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Levels: POPA POPB POPC
>
>
> #for single predictions
> myprofile2classify<-
data.frame(Locus01="GG",Locus02="AG",Locus03="CC",Locus04="AA",Locus05="AA",Locus06="CC",Locus07="GG",Locus08="CC",Locus09="CG",Locus10="GG",MH1="AGGCC/GGGCC",MH2="AG/
AG",MH3="ACC/TTT")
> predict(test,type="probs",na.action="na.exclude",newdata=myprofile2classify) #likelihoods for each population
      POPA      POPB      POPC
9.999999e-01 1.548406e-16 8.382124e-08
> predict(test,na.action="na.exclude",newdata=myprofile2classify) #predicted population
[1] POPA
Levels: POPA POPB POPC
>
>
> # for multiple predictions
> myprofiles<-read.xlsx("haplo_test.xlsx", sheet=1,na.strings=c("NN", ""))
> predict(test,type="probs",na.action="na.exclude",newdata=myprofiles) #likelihoods for each population
      POPA      POPB      POPC
1  1.000000e+00  1.211486e-22  4.172842e-16
2  1.000000e+00  3.987732e-20  8.321752e-17
3  1.000000e+00  2.905134e-14  1.766432e-18
4  1.000000e+00  1.403499e-17  1.309647e-16
5  1.271529e-35  1.000000e+00  2.280379e-26
6  5.117078e-29  9.999995e-01  5.366238e-07
7  1.127688e-44  1.000000e+00  5.090052e-35
8  4.309141e-29  1.000000e+00  6.582307e-22
9  4.195904e-21  2.922879e-11  1.000000e+00
10 1.247110e-15  6.519176e-08  9.999999e-01
11 8.973986e-20  1.855378e-19  1.000000e+00
12 1.008006e-19  3.918486e-19  1.000000e+00
> predict(test,na.action="na.exclude",newdata=myprofiles) #predicted populations
[1] POPA POPA POPA POPA POPB POPB POPB POPB POPC POPC POPC POPC
Levels: POPA POPB POPC
> myprofiles$Population #real populations
[1] "POPA" "POPA" "POPA" "POPA" "POPB" "POPB" "POPB" "POPB" "POPB" "POPC" "POPC" "POPC" "POPC"
> predict(test,na.action="na.exclude",newdata=myprofiles) == myprofiles$Population #compare predictions and real populations
[1] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE

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