ChiA-PET V3 tools install

simple introduce

Chromatin Interaction Analysis with Paired-End Tag (ChIA-PET) sequencing is a technology to study genome-wide long-range chromatin interactions bound by protein factors. ChIA-PET Tool V3, a software package for automatic processing of ChIA-PET sequence data, including:
0. linker detect (--stop_step 0, only run linker detect)

```
1.linker filtering
2.mapping the paired-end reads to a reference genome
3.purifying the mapped reads
4.dividing the reads into different categories
5.peak calling
6.interaction calling
7.visualizing the results
```

the software depends on the following softwares:

```
JDK>=1.8(https://www.oracle.com/technetwork/java/javase/downloads/index.html)
## conda base
BWA(http://bio-bwa.sourceforge.net/) ## conda install BWA -c bioconda
SAMtools(http://samtools.sourceforge.net/) ## conda install -c samtools
BEDTools(https://bedtools.readthedocs.io/en/latest/) ## conda install BEDTools
R(https://www.r-project.org/) ## install by apt-install R
R package grid(install.packages("grid")) ## install.packages("grid")
R package xtable(install.packages("xtable"))
R package RCircos(install.packages("RCircos"))
```

excute ChIA-PET_tool

Download the ChIA-PET Tool V3 package from https://github.com/GuoliangLi-HZAU/ChIA-PET_Tool_V3. Unpack the package using the following command in your selected directory:
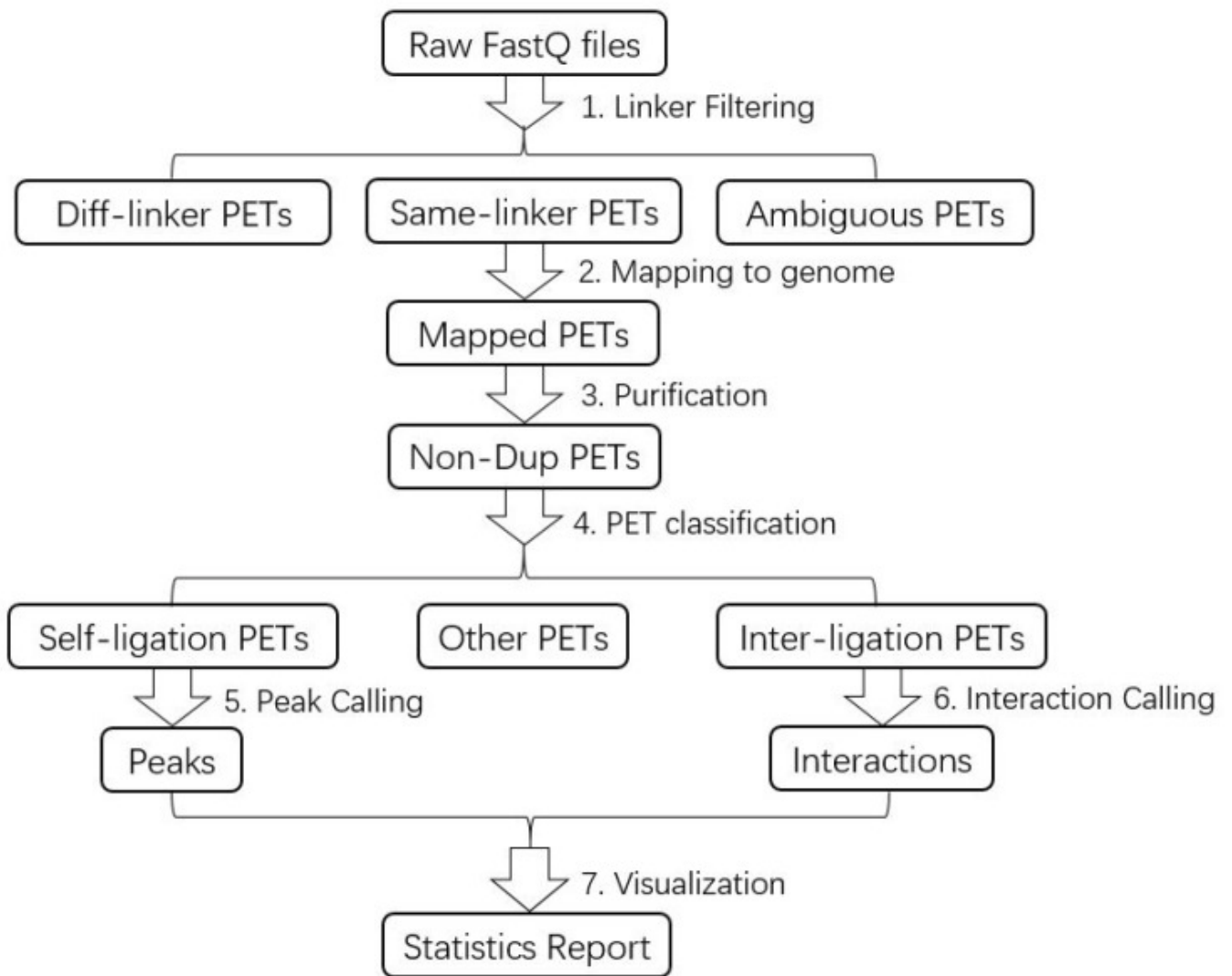$ unzip ChIA-PET_Tool_V3.zip

cd ChIA-PET_Tool_V3, the use ChIA-PET.jar to excute

###As the process was mapped with bwa, so need bulid index with bwa

```
bwa index ref.fa
```

pipeline of ChIA-PET

can uss "start_step" to choose corresponding steps