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load necessary software as modules

Add location of these modules

```
module use $RESIF_ROOTINSTALL/lcsb/modules/all
module use /home/users/aginolhac/.local/easybuild/modules/all/
```

Load the modules

```
module load bio/FastQC
module load bio/AdapterRemoval
module load bio/pysam
module load bio/paleomix
module load bio/SAMtools/0.1.19-goolf-1.4.10
module load bio/BWA
module load bio/mapDamage
module load bio/MACS2
```

Tweak for the `picard-tools`

To get all jars available

```
mkdir -p ~/install/jar_root/
cp /opt/apps/sources/p/picard/picard-tools-1.100.zip ~/install/jar_root/
cd ~/install/jar_root/
unzip picard-tools-1.100.zip
mv picard-tools-1.100/*.jar .
cd
```

you need to see `yes` to overwrite one file.

Final tweak for `Gatk`

```
cp /home/users/aginolhac/install/jar_root/GenomeAnalysisTK.jar ~/install/jar_root/
```

prepare your working environment

go to your home directory: `cd` create a new folder to work in: `mkdir chip-seq` go inside: `cd chip-seq` create and go in a sub-folder: `mkdir raw ; cd raw` symbolic link the fastq files: `ln -s /work/users/aginolhac/chip-seq/raw/C* .`

check integrity of files

Just as a side note, such large files are usually a pain to download. Since they are the very raw files after the sequencer (despite basecalling) checking their integrity is worth doing.

Computing the `md5sum` ensure you have the same file as your sequence provider. Then `pale`

`omix` will check the FASTQ are correct, *i. e* have 4 lines in a correct format.

```
md5sum -c C53CYACXX_TC1-I-A-D3_14s006682-1-1_Sinkkonen_lane114s006682_sequence.txt.md5
```

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