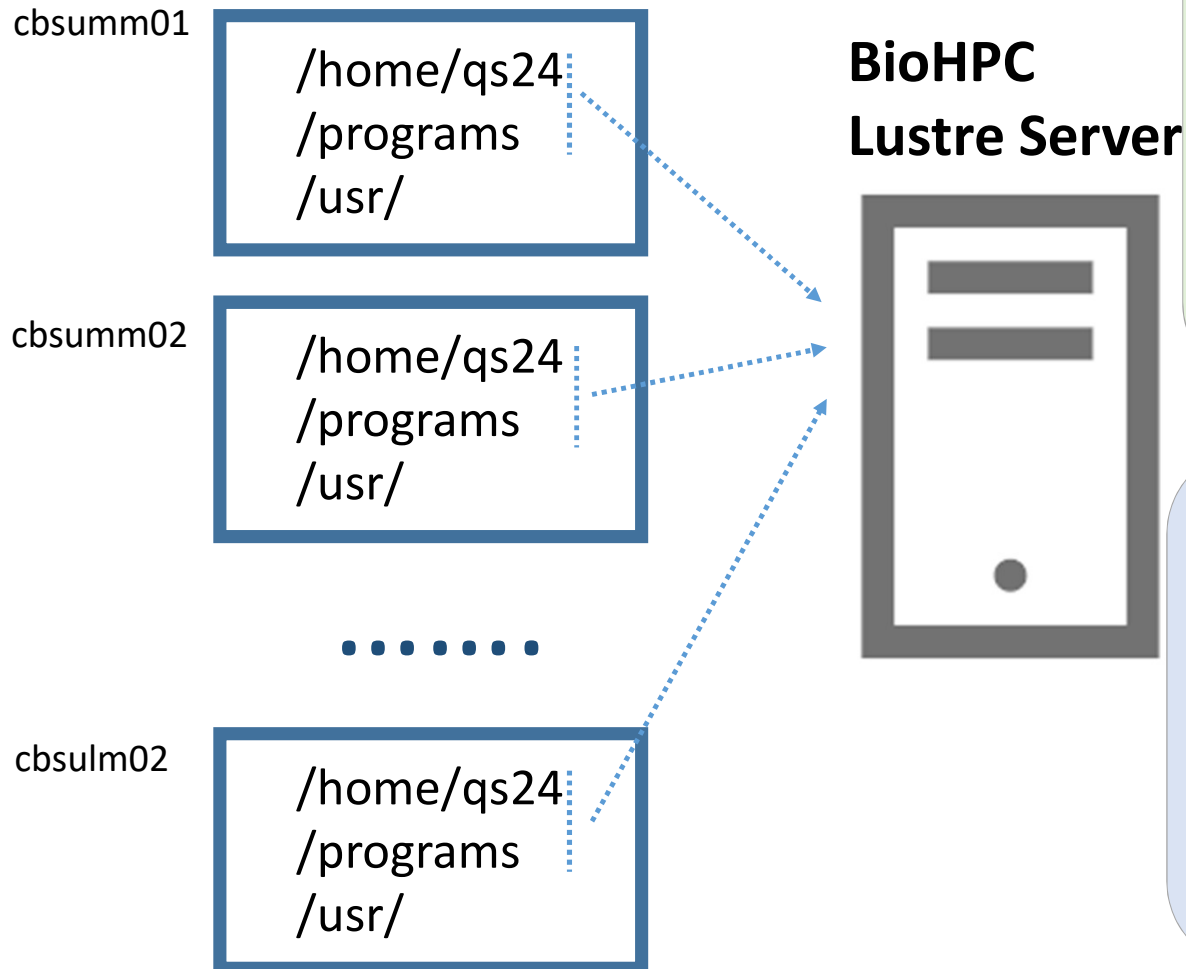


Software Locations on BioHPC



/usr or /usr/local

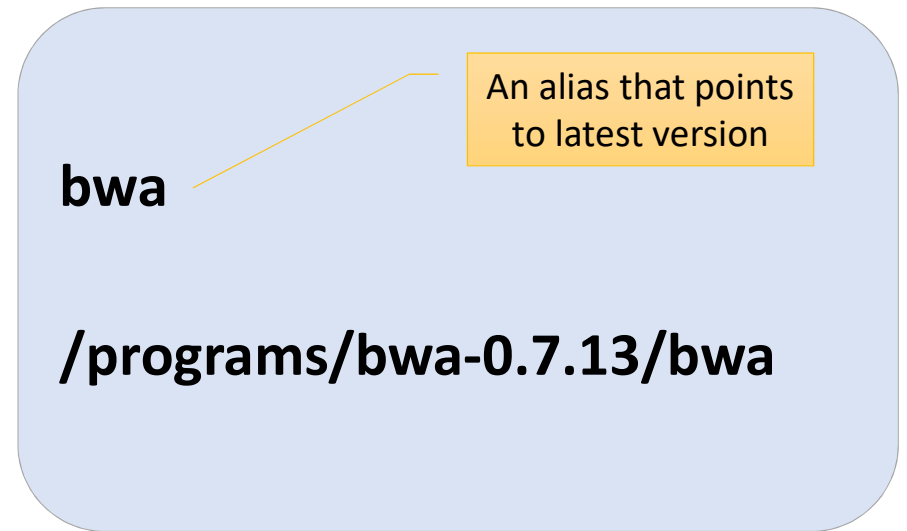
- Fast to load;
- Each computer might have different versions;

/programs

- A single copy is used by all machines;
- Slow to load;
- All versions kept;

All historic versions are kept in /programs/

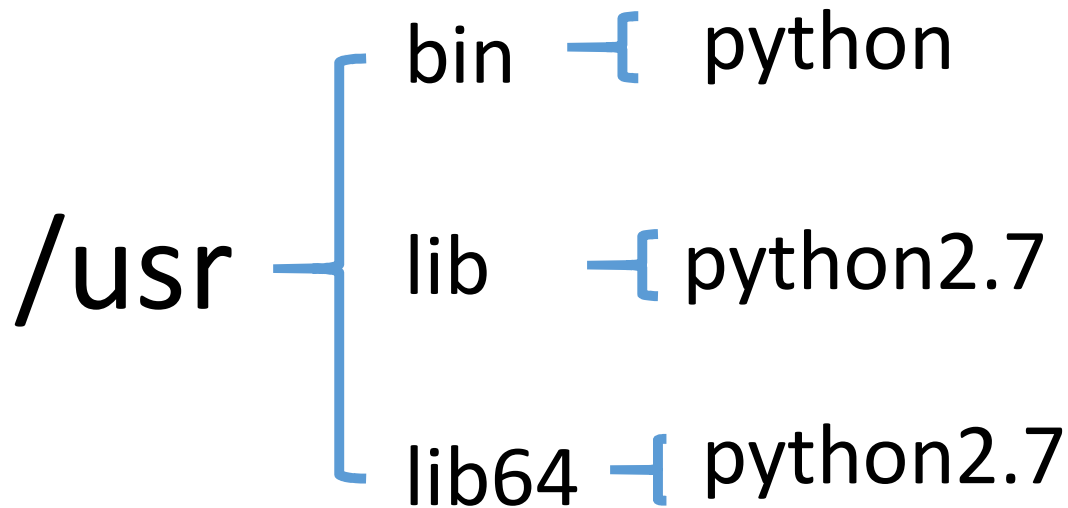
/programs {
 bwa-0.5.8c
 bwa-0.5.9
 bwa-0.6.1
 bwa-0.6.1.tar.bz2
 bwa-0.6.2
 bwa-0.6.2.tar
 bwa-0.7.13
 bwa-0.7.3a
 bwa-0.7.5a
 bwa-0.7.5a.tar
 bwa-0.7.7
 bwa-0.7.8



PYTHON



On a Brand New Server

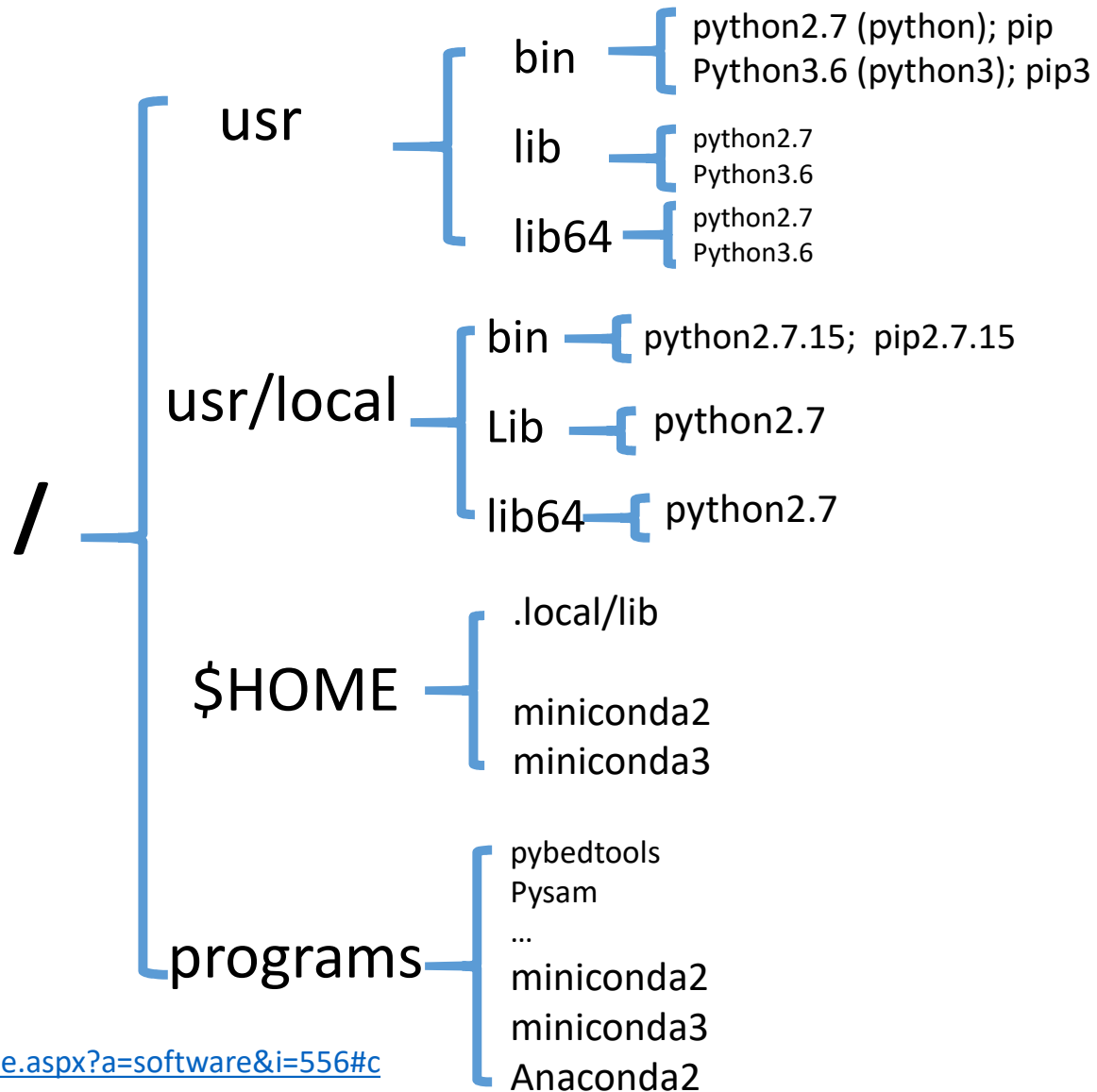
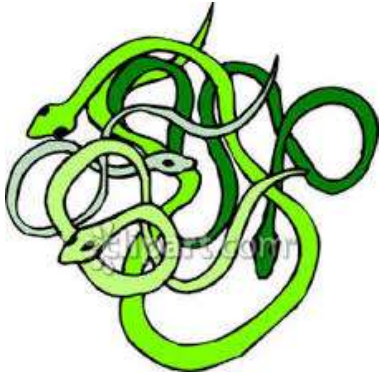


Executable

Libraries

PYTHON

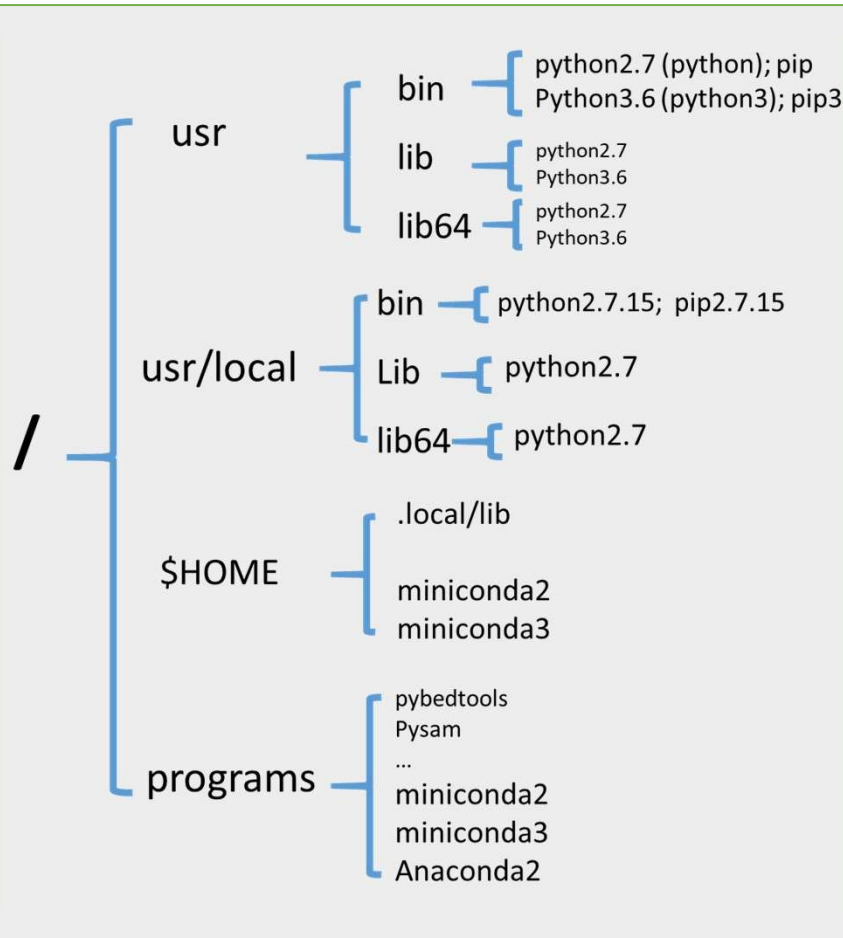
After a while



Instructions for Python on BioHPC

<https://biohpc.cornell.edu/lab/userguide.aspx?a=software&i=556#c>

PYTHON



Precedence

Executables

\$PATH

➤ /usr/local/bin

➤ /usr/bin

Libraries

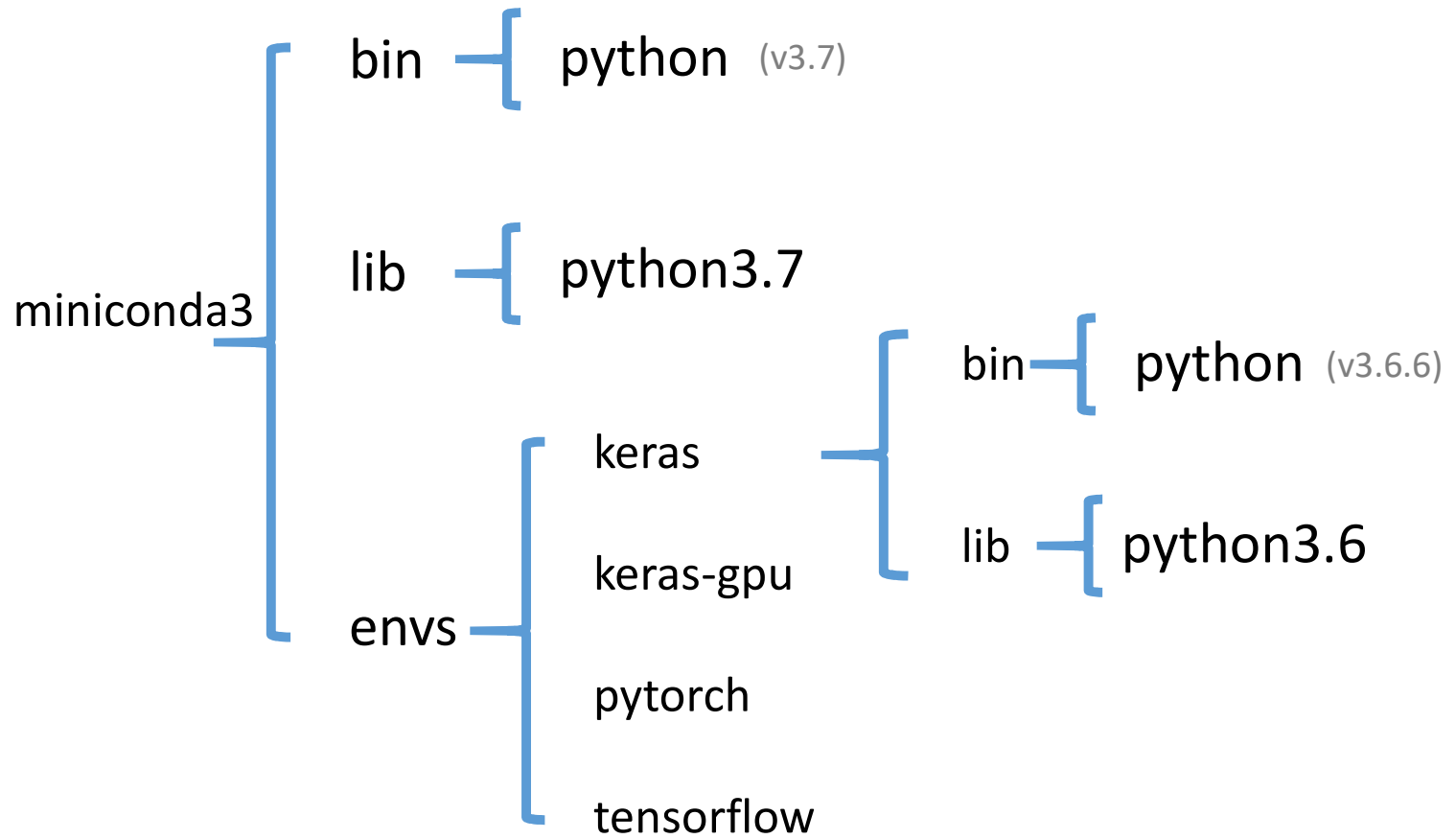
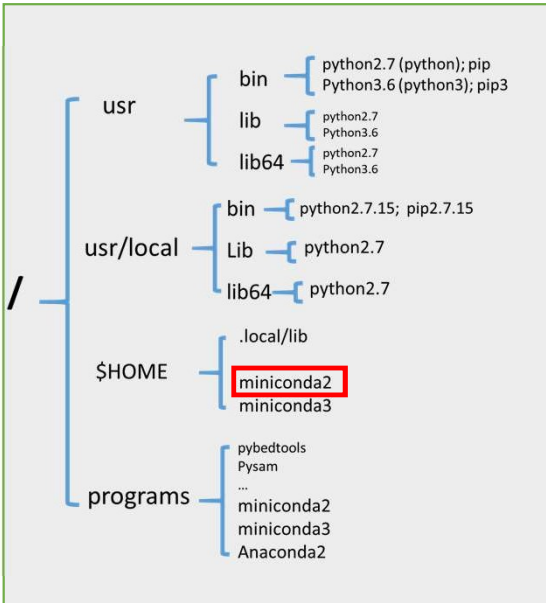
\$PYTHONPATH

➤ sys.path (installation-
dependent default)

- export PATH=/programs/pybedtools/bin:\$PATH
- export PYTHONPATH=/programs/pybedtools/lib64
- unset PYTHONPATH

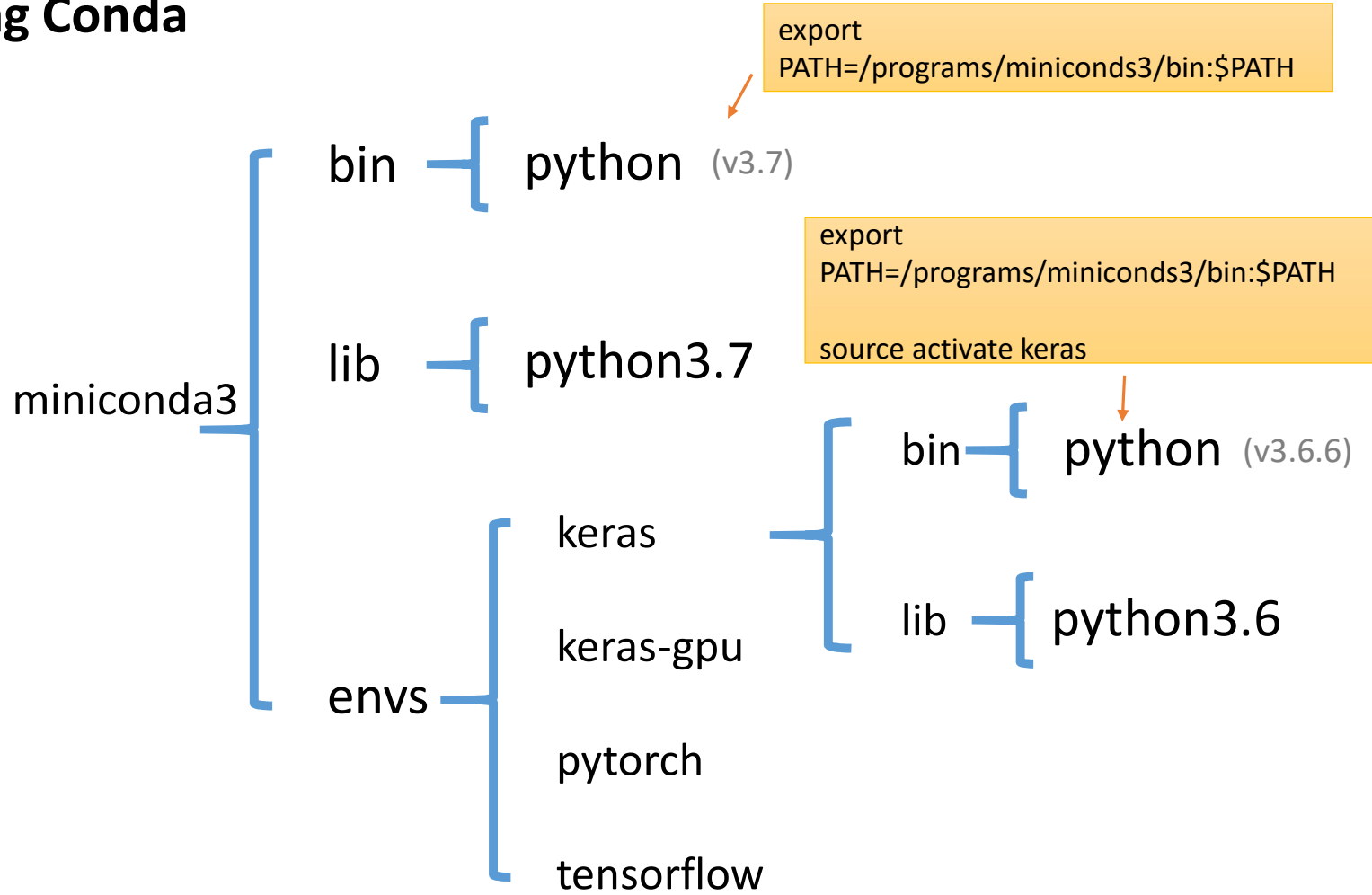
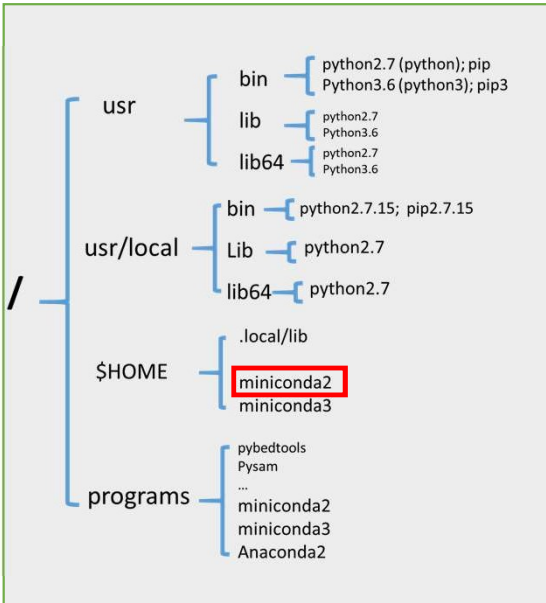
PYTHON

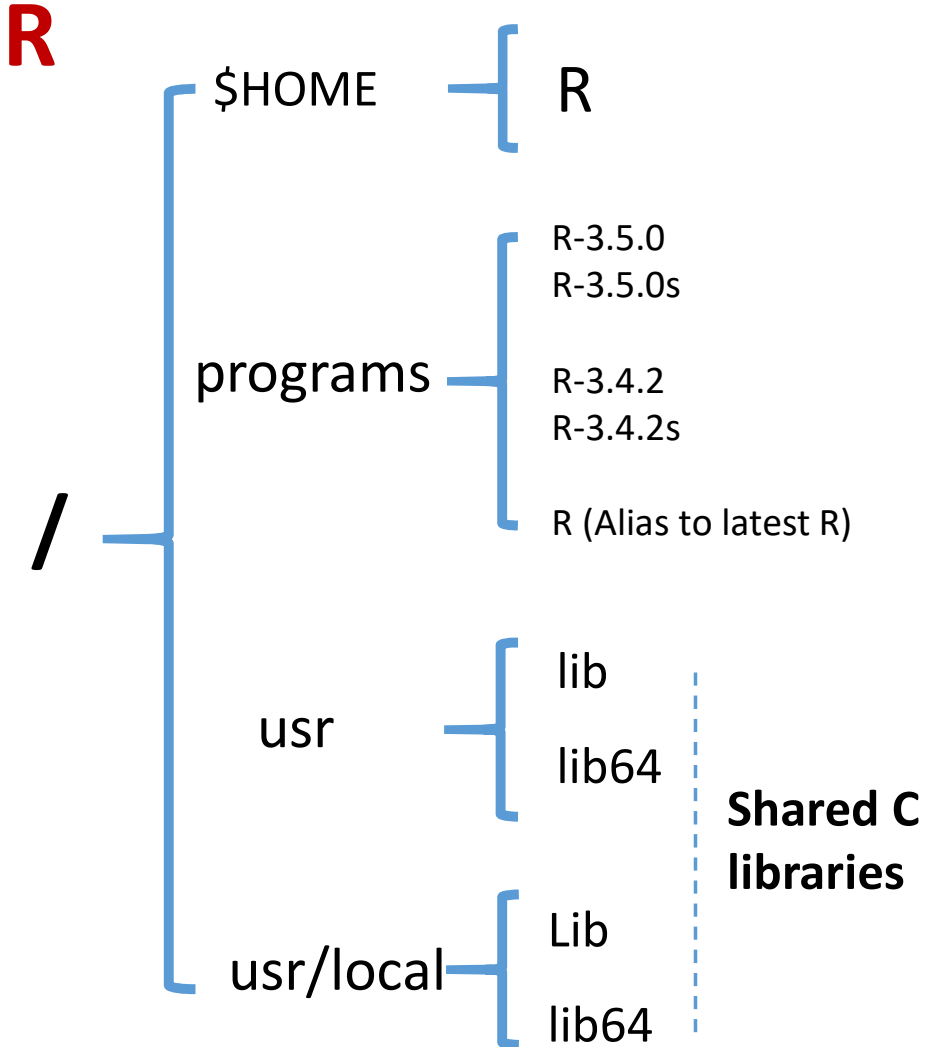
Using Conda



PYTHON

Using Conda





Note 1. Two separate installation for each version

R

- Using parallel BLAS library
- Location: /programs/R/bin/R

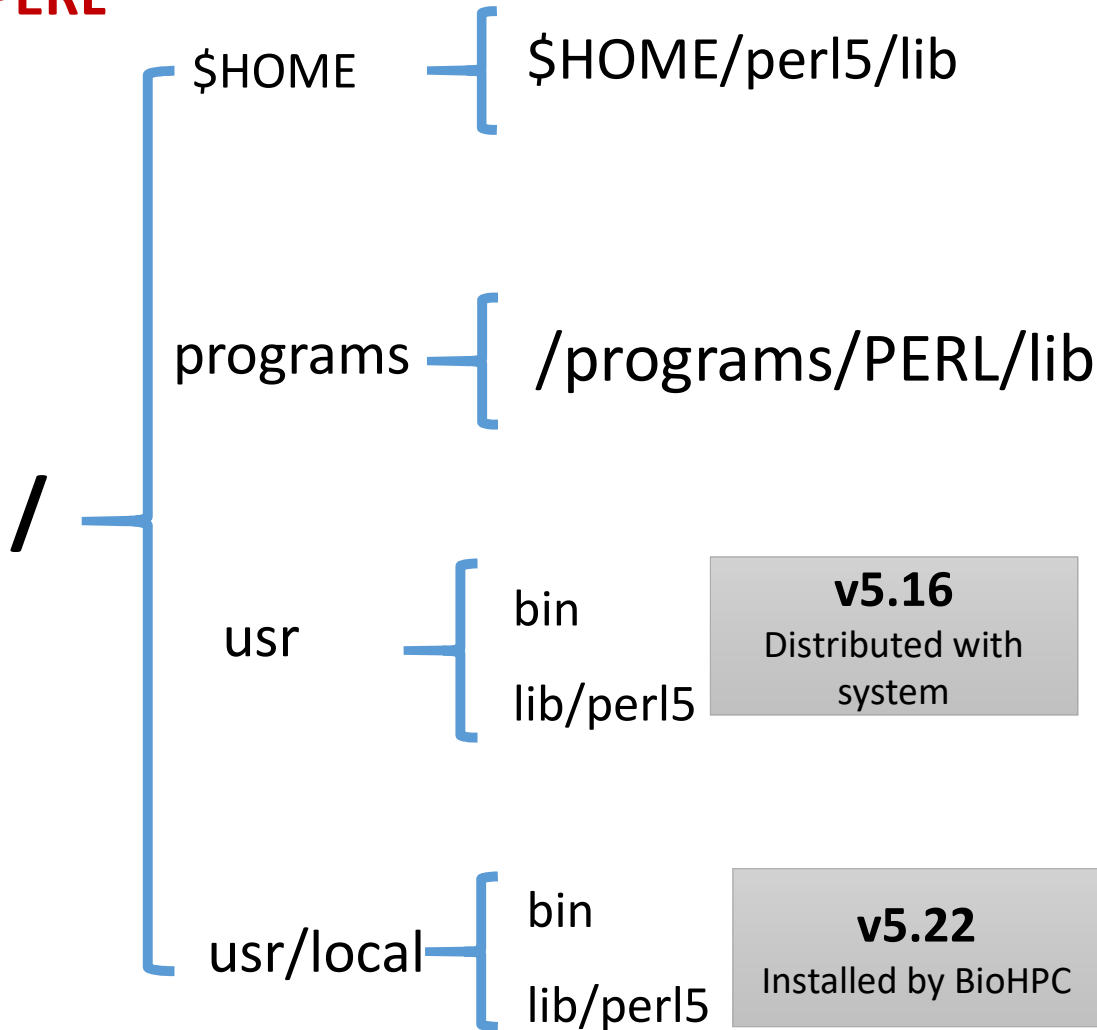
/programs/R-3.5.0s/bin/R

- Using built-in BLAS library

R in Conda Environment

Libraries in \$HOME/R has precedence over conda environment.

PERL



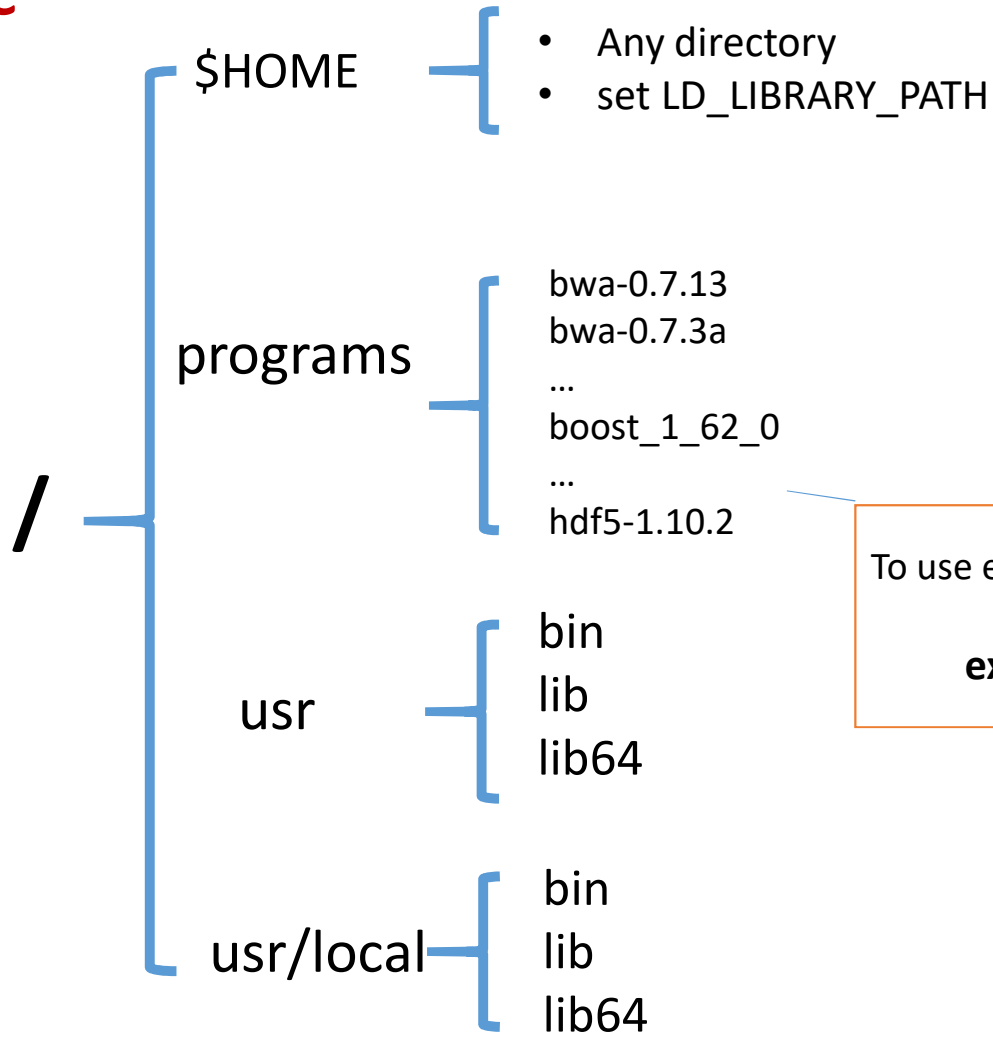
Use PERL5LIB to set library path

```
export PERL5LIB=/programs/PERL/lib/perl5
```

(perl in /usr/bin is alias to /usr/local/bin/perl)

Default PERL

C



To use extra libraries:

```
export LD_LIBRARY_PATH=/programs/ hdf5-1.10.2/lib
```

Compiler

Default: `/usr/bin/gcc` (v.4.8.5)

Updated versions:

- `/usr/local/gcc-5.5.0`
- `/usr/local/gcc-7.3.0`

```
export LD_LIBRARY_PATH=/usr/local/gcc-7.3.0/lib:/usr/local/gcc-7.3.0/lib64
```

```
export PATH=/usr/local/gcc-7.3.0/bin:$PATH
```

C

CPU/GPU Types

	AVX	AVX2
General	X	X
Gen1 (Medium and Large mem.)	✓	X
Gen2 & Extra large.	✓	✓

Software compiled on one type of computers might not run on a different type.

What if something goes wrong?

Which executable?

```
which python
```

Which library?

```
echo $PYTHONPATH
```

```
echo $LD_LIBRARY_PATH
```

```
echo $PERL5LIB
```

```
python
```

```
>import numpy
```

```
>numpy.__file__
```

```
C programs:
```

```
ldd /programs/bin/bwa/bwa
```

Check the .bashrc file

```
more $HOME/.bashrc
```

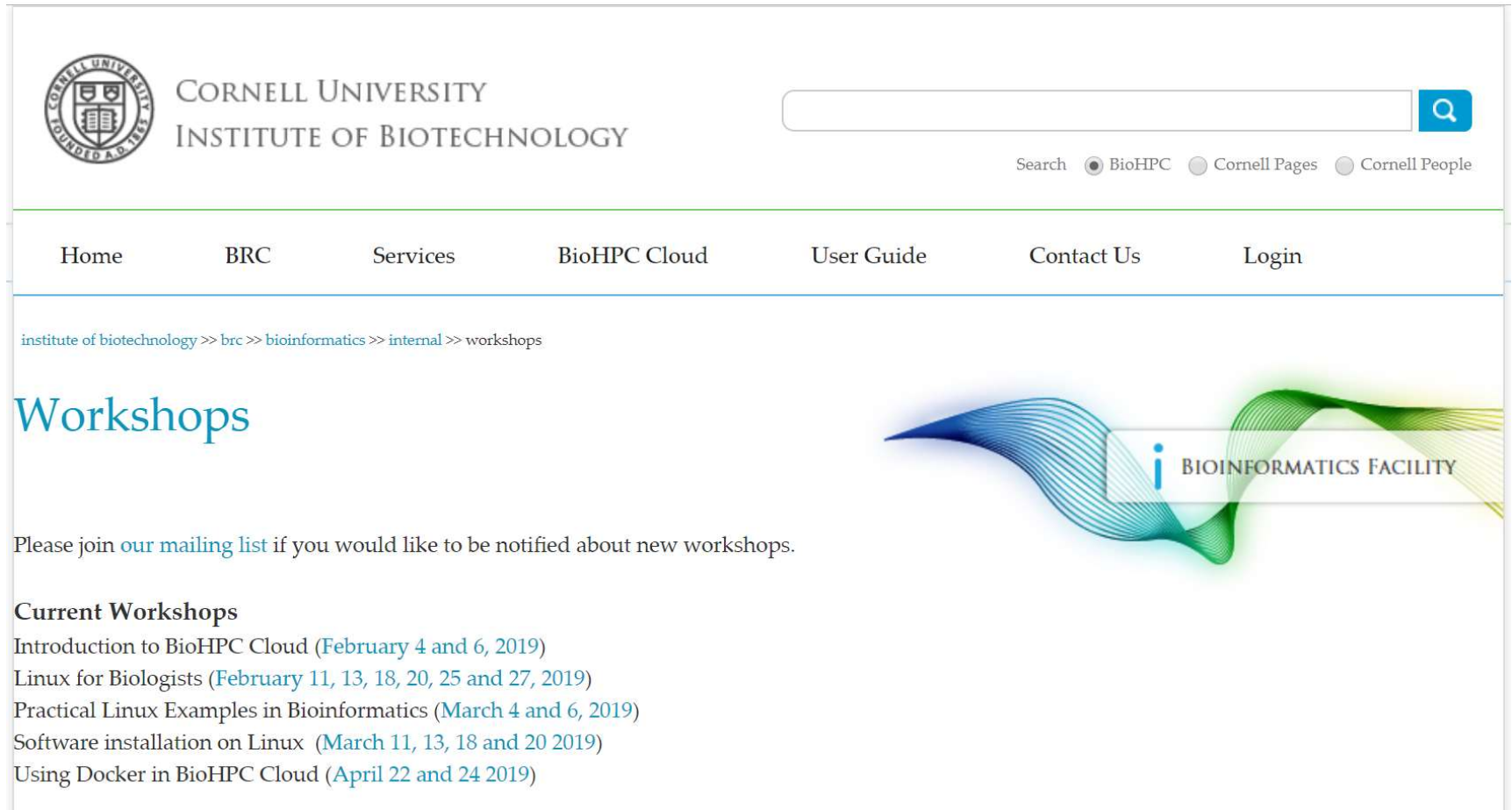
Software instruction page on BioHPC web site

Details for TensorFlow (hide)	
Name:	TensorFlow
Version:	1.12.0
OS:	Linux
About:	Software library for numerical computation using data flow graphs
Added:	10/14/2016 1:06:23 PM
Updated:	1/18/2019 11:05:00 AM
Link:	https://www.tensorflow.org/
Notes:	<p>TensorFlow is installed with conda (Python 3 version). To use it:</p> <pre>export PATH=/programs/miniconda3/bin:\$PATH source activate tensorflow-gpu python >>import tensorflow as tf</pre> <p>After you are done, exit python and run this command the deactivate the environment:</p> <pre>source deactivate</pre> <p>Please note: The tensorflow installed with conda works with BioHPC's GPU machines, as well as CPU machines that support avx2 (including Medium Memory Gen2, Large Memory Gen2 and Extra Large Memory machines).</p> <p>If you want to use Tensorflow through Keras, please follow instructions in this page (https://biohpc.cornell.edu/lab/userguide.aspx?a=software&i=550#c). If you need to use Tensorflow together with other python libraries, We recommend you to install your own tensorflow in your home directory, using conda. The installation procedure is simple, and compatible cuda is included. Here are the steps to install Tensorflow:</p> <ol style="list-style-type: none">1. If you do not have miniconda installed in your home directory, following these instructions to install

We do not support the “module” function to configure the shell.

Container and Software Installation Workshops

<https://biohpc.cornell.edu/workshops.aspx>



The screenshot shows the Cornell University Institute of Biotechnology website. At the top left is the Cornell University logo and the text "CORNELL UNIVERSITY INSTITUTE OF BIOTECHNOLOGY". To the right is a search bar with a magnifying glass icon and radio buttons for "BioHPC" (selected), "Cornell Pages", and "Cornell People". Below the search bar is a navigation menu with links: Home, BRC, Services, BioHPC Cloud, User Guide, Contact Us, and Login. The main content area has a breadcrumb trail: "institute of biotechnology >> brc >> bioinformatics >> internal >> workshops". The word "Workshops" is displayed in a large blue font. To the right is a graphic with a blue and green wavy line and the text "i BIOINFORMATICS FACILITY". Below the graphic, it says "Please join our mailing list if you would like to be notified about new workshops." Under the heading "Current Workshops", there is a list of workshop topics with dates in parentheses: "Introduction to BioHPC Cloud (February 4 and 6, 2019)", "Linux for Biologists (February 11, 13, 18, 20, 25 and 27, 2019)", "Practical Linux Examples in Bioinformatics (March 4 and 6, 2019)", "Software installation on Linux (March 11, 13, 18 and 20 2019)", and "Using Docker in BioHPC Cloud (April 22 and 24 2019)".


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Workshops

 BIOINFORMATICS FACILITY

Please join [our mailing list](#) if you would like to be notified about new workshops.

Current Workshops

- Introduction to BioHPC Cloud (February 4 and 6, 2019)
- Linux for Biologists (February 11, 13, 18, 20, 25 and 27, 2019)
- Practical Linux Examples in Bioinformatics (March 4 and 6, 2019)
- Software installation on Linux (March 11, 13, 18 and 20 2019)
- Using Docker in BioHPC Cloud (April 22 and 24 2019)