

先放到Linux的.sh文件里面编辑，不然会有因为win和linux的空格格式不同而产生的报错。

执行：（以run.sh为文件名为例，数据来源为：genome5 数据ID为：a01）

在终端中输入：

```
nohup sh run.sh genome5 a01 &  
(然后敲两次回车)
```

run.sh 中的代码

设定变量名

数据来源

SOURCE=\$1

数据ID

ID=\$2

assembly 的存储路径

ASSEMBLY=/home/liucongcong/data/testAllMethods/datasets/\${SOURCE}-\${ID}.assembly

bam 的存储路径

BAM=/home/liucongcong/data/testAllMethods/datasets/\${SOURCE}-\${ID}.*.bam

为所有bam文件建立索引, 生成bai文件

```
for bam in `ls ${BAM}`  
do  
    samtools index ${bam}  
done
```

CONCOCT - v1.0.0

创建CONCOCT - v1.0.0对应临时文件夹并进入该文件夹

```
mkdir ${SOURCE}-${ID}.concoct-1.0.0 && cd ${SOURCE}-${ID}.concoct-1.0.0
```

执行软件CONCOCT - v1.0.0

```
cut_up_fasta.py ${ASSEMBLY} -c 10000 -o 0 --merge_last -b contigs_10K.bed > contigs_10K.fa  
concoct_coverage_table.py contigs_10K.bed ${BAM} > coverage_table.tsv  
concoct -t 50 --composition_file contigs_10K.fa --coverage_file coverage_table.tsv -b concoct_output/  
merge_cutup_clustering.py concoct_output/clustering_gt1000.csv > concoct_output/clustering_merged.csv  
mkdir concoct_output/fasta_bins  
extract_fasta_bins.py ${ASSEMBLY} concoct_output/clustering_merged.csv --output_path concoct_output/fasta_bins
```

将需要保留的文件留在临时文件夹的上一层

```
mv coverage_table.tsv ../${SOURCE}-${ID}.concoct-1.0.0.coverage  
mv concoct_output/fasta_bins ../${SOURCE}-${ID}.concoct-1.0.0.clusters  
cd ..
```

移除临时文件夹

```
rm -rf ${SOURCE}-${ID}.concoct-1.0.0
```

Metabat2

创建Metabat2对应临时文件夹并进入该文件夹

```
mkdir ${SOURCE}-${ID}.metabat2-2.12.1 && cd ${SOURCE}-${ID}.metabat2-2.12.1
```

执行软件

```
runMetaBat.sh ${ASSEMBLY} ${BAM}
```

将需要保留的文件留在临时文件夹的上一层

```
mv *.depth.txt ../${SOURCE}-${ID}.metabat2-2.12.1.depth
```

```
mv *.metabat-bins ../${SOURCE}-${ID}.metabat2-2.12.1.clusters
```

```
cd ..
```

移除临时文件夹

```
rm -rf ${SOURCE}-${ID}.metabat2-2.12.1
```

SemiBin2 - v1.5.1

创建SemiBin2文件夹

```
mkdir ${SOURCE}-${ID}.semibin2-1.5.1
```

跑程序

```
SemiBin2 single_easy_bin -i ${ASSEMBLY} -b ${BAM} --self-supervised -o ${SOURCE}-${ID}.semibin2-1.5.1
```

只保留contig_bins.tsv文件 储存为.clusters

```
mv ${SOURCE}-${ID}.semibin2-1.5.1/contig_bins.tsv ${SOURCE}-${ID}.semibin2-1.5.1.clusters
```

删除临时文件夹

```
rm -rf ${SOURCE}-${ID}.semibin2-1.5.1
```

MetaDecoder - v1.0.3

#创建MetaDecoder对应的文件夹并进入

```
mkdir ${SOURCE}-${ID}.metadecoder-1.0.3 && cd ${SOURCE}-${ID}.metadecoder-1.0.3
```

#处理数据

```
for bam in `ls ${BAM}`
```

```
do
```

```
samtools view -@ 30 -h -o `date -u +%Y%m%d%H%M%S`.sam ${bam}
```

```
done
```

#执行程序

```
metadecoder coverage -s *.sam -o coverage
```

```
metadecoder seed --threads 50 -f ${ASSEMBLY} -o seed
```

```
metadecoder cluster --no -f ${ASSEMBLY} -s seed -c coverage -o metadecoder-1.0.3
```

```
mv coverage ../${SOURCE}-${ID}.metadecoder-1.0.3.coverage
mv metadecoder-1.0.3.cluster ../${SOURCE}-${ID}.metadecoder-1.0.3.clusters
cd ..
rm -rf ${SOURCE}-${ID}.metadecoder-1.0.3
```

VAMB - v4.1.3#

#VAMB要用新的数据集:

SOURCE=genome100

ID=a01

ASSEMBLY=/home/liucongcong/data/testAllMethods/datasets/\${SOURCE}-\${ID}.assembly

BAM=/home/liucongcong/data/testAllMethods/datasets/\${SOURCE}-\${ID}.*.bam

创建vamb对应临时文件夹

```
mkdir ${SOURCE}-${ID}.vamb-4.1.3 && cd ${SOURCE}-${ID}.vamb-4.1.3
```

运行程序

```
vamb --cuda --outdir ./out --fasta ${ASSEMBLY} --bamfiles ${BAM} -o C
```

保留abundance.npz文件

```
mv ./out/abundance.npz ../${SOURCE}-${ID}.vamb-4.1.3.abundance.npz
```

#保留vae_clusters.tsv文件为 .cluster

```
mv ./out/vae_clusters.tsv ../${SOURCE}-${ID}.vamb-4.1.3.clusters
```

#移除文件夹

```
cd ..
```

```
rm -rf ${SOURCE}-${ID}.vamb-4.1.3
```