## AnalisisSensibilidad

Análisis de sensibilidad de la mortalidad natural

```
system('~/admb-12.2/admb LBPA')
system('./LBPA')
data <-read.rep('LBPA.rep')</pre>
dat <- readLines("lbpa.dat",encoding="UTF-8")</pre>
dat2<-dat
M \leftarrow c(seq(0.1, 0.38, 0.02), 0.24)
par<-as.numeric(strsplit(dat[3],"\t")[[1]])</pre>
par [3]
## [1] 0.24
for(i in 1:length(M)){
dat2[3]<-paste(60.400, 0.250, M[i], -7.825, 2.950, 43.500, 53.000, 0.875,sep="\t")
cat(dat2,file=(can<-file("lbpa.dat","wb",encoding="UTF-8")),sep="\n")</pre>
close(can)
system('./LBPA')
rep<-readLines("LBPA.rep",encoding="UTF-8")</pre>
cat(rep,file=(can<-file(paste("LBPA",i,".rep",sep=""),"wb",encoding="UTF-8")),sep="\n")</pre>
close(can)
}
tabla <- matrix(ncol=7,nrow=16)</pre>
for(i in 1:16){
data <-read.rep(paste('LBPA',i,'.rep',sep=""))</pre>
tabla[i,] <- round(data$F_L50_slope_a0_cv_Lr_Ftar,2)</pre>
tablafin<-cbind(M,tabla)
colnames(tablafin) <- c("M","F Current", "L50", "Slope", "a0", "cv", "Lr", "F Target")</pre>
kable(tablafin)
```

M	F Current	L50	Slope	a0	cv	Lr	F Target
0.10	2.95	55.47	9.00	0	0.1	34.37	0.30
0.12	3.00	55.68	8.99	0	0.1	34.39	0.39
0.14	3.07	55.90	8.98	0	0.1	34.41	0.50
0.16	3.14	56.13	8.96	0	0.1	34.43	0.63
0.18	3.21	56.35	8.94	0	0.1	34.45	0.78
0.20	3.29	56.58	8.93	0	0.1	34.48	0.96

M	F Current	L50	Slope	a0	$\operatorname{cv}$	$\operatorname{Lr}$	F Target
0.22	2.43	56.16	9.50	0	0.1	31.30	0.92
0.24	3.47	57.05	8.89	0	0.1	34.53	1.44
0.26	3.57	57.28	8.87	0	0.1	34.56	1.75
0.28	3.68	57.52	8.85	0	0.1	34.58	2.13
0.30	3.80	57.77	8.82	0	0.1	34.61	2.59
0.32	3.93	58.01	8.80	0	0.1	34.64	3.15
0.34	1.91	53.29	6.75	0	0.1	39.65	1.85
0.36	2.04	53.20	6.46	0	0.1	40.06	1.79
0.38	4.38	58.76	8.72	0	0.1	34.74	5.65
0.24	3.47	57.05	8.89	0	0.1	34.53	1.44

```
age <- seq(1,10) #this age depend of your specie

BinLen <- data$Length_bins

NObsFre <- length(data$Observed_frequencies[,1]) #this numbers of observations depend of the own data

ObsFre <- data$Observed_frequencies

PredFre <- data$Predicted_frequency

CatchLFre<- data$Catch_length_frequency

ProbLen <- data$Probability_of_length

Nage <- length(data$Probability_of_length[,1])
```

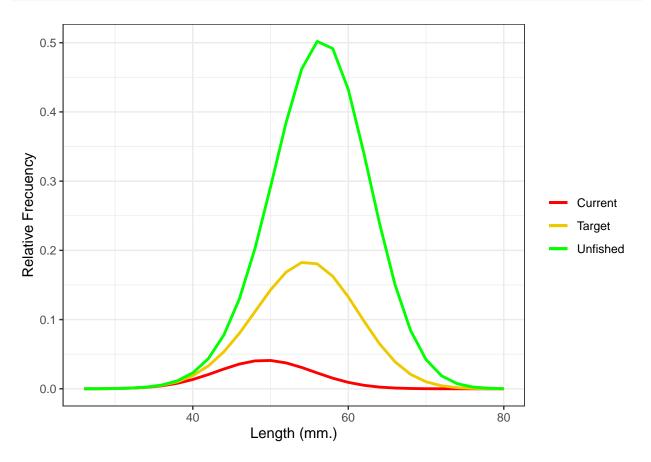


Figure 1: Outputs of different relative Length estimated in LBPA

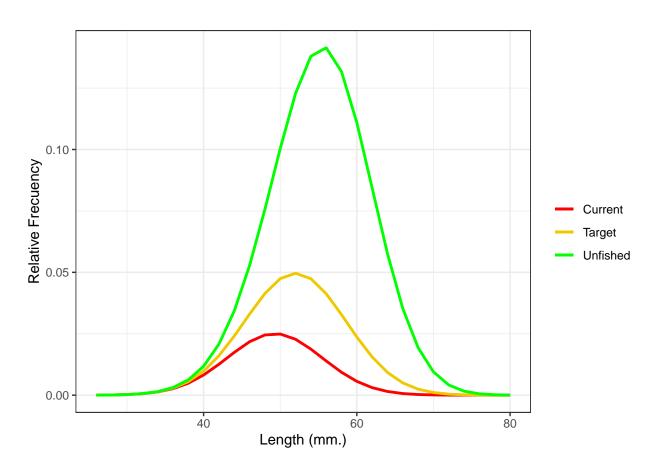


Figure 2: Outputs of different relative Length estimated in LBPA

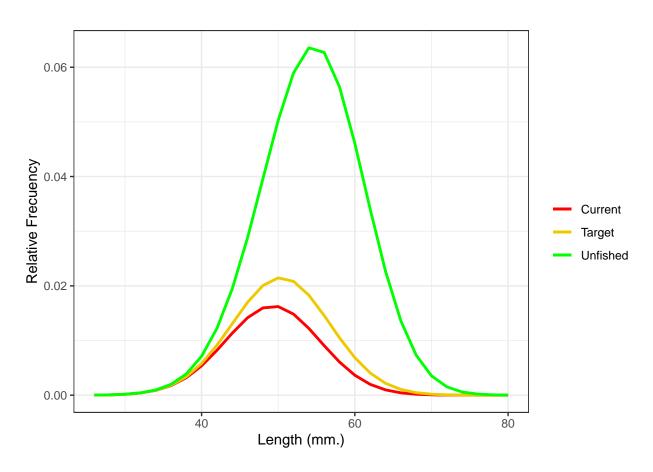


Figure 3: Outputs of different relative Length estimated in LBPA