

Fermitools/Conda Shared Installation at SLAC

SLAC has a shared installation of [conda](#) with [Fermitools](#), [Fermipy](#), and [3ML](#) environments for general use.

The currently available environments are:

- fermitools-2.2.0 - latest version, released 2022-06-21 ([Release Notes](#)) with Fermipy 1.2.0 ([Release Notes](#))
- fermitools-2.0.8 - previous version, released 2021-01-20 ([Release Notes](#)) with Fermipy 1.0.1 ([Release Notes](#))
- fermitools-2.0 - previous version, released 2020-09-21 ([Release Notes](#))
- fermitools-1.2.23 - previous version, released 2020-02-11 ([Release Notes](#))
- threeML-2.4.0 - latest version ([Release Notes](#)) with Fermitools 2.2.0
- threeML-1.1.1 - previous version ([Release Notes](#))

Running the Tools

You can activate one of the environments listed above by running the conda activate command (from a bash shell, which may not be your default shell):

```
source <path>/conda/bin/activate <environment>
```

The path is different depending on which machine you are on.

Old cluster

On the old cluster (e.g., bullet) or the rhel6 or centos7 pools, run, e.g.,

```
source /nfs/farm/g/glast/software/conda/bin/activate fermitools-2.2.0
```

Again, make sure you are using bash and not tcsh.

SDF

On SDF, run, e.g.,

```
source /sdf/group/fermi/software/conda/bin/activate fermitools-2.2.0
```

S3DF

[S3DF](#) currently has the fermitools 2.2.0 with fermipy 1.2.0 and 3ML 2.4.0 environment but not the older ones. To activate them, use, e.g.,

```
source /sdf/group/fermi/sw/conda/bin/activate fermitools-2.2.0
```

Finding Out What's Available

If you suspect the list on this page is not up-to-date, you can also first activate the conda base environment, e.g.,

```
source /nfs/farm/g/glast/software/conda/bin/activate
```

and see a list of installed environments

```
conda env list
```

which will give you output like

```
# conda environments:
#
base * /nfs/farm/g/glast/software/conda
fermitools-1.2.23 /nfs/farm/g/glast/software/conda/envs/fermitools-1.2.23
fermitools-2.0 /nfs/farm/g/glast/software/conda/envs/fermitools-2.0
fermitools-2.0.8 /nfs/farm/g/glast/software/conda/envs/fermitools-2.0.8
threeML-1.1.1 /nfs/farm/g/glast/software/conda/envs/threeML-1.1.1
```

which can then be activated with, e.g.,

```
conda activate fermitools-2.0.8
```

Troubleshooting

If the activation fails with an error like:

```
_CONDA_ROOT=/nfs/farm/g/glast/software/conda: Command not found.  
_CONDA_ROOT: Undefined variable.
```

You are likely not in a bash shell.

If the problem seems to be with the conda installation at SLAC, message Don.

If the problem seems to be with the FermiTools, see the [Troubleshooting](#) and [Error Reporting](#) pages.

Adding New Environments

The conda directories are owned by the glast user. You will need permission to access this account if you want to add or change the existing environments. You can then ssh into a machine as glast (which should not prompt you for a password) or "ksu glast" to change to the glast user on the machine you are currently logged into. You may then want to run "bash" to make sure you are using the bash shell since the glast account defaults to tcsh on the old clusters.

If you need to install conda itself, you will need to put it somewhere accessible for fermi users. For example, on S3DF, conda was installed under /sdf/group/fermi/sw following [their instructions](#):

```
wget https://repo.anaconda.com/miniconda/Miniconda3-latest-Linux-x86_64.sh -O /tmp/Miniconda3-latest-Linux-x86_64.  
sh  
bash /tmp/Miniconda3-latest-Linux-x86_64.sh -p /sdf/group/fermi/sw/conda/
```

You can then activate conda, e.g.,

```
source /sdf/group/fermi/sw/conda/bin/activate
```

and begin install software with the normal conda commands.