**ABBA BABA analysis on RAD data to test for admixture between populations**

Open a PUTTY terminal with the following configuration:

**Host Name**: maccolllab.life.nottingham.ac.uk

**Port:** 22

**Connection type**: SSH

***On the maccolllab.life.nottingham.ac.uk server:***

***To make the alignment file with the correct populations in it:***

FOR OBSE SCAD OBSM BEPA:

screen-S pop

screen-r pop

ref\_map.pl \

-b 4 \

-T 8 \

-O /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_OBSE\_SCAD\_OBSM\_BEPA/popmap\_population\_OBSE\_SCAD\_OBSM\_BEPA.txt \

-o /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_OBSE\_SCAD\_OBSM\_BEPA \

--samples /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/Isabels\_data/BAM\_files \

-S \

-m 3

populations \

-P /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_OBSE\_SCAD\_OBSM\_BEPA \

--popmap /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_OBSE\_SCAD\_OBSM\_BEPA/popmap\_population\_OBSE\_SCAD\_OBSM\_BEPA.txt \

-t 8 \

-k \

-O /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_OBSE\_SCAD\_OBSM\_BEPA \

--fstats \

--fst\_correction p\_value \

--min\_maf 0.05 \

-p 4 \

-r 1 \

--vcf \

--vcf\_haplotypes \

--genepop \

--ordered\_export

cd /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/PGDspider\_file\_conversion

java -Xmx1024m -Xms512m -jar PGDSpider2-cli.jar \

-inputfile /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_OBSE\_SCAD\_OBSM\_BEPA/batch\_4.vcf \

-inputformat VCF \

-outputfile /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_OBSE\_SCAD\_OBSM\_BEPA/batch\_4.fasta \

-outputformat FASTA \

-spid VCF\_to\_FASTA.spid

cd /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_OBSE\_SCAD\_OBSM\_BEPA

esl-sfetch --index batch\_4.fasta

esl-sfetch -o batch\_4\_ordered.fasta -f batch\_4.fasta list\_OBSE\_SCAD\_OBSM\_BEPA.list

FOR OBSE FADA OBSM BEPA:

screen-S popF

screen -r popF

ref\_map.pl \

-b 5 \

-T 8 \

-O /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_OBSE\_FADA\_OBSM\_BEPA/popmap\_population\_OBSE\_FADA\_OBSM\_BEPA.txt \

-o /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_OBSE\_FADA\_OBSM\_BEPA \

--samples /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/Isabels\_data/BAM\_files \

-S \

-m 3

populations \

-P /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_OBSE\_FADA\_OBSM\_BEPA \

--popmap /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_OBSE\_FADA\_OBSM\_BEPA/popmap\_population\_OBSE\_FADA\_OBSM\_BEPA.txt \

-t 8 \

-k \

-O /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_OBSE\_FADA\_OBSM\_BEPA \

--fstats \

--fst\_correction p\_value \

--min\_maf 0.05 \

-p 4 \

-r 1 \

--vcf \

--vcf\_haplotypes \

--genepop \

--ordered\_export

cd /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/PGDspider\_file\_conversion

java -Xmx1024m -Xms512m -jar PGDSpider2-cli.jar \

-inputfile /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_OBSE\_FADA\_OBSM\_BEPA/batch\_5.vcf \

-inputformat VCF \

-outputfile /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_OBSE\_FADA\_OBSM\_BEPA/batch\_5.fasta \

-outputformat FASTA \

-spid VCF\_to\_FASTA.spid

cd /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_OBSE\_FADA\_OBSM\_BEPA

esl-sfetch --index batch\_5.fasta

esl-sfetch -o batch\_5\_ordered.fasta -f batch\_5.fasta list\_OBSE\_FADA\_OBSM\_BEPA.list

FOR SCAD OBSE OBSM BEPA:

screen-S popS

screen -r popS

ref\_map.pl \

-b 6 \

-T 8 \

-O /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_SCAD\_OBSE\_OBSM\_BEPA/popmap\_population\_SCAD\_OBSE\_OBSM\_BEPA.txt \

-o /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_SCAD\_OBSE\_OBSM\_BEPA \

--samples /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/Isabels\_data/BAM\_files \

-S \

-m 3

populations \

-P /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_SCAD\_OBSE\_OBSM\_BEPA \

--popmap /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_SCAD\_OBSE\_OBSM\_BEPA/popmap\_population\_SCAD\_OBSE\_OBSM\_BEPA.txt \

-t 8 \

-k \

-O /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_SCAD\_OBSE\_OBSM\_BEPA \

--fstats \

--fst\_correction p\_value \

--min\_maf 0.05 \

-p 4 \

-r 1 \

--vcf \

--vcf\_haplotypes \

--genepop \

--ordered\_export

cd /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/PGDspider\_file\_conversion

java -Xmx1024m -Xms512m -jar PGDSpider2-cli.jar \

-inputfile /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_SCAD\_OBSE\_OBSM\_BEPA/batch\_6.vcf \

-inputformat VCF \

-outputfile /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_SCAD\_OBSE\_OBSM\_BEPA/batch\_6.fasta \

-outputformat FASTA \

-spid VCF\_to\_FASTA.spid

cd /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_SCAD\_OBSE\_OBSM\_BEPA

esl-sfetch --index batch\_6.fasta

esl-sfetch -o batch\_6\_ordered.fasta -f batch\_6.fasta list\_SCAD\_OBSE\_OBSM\_BEPA.list

FOR OBSE GILL OBSM ARRO:

screen-S popS

screen -r popS

ref\_map.pl \

-b 7 \

-T 8 \

-O /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_OBSE\_GILL\_OBSM\_ARRO/popmap\_population\_OBSE\_GILL\_OBSM\_ARRO.txt \

-o /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_OBSE\_GILL\_OBSM\_ARRO \

--samples /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/Isabels\_data/BAM\_files \

-S \

-m 3

populations \

-P /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_OBSE\_GILL\_OBSM\_ARRO \

--popmap /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_OBSE\_GILL\_OBSM\_ARRO/popmap\_population\_OBSE\_GILL\_OBSM\_ARRO.txt \

-t 8 \

-k \

-O /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_OBSE\_GILL\_OBSM\_ARRO \

--fstats \

--fst\_correction p\_value \

--min\_maf 0.05 \

-p 4 \

-r 1 \

--vcf \

--vcf\_haplotypes \

--genepop \

--ordered\_export

cd /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/PGDspider\_file\_conversion

java -Xmx1024m -Xms512m -jar PGDSpider2-cli.jar \

-inputfile /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_OBSE\_GILL\_OBSM\_ARRO/batch\_7.vcf \

-inputformat VCF \

-outputfile /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_OBSE\_GILL\_OBSM\_ARRO/batch\_7.fasta \

-outputformat FASTA \

-spid VCF\_to\_FASTA.spid

cd /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_OBSE\_GILL\_OBSM\_ARRO

esl-sfetch --index batch\_7.fasta

esl-sfetch -o batch\_7\_ordered.fasta -f batch\_7.fasta list\_OBSE\_GILL\_OBSM\_ARRO.list

FOR OBSE OBSM SCAD BEPA:

screen-S popF

screen -r popF

ref\_map.pl \

-b 8 \

-T 8 \

-O /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_OBSE\_OBSM\_SCAD\_BEPA/popmap\_population\_OBSE\_OBSM\_SCAD\_BEPA.txt \

-o /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_OBSE\_OBSM\_SCAD\_BEPA \

--samples /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/Isabels\_data/BAM\_files \

-S \

-m 3

populations \

-P /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_OBSE\_OBSM\_SCAD\_BEPA \

--popmap /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_OBSE\_OBSM\_SCAD\_BEPA/popmap\_population\_OBSE\_OBSM\_SCAD\_BEPA.txt \

-t 8 \

-k \

-O /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_OBSE\_OBSM\_SCAD\_BEPA \

--fstats \

--fst\_correction p\_value \

--min\_maf 0.05 \

-p 4 \

-r 1 \

--vcf \

--vcf\_haplotypes \

--genepop \

--ordered\_export

cd /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/PGDspider\_file\_conversion

java -Xmx1024m -Xms512m -jar PGDSpider2-cli.jar \

-inputfile /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_OBSE\_OBSM\_SCAD\_BEPA/batch\_8.vcf \

-inputformat VCF \

-outputfile /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_OBSE\_OBSM\_SCAD\_BEPA/batch\_8.fasta \

-outputformat FASTA \

-spid VCF\_to\_FASTA.spid

cd /home/mbzlld/lauras\_files/Post-doc\_work\_2018/RAD\_analysis/my\_RAD\_analysis/ABBA\_BABA/Populations\_OBSE\_OBSM\_SCAD\_BEPA

esl-sfetch --index batch\_8.fasta

esl-sfetch -o batch\_8\_ordered.fasta -f batch\_8.fasta list\_OBSE\_OBSM\_SCAD\_BEPA.list