Planemo is a python project, which help you build and publish Galaxy tool.

Here we should you is how to install planemo in centos7.

Install Planemo has two ways: using pip or conda.

Pip install Planemo

That is our system install enviroment:

- · centos 7
- python 2.7
- python 3.5

1.In order no ERROR, I suggest it uses python3 to create virtual environment:

Use following code will auto create a virtual environment $venv_dir$ and a folder name $venv_dir$. If you want to hide folder, you add . before $venv_dir$.

```
python3 -m venv venv_dir
```

```
[xiaowei@localhost Galaxy]$ python3 -m venv venv_dir
[xiaowei@localhost Galaxy]$ cd venv_dir/
[xiaowei@localhost venv_dir]$ ls
pin include lib lib64 pyvenv.cfg
```

2.Activate this virtual environment:

```
cd venv_dir/
source ./bin/activate
```

After you enable your virtual environment, all your operation will be in this virtual environment. If you are not in virtual environment, you shall be input deactivate to terminal window for end this virtual environment.

3.Update pip

Pip version must be \geq =7 before install planemo. If pip version not \geq =7, please run this command to update pip:

```
pip install "pip>=7"
pip install --upgrade pip
```

```
[xiaowei@localhost venv_dir]$ source ./bin/activate

(venv_dir) [xiaowei@localhost venv_dir]$ pip install "pip>=7"

Requirement already satisfied (use --upgrade to upgrade): pip>=7 in ./lib/python3.5/site-packages

You are using pip version 7.1.2, however version 20.1.1 is available.

You should consider upgrading via the 'pip install --upgrade pip' command.

(venv dir) [xiaowei@localhost venv dir]$ pvthon

Python 3.5.0 (default, Jul 2 2020, 04:06:50)

[GCC 4.8.5 20150623 (Red Hat 4.8.5-39)] on linux

Type "help", "copyright", "credits" or "license" for more information.

>>>
```

4.Install planemo

```
pip install planemo
```

When installed this way, planemo can be upgraded use command

pip install -U planemo or pip install -U git+git://github.com/galaxyproject/planemo.git.

5. ERROR

When you use pip install planemo, it maybe show you some ERROR. So you can see the \underline{link} (ERROR when planemo install.ipynb) to solve your ERROR. This link is some ERROR when I used pip install planemo.

Conda install planemo

Conda is an open-source package management system and environment management system that runs on Windows, macOS, and Linux.

Conda quickly install, runs, and updates packages and their dependencies.

Conda easily creates, saves, loads, and switches between environments on your local computer.

Conda play an important role in building Galaxy tools because some Galaxy tools requirment packages are installed by conda. If you are interest in conda, you can see <u>user guide of conda</u> (https://docs.conda.io/projects/conda/en/latest/user-guide/index.html).

1.Install conda

Conda install on linux, you can choose install Miniconda or Anaconda. Here I chose Anaconda to install.

Step1: Download Anaconda:

```
curl -0 https://repo.anaconda.com/archive/Anaconda3-2020.02-Linux-x86_64.sh
```

Step2: in your terminal window,run:

bash Anaconda3-2020.02-Linux-x86 64.sh

Step3: Activate conda before use conda

```
cd /anaconda3/bin/ #go to Anaconda installed directory
source activate #activate Anaconda
```

Step4: check whether conda install

just input conda in your terminal:

conda

2. Conda install planemo

Input following codes in terminal:

```
conda config --add channels bioconda

conda config --add channels conda-forge

conda install planemo
```

Check whether it install planemo

Just run:

```
planemo --help
```

```
(base) [xiaowei@localhost bin]$ planemo --help
Usage: planemo [OPTIONS] COMMAND [ARGS]...
 A command-line toolkit for building tools and workflows for Galaxy.
 Check out the full documentation for Planemo online
                                               `planemo docs``.
 http://planemo.readthedocs.org or open with `
 All the individual planemo commands support the ``--help`` option, for
 example use ``planemo lint --help`` for more details on checking tools.
ptions:
                   Show the version and exit.
 --version
 -v, --verbose
                   Enables verbose mode.
 --config TEXT
                   Planemo configuration YAML file.
  --directory TEXT Workspace for planemo.
                   Show this message and exit.
 --help
ommands:
 bioc_conda_recipe_init
                             Make a bioconda recipe, given a R or...
 bioc_tool_init
                             Generate a bioconductor tool outline from...
                             Install tool requirements using brew.
 brew
 brew env
                             List commands to inject brew dependencies.
 brew_init
                             Download linuxbrew install & run it in ruby.
 ci_find_repos
                             Find all shed repositories in one or more...
                              Find all tools in one or more directories.
 ci_find_tools
                             Short-cut to quickly clone, fork, and branch
 clone
                             Perform conda build with Planemo's conda.
 conda_build
 conda_env
                             Activate a conda environment for tool.
 conda_init
                             Download and install conda.
```

reference

- 1. conda (https://docs.conda.io/projects/conda/en/latest/index.html)
- 2. planemo project description (https://pypi.org/project/planemo/)
- 3. planemo installation (https://planemo.readthedocs.io/en/latest/installation.html)