<http://slowkow.com/notes/snakemake-tutorial/>

<http://snakemake.bitbucket.org/snakemake-tutorial.html>

|  |  |
| --- | --- |
| skewer | Trimming & quality filter |
| fastqc | Visualize quality |
| Bwa mem  Samtools  IGV | Mapping to reference  Alignment  Visualize alignment |
| (BCFtools)  Freebayes / gatk | For SNP calling |
| Bedtools | Get coverage |

# skewer

skewer -m pe -t 10 /home/ubuntu/Desktop/Files/Documents/Projects/Gre-Net\_project/MPI\_field/data/GT10\_samples\_2016/fastaq\_files/francoisfield\_S1\_L005\_R1\_001.fastq.gz /home/ubuntu/Desktop/Files/Documents/Projects/Gre-Net\_project/MPI\_field/data/GT10\_samples\_2016/fastaq\_files/francoisfield\_S1\_L005\_R2\_001.fastq.gz

# FastQC

~/Desktop/Files/Software/fastqc/FastQC/fastqc /home/ubuntu/Desktop/Files/Documents/Projects/Gre-Net\_project/MPI\_field/data/GT10\_samples\_2016/fastaq\_files/trimmed\_pairedend\_S1/francoisfield\_S1\_L005\_R1\_001.fastq-trimmed-pair1.fastq /home/ubuntu/Desktop/Files/Documents/Projects/Gre-Net\_project/MPI\_field/data/GT10\_samples\_2016/fastaq\_files/trimmed\_pairedend\_S1/francoisfield\_S1\_L005\_R1\_001.fastq-trimmed-pair2.fastq --extract -o /home/ubuntu/Desktop/Files/Documents/Projects/Gre-Net\_project/MPI\_field/data/GT10\_samples\_2016/fastaq\_files/fastqc/paired-end/

# BWA

bwa index /home/ubuntu/Desktop/index/TAIR10\_chr\_all.fas index\_prefix

bwa mem /home/ubuntu/Desktop/index/TAIR10\_chr\_all.fas /home/ubuntu/Desktop/Files/Documents/Projects/Gre-Net\_project/MPI\_field/data/GT10\_samples\_2016/fastaq\_files/trimmed\_pairedend\_S1/francoisfield\_S1\_L005\_R1\_001.fastq-trimmed-pair1.fastq /home/ubuntu/Desktop/Files/Documents/Projects/Gre-Net\_project/MPI\_field/data/GT10\_samples\_2016/fastaq\_files/trimmed\_pairedend\_S1/francoisfield\_S1\_L005\_R1\_001.fastq-trimmed-pair2.fastq > FieldExp\_S1.sam

# samtools

samtools view -S -b FieldExp\_S1.sam > FieldExp\_S1.bam

samtools sort FieldExp\_S1.bam FieldExp\_S1.sorted

samtools index FieldExp\_S1.sorted.bam

# Freebayes

/home/ubuntu/Desktop/Files/Software/freebayes/bin/freebayes -f /home/ubuntu/Desktop/Analysis\_FieldExp\_sequences/index/TAIR10\_chr\_all.fas /home/ubuntu/Desktop/Analysis\_FieldExp\_sequences/S1/FieldExp\_S1.sorted.bam > FieldExp\_S1.freebayes.vcf