conda init 初始化到 conda base环境

conda config --set auto\_activate\_base false

wget https://repo.anaconda.com/archive/Anaconda3-2020.07-Linux-x86\_64.sh -O anaconda3.sh

sh anaconda3.sh -b -p /mnt/sdb/zengl/lib/anaconda

export PATH="$HOME/miniconda/bin:$PATH";

hash -r;

conda config --add channels conda-forge

conda config --add channels r

conda config --add channels bioconda

conda config --set show\_channel\_urls yes 的意思是从channel中安装包时显示channel的url，这样就可以知道包的安装来源了

conda info -a # 查看所有信息

conda info --envs # 查看环境

conda create -q -n test-environment python=3.6 numpy scipy matplotlib sphinx tabulate;

建议安装完Anaconda后，添加清华大学的源，方便更新，代码如下：

conda config --add channels https://mirrors.tuna.tsinghua.edu.cn/anaconda/pkgs/free/

conda install -c bioconda perl-bioperl

conda install -c bioconda perl-bioperl-core

conda install biopython

conda install -y -c bioconda r-sleuth

conda install -c bioconda blast

conda install -c bioconda pbmm2

conda install -c bioconda pbsv

conda install -c bioconda pbbam

conda install -c atgc-montpellier lordec

conda install -n py2.7 -c bioconda faststructure

source activate py2.7

conda install -c bioconda genomicconsensus

conda install -c bioconda pbalign

conda install -c bioconda pbccs

conda install -c bioconda lima

conda install -c bioconda pbcoretools

conda install -c bioconda isoseq3

https://zhuanlan.zhihu.com/p/89356758

安装-kobas

source activate py2.7

conda install -c bioconda kobas

kobas-annotate -i C1\_5.vs.kobas.m8 -t blastout:tab -s ko -o pathway2.txt

kobas-identify -f HBV-ETOH-NK\_vs\_HBV-ETOH.DEG.Ko -n BH -b ref\_gene.pathway.txt -o enrich.xls

配置：/home/zengl/.kobasrc

conda create -n qiime1 python=2.7 qiime matplotlib=1.4.3 mock nose -c bioconda

source activate qiime1

conda install psutil

conda install -c bioconda qiime

设置数据库路径：checkm data setRoot /home/taoye/mybin/Module\_Meta/checkm\_db

conda create -n checkv -c conda-forge -c bioconda checkv

conda create -n checkm python=2.7

conda create -n unicycler -c bioconda unicycler

conda create -n masurca -c bioconda masurca

conda create -n circlator -c bioconda circlator

conda install -c bioconda trnascan-se

source activate checkm

conda install -c bioconda checkm-genome

conda create -n cat -c bioconda cat

conda create -n virsorter -c bioconda virsorter

conda create -n vs2 -c conda-forge -c bioconda virsorter=2

conda create -n denovo trinity 创建环境并安装包

conda create -n qiime1 python=2.7 qiime matplotlib=1.4.3 mock nose -c bioconda

wget https://data.qiime2.org/distro/core/qiime2-2018.8-py35-linux-conda.yml

conda env create -n qiime2-2018.8 --file qiime2-2018.8-py35-linux-conda.yml

conda install -c bioconda blast

conda install -c bioconda trinity

conda install fastqc

conda install paml

conda install -c bioconda r-virfinder

conda create -q -n py2.7 python=2.7

conda create -n R33 创建名为R3.3.2的环境

source activate R33

conda install -c r r=3.3.2

conda create -n R363 r=3.6.3

conda install r-base #安装R语言

conda install -c r r-essentials

conda install r-units

conda install -c conda-forge r-rgdal

conda install -c r rpy2

conda install r-stringi # R包 以 r- 开头

conda deactivate

conda remove -n py2.7 --all

https://zhuanlan.zhihu.com/p/89356758

conda list #查看当前安装的软件

conda list -n env\_name #特定环境安装包

conda search ruby 搜索软件包包含的版本

conda update r r=3.5.3 包更新

防止包更新

conda update fastqc --no-pin

conda install -c r r-dplyr

conda install -c r Cairo

conda create -n my-r-env -c r r-essentials

完成后，将是一个自动配置好“R essentials”的环境！包含了dplyr, shiny, ggplot2, tidyr,caret 和 nnet等等常用包。（可以通过 conda list查看）

install.packages('udunits2', type = 'source', repo = 'cran.rstudio.com', configure.args = "--with-udunits2-lib=/usr/local/lib")

conda create -q -n test-environment python=3.6 numpy scipy matplotlib sphinx tabulate

conda install numpy scipy matplotlib sphinx tabulate

conda 切换python版本

source activate py2.7

run\_lefse.py /mnt/sdb/miudong/work/2019/201907/lizhipeng\_190718/All/Lefse/lefse\_format.txt lefse\_LDA.xls -y 1

source deactivate py2.7

conda create -n orthofinder -c bioconda orthofinder

conda create -n abyss -c bioconda abyss

conda create -n mummer4 -c bioconda mummer4

conda create -n antismash antismash

conda activate antismash

download-antismash-databases

conda deactivate

conda create -n plasflow python=3.5

source activate plasflow

conda install -c jjhelmus tensorflow

conda install plasflow -c smaegol

# 下载qiime2的conda安装配置文件

wget https://data.qiime2.org/distro/core/qiime2-2020.2-py36-linux-conda.yml --no-check-certificate

# 创建一个名为 qm2-2020.2的环境，按照qiime2文件安装

conda env create -n qm2-2020.2 --file qiime2-2020.2-py36-linux-conda.yml

gtdbtk-数据库路径修改

conda create -n gtdbtk -c bioconda gtdbtk=1.5.0

/lustre/sdb/taoye/miniconda3/envs/GTDB-Tk/etc/conda/activate.d/gtdbtk.sh