SeqApiPop analyses: admixture

Following the MAF and LD pruning analysis, the 601,945 SNPs from the plink files SeqApiPop_629_maf001_LD03_pruned.* were used for the Admixture analysis.

Fifty runs of admixture were done, using a random seed. The 50 folders and the corresponding scripts for running admixture were generated by the script launchAdmixtureRunsWriteScriptsMAF001.bash

```
#!/bin/bash
#launchAdmixtureRunsWriteScriptsMAF001.bash
LD=LD03
for i in $(seq 00 49)
mkdir SeqApiPop_629_MAF001_${LD}rep${i}
echo \#!/bin/bash > SeqApiPop_629_MAF001_${LD}rep${i}/admixtureAnalysis.sh
echo >> SeqApiPop_629_MAF001_${LD}rep${i}/admixtureAnalysis.sh
echo module load -f /home/gencel/vignal/save/000_ProgramModules/program_module >> SeqApiPop_629_MAF001_${LD}
echo >> SegApiPop_629_MAF001_${LD}rep${i}/admixtureAnalysis.sh
echo IN=SeqApiPop_629_maf001_${LD}_pruned.bed >> SeqApiPop_629_MAF001_${LD}rep${i}/admixtureAnalysis.sh
echo >> SegApiPop_629_MAF001_${LD}rep${i}/admixtureAnalysis.sh
echo "for K in 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16;" >> SeqApiPop_629_MAF001_\$\{LD\}rep\$\{i\}/admixtureAnalysis.
echo do >> SeqApiPop_629_MAF001_${LD}rep${i}/admixtureAnalysis.sh
echo -en " -s ${RANDOM}" >> SeqApiPop_629_MAF001_${LD}rep${i}/admixtureAnalysis.sh
echo -e ' ../../\{IN\} \{K\} -j4 | tee \{IN\}.log\{K\}"' >> SeqApiPop_629_MAF001_\{LD\}rep\{i\}/admixtureAnalysis.
echo done >> SeqApiPop_629_MAF001_${LD}rep${i}/admixtureAnalysis.sh
done
```

```
#!/bin/bash
#admixtureAnalysis_multiThread.sh

module load -f /home/gencel/vignal/save/000_ProgramModules/program_module

IN=SeqApiPop_629_maf001_LD03_pruned.bed

for K in 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16;

do

sbatch --cpus-per-task=4 --mem-per-cpu=46 \
    -J ${K}admixt -o ${IN}.${K}.o -e ${IN}.${K}.e \
    --wrap="admixture --cv -s 20145 ../../${IN} ${K} -j4 | tee ${IN}.log${K}"

done
```

Obtain the CV values for plotting:

```
#!/bin/bash
#obtainCVerrorAllSeqApiPop.bash
for i in `ls | grep ^SeqApiPop`
do
```

```
grep CV ${i}/*log* | \
   awk -v var="$i" 'BEGIN{0FS="\t"}{print $3,$4, var}' | \
   sed 's/(K=//' | \
   sed 's/)://' | \
   awk 'BEGIN{FS="_";0FS="\t"}{print $1,$4,$3}' | \
   awk 'BEGIN{0FS="\t"}{print $1,$2,$4,$5}'
done
```

Collect and rename all Q matrix Files, for Pong analysis

Pong analysis: on PC

From Admixture Qfiles to Pong format

```
ls ../Qfiles/* | \
   grep LD0 | \
   awk 'BEGIN{FS="\";0FS="\t"}{print $3, $0}' | \
   awk 'BEGIN{FS=".";0FS="\t"}{print $1"_"$2"_"$3"_"$4, $2, ".."$6"."$7"."$8"."$9}' | \
   awk 'BEGIN{0FS="\t"}{print $1,$2,$3}'
```

Pong couldn't run on All Ka values computed. As the CV values suggest K=8 or K=9 as the optimum, results for K = 2 to 12 were analysed.

```
conda activate Py27Pong
pong -m Q_fileMaps_MAF001LD03_K2K12_50samples \
    -n pop0rder.list \
    -i ind2pop.list \
    -s 0.98 # Similarity threshold. Default = 0.97
```

With:

```
$ head popOrder.list
Spain IbericaSpain
Ouessant MelliferaOuessant
UK MelliferaColonsay
```

Porquerolles MelliferaPorquerolles

Sollies MelliferaSollies Savoy SavoyConservatory Italy LigusticaItaly

Slovenia CarnicaSlovenia CarGermany CaricaGermany CarFrance CaricaFrance

>head ind2pop.list

Corsica

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