

Uni.lu HPC School 2018

PS3b: Software Build and Customization using Easybuild



Uni.lu High Performance Computing (HPC) Team

S. Peter

University of Luxembourg (UL), Luxembourg

<http://hpc.uni.lu>



Latest versions available on Github:



UL HPC tutorials:

<https://github.com/ULHPC/tutorials>

UL HPC School:

<http://hpc.uni.lu/hpc-school/>

PS3b tutorial sources:

ulhpc-tutorials.rtfid.io/en/latest/tools/easybuild/





Summary

1 Introduction

2 Software/Modules Management

Main Objectives of this Session

- **Discover** Environment Modules and Lmod
- **Installation** of EasyBuild
- Understanding **local vs. global** installation
- **Build your own software** on top of the provided software set
 - ↪ local installation of HPL
 - ↪ using **existing** easyconfigs
- **Write your own easyconfig** file
 - ↪ build the latest version of CMake

Part 1

Part 2 (a)

Part 2 (b)

Part 2 (c)

Part 2 (d)



Summary

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Software/Modules Management

<https://hpc.uni.lu/users/software/>

- Based on **Environment Modules / LMod**
 - ↪ convenient way to dynamically change the users environment \$PATH
 - ↪ permits to easily load software through module command
- Currently on **UL HPC**:
 - ↪ > **163 software packages**, in *multiple* versions, within **18 categ.**
 - ↪ reworked software set for iris cluster and now deployed everywhere
 - ✓ RESIF v2.0, allowing [real] semantic versioning of released builds
 - ↪ hierarchical organization **Ex:** toolchain/{foss,intel}

```
$> module avail
```

List available modules

```
$> module load <category>/<software>[/<version>]
```

Software/Modules Management

- Key module variable: `$MODULEPATH` / where to look for modules
↳ altered with `module use <path>`. **Ex:**

```
export EASYBUILD_PREFIX=$HOME/.local/easybuild
export LOCAL_MODULES=$EASYBUILD_PREFIX/modules/all
module use $LOCAL_MODULES
```

Software/Modules Management

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 ↳ altered with module use <path>. **Ex:**

```
export EASYBUILD_PREFIX=$HOME/.local/easybuild
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module use $LOCAL_MODULES
```

Main modules commands:

Command	Description
<code>module avail</code>	Lists all the modules which are available to be loaded
<code>module spider <pattern></code>	Search for among available modules (Lmod only)
<code>module load <mod1> [mod2...]</code>	Load a module
<code>module unload <module></code>	Unload a module
<code>module list</code>	List loaded modules
<code>module purge</code>	Unload all modules (purge)
<code>module display <module></code>	Display what a module does
<code>module use <path></code>	Prepend the directory to the <code>MODULEPATH</code> environment variable
<code>module unuse <path></code>	Remove the directory from the <code>MODULEPATH</code> environment variable

Software/Modules Management

<http://hpcugent.github.io/easybuild/>

- **Easybuild**: open-source framework to (automatically) build scientific software
- **Why?**: *"Could you please install this software on the cluster?"*
 - Scientific software is often **difficult** to build
 - ✓ non-standard build tools / incomplete build procedures
 - ✓ hardcoded parameters and/or poor/outdated documentation
 - EasyBuild helps to facilitate this task
 - ✓ **consistent** software **build and installation** framework
 - ✓ includes testing step that helps validate builds
 - ✓ **automatically generates LMod modulefiles**

```
$> module use $LOCAL_MODULES
$> module load tools/EasyBuild
$> eb -S HPL      # Search for recipes for HPL software
$> eb HPL-2.2-intel-2017a.eb # Install HPL 2.2 w. Intel toolchain
```

Software/Modules Management

- **RESIF**: Revolutionary EasyBuild-based Software Installation Framework
 - ↪ Automatic Management of **software sets**
 - ↪ Fully automates software builds and supports all available toolchains
 - ↪ Clean (hierarchical) modules layout to facilitate its usage
 - ↪ **Versioning** of software set builds
 - ↪ Easyconfig files from multiple sources
 - ↪ Define options and software in easy to read **yaml** files
 - ↪ Targeted at ULHPC sysadmins use case to build many softwares in one go

Available software sets

- Gaia

→ **default**: available by default

→ **bioinfo**: load with

```
module use $RESIF_ROOTINSTALL/bioinfo/modules/all
```

- Iris

→ **default**: available by default

→ **bioinfo**: load with

```
module use /opt/apps/resif/data/stable/bioinfo/modules/all
```

Policies

- **We provide** software that is used by many users on the cluster
- What the **users** should install themselves:
 - ↪ Python packages
 - ↪ R packages
 - ↪ Perl modules
 - ↪ software only used by 1 or 2 persons

DIY

We provide several how-tos and tutorials for installing software as a user on the [ULHPC website](#) and in our [HPC school tutorials](#):

- Installation with **EasyBuild**
- Installation from source with `configure` and `make`
- Installation of Python packages and usage of virtual environments
- Installation of Perl modules and how to set up a local library

Or just download precompiled binaries (see Bioinformatics tutorial)
;-)

Questions?

<http://hpc.uni.lu>

High Performance Computing @ uni.lu

Prof. Pascal Bouvry
Dr. Sebastien Varrette
Valentin Plugaru
Sarah Peter
Hyacinthe Cartiaux
Clement Parisot

University of Luxembourg, Belval Campus
Maison du Nombre, 4th floor
2, avenue de l'Université
L-4365 Esch-sur-Alzette
mail: hpc@uni.lu



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