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:

Raw input data files ("EBM_ceattlenew.Rdata" and "data.zip") can be downloaded from Marine Data Archive [add link] and should be unzipped (if applicable) and placed in the main directory (i.e., "EBM_Holsman_NatComm/EBM_ceattlenew.Rdata"" and "EBM_Holsman_NatComm/data").

Intermediate data:

Intermediate data can be found in the main EBM_Holsman_NatComm in the form of .Rdata files.

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:

```r
## -----------------------------------------------
## 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)
   library(dplyr)
   library(ggplot2)
   library(svMisc)  #install.packages("svMisc")
   library( quantmod)

   main  <-  path.expand("~/Documents/D_AFSC_Files/Manuscripts/00_EBM_ACLIM_CEATTLE/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


   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){
       load("EBM_ceattlenew.Rdata")
   }else{
       source("SUB_EBM_paper.R")
```

```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")) # K
    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])
```

```r
    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,
      ylabb=expression(paste("Bottom temperature",'(',^{o},"C)")),
      ltyy=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,
      xlabb="",lgnpos= "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),
```

```r
        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),lgnpos= "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,
        ylimm_up=c(100,100,100),ylimm_dwn=c(-200,-200,-200),
        plot_marginIN=c(-15,5,-10,5),alpha=c(0,0),lwdd=c(.7,.3),plotpersist = FALSE,
        coll = coll_use,
        ylabb   = expression(paste(Delta," Catch (%)")),
        xlimmIN = 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),
        lgnpos= "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),
        lgnpos= "bottom",RISKTYPES = riskTypes[c(1,2,3)],ltyy=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,
```

```r
  ylimmIN =c(-1,1.5),
  xlimmIN =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),
        ylabb  = "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",lwdd=c(.7,.4,.4),rcpIN=c("RCP 8.5"="rcp85"),pchh=c(16,1
```

```r
        lgnpos= "bottom",RISKTYPES = riskTypes[c(1,3)],ltyy=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),
  #xlimmIN =c(.5,7),
  ylimmIN =c(-1,1.5),
  xlimmIN =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)
```