

EBM Nature Communications main script

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Code used to generate intermediate and final data for Holsman et al. in review Nature Communications paper

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Input data:

Option 1: Re-generate final data for plots

If running plotting code below (recommended) you will need to download the final data “EBM_ceattlenew.Rdata” from figshare and place it in the main directory: “EBM_Holsman_NatComm/EBM_ceattlenew.Rdata”.

- access EBM_ceattlenew.Rdata here: <https://figshare.com/s/6dea7722df39e07d79f0> and place it in the directory: EBM_Holsman_NatComm/EBM_ceattlenew.Rdata. (Data DOI:10.6084/m9.figshare.11864505)

Option 2: Re-running the intermediate data (not recommended)

If re-running the intermediate data analysis (not recommended) the following files will need to be downloaded unzipped and placed in the assesment_files folder:

- access aclim_00_JunV2_2019_2.zip here: <https://figshare.com/s/3a1aaa86837b79d6aa07> and place it in the EBM_Holsman_NatComm/data/runs/aclim_00_JunV2_2019_2.zip and unzip. (Data DOI: 10.6084/m9.figshare.11864586)
- access aclim_00_JunV2_2019_0.zip here: <https://figshare.com/s/d9c35dbe0880f4169041> and place it in the EBM_Holsman_NatComm/data/runs/aclim_00_JunV2_2019_0.zip and unzip (Data DOI: 10.6084/m9.figshare.11864577)

Intermediate data:

Intermediate data can be found in the main EBM_Holsman_NatComm in the form of .Rdata files but can be recreated from the ADMB model using the EBM_Holsman_NatComm/assessment_scripts/README_EBM_Holsman_An (not recommended; see below).

Figures and tables:

Final figures and tables (including illustrator files that were used to add fish icons) can be found in the **Figures** folder.

This is the main script for running analysis and plotting results and requires R version 3.5.3 (available at <https://cran.r-project.org/bin/macosx/el-capitan/base/>). To update the analysis using .Rdata outputs run the R() code below as is currently configured. If you want to update the intermediate data, set “readdat” to TRUE in line 80 below. The CEATTLE stock assessment is also included but requires AD Model builder (<http://www.admb-project.org>). To run the assessment scripts (not recommended or tested outside of macOSX) see “README_EBM_Holsman_Analysis.pdf”.

EMB_paper.R script:

```
## -----
## plotting code for EBM paper
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## Feb 2020
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## -----

# 1. Set up
# 2. load data
# 3. make figures

rm(list=ls())
graphics.off()

#-----
# 1. SET THINGS UP
#-----

# library(RmarineHeatWaves)
# library(plyr)
if(!require(dplyr)){ install.packages(dplyr)}else{library(dplyr)}
if(!require(ggplot2)){ install.packages(ggplot2)}else{library(ggplot2)}
if(!require(svMisc)){ install.packages(svMisc)}else{library(svMisc)}
if(!require(quantmod)){ install.packages(quantmod)}else{library(quantmod)}

main <- path.expand("~/GitHub_new/EBM_Holsman_NatComm/")
setwd(main)

update.figs <- FALSE
fldr <- "aclim_00_JunV2_2019" # folder with the CEATTLE assessment runs
UpdateMCMC <- 1 # update MCMC?
readdat <- FALSE # re-read in new data?
status <- TRUE # print updates
dpiIN <- 150
update.simlist <- FALSE # only TRUE when re-running enitre CEATTLE fitting

getnm<-function(nm=mclist0[1]){
  nmi<-strsplit(nm,split=paste0("Summary_proj_",fldr))[[1]][2]
  nmi<-strsplit(nmi,split="_mc")[[1]][1]
```

```

    return(paste0("dat",nmi,"_mc"))
  }

#-----
# 2. LOAD DATA
#-----

source("FUN_GG_EBM_paper.R")
source("FUN_EBM_paper.R")

if(readdat==FALSE){

  if(!any(dir()%in%"EBM_ceattlenew.Rdata"))
    download.file("https://figshare.com/s/6dea7722df39e07d79f0",destfile="EBM_ceattlenew.Rdata")
    load("EBM_ceattlenew.Rdata")
}else{
  source("SUB_EBM_paper.R")
  save.image(file = "EBM_ceattlenew.Rdata")
}

riskTypes      <- c("10% decline","50% decline","80% decline")
RISK            <- list("no cap" = risk12,"2 MT cap" = risk13)
timeF          <- levels(risk12$timeframe)

flList         <- dir("data/runs",paste0(fldr,"_0"))
txt            <- c("no cap"="_219_CENaivecf_2_5_12","2MT cap"="_2MT_219_CENaivecf1_2_5_13")
fldin          <- (paste0("data/runs/",fldr,"_2/projections/",fldr,txt,"/",fldr,txt,".ctl")) # KE
target_B_2     <- rbind(
  getBtarget(fldrIN=fldin[1],nm="B0_set"),
  getBtarget(fldrIN=fldin[2],nm="B0_set"))
rownames(target_B_2) <- names(txt)
txt            <- c("no cap"="_019_CENaivecf_0_5_12","2MT cap"="_2MT_019_CENaivecf1_0_5_13")
fldin          <- (paste0("data/runs/",fldr,"_0/projections/",fldr,txt,"/",fldr,txt,".ctl")) # KE
target_B_0     <- rbind(
  getBtarget(fldrIN=fldin[1],nm="B0_set"),
  getBtarget(fldrIN=fldin[2],nm="B0_set"))
rownames(target_B_0) <- names(txt)

# set the color scheme
coll_use       <- c(colors()[320],col2(6)[c(2,3,4)],col3(6)[c(3,4,6)])

# set up some plotting labels
A1B_n_sim     <- grep("A1B",simnames)
bio_n_sim     <- grep("bio",simnames)
rcp45_n_sim   <- grep("rcp45",simnames)
rcp85_n_sim   <- grep("rcp85",simnames)
rcp85NoBio_n_sim <- setdiff(rcp85_n_sim,bio_n_sim)
meanhistT     <- mean(TempC_219_CENaivecf_2_5_12_mc[s,,1][1,][hind_yrs])

```

```

# get target biomass from ctl files:
cumlyr <- function(x,sumyr=3){

  x<-as.numeric(x)
  x2<-x*0
  for(i in sumyr:length(x)){
    x2[i]<-ifelse(sum(x[i-(1:sumyr)+1])==sumyr,1,0)
  }
  return(x2==1)

}

# plot cumulative years above threshold:
plot_figS6<-function(){
  dev.new(height=3.25*1.3,width=4.5*1.3)
  head(TempC_019_CENaivecf_0_5_3_mc[1,1,,])
  above <- TempC_019_CENaivecf_0_5_3_mc[1,1,,]>2.16
  tt1 <- apply(above,2,cumlyr,sumyr=5)
  tt <- apply(tt1,2,cumsum)/length(above[,1])
  yrs2 <- as.numeric(rownames(above))
  findthrsh <- function(x,thrsh=.25,yrsIN=yrs2){
    yrsIN[as.numeric(x)>thrsh][1]
  }

  yrt <- apply(tt,2,findthrsh)
  plot(yrs2,tt)
  yrt[rcp85NoBio_n-1]
  yrt[rcp45_n-1]
  nscen <- length(c(rcp45_n,rcp85NoBio_n))
  plot(yrs2,tt[,2],ylim=c(0,nscen*1.2),xlim=c(1965,2100),type="l",col=NA,axes=F,ylab="",xlab="")
  axis(1)
  firstY<-rep(2017,nscen);names(firstY)<-colnames(tt1)[c(rcp45_n,rcp85NoBio_n)-1]

  for(i in 1:nscen){
    cc <- (c(rcp45_n,rcp85NoBio_n)-1)[i]
    ll <- NA*tt1[,cc]
    ll[tt1[,cc]] <- i
    suby <- yrs2[tt1[,cc]]
    if(any(suby>2017))
      firstY[i] <- suby[suby>2017][1]
    points(yrs2,ll,pch=16,cex=1.5,col=makeTransparent((wes(6))[i],alpha=250))
  }

  text(rep(1980,nscen),1:nscen,colnames(tt1)[c(rcp45_n,rcp85NoBio_n)-1],cex=.8,col=(wes(6))[1:nscen])
  mean(firstY[1:3],na.rm=T)
  mean(firstY[4:6],na.rm=T)
}

#-----
# 3. Final figures:
#-----
#fig 2: temperature

```

```

graphics.off()
GGplot_aclimTS(dat=allDat,h=2*1.3,w=4.75*1.3,
  ylab=expression(paste("Bottom temperature",'\^{o}','C'))),
  lty=c("solid",rep("solid",6)),
  subtitle_face="plain",
  plotSet=list(c(1,rcp45_n),c(1,rcp85NoBio_n)),
  coll=coll_use,tline=2,talpha=.5,
  xlab="",lgpos= "right",plot_marginIN=c(-10,-1,-10,1))

if(update.figs) ggsave(file=paste0("Figures/Fig2.tiff"), device = "tiff",
  scale = 1, width = NA, height = NA, units = "in",
  dpi = dpiIN)

#fig 3: delta B
# 50% quantiles
graphics.off()
GGplot_aclimCEATTLE_delta(h=4.75*1.3,w=4.75*1.3,
  nmLIST = list("SSB0"="dat_219_CENaivecf_2_5_12","SSB0"="dat_219_CENaivecf_2_5_12"),
  datLIST = list(dat1=B0_219_CENaivecf_2_5_12_mc,dat2=B0_219_CENaivecf_2_5_12_mc),
  valLIST = list(valIn1="SSB0_total_biom", valIn2="SSB0_total_biom"),
  prob=c(.01,.50,.9),plot_marginIN=c(-15,5,-10,5),alpha=c(10,5),lgpos= "bottom",coll=coll_use)

if(update.figs) ggsave(file=paste0("Figures/Fig3.tiff"), device = "tiff",
  scale = 1, width = NA, height = NA, units = "in",
  dpi = dpiIN)

#fig 4: delta C
# 50% quantiles

graphics.off()
GGplot_aclimCEATTLE_delta(deltaIN=TRUE,h=4.75*1.3,w=4.75*1.3,ydiv=1,
  ylim_up=c(100,100,100),ylim_down=c(-200,-200,-200),
  plot_marginIN=c(-15,5,-10,5),alpha=c(0,0),lwdd=c(.7,.3),plotpersist = FALSE,
  coll = coll_use,
  ylab = expression(paste(Delta," Catch (%)")),
  xlimIN = c(2010,2100),
  nmLIST = list("2 MT cap"="dat_2MT_219_CENaivecf1_2_5_13","no cap"="dat_219_CENaivecf_2_5_12"),
  valLIST = list(valIn1="Catch_total_biom", valIn2="Catch_total_biom"),
  datLIST = list(dat1=B_219_CENaivecf_2_5_12_mc,dat2=B_219_CENaivecf_2_5_12_mc),
  lgpos= "bottom",scalesIN="fixed")

if(update.figs) ggsave(file=paste0("Figures/Fig4.tiff"), device = "tiff",
  scale = 1, width = NA, height = NA, units = "in",
  dpi = dpiIN)

#fig 5: risk
graphics.off()
GGplot_aclimCEATTLE_risk(h=2*1.3,w=4*1.3,coll= c(col2(6)),sp=1,colvar="type",rowvar="sp",alpha=c(
  plot_marginIN=c(-15,0,-10,5),mode="MSM",lwdd=c(.7,.4,.4),rcpIN=c("RCP 8.5"="rcp85"),
  nrowlg = c(1,1),pchh=c(16,15),
  lgpos= "bottom",RISKTYPES = riskTypes[c(1,2,3)],lty=c("solid","solid","solid"))

```

```

    grid.force()
    # change shape of arrows
    grid.gedit("segments", gp=gpar(linejoin='mitre'))
    # change the shape in legend also
    grid.gedit("layout", gp=gpar(linejoin='mitre'))

if(update.figs) ggsave(file=paste0("Figures/Fig5.tiff"), device = "tiff",
    scale = 1, width = NA, height = NA, units = "in",
    dpi = dpiIN)

#fig 6: Threshold

dev.new(height=4.75*1.3,width=4.5*1.3)
PLOT_THRESHOLD2(
  multIN=10,
  firstdiff=T,
  ntemps=3,
  ylimIN =c(-1,1.5),
  xlimIN =c(1,7),
  trndln  = "white",
  trndln2 = Ornjazz[3],
  tipping = Ornjazz[5],
  sizeIN=c(0.1,.3,.75,2))

if(update.figs) ggsave(file=paste0("Figures/Fig6.tiff"), device = "tiff",
    scale = 1, width = NA, height = NA, units = "in",
    dpi = dpiIN)

# Fig S1: HCR

graphics.off()
GG_HCRplot(h=3.5,w=8,futScen="GFDL_rcp45",fontSize=3,yfont=c(2070,2073))

if(update.figs) ggsave(file=paste0("Figures/FigS1.tiff"), device = "tiff",
    scale = 1, width = NA, height = NA, units = "in",
    dpi = dpiIN)

# Fig S2: SSB with and without cap

GGplot_aclimCEATTLE_delta(deltaIN=F,h=4.75*1.3,w=4.75*1.3,ydiv=1e6,
  plot_marginIN=c(-15,5,-10,5),alpha=c(0,0),lwdd=c(.7,.3),
  ylabbb  = "Spawning biomass (million tons)",
  nmLIST  = list("2 MT cap"="dat_2MT_219_CENaivecf1_2_5_13","no cap"="dat_219_CENaivecf_2_5_12"),
  valLIST = list(valIn1="SSB_total_biom", valIn2="SSB_total_biom"),
  datLIST = list(dat1=B_219_CENaivecf_2_5_12_mc,dat2=B_219_CENaivecf_2_5_12_mc),
  lgnpos= "bottom",scalesIN="free_y")
if(update.figs) ggsave(file=paste0("Figures/FigS2.tiff"), device = "tiff",
    scale = 1, width = NA, height = NA, units = "in",
    dpi = dpiIN)

```

```
# Fig S3: effective F
```

```
graphics.off()
dev.new(height=3.5,weight=5)
plot_Feffective()
```

```
if(update.figs) ggsave(file=paste0("Figures/FigS3.tiff"), device = "tiff",
  scale = 1, width = NA, height = NA, units = "in",
  dpi = dpiIN)
```

```
# Fig S4: risk plot
```

```
graphics.off()
GGplot_aclimCEATTLE_risk(h=4.75*1.3,w=3.2*1.3,coll= c(col2(6)),colvar="type",rowvar="sp",alpha=c(
  plot_marginIN=c(-15,5,-10,5),mode="MSM",lwd=c(.7,.4,.4),rcpIN=c("RCP 8.5"="rcp85"),pchh=c(16,1),
  lgnpos= "bottom",RISKTYPES = riskTypes[c(1,3)],lty=c("solid","solid"))
```

```
grid.force()
# change shape of arrows
grid.gedit("segments", gp=gpar(linejoin = 'mitre'))
# change the shape in legend also
grid.gedit("layout", gp=gpar(linejoin = 'mitre'))
```

```
if(update.figs) ggsave(file=paste0("Figures/FigS4.tiff"), device = "tiff",
  scale = 1, width = NA, height = NA, units = "in",
  dpi = dpiIN)
```

```
# Fig S5: threshold 1
```

```
graphics.off()
dev.new(height=3*1.3,width=4.75*1.3)
```

```
PLOT_THRESHOLD(
  dataIN_1=tmpall12_1,
  dataIN_2=tmpall12_2,
  dataIN_3=tmpall12_3,
  firstdiff=F,
  ntemps=3,
  multIN=10,
  #ylimmIN =c(-1.5,1.5),
  #xlimIN =c(.5,7),
  ylimIN =c(-1,1.5),
  xlimIN =c(1,7),
  trndln = "white",
  trndln2 = Ornjazz[3],
  tipping = Ornjazz[5],
  sizeIN=c(0.1,.3,.75,2))
```

```
if(update.figs) ggsave(file=paste0("Figures/FigS5.tiff"), device = "tiff",
```

```
scale = 1, width = NA, height = NA, units = "in",  
dpi = dpiIN)  
  
# Fig S6: hindcast years  
plot_figS6()  
if(update.figs) quartz.save(file=paste0("Figures/Figs6_delta.pdf"), type = "pdf",  
width = 4.5*1.3, height = 3.25*1.3,dpi = dpiIN)
```