Farm MS figures

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```
knitr::opts_chunk$set(echo = TRUE,warning=FALSE,message=FALSE)

library(tidyverse)
library(spasm)
library(patchwork)
library(paletteer)
library(knitr)
library(beyonce)
```

Figures for ocean aquaculture impacts manuscript. First, one to define the model (fig 1), then represent general results and finally to give and idea of how changing key parameters like movement, attraction, farm size and impacts on the population change the results. Figure 1 will be a diagram of a farm that highlights and explains the parameters I mess with.

Figure 1: Farm diagram

Figure 2: Equilibrium catches at different MPA and farm sizes

Attraction is varied and benefits from the farm are included but held constant. The committee liked the catches plot since it was most dynamic, but wanted it pulled apart to make the message that breaking the farms up into smaller spaces makes a difference, so this figure will have 2 panels, one with one large farm (A) and a second with farms broken up into smaller spaces (B).

```
msAttrOA<-read_csv("runs/openAccess/farmEq_msAttrOALg.csv")

msAttrOAxs<-read_csv("runs/openAccess/farmEq_msAttrOAXSm.csv") # 4 farms at 5 patches each
nullOA<-read_csv("runs/openAccess/nullOA.csv")


### Calculate biomass and catch differences
msAttrOA2<-msAttrOA%>%
  mutate(diffBm=biomass-as.numeric(nullOA[1,"biomass"]),
         diffCtch=catch-as.numeric(nullOA[1,"catch"]))

msAttrOAxs2<-msAttrOAxs%>%
  mutate(diffBm=biomass-as.numeric(nullOA[1,"biomass"]),
         diffCtch=catch-as.numeric(nullOA[1,"catch"]))

### plot mpaSize by attraction

attrCols<-beyonce_palette(19)[c(5,2:4)]
names(attrCols)<-c("1","3","9","15")
```
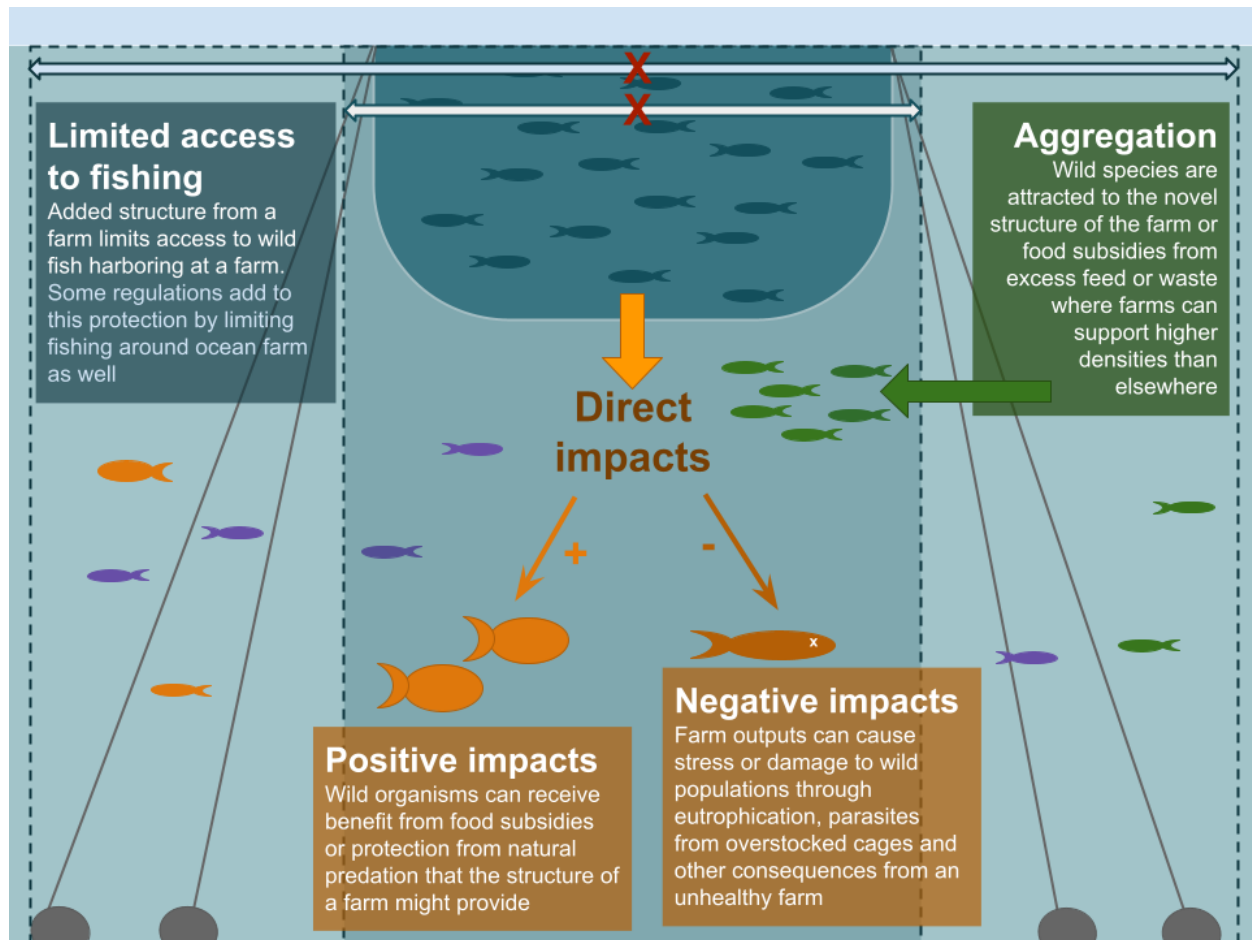
Figure 1: Figure 1: Diagram of ocean farm with key parameters indicated.

```r
sizeAttrCatch<-ggplot(msAttrOA2,aes(x=mpaSize,y=diffCtch,group=as.factor(attr),color=as.factor(attr)))+
  geom_hline(yintercept = 0,color="gray66")+
  geom_smooth(size=0.8,se=FALSE)+
  labs(title = "One large farm",y="Catch biomass",x="")+
  scale_y_continuous(limits = c(-1750,1000))+
  scale_x_continuous(breaks = seq(0.2,0.8,by=0.2),labels = seq(0.2,0.8,by=0.2)*100)+
  scale_color_manual(values = attrCols,name="Attraction",labels=c("None","Low","Moderate","High"))+
  theme_bw()+
    theme(axis.text=element_text(size=12),
          axis.title = element_text(size=16),
          legend.text = element_text(size=12),
        legend.title = element_text(size=16))

sizeAttrCatchS<-ggplot()+ ## replaced sm with xsm to accentuate differences (smaller farms)
  geom_hline(yintercept = 0,color="gray66")+
  geom_smooth(data=msAttrOAxs2,aes(x=mpaSize,y=diffCtch,group=as.factor(attr),color=as.factor(attr)),si
  labs(title = "Several smaller farms",y="",x="")+
  scale_y_continuous(limits = c(-1750,1000))+
  scale_x_continuous(breaks = seq(0.2,0.8,by=0.2),labels = seq(0.2,0.8,by=0.2)*100)+
  scale_color_manual(values = attrCols,name="Attraction",labels=c("None","Low","Moderate","High"))+
  theme_bw()+
    theme(axis.text=element_text(size=12),
          axis.title = element_text(size=16),
          legend.text = element_text(size=12),
        legend.title = element_text(size=16))

## combined x-lab
x_lab <-
  ggplot() +
  annotate(geom = "text", x = 1, y = 1, label = "Total farm area (% of total range)", size=6) +
  theme_void()

fig1Plts<-sizeAttrCatch+sizeAttrCatchS+plot_layout(guides = "collect")+plot_annotation(tag_levels = "A"

(fig1Plts/x_lab) + plot_layout(heights = c(1,0.05))
```
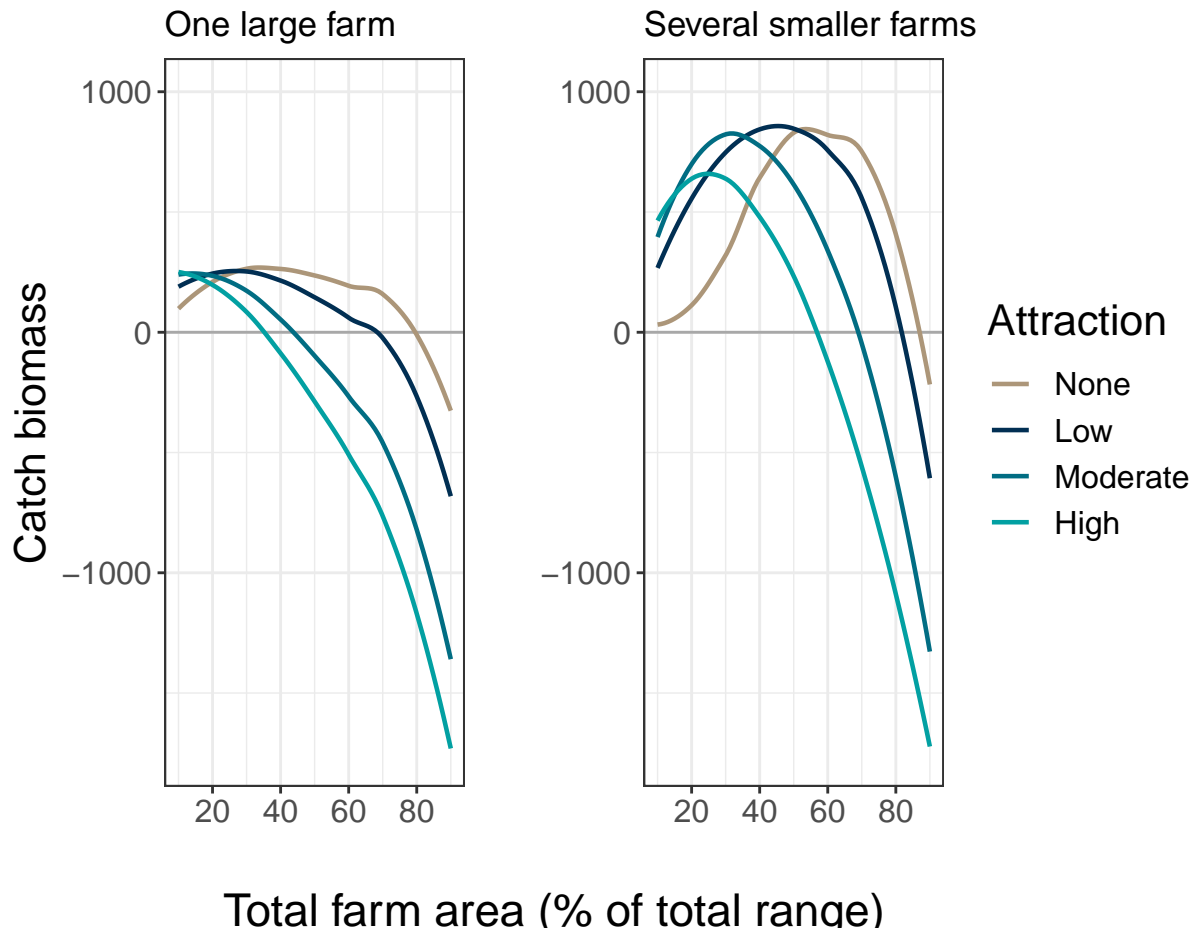
Figure 3: Equilibrium catches with positive and negative impacts to wild populations

Relative differences in catch biomass compared to no farm over a range of total farm areas. Farms are all divided into several smaller farms. Farm scenarios with positive (A, C) and negative impacts to the wild population (C, D), under strong (A, B) and weak (B, D) fishery management.

```
### Farm size colors:
szCols<-c(beyonce_palette(129)[c(1,2,4)],beyonce_palette(6)[5])#paletteer_d("ghibli::PonyoMedium")[c(1,
names(szCols)<-c("60","20","3","0")

### control CE data
nullCE<-read_csv("runs/constantEffortMSY/nullCE.csv")

### Benefits to wild population

szMgmtBen<-read_csv("runs/movement/farmEq_mpaMgmtAMBen.csv")

szMgmtBen2<-szMgmtBen%>%
  mutate(diffBm=case_when(mgmt == "oa" ~  biomass/as.numeric(nullOA[1,"biomass"]),
                          TRUE ~ biomass/as.numeric(nullCE[1,"biomass"])),
```

```r
        diffCtch=case_when(mgmt=="oa" ~  catch/as.numeric(nullOA[1,"catch"]),
                           TRUE ~ catch/as.numeric(nullCE[1,"catch"]))))

zeros<-data.frame(mpaSz=0,
                  aMove=rep(c(0,3,20,60),2),
                  mgmt=rep(c("oa","ce"),each=4),
                  diffBm=1,
                  diffCtch=1)

szMgmtBen3<-szMgmtBen2%>%
  bind_rows(.,zeros)

### open access

szMgmtBenCtchOA<-ggplot(szMgmtBen3[szMgmtBen3$mgmt=="oa",],aes(x=mpaSz*100,y=diffCtch*100,group=aMove,co
  geom_hline(yintercept = 100,color="gray66")+
  geom_smooth(size=0.8,se=FALSE)+#geom_line(size=0.8)+
  scale_color_manual(values = szCols,name="Adult\nmovement",labels=c("None","Low","Moderate","High"))+
  scale_y_continuous(limits = c(9,215))+
  labs(x="",y="\n\n",title = "")+
  theme_bw()+
  theme(plot.title = element_text(hjust = 0.5, size = 16),
        axis.text=element_text(size=12),
        axis.title = element_text(size=16),
        legend.text = element_text(size=12),
        legend.title = element_text(size=16))

### constant effort at MSY

szMgmtBenCtchCE<-ggplot(szMgmtBen3[szMgmtBen3$mgmt=="ce",],aes(x=mpaSz*100,y=diffCtch*100,group=aMove,co
  geom_hline(yintercept = 100,color="gray66")+
  geom_smooth(size=0.8,se=FALSE)+#geom_line(size=0.8)+
  scale_color_manual(values = szCols,name="Adult\nmovement",labels=c("None","Low","Moderate","High"))+
  scale_y_continuous(limits = c(9,215))+
  labs(x="",y="\n\n",title = "Positive impacts\n")+
  theme_bw()+
  theme(plot.title = element_text(hjust = 0.5, size = 16),
        axis.text=element_text(size=12),
        axis.title = element_text(size=16),
        legend.text = element_text(size=12),
        legend.title = element_text(size=16))

goodPlt<-szMgmtBenCtchOA + szMgmtBenCtchCE
  # plot_annotation(title = "Adult movement by number of farms - benefits", theme = theme(plot.title =

### Stress/damage to wild population

szMgmtNeg<-read_csv("runs/movement/farmEq_mpaMgmtAMNeg.csv")

szMgmtNeg2<-szMgmtNeg%>%
  mutate(diffBm=case_when(mgmt == "oa" ~  biomass/as.numeric(nullOA[1,"biomass"]),
                          TRUE ~ biomass/as.numeric(nullCE[1,"biomass"])),
         diffCtch=case_when(mgmt=="oa" ~  catch/as.numeric(nullOA[1,"catch"]),
```

```r
                            TRUE ~ catch/as.numeric(nullCE[1,"catch"])))

szMgmtNeg3<-szMgmtNeg2%>%
  bind_rows(.,zeros)


### Open access

szMgmtNegCtchOA<-ggplot(szMgmtNeg3[szMgmtNeg3$mgmt=="oa",],aes(x=mpaSz*100,y=diffCtch*100,group=aMove,co
  geom_hline(yintercept = 100,color="gray66")+
  geom_smooth(size=0.8,se=FALSE)+#geom_line(size=0.8)+
  scale_color_manual(values = szCols,name="Adult\nmovement",labels=c("None","Low","Moderate","High"))+
  scale_y_continuous(limits = c(9,215))+
  labs(x="",y="\n\n",title = "")+
  theme_bw()+
  theme(plot.title = element_text(hjust = 0.5, size = 16),
        axis.text=element_text(size=12),
        axis.title = element_text(size=16),
        legend.text = element_text(size=12),
        legend.title = element_text(size=16))


#constant effort at MSY

szMgmtNegCtchCE<-ggplot(szMgmtNeg3[szMgmtNeg3$mgmt=="ce",],aes(x=mpaSz*100,y=diffCtch*100,group=aMove,co
  geom_hline(yintercept = 100,color="gray66")+
  geom_smooth(size=0.8,se=FALSE)+#geom_line(size=0.8)+
  scale_color_manual(values = szCols,name="Adult\nmovement",labels=c("None","Low","Moderate","High"))+
  scale_y_continuous(limits = c(9,215))+
  labs(x="",y="\n\n",title = "Negative impacts\n")+
  theme_bw()+
  theme(plot.title = element_text(hjust = 0.5, size = 16),
        axis.text=element_text(size=12),
        axis.title = element_text(size=16),
        legend.text = element_text(size=12),
        legend.title = element_text(size=16))

fig3Plts<-((szMgmtBenCtchCE + szMgmtNegCtchCE)/(szMgmtBenCtchOA + szMgmtNegCtchOA )) +
  plot_annotation(tag_levels = 'A') +
  plot_layout(guides="collect")


fig3Plts
```
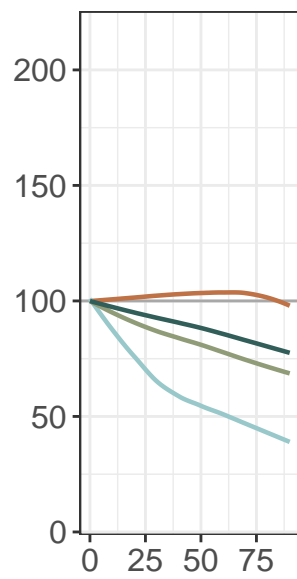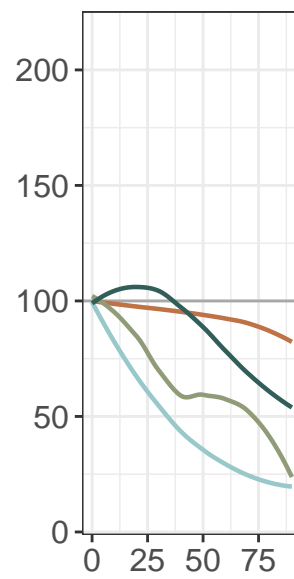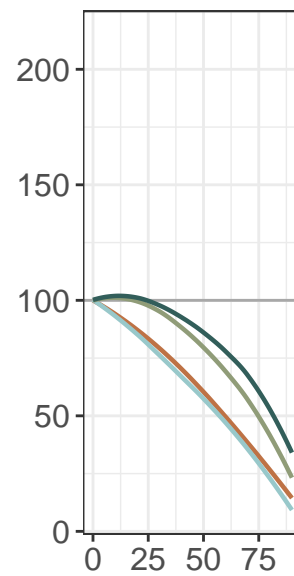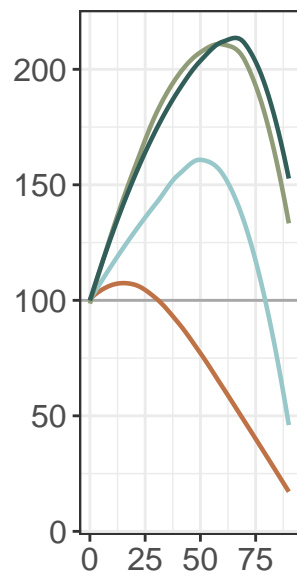
A Positive impact
B Negative impacts

C

D

Adult movement

— None
— Low
— Moderate
— High

```
# (fig2Plts/x_lab2) + plot_layout(heights = c(1,0.05))
```