without-debug --with-mt"
sanity_check_paths = {
    'files': ['bin/blastn', 'bin/blastp', 'bin/blastx'],
    'dirs': []
}

moduleclass = 'bio'
```

# Easybuild

## Process of installation

- Command to run easybuild:

```
$ eb [path]/<recipe> [options]
```

- Download the source file
- Compare checksum to check if downloaded files altered or corrupted
- Apply patch files
- Build (compile)
- Copy the executables to installation path, `%(installdir)s`
- Check to see if expected executable file exist
- Make module
- End

## Useful Template names/values

<code>%(name)s</code>	Name of the software
<code>%(namelower)s</code>	lower case of name
<code>%(version)s</code>	Version of the software
<code>%(version_major)s</code>	major version
<code>%(version_minor)s</code>	minor version
<code>%(builddir)s</code>	Build directory
<code>%(installdir)s</code>	Installation directory

Example: `name='FastANI'`  
`Version='3.2.1'`

```
%(namelower)s : 'fastani'  
%(version_major)s : '3.2'
```

## Module command

- to load a software
  - Add "%(installdir)s/bin" where executable files are located to default searching path (PATH)
  - Add "%(installdir)s/lib" to LIBRARY\_PATH variable
  - And some other variables....
- Upon a successful module command the following environmental variable is also setup:

**EBROOT**<name of the software in capital>

And it will contain the path to install dir.

## Example:

```
$ module load gcc/9.3.0 openmpi/4.0.3 gromacs/2021.4
$ echo $EBROOTGROMACS
$/cvmfs/soft.computecanada.ca/easybuild/software/2020/avx2/MPI/gcc9/openmpi4/gromacs/2021.4
```

In this example we loaded gromacs-2021.4 that is installed globally using module command

# Exercises

1. Reinstalling a software in user's home
2. Upgrading a software in user's home
3. Modifying a software in user's home

## 1. Reinstalling a software

- The software is already installed globally in /cvmfs
- Install the software on \$HOME/.local/easybuild/as well
- We need a copy of software recipe and patch files to run easybuild

# reinstalling software orthomcl

- **Load the software, orthomcl**

```
$ module spider orthomcl
# the output shows that orthomcl-2.0.9 is the latest
$ module spider orthomcl/2.0.9
# orthomcl/2.0.9 has no dependency modules
$ module load orthomcl/2.0.9
```

- **Find install directory**

```
$ echo $EBROOTORTHOMCL
/cvmfs/soft.computecanada.ca/easybuild/software/2020/Core/orthomcl/2.0.9
```

- **Locating easybuild recipe**

```
$ ls $EBROOTORTHOMCL/easybuild/*.eb
/cvmfs/soft.computecanada.ca/easybuild/software/2020/Core/orthomcl/2.0.9/easybuild/orthomcl-
2.0.9.eb
```

- **Creating a directory and copy the recipe and patch files**

```
$ mkdir -p ~/easybuild/reinstall
$ cp /cvmfs/soft.computecanada.ca/easybuild/software/2020/Core/orthomcl/2.0.9/easybuild/orthomcl-2.0.9.eb ~/easybuild/reinstall
$ cp /cvmfs/soft.computecanada.ca/easybuild/software/2020/Core/orthomcl/2.0.9/easybuild/*.patch ~/easybuild/reinstall
```

# reinstalling software orthomcl

- run easybuild to build and install the software

```
$ cd ~/easybuild/reinstall
$ eb -f ./orthomcl-2.0.9.eb
# option -f is used to force easybuild to install on home
== Temporary log file in case of crash /tmp/eb-dydsorh6/easybuild-cdf1oxk5.log
== Running parse hook for orthomcl-2.0.9.eb...
== Running parse hook for GCC-9.3.0.eb...
== Running parse hook for GCCcore-9.3.0.eb...
Changing postinstallcmds from: []
New postinstallcmds: ["find %(installdir)s -name '*.la' -delete"]
== Running parse hook for MCL-14.137-GCC-9.3.0.eb...
== Running parse hook for GCC-9.3.0.eb...
== processing EasyBuild easyconfig /home/aroudgar/easybuild-recipes/orthomcl-2.0.9.eb
== building and installing Core/orthomcl/2.0.9...
== fetching files...
== creating build dir, resetting environment...
== unpacking...
== patching...
== preparing...
== Running pre-prepare hook...
== Running post-prepare hook...
== ... (took 3 secs)
== configuring [skipped]
== building [skipped]
== testing...
== installing...
== taking care of extensions...
== restore after iterating...
== postprocessing...
== sanity checking...
== ... (took 7 secs)
== cleaning up...
== creating module...
== Running post-module hook...
== ... (took 7 secs)
== permissions...
== packaging...
== COMPLETED: Installation ended successfully (took 22 secs)
== Results of the build can be found in the log file(s) /home/aroudgar/.local/easybuild/software/2020/Core/orthomcl/2.0.9/easybuild/easybuild-orthomcl-2.0.9-20211117.155541.log
== Build succeeded for 1 out of 1
== Running end hook...
== Temporary log file(s) /tmp/eb-dydsorh6/easybuild-cdf1oxk5.log* have been removed.
== Temporary directory /tmp/eb-dydsorh6 has been removed.
```

# reinstalling software orthomcl

We now have two copies of orthomcl, one installed in home, and one installed in cvmfs

We run:

```
$ module unload orthomcl/2.0.9  
$ module load orthomcl/2.0.9
```

Which one is loaded?

```
$ echo $EBROOTORTHOMCL  
/home/aroudgar/.local/easybuild/software/2020/Core/orthomcl/2.0.9
```

home installed softwares have more priority to be loaded by module command

## 2. Upgrading a software, FastANI

- Recipe

FastANI-1.32-GCC-9.3.0.eb

```
name = 'FastANI'
version = '1.32'

source_urls = ['https://github.com/ParBLISS/FastANI/archive']
sources = ['v%(version)s.zip']
patches = ['FastANI-1.32-memcpy.patch']
checksums = [
    '06a3bd38840526eabf7a99d4f10b8f05edbf5b96bf4301e37afd89f4c1ff6d81', # v1.32.zip
    'eebcf0b64c31ee360ca79136f644157064ac69747ed13cff70f5c9932c6bb0d5', # FastANI-1.32-memcpy.patch
]
```

# Upgrading a software

## Checksum:

- Every file has a unique digital signature
- Command **sha256sum** is used to calculate the checksum of a file

```
$ sha256sum <file name>
```

- Download the source file. E.g., <https://github.com/ParBLiSS/FastANI/archive/v1.32.zip>

- Run the command

```
$ sha256sum v1.32.zip
```

```
06a3bd38840526eabf7a99d4f10b8f05edbf5b96bf4301e37afd89f4c1ff6d81 v1.32.zip
```

- Add the output of the command to your recipe
- Checksum in recipe contains the digital signature of source and patch files. The first one belong to the source code, the rest belongs to patch files

# Upgrading software, FastANI

- **Load the latest version of software "FastANI"**

```
$ mkdir ~/easybuild/upgrade
$ cd ~/easybuild/upgrade
$ module spider fastani
# the output shows that fastani/1.32 is the latest
$ module spider fastani/1.32
.
.
StdEnv/2020 gcc/9.3.0
StdEnv/2020 intel/2020.1.217
.
.

# FastANI compiled with two compiler, GCC and INTEL
$ module load gcc/9.3.0 fastani/1.32
```

# Upgrading software, FastANI

- **Find install directory**

```
$ echo $EBROOTFASTANI  
/cvmfs/soft.computecanada.ca/easybuild/software/2020/avx2/Compiler/gcc9/fastani/1.32
```

- **Locating easybuild recipe**

```
$ ls $EBROOTSPADES/easybuild/*.eb  
/cvmfs/soft.computecanada.ca/easybuild/software/2020/avx2/Compiler/gcc9/fastani/1.32/easybuild  
/FastANI-1.32-GCC-9.3.0.eb
```

- **Copy the recipe and patch files**

```
$ cp /cvmfs/soft.computecanada.ca/easybuild/software/2020/avx2/Compiler/gcc9/fastani/1.32/easybuild/*.eb ./  
$ cp /cvmfs/soft.computecanada.ca/easybuild/software/2020/avx2/Compiler/gcc9/fastani/1.32/easybuild/*.patch  
./
```

# Upgrading software, FastANI

- Inspect the recipe using "vi" and modify it. The current version of fastANI software is **1.33**

## I. Checksum

- Download the source code using **wget** command

```
$ wget https://github.com/ParBLiSS/FastANI/archive/v1.33.zip
```

- Calculate checksum

```
$ sha256sum v1.33.zip
```

```
fb392ffa3c7942091a06de05c56c8e250523723c39da65ae8f245e65e440a74b v1.33.zip
```

- Insert it in the recipe

```
checksums = [  
    'fb392ffa3c7942091a06de05c56c8e250523723c39da65ae8f245e65e440a74b', # v1.33.zip  
    'eebcf0b64c31ee360ca79136f644157064ac69747ed13cff70f5c9932c6bb0d5', # FastANI-1.32 memcpy.patch  
]
```

- version=1.32 -> version=1.33

- Save it under the name **FastANI-1.33-GCC-9.3.0.eb**

- run easybuild to build and install the software

```
$ eb -f ./FastANI-1.33-GCC-9.3.0.eb
```

### 3. Modifying and installing a software, FastANI

FastANI-1.32-GCC-9.3.0.eb

```
name = 'FastANI'
version = '1.32'

source_urls = ['https://github.com/ParBLiSS/FastANI/archive']
sources = ['v%(version)s.zip']
patches = ['FastANI-1.32-memcpy.patch']
checksums = [
    '06a3bd38840526eabf7a99d4f10b8f05edbf5b96bf4301e37afd89f4c1ff6d81', # v1.32.zip
    'eebcf0b64c31ee360ca79136f644157064ac69747ed13cff70f5c9932c6bb0d5', # FastANI-1.32-memcpy.patch
]
```

#### Patch file

- A patch file is a text file that consists of a list of differences
- Command `diff` is used to generate the list of differences with respect to original file name (1<sup>st</sup> argument)  
`$ diff -u <original file name> <recent file name>`
- Example of a patch file:  
`$ cat FastANI-1.32-memcpy.patch`

# Modifying and installing software, FastANI

```
--- Makefile.in.orig      2019-07-25 18:01:28.000000000 +0200
+++ Makefile.in           2019-10-17 15:49:27.034833116 +0200
@@ -6,7 +6,7 @@
ifeq ($(UNAME_S), Darwin) #macOS clang
    CXXFLAGS += -mmacosx-version-min=10.7 -stdlib=libc++ -Xpreprocessor -fopenmp -lomp
else
-    CXXFLAGS += -include src/common/memcpyLink.h -Wl,--wrap=memcpy
+    CXXFLAGS += -include src/common/memcpyLink.h
    CFLAGS += -include src/common/memcpyLink.h
endif
```

# Modifying and installing a software, FastANI

- I. Prepare recipe, directory and original source files
- II. Modify file(s)
- III. Use command `diff` to generate a patch file
- IV. Calculate checksum of the patch file using `sha256sum` command
- V. Add patch file in the recipe
- VI. Install the modified version of the software

## I. Prepare original recipe, directory and source files

```
$ mkdir ~/easybuild/modify
$ cd ~/easybuild/modify
```

# We copy `FastANI-1.32-GCC-9.3.0.eb` and `FastANI-1.32-memcpy.patch` from install directory to this directory (exactly as we did for exercise 2)

```
$ module load gcc/9.3.0 fastani/1.32
$ cp $EBROOTFASTANI/easybuild/*.eb ./
$ cp $EBROOTFASTANI/easybuild/*.patch ./
```

# Modifying and installing software, FastANI

```
# using command wget to download the source file
$ wget https://github.com/ParBLiSS/FastANI/archive/v1.32.zip
# unzip the file using command unzip
$ unzip v1.32.zip
$ ls -l
drwxr-x--- 5 aroudgar aroudgar 4096 Sep 30 2020 FastANI-1.32
$ cd FastANI-1.32/src/cgi
$ ls -l
rw-r----- 1 aroudgar aroudgar 4234 Sep 30 2020 core_genome_identity.cpp
```

## II. Modify the file `core_genome_identity.cpp`

# first, we make a copy of the original file

```
$ cp core_genome_identity.cpp core_genome_identity.cpp.orig
```

```
$ vi core_genome_identity.cpp
```

# Line 32 we add

```
unsetenv((char *) "MALLOC_ARENA_MAX");  
/* This is just a test*/  
CommandLineProcessing::ArgvParser cmd;
```

# Save the file and go back to top directory of the source file

```
$ cd ../../
```

# Modifying and installing software, FastANI

## III. Use command diff to generate a patch file

```
$ diff -u src/cgi/core_genome_identity.cpp.orig src/cgi/core_genome_identity.cpp > ../FastANI-test-1.32.patch  
$ cd ..  
$ ls -l
```

```
drwxr-x--- 5 aroudgar aroudgar 4096 Sep 30 2020 FastANI-1.32  
-rw-r----- 1 aroudgar aroudgar 394 Dec 2 15:38 FastANI-test-1.3.patch  
-rw-r----- 1 aroudgar aroudgar 519 Dec 5 23:38 FastANI-1.32-memcpy.patch  
-rw-r----- 1 aroudgar aroudgar 2965327 Dec 5 23:41 v1.32.zip
```

# Modifying and installing software, FastANI

- `$ cat FastANI-test-1.32.patch`

```
--- src/cgi/core_genome_identity.cpp.orig      2021-12-05 23:42:18.000000000 -0800
+++ src/cgi/core_genome_identity.cpp          2021-12-05 23:43:30.000000000 -0800
@@ -29,7 +29,7 @@
     * for efficient multi-threaded execution
     */
     unsetenv((char *)"MALLOC_ARENA_MAX");
-
+ /* This is just a test*/
     CommandLineProcessing::ArgvParser cmd;
     using namespace std::placeholders; // for _1, _2, _3...
```

## IV. Calculate checksum of the patch file using sha256sum command

```
$ sha256sum FastANI-test-1.3.patch  
e2c71fe73fc66e00d9af2842d7edc2232136ecb5bb99a2a1857796c3b7900fea FastANI-test-1.3.patch
```

# Modifying and installing a software, FastANI

## V. Add patch file to the recipe

### FastANI-1.32-GCC-9.3.0.eb

```
easyblock = 'ConfigureMake'

name = 'FastANI'
version = '1.32'

homepage = "https://github.com/ParBLiSS/FastANI"
description = """FastANI is developed for fast alignment-free computation of
whole-genome Average Nucleotide Identity (ANI). ANI is defined as mean
nucleotide identity of orthologous gene pairs shared between two microbial
genomes. FastANI supports pairwise comparison of both complete and draft
genome assemblies."""

toolchain = {'name': 'GCC', 'version': '9.3.0'}

source_urls = ['https://github.com/ParBLiSS/FastANI/archive']
sources = ['v%(version)s.zip']
patches = ['FastANI-test-1.3.patch', 'FastANI-1.32-memcpy.patch']
checksums = [
    '06a3bd38840526eabf7a99d4f10b8f05edbf5b96bf4301e37afd89f4c1ff6d81', # v1.32.zip
    'e2c71fe73fc66e00d9af2842d7edc2232136ecb5bb99a2a1857796c3b7900fea', #FastANI-test-1.3.patch
    'eebcf0b64c31ee360ca79136f644157064ac69747ed13cff70f5c9932c6bb0d5', # FastANI-1.32-memcpy.patch
]
```

## VI. Install the modified version of the software

```
$ eb -f ./FastANI-1.32-GCC-9.3.0.eb
```

Questions?