Casal2 krill modeling

Doug Kinzey, NOAA Southwest Fisheries Science Center

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Read Casal2 R libraries

```
R.libr.path <- 'c:/zot/Casal2/2023/R-Libraries/R/'
# local path to R libraries for Casal2
mpd.path <- 'c:/zot/Casal2/2023/6jun/jun9_github/krill.e.txt'
# AMLR biomass model outputs ('krill.e.txt')
nasc.path <- 'c:/zot/Casal2/2023/6jun/jun9_github/krill.nasc.txt'
# AMLR NASC model outputs ('krill.nasc.txt')
output.path <- 'c:/zot/Casal2/2023/6jun/jun9_github/'

r.scrpts <- dir(R.libr.path)
for(i in 1:length(r.scrpts)) # read Casal2 R libraries
  source(paste(R.libr.path,r.scrpts[i],sep=''))
```

Extract Casal2 mpd outputs, create and set working directory

```
krill.b <- extract.mpd(mpd.path)  # AMLR acoustic biomass model
krill.n <- extract.mpd(nasc.path) # AMLR acoustic NASC model

setwd(output.path)
if(!dir.exists('krill_figs')){
    dir.create('krill_figs')
    }

setwd(paste(output.path,'krill_figs',sep=''))
```

Figure 1: Krill catches

```
Fig1 <- function(){
par(cex=1.2)
plot(krill.b$Instantaneous_Mortality$year,krill.b$Instantaneous_Mortality$`catch[K48.1]`,
  ylab = 'Catch (tonnes)',xlab = 'Year', main='krill catch',type='l',lwd=3
  )
}
Fig1()
```
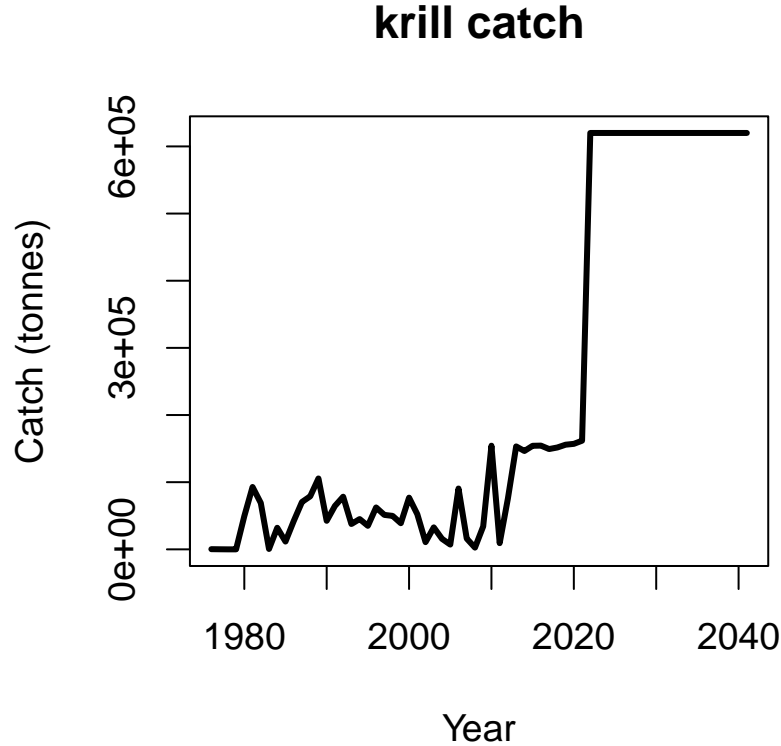
krill catch

Figure 1. Krill catches from 1976 to 2021 for Subarea 48.1, and projected catches of 620,000 tonnes from 2022 to 2041 for the combined AMLR sampling strata.

Figure 2a: SSB, AMLR biomass surveys

```
Fig2a <- function(){
par(cex=1.2)
y.lim <- c(0,max(krill.b$AMLRsrv$Values$observed / krill.b$AMLRsrv$Values$error_value,
  krill.b$synop_biom$Values$observed / krill.b$synop_biom$Values$error_value,
  krill.b$synop_biom$Values$observed * krill.b$synop_biom$Values$error_value,
  krill.b$AMLRsrv$Values$expected / krill.b$AMLRsrv$Values$error_value,
  krill.b$synop_biom$Values$expected / krill.b$synop_biom$Values$error_value,
  krill.b$synop_biom$Values$expected * krill.b$synop_biom$Values$error_value))
plot(1996:2021, krill.b$AMLRsrv$Values$expected[match(1996:2021,
  krill.b$AMLRsrv$Values$year)],ylab='Survey biomass (tonnes)',xlab='Year',
  main='observed 95% CI',type='l',lwd=5,ylim=y.lim,col='#95D840FF'
  )
points(1996:2021, krill.b$AMLRsrv$Values$observed[match(1996:2021,
  krill.b$AMLRsrv$Values$year)],pch=19)
lines(krill.b$FsrvBiomass$Values$year[match(1996:2021,krill.b$FsrvBiomass$Values$year)],
  krill.b$FsrvBiomass$Values$expected[match(1996:2021,krill.b$FsrvBiomass$Values$year)],
  col='#95D840FF',lwd=5)
points(krill.b$FsrvBiomass$Values$year[match(1996:2021,krill.b$FsrvBiomass$Values$year)],
```

```
    krill.b$FsrvBiomass$Values$observed[match(1996:2021,krill.b$FsrvBiomass$Values$year)]
    ,pch=19)
segments(
  krill.b$AMLRsrv$Values$year, krill.b$AMLRsrv$Values$observed *
  krill.b$AMLRsrv$Values$error_value,
  krill.b$AMLRsrv$Values$year, krill.b$AMLRsrv$Values$observed /
  krill.b$AMLRsrv$Values$error_value,
  lwd=4)
segments(
  krill.b$FsrvBiomass$Values$year[match(1996:2021,krill.b$FsrvBiomass$Values$year)],
  krill.b$FsrvBiomass$Values$observed[match(1996:2021,krill.b$FsrvBiomass$Values$year)] *
  krill.b$FsrvBiomass$Values$error_value[match(1996:2021,krill.b$FsrvBiomass$Values$year)],
  krill.b$FsrvBiomass$Values$year[match(1996:2021,krill.b$FsrvBiomass$Values$year)],
  krill.b$FsrvBiomass$Values$observed[match(1996:2021,krill.b$FsrvBiomass$Values$year)] /
  krill.b$FsrvBiomass$Values$error_value[match(1996:2021,krill.b$FsrvBiomass$Values$year)],
  lwd=4)
points(krill.b$synop_biom$Values$year,krill.b$synop_biom$Values$observed,pch= 2,
  col='#95D840FF',cex=1.5,lwd=4)
segments(
  krill.b$synop_biom$Values$year,krill.b$synop_biom$Values$observed *
  krill.b$synop_biom$Values$error_value,
  krill.b$synop_biom$Values$year,krill.b$synop_biom$Values$observed /
  krill.b$synop_biom$Values$error_value,
  col='#95D840FF',lwd=5,lty=2
  )
}
Fig2a()
```
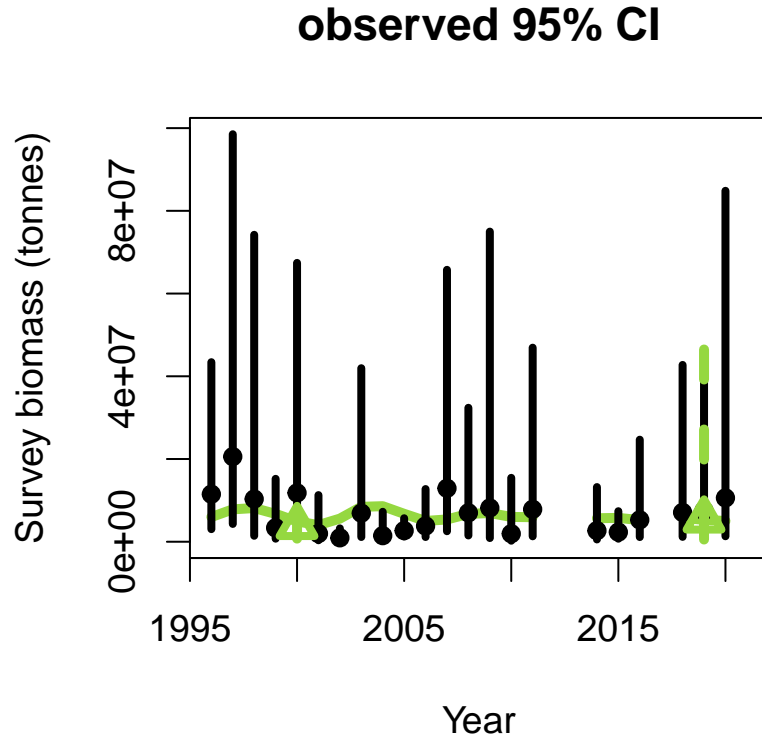
observed 95% CI

Figure 2. (A) Observed acoustic survey biomasses from U. S. AMLR (1996 to 2011) and fishery surveys (2014-2016, 2018-2020). Dark points represent annual mean biomasses with vertical dark line segments representing 95% lognormal CIs (WG-EMM-2021-05r1). Green horizontal lines are the fitted values to the data. Green triangles and dashed vertical lines in 2000 and 2019 represent mean biomasses with 95% lognormal CIs for the synoptic surveys. (B) Observed U. S. AMLR acoustic survey (1996 to 2011) NASC attributed to krill. Fisheries and synoptic survey values remain as biomass.
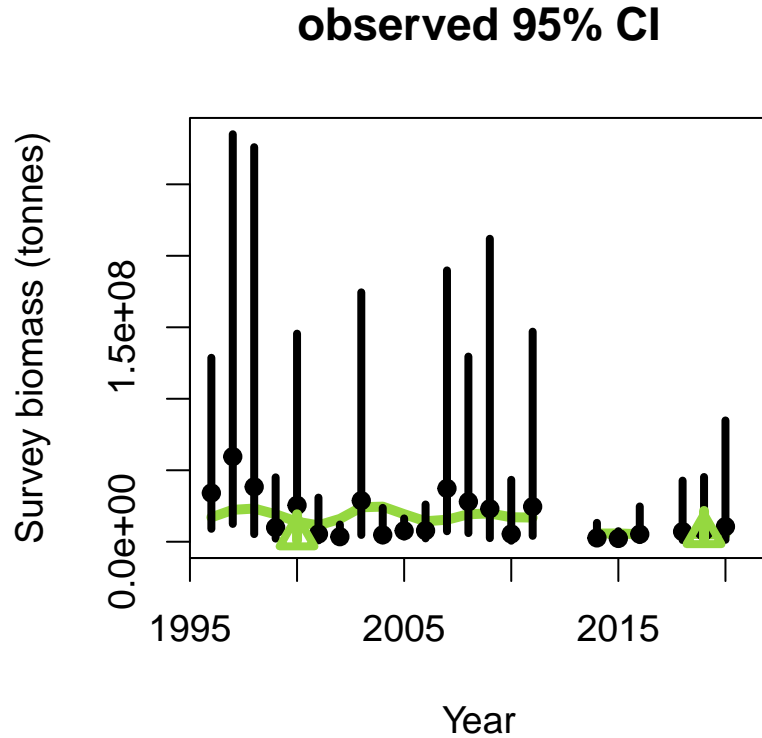
Figure 2b

```
Fig2b <- function(){
par(cex=1.2)
y.lim <- c(0,max(krill.n$AMLRsrv$Values$observed / krill.n$AMLRsrv$Values$error_value,
  krill.n$synop_biom$Values$observed / krill.n$synop_biom$Values$error_value,
  krill.n$synop_biom$Values$observed * krill.n$synop_biom$Values$error_value,
  krill.n$AMLRsrv$Values$expected / krill.n$AMLRsrv$Values$error_value,
  krill.n$synop_biom$Values$expected / krill.n$synop_biom$Values$error_value,
  krill.n$synop_biom$Values$expected * krill.n$synop_biom$Values$error_value))
plot(1996:2021, krill.n$AMLRsrv$Values$expected[match(1996:2021,
  krill.n$AMLRsrv$Values$year)],ylab='Survey biomass (tonnes)',xlab='Year',
  main='observed 95% CI',type='l',lwd=5,ylim=y.lim,col='#95D840FF'
  )
points(1996:2021, krill.n$AMLRsrv$Values$observed[match(1996:2021,
  krill.n$AMLRsrv$Values$year)],pch=19)
lines(krill.n$FsrvBiomass$Values$year[match(1996:2021,krill.n$FsrvBiomass$Values$year)],
```

```
    krill.n$FsrvBiomass$Values$expected[match(1996:2021,krill.n$FsrvBiomass$Values$year)],
    col='#95D840FF',lwd=5)
points(krill.n$FsrvBiomass$Values$year[match(1996:2021,krill.n$FsrvBiomass$Values$year)],
    krill.n$FsrvBiomass$Values$observed[match(1996:2021,krill.n$FsrvBiomass$Values$year)],
    pch=19)
segments(
    krill.n$AMLRsrv$Values$year, krill.n$AMLRsrv$Values$observed *
    krill.n$AMLRsrv$Values$error_value,
    krill.n$AMLRsrv$Values$year, krill.n$AMLRsrv$Values$observed /
    krill.n$AMLRsrv$Values$error_value,lwd=4)
segments(
    krill.n$FsrvBiomass$Values$year[match(1996:2021,krill.n$FsrvBiomass$Values$year)],
    krill.n$FsrvBiomass$Values$observed[match(1996:2021,krill.n$FsrvBiomass$Values$year)] *
    krill.n$FsrvBiomass$Values$error_value[match(1996:2021,krill.n$FsrvBiomass$Values$year)],
    krill.n$FsrvBiomass$Values$year[match(1996:2021,krill.n$FsrvBiomass$Values$year)],
    krill.n$FsrvBiomass$Values$observed[match(1996:2021,krill.n$FsrvBiomass$Values$year)] /
    krill.n$FsrvBiomass$Values$error_value[match(1996:2021,krill.n$FsrvBiomass$Values$year)],
    lwd=4)
points(krill.n$synop_biom$Values$year,krill.n$synop_biom$Values$observed,pch= 2,
    col='#95D840FF',cex=1.5,lwd=4)
segments(
    krill.n$synop_biom$Values$year,krill.n$synop_biom$Values$observed *
    krill.n$synop_biom$Values$error_value,
    krill.n$synop_biom$Values$year,krill.n$synop_biom$Values$observed /
    krill.n$synop_biom$Values$error_value,
    col='#95D840FF',lwd=5,lty=2
    )
}
Fig2b()
```

observed 95% CI

Order length-frequency datasets by year for Figures 3-5

```
df <- krill.b$ProportionAtLength_Fshry$Values[order(
  krill.b$ProportionAtLength_Fshry$Values[,'length'],
  krill.b$ProportionAtLength_Fshry$Values[,'year']),]
dfAMLR <- krill.b$ProportionAtLength_trawl$Values[order(
  krill.b$ProportionAtLength_trawl$Values[,'length'],
  krill.b$ProportionAtLength_trawl$Values[,'year']),]
dfGerman <- krill.b$ProportionAtLength_German$Values[order(
  krill.b$ProportionAtLength_German$Values[,'length'],
  krill.b$ProportionAtLength_German$Values[,'year']),]
```

Figure 3a

```
Fig3a <- function(){
par(cex=1.2)
plot(dfAMLR$year,as.numeric(as.character(dfAMLR$length)),cex=dfAMLR$observed*10,pch=19,
     col=ifelse(dfAMLR$observed>0,'black','white'),
     main= 'AMLR observed length frequencies',
     ylim=c(0,64),ylab= 'length (proportion X 10)', xlab= 'Year')
```

```
}
Fig3a()
```

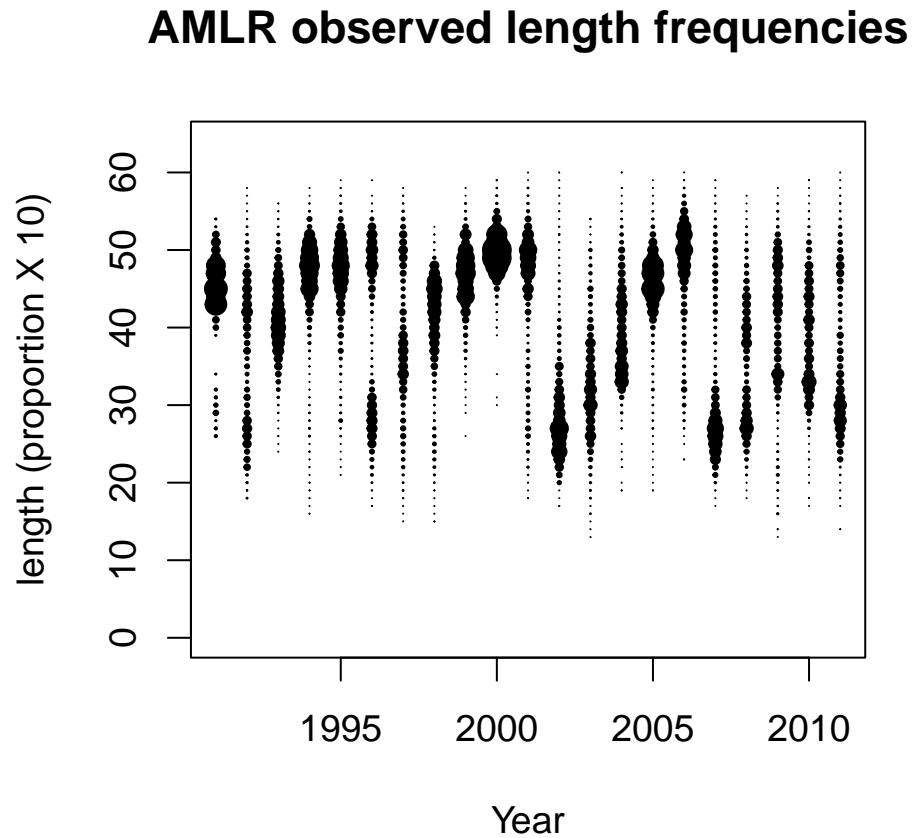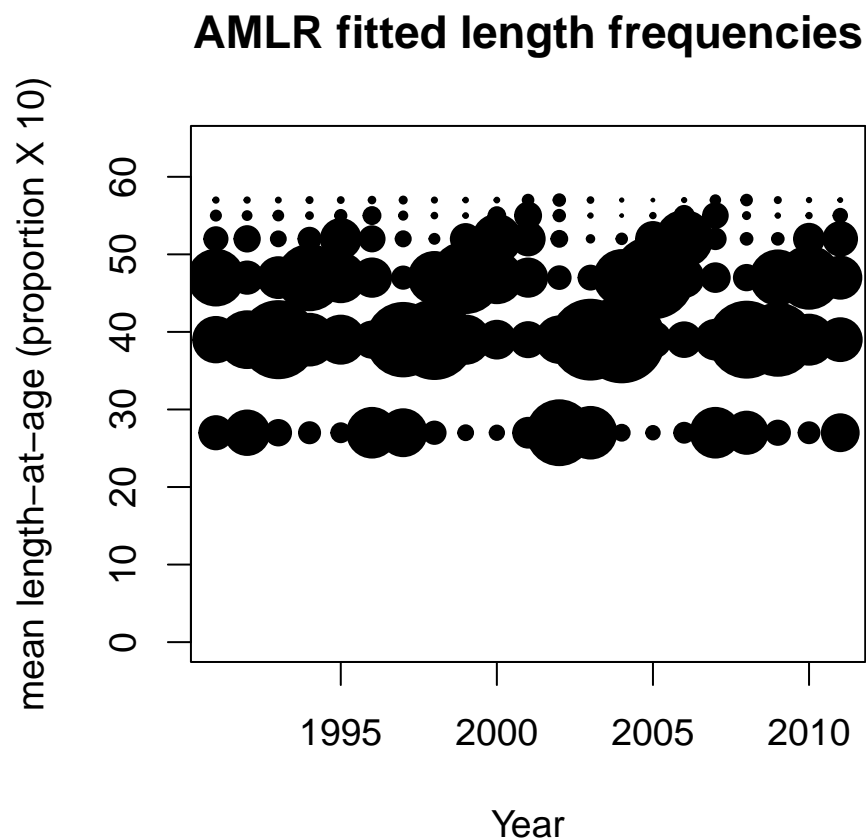# AMLR observed length frequencies

Figure 3. (A) Observed length-frequencies from AMLR surveys from 1992 to 2011. (B) Casal2 fitted length-frequencies. The fitted frequencies are for the mean lengths-at-age from the von Bertalanffy growth curve for ages one to six each year.

Figure 3b

```
Fig3b <- function(){
par(cex=1.2)
plot(dfAMLR$year,as.numeric(as.character(dfAMLR$length)),cex=dfAMLR$expected*10,pch=19,
    col=ifelse(dfAMLR$expected>0,'black','white'),
    main= 'AMLR fitted length frequencies',
    ylim=c(0,64),ylab= 'mean length-at-age (proportion X 10)', xlab= 'Year')
}
Fig3b()
```

AMLR fitted length frequencies

Figure 4. (A) Observed length-frequencies from the observer database for fishery surveys from 2014 to 2016 and 2018 to 2020. (B) Casal2 fitted length-frequencies. The fitted frequencies are from the von Bertalanffy growth curve as in Figure 2.

Figure 4a fishery observed lfs

```
Fig4a <- function(){
par(cex=1.2)
plot(df$year,as.numeric(as.character(df$length)),cex=df$observed*10,pch=19,
    col=ifelse(df$observed>0,'black','white'),
    main= 'Fishery observed length frequencies',
    ylim=c(0,64),ylab= 'length (proportion X 10)', xlab= 'Year')
}
Fig4a()
```

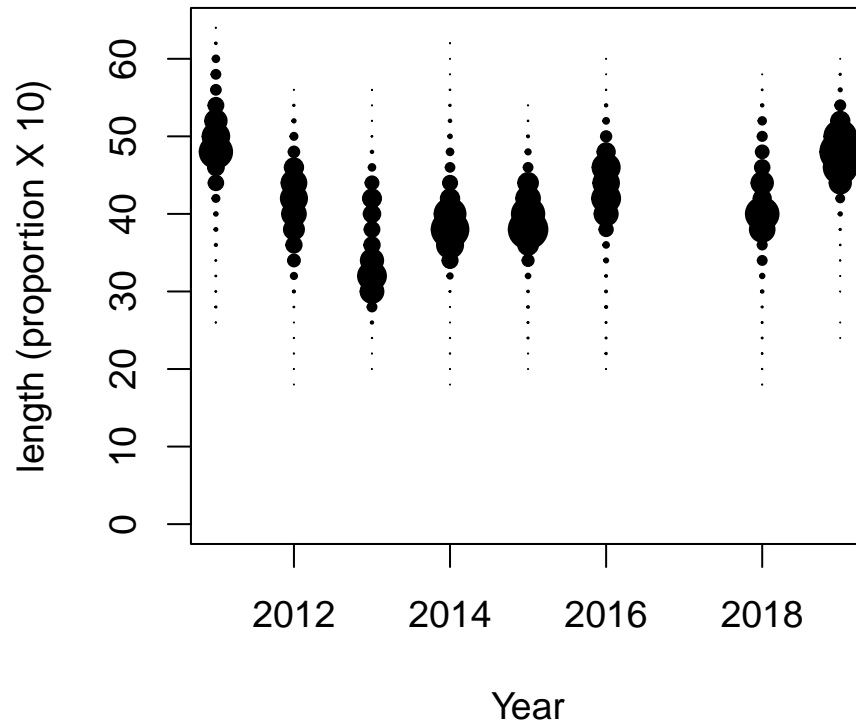# Fishery observed length frequencies

Figure 4b Fishery fitted lfs

```
Fig4b <- function(){
par(cex=1.2)
plot(df$year,as.numeric(as.character(df$length)),cex=df$expected*10,pch=19,
    col=ifelse(df$expected>0,'black','white'),
    main= 'Fishery fitted length frequencies',
    ylim=c(0,64),ylab= 'mean length-at-age (proportion X 10)', xlab= 'Year')
}
Fig4b()
```
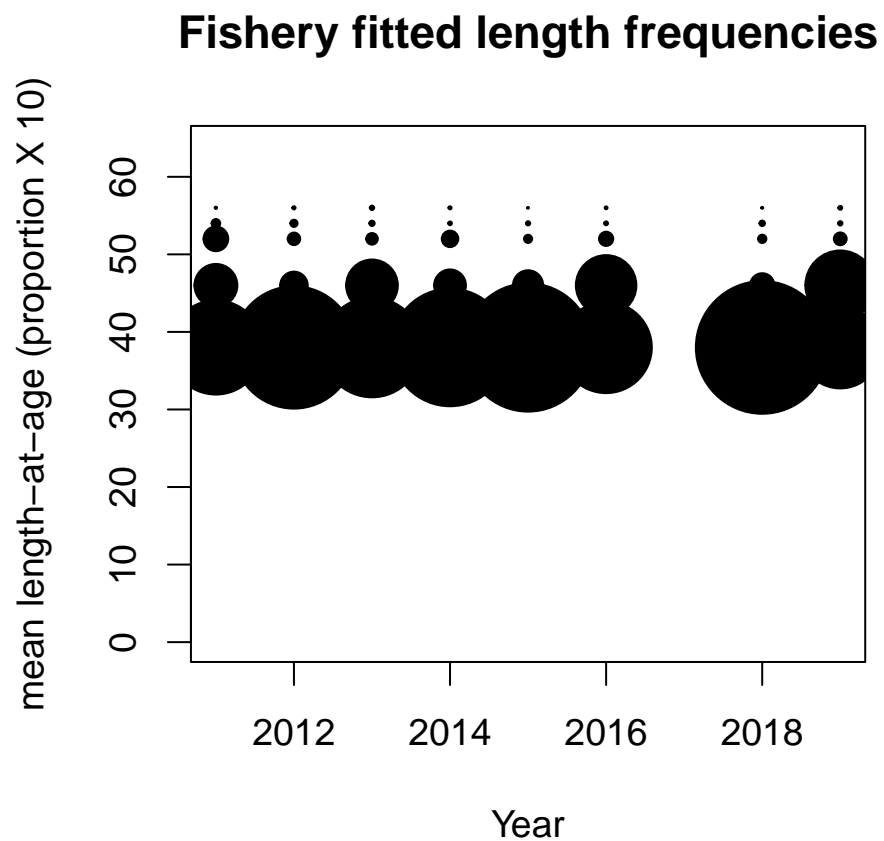
Figure 5a

```r
Fig5a <- function(){
par(cex=1.2)
plot(dfGerman$year,as.numeric(as.character(dfGerman$length)),cex=dfGerman$observed*10,
  pch=19,col=ifelse(dfGerman$observed>0,'black','white'),ylim=c(0,64),
    main= 'German observed length frequencies',
    ylab= 'Age (proportion X 10)', xlab= 'Year')
}
Fig5a()
```
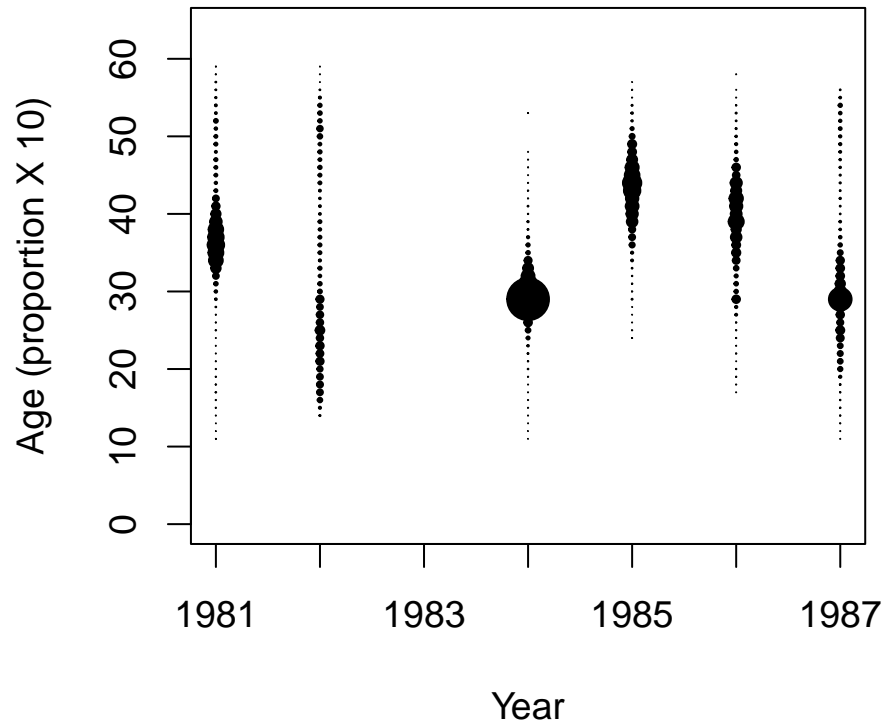
German observed length frequencies

Figure 5. (A) Observed length-frequencies from German research surveys in 1981, 1982, and 1984-1987. (B) Casal2 fitted length-frequencies. The fitted frequencies are from the von Bertalanffy growth curve as in Figure 2.

Figure 5b

```
Fig5b <- function(){
par(cex=1.2)
plot(dfGerman$year,as.numeric(as.character(dfGerman$length)),cex=dfGerman$expected*10,
  pch=19,col=ifelse(dfGerman$expected>0,'black','white'),ylim=c(0,64),
    main= 'German fitted length frequencies',
    ylab= 'mean length-at-age (proportion X 10)', xlab= 'Year')
}
Fig5b()
```
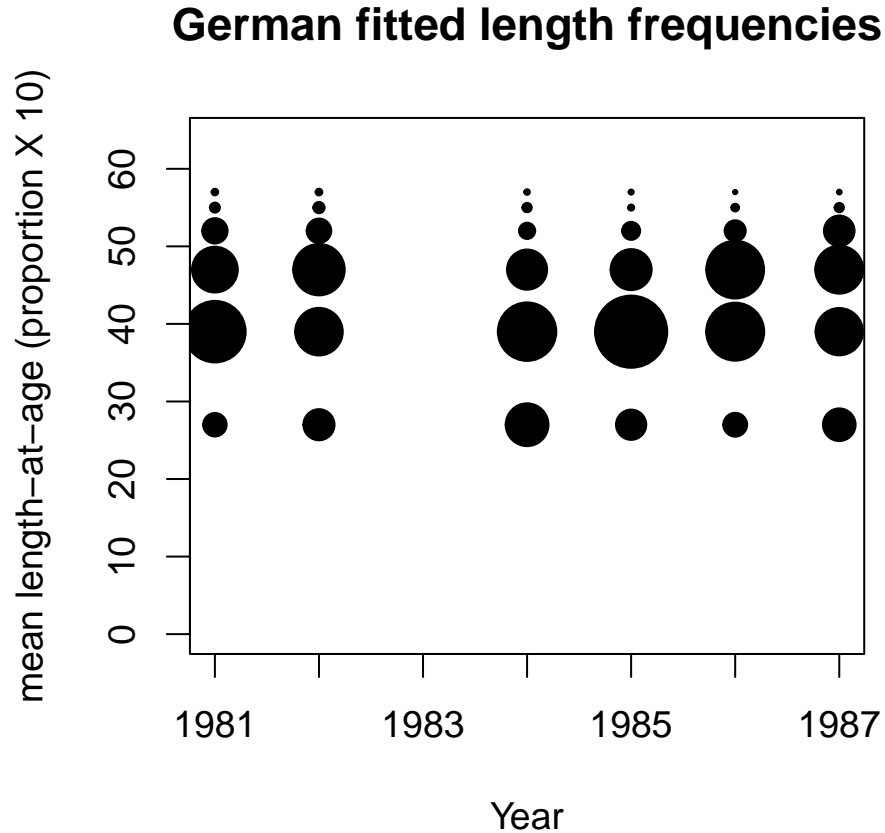
German fitted length frequencies

Figure 6 selectivities (AMLR biomass)

```
Fig6 <- function(){
plot(names(krill.b$krillFSel$Values),krill.b$krillFSel$Values,
  main='Krill Selectivities (A<LR biomass)',xlab = 'Length (mm)',ylab = 'Length Selectivity',type='l',
  lwd=3,col='#95D840FF')
  lines(names(krill.b$trawlSel$Values),krill.b$trawlSel$Values,col='#404788FF',lwd=3,lty=1)
  lines(names(krill.b$AMLR_Sel$Values),krill.b$AMLR_Sel$Values,col='#404788FF',lwd=3,lty=2)
  lines(names(krill.b$FbiomSel$Values),krill.b$FbiomSel$Values,col='#95D840FF',lwd=3,lty=2)
  legend(3,0.4,lty=c(1,1,2,2),col=c('#95D840FF','#404788FF','#404788FF','#95D840FF'),
    c('Fishery_lfs','AMLR_lfs','AMLRacoustics','FisheryAcoustics'),lwd=3,cex=0.8)
}
Fig6()
```
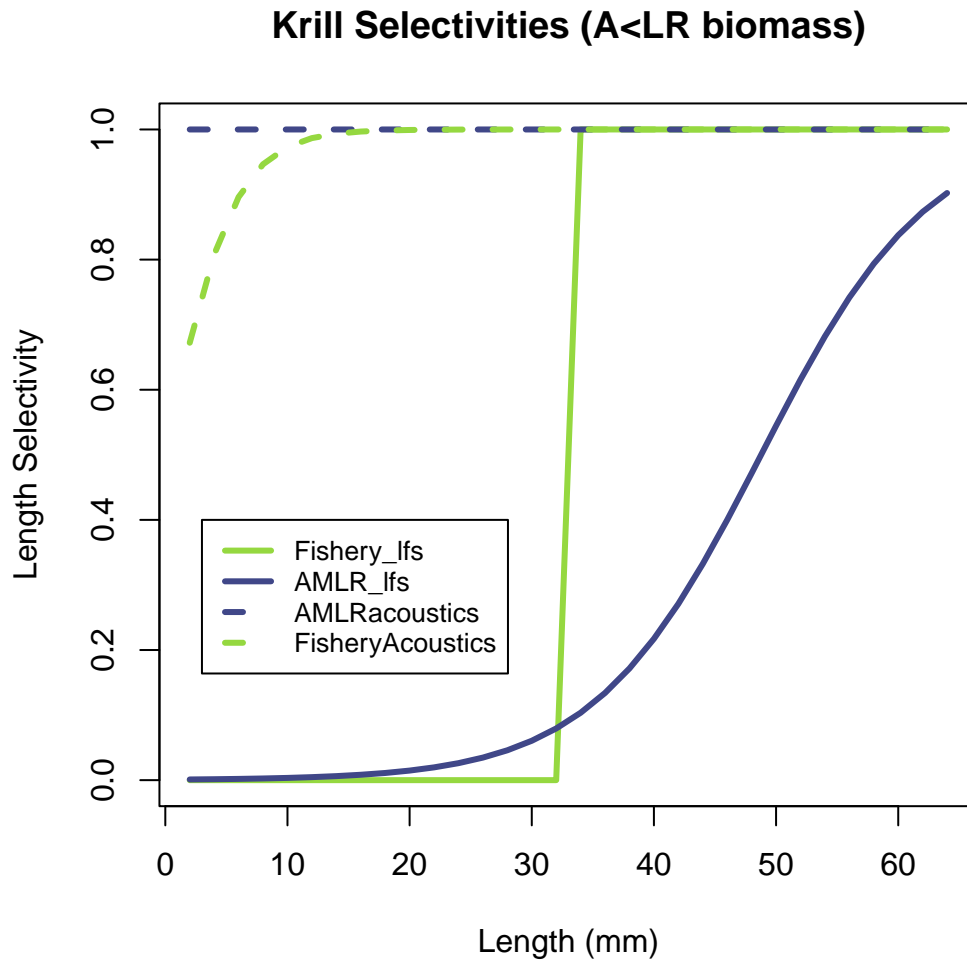
Krill Selectivities (A<LR biomass)

Figure 6. Estimated selectivities for length-frequencies and acoustic survey data from AMLR and fisheries.

Figure 6 selectivities (AMLR NASC)

```
Fig6nasc <- function(){
plot(names(krill.n$krillFSel$Values),krill.n$krillFSel$Values,
  main='Krill Selectivities (AMLR NASC)',xlab = 'Length (mm)',ylab = 'Length Selectivity',
  type='l',lwd=3,col='#95D840FF')
  lines(names(krill.n$trawlSel$Values),krill.n$trawlSel$Values,col='#404788FF',lwd=3,lty=1)
  lines(names(krill.n$AMLR_Sel$Values),krill.n$AMLR_Sel$Values,col='#404788FF',lwd=3,lty=2)
  lines(names(krill.n$FbiomSel$Values),krill.n$FbiomSel$Values,col='#95D840FF',lwd=3,lty=2)
  legend(3,0.4,lty=c(1,1,2,2),col=c('#95D840FF','#404788FF','#404788FF','#95D840FF'),
    c('Fishery_lfs','AMLR_lfs','AMLRacoustics','FisheryAcoustics'),lwd=3,cex=0.8)
}
Fig6nasc()
```
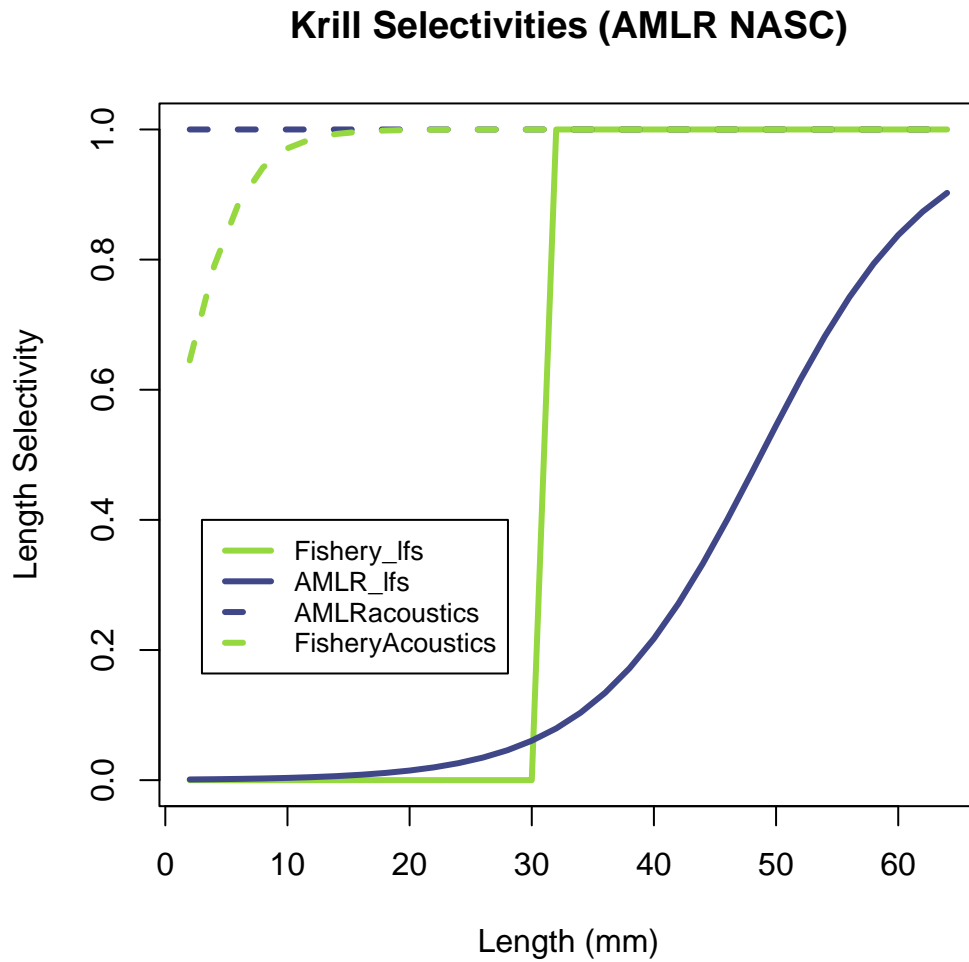
Krill Selectivities (AMLR NASC)

Figure 7 recruits

```
Fig7 <- function(){
par(cex=1.2)
plot(krill.b$Recruitment$model_year,krill.b$Recruitment$recruits,
  ylab='Recruits',xlab='Year',main='Estimate',type='l',lwd=3,col='#95D840FF'
  )
lines(krill.n$Recruitment$model_year,krill.n$Recruitment$recruits,lwd=3,
  lty=2,col='#404788FF')
legend(1976,3.0e+13,c('Biomass','NASC'),lty=c(1,2),col=c('#95D840FF','#404788FF'),lwd=3,
  cex=0.9)
}
Fig7()
```
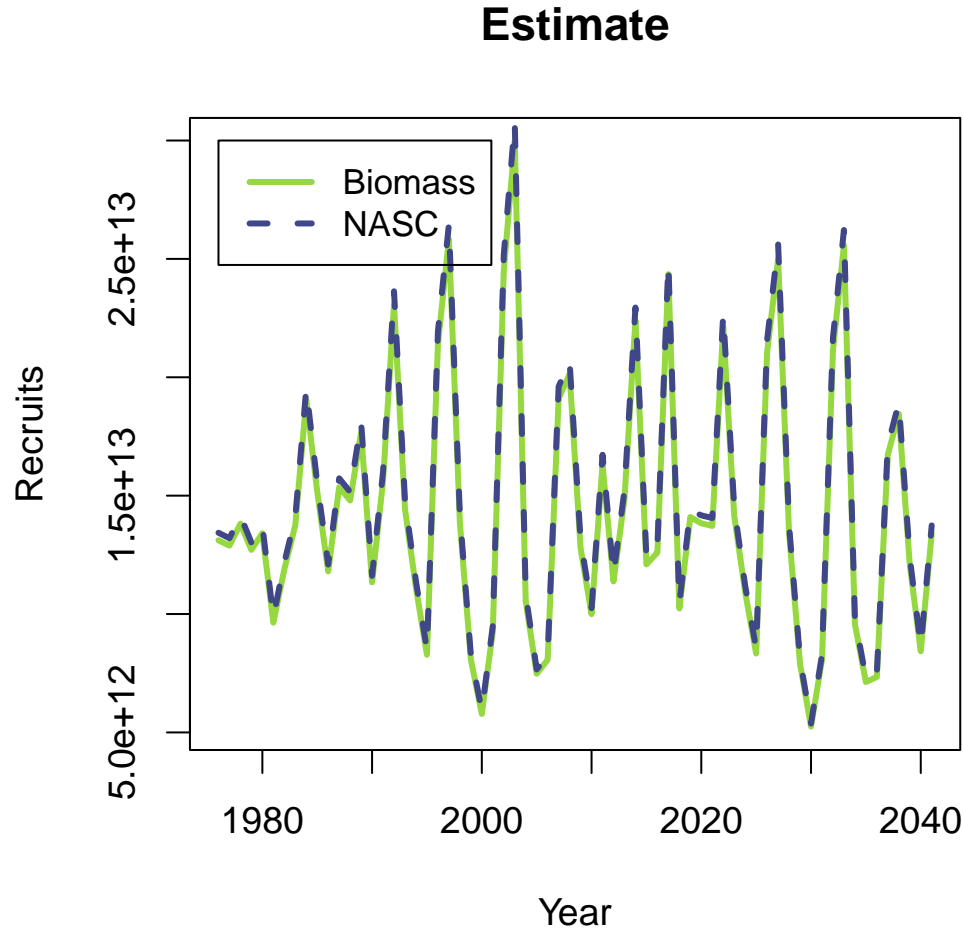
Estimate

Figure 7. Recruitment estimates for 1976-2041. Recruitment for 2022-2041 is assigned based on standardized recruitment multipliers estimated for 1992-2011.

Figure 8a spawning stock biomass with synoptic survey 95% CIs

```
Fig8a <- function(){
par(cex=1.2)
y.lim <- c(0,max(c(krill.b$SSB$SSB$values,
  krill.b$synop_biom$Values$observed * krill.b$synop_biom$Values$error_value,
  krill.b$synop_biom$Values$observed / krill.b$synop_biom$Values$error_value)))
plot(names(krill.b$SSB$SSB$values),krill.b$SSB$SSB$values,
  ylab='SSB',xlab='Year',main='Estimate',type='l',lwd=4,
  ylim=y.lim
  )
points(krill.b$synop_biom$Values$year,krill.b$synop_biom$Values$observed,
  col='#95D840FF',lwd=4,pch=2)
segments(
  krill.b$synop_biom$Values$year,krill.b$synop_biom$Values$observed *
```

```
    krill.b$synop_biom$Values$error_value,
    krill.b$synop_biom$Values$year,krill.b$synop_biom$Values$observed /
    krill.b$synop_biom$Values$error_value,
    col='#95D840FF',lwd=4
    )
abline(h= krill.b$SSB$SSB$`initialisation_phase[1]`,lty=2,lwd=4)
}
Fig8a()
```
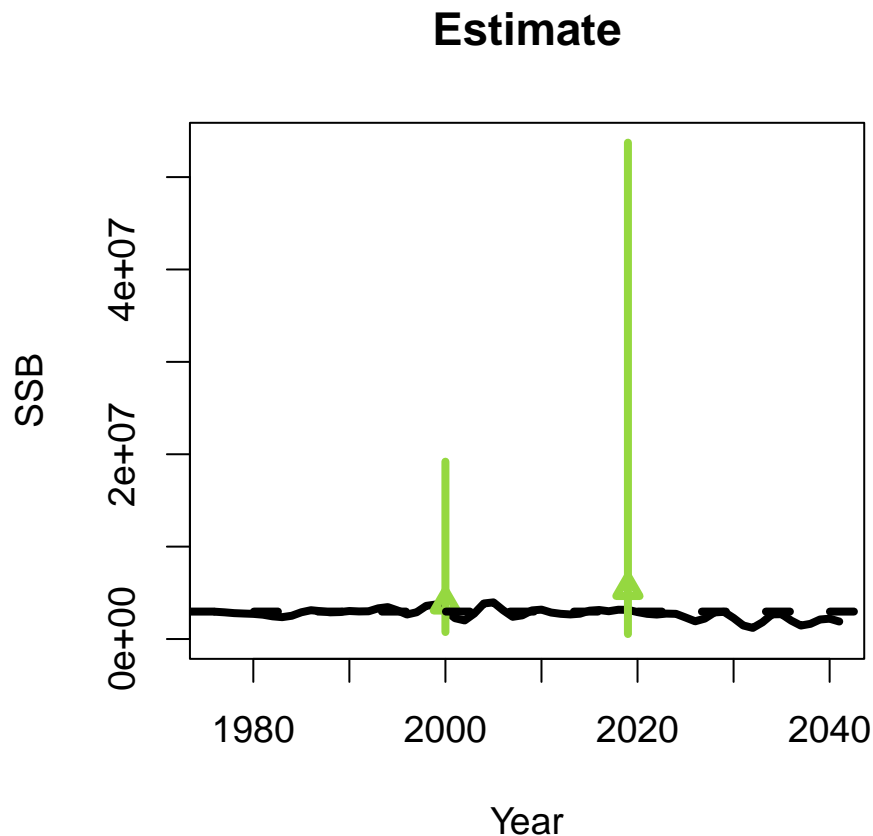
Estimate

Figure 8. (A) Spawning biomass estimates during 1992-2021 and projected for 2022-2041 (based on 620,000 tonnes annual catches) from the Casal2 model. Synoptic survey means (triangles) and 95% CIs (lines) are in green. Dashed line is unexploited spawning biomass. (B) Same spawning biomass estimates without synoptic survey scaling using AMLR biomass and NASC as model inputs.

Figure 8b spawning stock biomass

```
Fig8b <- function(){
par(cex=1.2)
y.lim <- c(0,max(c(krill.b$SSB$SSB$values
  )))
```

```
plot(names(krill.b$SSB$SSB$values),krill.b$SSB$SSB$values,col='#95D840FF',
  ylab='SSB',xlab='Year',main='Estimate',type='l',lwd=3,
  ylim=y.lim
  )
lines(names(krill.n$SSB$SSB$values), krill.n$SSB$SSB$values,col='#404788FF',lwd=3,lty=2)
abline(h= krill.b$SSB$SSB$`initialisation_phase[1]`,lty=2,lwd=2)
legend(1977,1e+06,c('Biomass','NASC'),lty=c(1,2),col=c('#95D840FF','#404788FF'),lwd=3)
}
Fig8b()
```
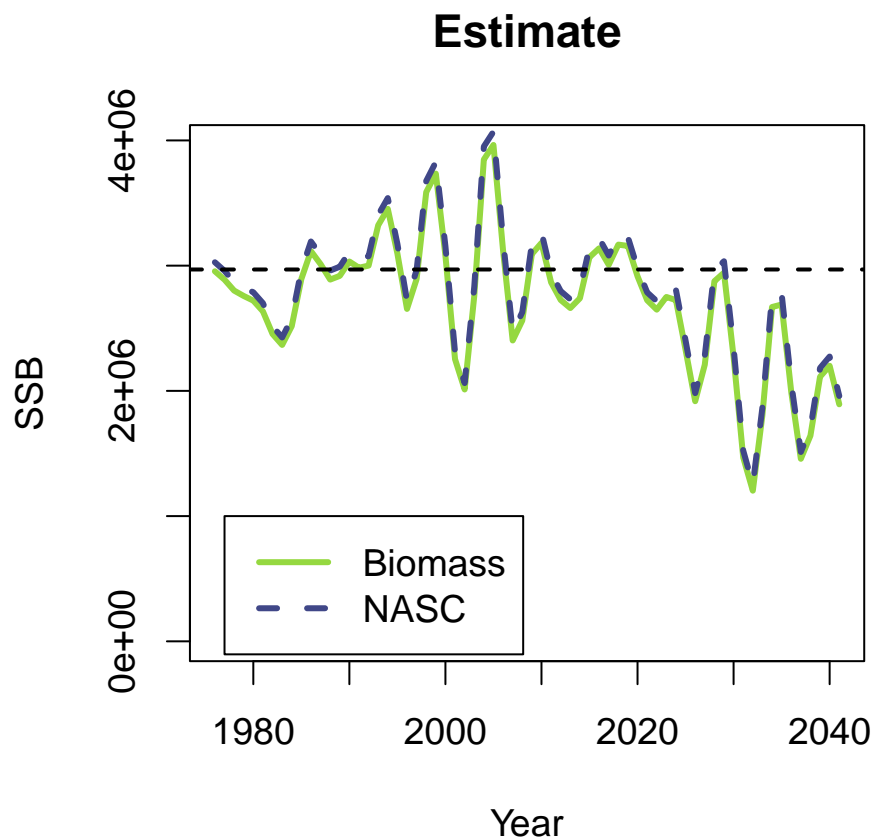

Figure 9 Fishing mortality

```
Fig9 <- function(){
par(cex=1.2)
plot(krill.b$Instantaneous_Mortality$year,krill.b$Instantaneous_Mortality$
  'exploitation_rate[K48.1]',ylab= 'Exploitation rate', xlab= 'Year',
   main = 'Estimate exploitation rate',type='l',lwd=3
  )
}
Fig9()
```
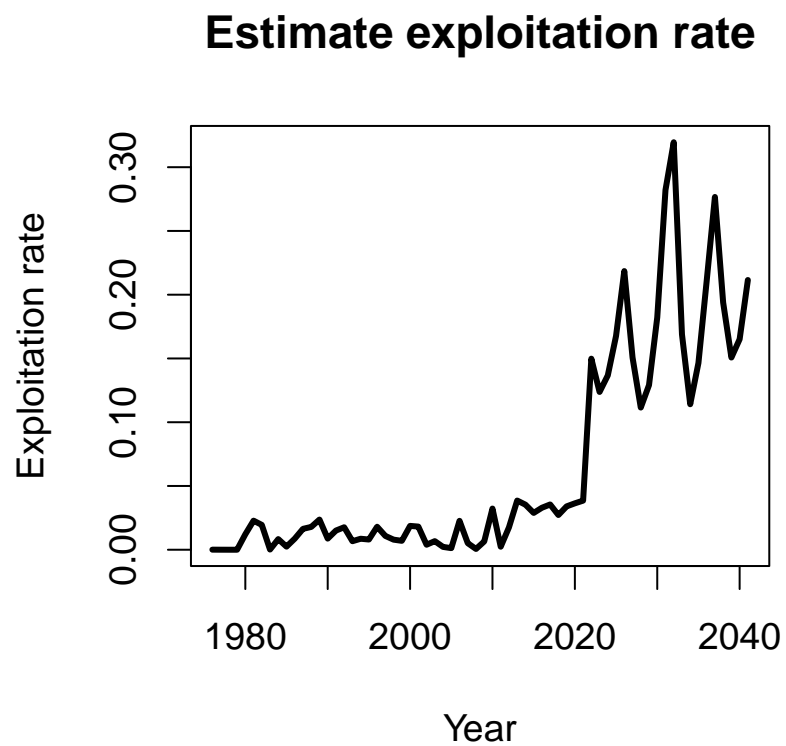
Estimate exploitation rate

Figure 9. Estimated annual exploitation rates with historical catches and with 620,000 tonnes/year future catches.