

File S1. R-script for the statistical analyses of bigeye and yellowfin tunas in the Indian Ocean. Information about the script (not run) are preceded by a hash symbol (#) and shaded in grey.

```
# Loading the packages into R environment
```

```
library(zoo)
library(tidyverse)
library(ggplot2)
library(mgcv)
```

```
# Set the working Directory
```

```
setwd("E:/1_Paper/IOD Paper/Data/use std cpue/")
```

```
#As the original DMI data is monthly, covert the data to quarterly to match the CPUE data
```

```
DMI<- read.csv ("DMI.csv", header = T, sep=",")
```

```
ym <- as.yearmon(paste(DMI$year, DMI$month), "%Y %m")
```

```
DMI$yq <- as.yearqtr(ym)
```

```
DMI_qtr <- DMI %>%
```

```
  group_by(yq) %>%
```

```
  summarise_all(mean)
```

```
write.table(DMI_qtr," DMI_qtr.csv",sep=",")
```

```
# Read data of bigeye and yellowfin tuna. Data include the CPUE and DMI.
```

```
Bigeye_IO<- read.csv("BET_IO.csv", header=T, sep=",")
```

```
Bigeye_R1<- read.csv("BET_R1.csv", header=T, sep=",")
```

```
Bigeye_R2<- read.csv("BET_R2.csv", header=T, sep=",")
```

```
Bigeye_R3<- read.csv("BET_R3.csv", header=T, sep=",")
```

```
Yellowfin_IO<- read.csv("YFT_IO.csv", header=T, sep=",")
```

```
Yellowfin_R1<- read.csv("YFT_R1.csv", header=T, sep=",")
```

```
Yellowfin_R2<- read.csv("YFT_R2.csv", header=T, sep=",")
```

```
Yellowfin_R3<- read.csv("YFT_R3.csv", header=T, sep=",")
```

```
Yellowfin_R4<- read.csv("YFT_R4.csv", header=T, sep=",")
```

```
# Run linear regression models
```

```
lm_bigeye_IO <- lm(CPUE ~ DMI, data = Bigeye_IO)
```

```
summary(lm_bigeye_IO)
```

```
lm_bigeye_R1 <- lm(CPUE ~ DMI, data = Bigeye_R1)
summary(lm_bigeye_R1)
```

```
lm_bigeye_R2<- lm(CPUE ~ DMI, data = Bigeye_R2)
summary(lm_bigeye_R2)
```

```
lm_bigeye_R3 <- lm(CPUE ~ DMI, data = Bigeye_R3)
summary(lm_bigeye_R3)
```

```
lm_yellowfin_IO <- lm(CPUE ~ DMI, data = Yellowfin_IO)
summary(lm_yellowfin_IO)
```

```
lm_yellowfin_R1 <- lm(CPUE ~ DMI, data = Yellowfin_R1)
summary(lm_yellowfin_R1)
```

```
lm_yellowfin_R2<- lm(CPUE ~ DMI, data = Yellowfin_R2)
summary(lm_yellowfin_R2)
```

```
lm_yellowfin_R3 <- lm(CPUE ~ DMI, data = Yellowfin_R3)
summary(lm_yellowfin_R3)
```

```
lm_yellowfin_R4 <- lm(CPUE ~ DMI, data = Yellowfin_R4)
summary(lm_yellowfin_R4)
```

```
#Plot results by ggplot2
```

```
p_bigeye_IO <- ggplot(Bigeye_IO, aes(x = DMI, y = CPUE)) +
  geom_point()+geom_smooth(method = "lm")+ggtitle("BET_IO")+
  labs(x= "DMI", y= "Standardized CPUE")+
  xlim(-0.5,1.25) + ylim(0,2.5)
```

```
p_bigeye_R1 <- ggplot(Bigeye_R1, aes(x = DMI, y = CPUE)) +
  geom_point()+geom_smooth(method = "lm")+ggtitle("BET_R1")+
  labs(x= "DMI", y= "Standardized CPUE")+
  xlim(-0.5,1.25) + ylim(0,2.5)
```

```
p_bigeye_R2 <- ggplot(Bigeye_R2, aes(x = DMI, y = CPUE)) +
  geom_point()+geom_smooth(method = "lm")+ggtitle("BET_R2")+
  labs(x= "DMI", y= "Standardized CPUE")+
  xlim(-0.5,1.25) + ylim(0,2.5)
```

```
p_bigeye_R3 <- ggplot(Bigeye_R3, aes(x = DMI, y = CPUE)) +
  geom_point()+geom_smooth(method = "lm")+ggtitle("BET_R3")+
  labs(x= "DMI", y= "Standardized CPUE")+
  xlim(-0.5,1.25) + ylim(0,2.5)
```

```
p_yellowfin_IO <- ggplot(Yellowfin_IO, aes(x = DMI, y = CPUE)) +
  geom_point()+geom_smooth(method = "lm")+ggtitle("YET_IO")+
  labs(x= "DMI", y= "Standardized CPUE")+
  xlim(-0.5,0.75) + ylim(0,1.75)
```

```
p_yellowfin_R1 <- ggplot(Yellowfin_R1, aes(x = DMI, y = CPUE)) +
  geom_point()+geom_smooth(method = "lm")+ggtitle("YET_R1")+
  labs(x= "DMI", y= "Standardized CPUE")+
  xlim(-0.5,0.75) + ylim(0,1.75)
```

```
p_yellowfin_R2 <- ggplot(Yellowfin_R2, aes(x = DMI, y = CPUE)) +
  geom_point()+geom_smooth(method = "lm")+ggtitle("YET_R2")+
  labs(x= "DMI", y= "Standardized CPUE")+
  xlim(-0.5,0.75) + ylim(0,1.75)
```

```
p_yellowfin_R3 <- ggplot(Yellowfin_R3, aes(x = DMI, y = CPUE)) +
  geom_point()+geom_smooth(method = "lm")+ggtitle("YET_R3")+
  labs(x= "DMI", y= "Standardized CPUE")+
  xlim(-0.5,0.75) + ylim(0,1.75)
```

```
p_yellowfin_R4 <- ggplot(Yellowfin_R4, aes(x = DMI, y = CPUE)) +
  geom_point()+geom_smooth(method = "lm")+ggtitle("YET_R4")+
  labs(x= "DMI", y= "Standardized CPUE")+
  xlim(-0.5,0.75) + ylim(0,1.75)
```

#Combine the plots

```
library(ggpubr)
```

```
ggarrange(p_bigeye_IO, p_bigeye_R1, p_bigeye_R2, p_bigeye_R3, ncol = 2, nrow = 2, labels =
c("a","b","c","d"))
```

```
ggarrange(p_yellowfin_IO, p_yellowfin_R1, p_yellowfin_R2, p_yellowfin_R3, p_yellowfin_R4,
ncol = 3, nrow = 2, labels = c("a","b","c","d","e",))
```

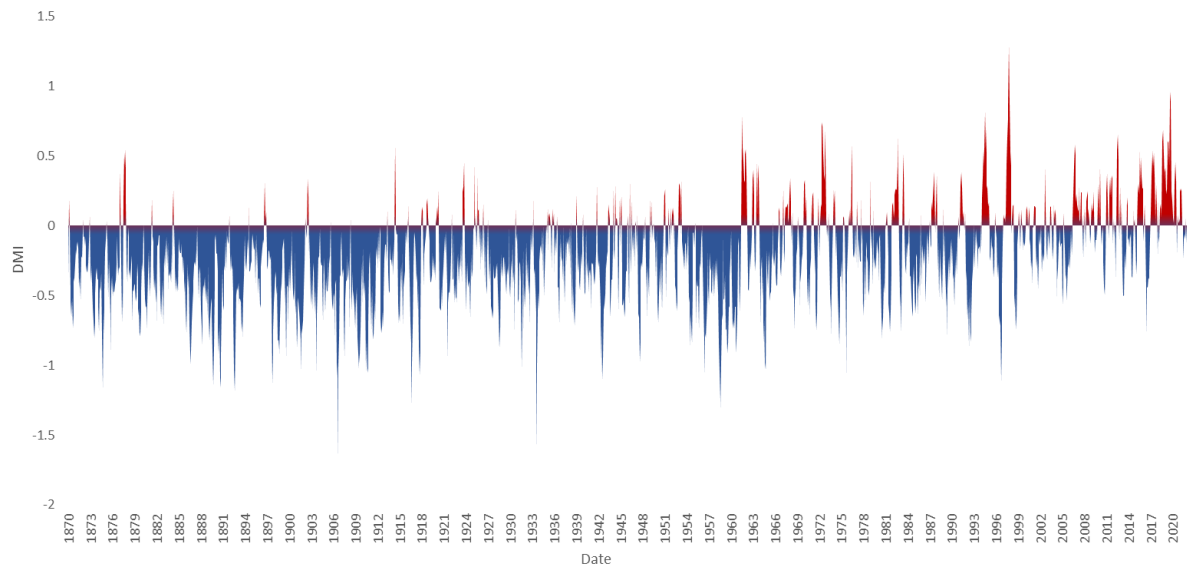


Figure S1. Distribution of DMI from 1870 to 2020. Positive DMI is referred to as positive IOD (red); negative DMI represents the negative IOD phenomenon (blue).