Linux安装conda

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#登录服务器
$ ssh bio01@182.42.145.90
bio01@182.42.145.90's password:xxxxxxxx

#设置清华镜像，安装conda
$ wget https://mirrors.tuna.tsinghua.edu.cn/anaconda/miniconda/M
--2024-06-09 13:13:48-- https://mirrors.tuna.tsinghua.edu.cn/an
Resolving mirrors.tuna.tsinghua.edu.cn (mirrors.tuna.tsinghua.ed
Connecting to mirrors.tuna.tsinghua.edu.cn (mirrors.tuna.tsinghu
HTTP request sent, awaiting response... 200 OK
Length: 143808873 (137M) [application/octet-stream]
Saving to: 'Miniconda3-latest-Linux-x86_64.sh'

Miniconda3-latest-Linux-x86_64.sh   100%[====================

2024-06-09 13:13:52 (36.7 MB/s) - 'Miniconda3-latest-Linux-x86_(

#安装conda
$ bash Miniconda3-latest-Linux-x86_64.sh

Welcome to Miniconda3 py312_24.4.0-0

In order to continue the installation process, please review the

```
agreement.
Please, press ENTER to continue
>>>
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Do you accept the license terms? [yes|no]
>>> yes

Miniconda3 will now be installed into this location:
/home/bio01/miniconda3

  - Press ENTER to confirm the location
  - Press CTRL-C to abort the installation
  - Or specify a different location below

[/home/bio01/miniconda3] >>>
PREFIX=/home/bio01/miniconda3
Unpacking payload ...

Installing base environment...

Downloading and Extracting Packages:

Downloading and Extracting Packages:

Preparing transaction: done
Executing transaction: done
installation finished.
Do you wish to update your shell profile to automatically initi
This will activate conda on startup and change the command promp
If you'd prefer that conda's base environment not be activated (

```
    run the following command when conda is activated:

conda config --set auto_activate_base false


You can undo this by running `conda init --reverse $SHELL`? [ye
[no] >>> yes
no change     /home/bio01/miniconda3/condabin/conda
no change     /home/bio01/miniconda3/bin/conda
no change     /home/bio01/miniconda3/bin/conda-env
no change     /home/bio01/miniconda3/bin/activate
no change     /home/bio01/miniconda3/bin/deactivate
no change     /home/bio01/miniconda3/etc/profile.d/conda.sh
no change     /home/bio01/miniconda3/etc/fish/conf.d/conda.fish
no change     /home/bio01/miniconda3/shell/condabin/Conda.psm1
no change     /home/bio01/miniconda3/shell/condabin/conda-hook.
no change     /home/bio01/miniconda3/lib/python3.12/site-package
no change     /home/bio01/miniconda3/etc/profile.d/conda.csh
modified      /home/bio01/.bashrc

==> For changes to take effect, close and re-open your current

Thank you for installing Miniconda3!
#安装成功

#激活conda
source ~/.bashrc

#conda一下
conda
usage: conda [-h] [-v] [--no-plugins] [-V] COMMAND ...


conda is a tool for managing and deploying applications, enviro

options:
  -h, --help        Show this help message and exit.
  -v, --verbose     Can be used multiple times. Once for deta
```

```
    --no-plugins          Disable all plugins that are not built in
  -V, --version           Show the conda version number and exit.


commands:
  The following built-in and plugins subcommands are available.


  COMMAND
    activate            Activate a conda environment.
    clean               Remove unused packages and caches.
    compare             Compare packages between conda environment
    config              Modify configuration values in .condarc.
    content-trust       Signing and verification tools for Conda
    create              Create a new conda environment from a list
    deactivate          Deactivate the current active conda enviro
    doctor              Display a health report for your environme
    export              Export a given environment
    info                Display information about current conda in
    init                Initialize conda for shell interaction.
    install             Install a list of packages into a specifie
    list                List installed packages in a conda environ
    notices             Retrieve latest channel notifications.
    package             Create low-level conda packages. (EXPERIM
    remove (uninstall)
                        Remove a list of packages from a specifie
    rename              Rename an existing environment.
    repoquery           Advanced search for repodata.
    run                 Run an executable in a conda environment.
    search              Search for packages and display associate
    update (upgrade)    Update conda packages to the latest compa
```

#设置conda下载镜像
```
conda config --add channels https://mirrors.bfsu.edu.cn/anaconda
conda config --add channels https://mirrors.bfsu.edu.cn/anaconda
conda config --add channels https://mirrors.bfsu.edu.cn/anaconda
conda config --add channels https://mirrors.bfsu.edu.cn/anaconda
conda config --set show_channel_urls
```

```
#查看conda安装包
conda list
# packages in environment at /home/bio01/miniconda3:
#
# Name                        Version                     Build  Chann
_libgcc_mutex                 0.1                          main   de1
_openmp_mutex                 5.1                         1_gnu   de1
anaconda-anon-usage           0.4.4            py312hfc0e8ea_100    c
archspec                      0.2.3                  pyhd3eb1b0_0   de1


#安装了错误镜像地址：
conda config --add channels {{bfsu}}
#导致安装不成功
conda install fastqc -y
Channels:
 - {{bfsu}}
 - defaults
Platform: osx-arm64
Collecting package metadata (repodata.json): failed


UnavailableInvalidChannel: HTTP 404 NOT FOUND for channel {{bfsu


The channel is not accessible or is invalid.


You will need to adjust your conda configuration to proceed.
Use `conda config --show channels` to view your configuration's
and use `conda config --show-sources` to view config file locati


#删除路径
conda config --remove channels '{{bfsu}}'
#安装成功
conda install fastqc -y
Channels:
 - https://mirrors.bfsu.edu.cn/anaconda/pkgs/main
 - https://mirrors.bfsu.edu.cn/anaconda/pkgs/free
```

```
    - https://mirrors.bfsu.edu.cn/anaconda/cloud/conda-forge
    - https://mirrors.bfsu.edu.cn/anaconda/cloud/bioconda
    - defaults
Platform: osx-arm64
Collecting package metadata (repodata.json): done
Solving environment: done

## Package Plan ##

  environment location: /opt/anaconda3

  added / updated specs:
    - fastqc


The following packages will be downloaded:

    package                    |               build
    ---------------------------|----------------
    fastqc-0.12.1              |       hdfd78af_0        11.1 ME
    font-ttf-dejavu-sans-mono-2.37|       hd3eb1b0_0          335
    fontconfig-2.14.1          |       hee714a5_2        254 KE
    gdbm-1.18                  |       h8fe7016_4        141 KE
    openjdk-11.0.13            |       h98b2900_0       164.3 ME
    perl-5.34.0               |       h1a28f6b_2        14.0 ME
    ---------------------------------------------------------
                                       Total:       190.1 ME

The following NEW packages will be INSTALLED:

  fastqc            anaconda/cloud/bioconda/noarch::fastqc-0.12
  font-ttf-dejavu-s~ anaconda/pkgs/main/noarch::font-ttf-dejavu-
  fontconfig        anaconda/pkgs/main/osx-arm64::fontconfig-2
  gdbm              anaconda/pkgs/main/osx-arm64::gdbm-1.18-h8f
  openjdk           anaconda/pkgs/main/osx-arm64::openjdk-11.0
  perl              anaconda/pkgs/main/osx-arm64::perl-5.34.0-h
```

```
Downloading and Extracting Packages:

Preparing transaction: done
Verifying transaction: done
Executing transaction: done


#运行fastqc --help查看是否安装成功
fastqc --help


#查看conda环境
conda info --envs
# conda environments:
#
base                     *  /opt/anaconda3


# 新建conda环境，用python3
conda create -n rna-seq python=3 fastqc trimmomatic -y
Channels:
 - https://mirrors.bfsu.edu.cn/anaconda/pkgs/main
 - https://mirrors.bfsu.edu.cn/anaconda/pkgs/free
 - https://mirrors.bfsu.edu.cn/anaconda/cloud/conda-forge
 - https://mirrors.bfsu.edu.cn/anaconda/cloud/bioconda
 - defaults
Platform: osx-arm64
Collecting package metadata (repodata.json): done
Solving environment: done

## Package Plan ##

  environment location: /opt/anaconda3/envs/rna-seq
```

```
  added / updated specs:
    - fastqc
    - python=3
    - trimmomatic


The following packages will be downloaded:

    package                    |                 build
    ---------------------------|----------------
    bzip2-1.0.8                |            h80987f9_6         129 KB
    ca-certificates-2024.3.11  |            hca03da5_0         128 KB
    expat-2.6.2                |            h313beb8_0         150 KB
    freetype-2.12.1            |            h1192e45_0         570 KB
    icu-73.1                   |            h313beb8_0         25.4 MB
    libcxx-14.0.6              |            h848a8c0_0         965 KB
    libffi-3.4.4               |            hca03da5_1         120 KB
    libiconv-1.16              |            h80987f9_3         735 KB
    libpng-1.6.39              |            h80987f9_0         283 KB
    libxml2-2.10.4             |            h0b34f26_2         638 KB
    ncurses-6.4                |            h313beb8_0         884 KB
    openssl-3.0.13             |            h1a28f6b_2         4.3 MB
    pip-24.0                   |      py312hca03da5_0         3.3 MB
    python-3.12.3              |            h99e199e_1         14.0 MB
    readline-8.2               |            h1a28f6b_0         353 KB
    setuptools-69.5.1          |      py312hca03da5_0         1.3 MB
    sqlite-3.45.3              |            h80987f9_0         1.2 MB
    tk-8.6.14                  |            h6ba3021_0         3.3 MB
    trimmomatic-0.39           |            hdfd78af_2         144 KB
    tzdata-2024a               |            h04d1e81_0         116 KB
    wheel-0.43.0               |      py312hca03da5_0         140 KB
    xz-5.4.6                   |            h80987f9_1         371 KB
    zlib-1.2.13                |            h18a0788_1          91 KB
    ------------------------------------------------------------
                                           Total:         58.4 MB
```

```
The following NEW packages will be INSTALLED:

  bzip2              anaconda/pkgs/main/osx-arm64::bzip2-1.0.8-h
  ca-certificates    anaconda/pkgs/main/osx-arm64::ca-certificat
  expat              anaconda/pkgs/main/osx-arm64::expat-2.6.2-h
  fastqc             anaconda/cloud/bioconda/noarch::fastqc-0.12
  font-ttf-dejavu-s~ anaconda/pkgs/main/noarch::font-ttf-dejavu-
  fontconfig         anaconda/pkgs/main/osx-arm64::fontconfig-2
  freetype           anaconda/pkgs/main/osx-arm64::freetype-2.12
  gdbm               anaconda/pkgs/main/osx-arm64::gdbm-1.18-h8f
  icu                anaconda/pkgs/main/osx-arm64::icu-73.1-h313
  libcxx             anaconda/pkgs/main/osx-arm64::libcxx-14.0.6
  libffi             anaconda/pkgs/main/osx-arm64::libffi-3.4.4
  libiconv           anaconda/pkgs/main/osx-arm64::libiconv-1.16
  libpng             anaconda/pkgs/main/osx-arm64::libpng-1.6.39
  libxml2            anaconda/pkgs/main/osx-arm64::libxml2-2.10
  ncurses            anaconda/pkgs/main/osx-arm64::ncurses-6.4-h
  openjdk            anaconda/pkgs/main/osx-arm64::openjdk-11.0
  openssl            anaconda/pkgs/main/osx-arm64::openssl-3.0.1
  perl               anaconda/pkgs/main/osx-arm64::perl-5.34.0-h
  pip                anaconda/pkgs/main/osx-arm64::pip-24.0-py31
  python             anaconda/pkgs/main/osx-arm64::python-3.12.3
  readline           anaconda/pkgs/main/osx-arm64::readline-8.2
  setuptools         anaconda/pkgs/main/osx-arm64::setuptools-69
  sqlite             anaconda/pkgs/main/osx-arm64::sqlite-3.45.3
  tk                 anaconda/pkgs/main/osx-arm64::tk-8.6.14-h6b
  trimmomatic        anaconda/cloud/bioconda/noarch::trimmomatic
  tzdata             anaconda/pkgs/main/noarch::tzdata-2024a-h04
  wheel              anaconda/pkgs/main/osx-arm64::wheel-0.43.0-
  xz                 anaconda/pkgs/main/osx-arm64::xz-5.4.6-h809
  zlib               anaconda/pkgs/main/osx-arm64::zlib-1.2.13-h


Downloading and Extracting Packages:
```

```
Preparing transaction: done
Verifying transaction: done
Executing transaction: done
#
# To activate this environment, use
#
#     $ conda activate rna-seq
#
# To deactivate an active environment, use
#
#     $ conda deactivate


#创建成功
conda info --envs
# conda environments:
#
base                  *  /opt/anaconda3
rna-seq                  /opt/anaconda3/envs/rna-seq


#激活新环境
conda activate rna-seq

#关闭
rna-seq ~ git: (master)‡58 (0.098s)
conda deactivate
```