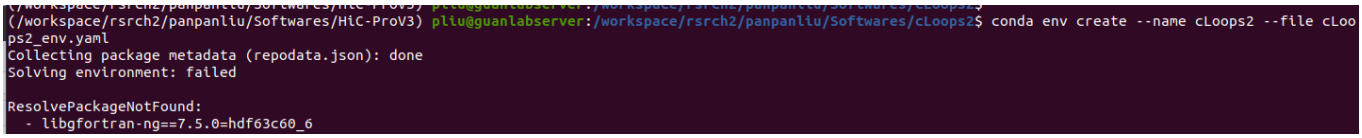
ChiA-Pet V3 get .hic file by cLoops2

#As cLoops2 are based on python 3.8, so we convert into conda activate /workspace/rsrch2/panpanliu/Softwares/HiC-ProV3 to change in to python 3.8

then install cLoops2 as following steps

```
git clone --depth=1 https://github.com/YaqiangCao/cLoops2
cd cLoops2
conda env create --name cLoops2 --file cLoops2_env.yaml ## may have erro with
```



solved by change cLoops2_env.yaml "libgfortran-ng==7.5.0=hdf63c60_6" to "libgfortran-ng==7.5.0"

```
conda activate cLoops2
python3 setup.py install
```

add juicer_tools into enviroment path

conda activate cLoops2

```
cp /workspace/rsrch2/panpanliu/Softwares/ChIA-pipe_newversion/ChIA-
PIPE/util/juicer_tools.1.7.5_linux_x64_jcuda.0.8.jar
/workspace/rsrch2/panpanliu/Softwares/miniconda3/envs/cLoops2/bin

cd /workspace/rsrch2/panpanliu/Softwares/miniconda3/envs/cLoops2/bin
cat >juicer_tools
#!/bin/bash
java -Xmx2g -jar
/workspace/rsrch2/panpanliu/Softwares/miniconda3/envs/cLoops2/bin/juicer_tools.
1.7.5_linux_x64_jcuda.0.8.jar $@
(ctl+D)

chmod +x juicer_tools
```

Then can excute juicer_tools pre by juicer_tools, and can used to convert cloops file to .hic file

convert bedpe to hic(*bedpe.selected.unique.txt)

##from the log file, we can get that ChiA Pet V3 get .bedpe file from *.merge.bam file, and then do Removing redundancy in step3.
after this step, the
mapq filter: ../combined_3_times/ChIAPET.Tool.V3/S10/S10.bedpe.selected.txt
unique filter : ../combined_3_times/ChIAPET.Tool.V3/S10/S10.bedpe.selected.unique.txt used for downstream pet loop calling and peak calling.

```
cLoops2 pre -f S10.bedpe.selected.unique.txt -o trac ## output is a directory
named trac
cLoops2 dump -d ./trac/ -o hic_S10 -hic -hic_org mm10 -hic_res
25000000,20000000,15000000,10000000,5000000,1000000,500000,100000,5000 ##
output is a .hic file "-o" name
```

creat bigwig from .bedpe file

```
awk -F '\t' '{print $1"\t"$2"\t"$3"\n"$4"\t"$5"\t"$6}'
<S10.bedpe.selected.unique.txt >>S10.bedpe.selected.unique.split.bed
sort -k1,1 -k2,2n S10.bedpe.selected.unique.split.bed -o
S10.bedpe.selected.unique.split.bed.sorted

genomeCoverageBed -i S10.bedpe.selected.unique.split.bed.sorted -g
/workspace/rsrch2/common_data/Refgenome/mm10/ \ chr.GRCm38_mm10.normalChr.size
-bg >S10.bedpe.selected.unique.split.bedgraph -scale 1e7 ## scale is same with
homer

bedGraphToBigWig S10.bedpe.selected.unique.split.bedgraph
/workspace/rsrch2/common_data/Refgenome/mm10/ \
chr.GRCm38_mm10.normalChr.size S10.bedpe.selected.unique.split.bed.bigwig
```

creat pet counts >=3 loop to washU local track file (only extract the first 7 columns)

```
awk -F '\t' '{ if($7>2) print $1"\t"$2"\t"$3"\t"$4"\t"$5"\t"$6"\t"$7}'
<S10.cluster.FDRfiltered.txt >S10.cluster.FDRfiltered.txt.BE3
python  ~/Softwares/ChIA-pipe_newversion/ChIA-
PIPE/util/scripts/convert_loops_to_washu_format.py -l
S10.cluster.FDRfiltered.txt.BE3
```

will get the wash U file S10.cluster.FDRfiltered.txt.BE3.for_WashU.mid200.txt.gz