Human tissue biomass and cell density databases for medical research

Dr. M. Ivanov[1], Dr. A. Petrov[1], Dr. D. Smirnov[1], Dr. N. Volkov[1]*

[1] Department of Clinical Medicine and Biomedical Sciences, Saint Petersburg State University, Saint Petersburg, Russia

```
knitr::opts_chunk$set(echo = TRUE, warning=FALSE, message=FALSE)
knitr::opts_chunk$set(fig.width=5, fig.height=15)
```

#BenBIO database ## Loading benthic biomass dataset

```
require(ggplot2)
require(scales)
require(varhandle)
require(psych)
require(tidyverse)
require(gridExtra)
require(grid)
require(ggpubr)
require(openxlsx)
require(farver)

setwd("C:/Users/Mama/Desktop/manuscript version 6/resubmission")
benthic_biomass_data <- read.xlsx("BenBIO database.xlsx")  # read xlsx file

benthic_biomass_data <- benthic_biomass_data[c(2:4, 6, 8:9, 11)]
cols <- c("Ocean","Latitude", "Longitude", "Depth", "Biomass", "Unit",
"Benthos")
colnames(benthic_biomass_data) <- cols
head(benthic_biomass_data)
```

```
##               Ocean Latitude Longitude Depth Biomass    Unit      Benthos
## 1 Mediterranean Sea  44.2940    9.3228    60  0.7160 g C/ m2 macrobenthos
## 2 Mediterranean Sea  44.2881    9.3209    90  0.2870 g C/ m2 macrobenthos
## 3     Pacific Ocean  44.6417 -125.2417  2304  0.1810 g C/ m2  meiobenthos
## 4     Pacific Ocean  44.5697 -125.1467   785  0.2620 g C/ m2  meiobenthos
## 5     Pacific Ocean  44.5690 -125.1468   787  0.0614 g C/ m2  meiobenthos
## 6     Pacific Ocean  44.5647 -125.1382   852  0.2100 g C/ m2  meiobenthos
```

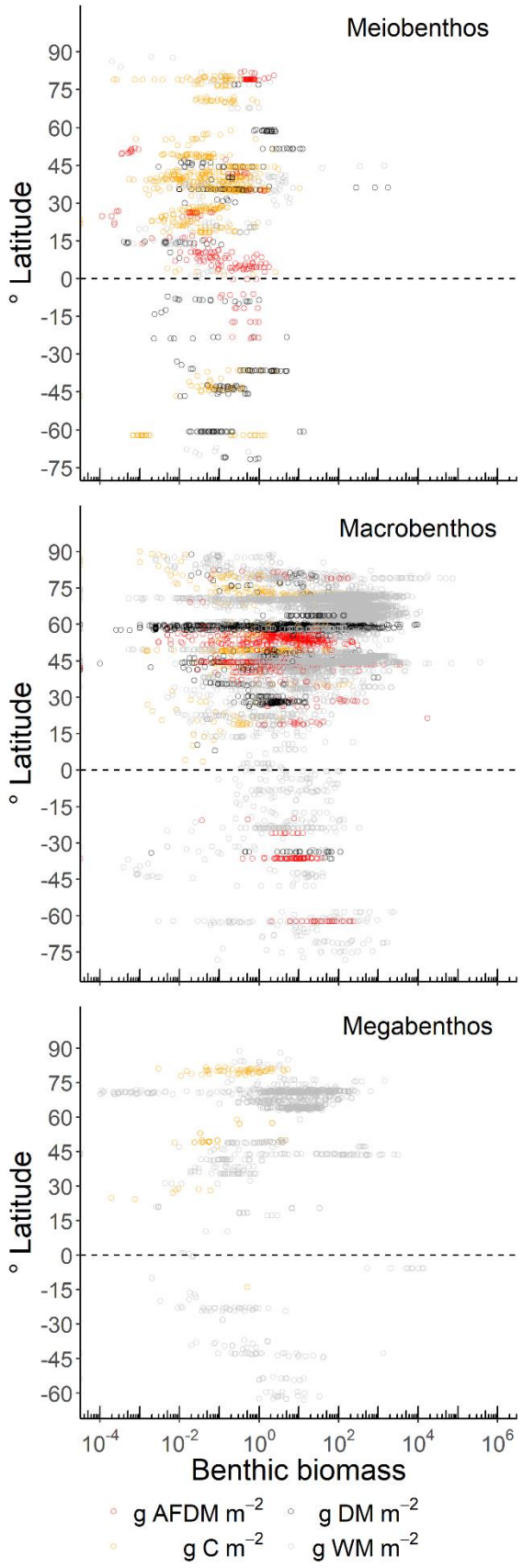
##Divide datasets for meiobenthos, macrobenthos, and megabenthos

```
meiobenthos_data <- benthic_biomass_data %>% filter(Benthos == "meiobenthos")

macrobenthos_data <- benthic_biomass_data %>% filter(Benthos ==
"macrobenthos")

megabenthos_data <- benthic_biomass_data %>% filter(Benthos == "megabenthos")
```

Preparing figure: Benthic biomasses along a latitudinal gradient

```
#Plot for meiobenthic biomass
lab1 <- c(expression(g~AFDM~m^-2),
          expression(g~C~m^-2),
          expression(g~DM~m^-2),
          expression(g~WM~m^-2))


p1 <- ggplot(data = meiobenthos_data, aes(x = Biomass, y = Latitude,
color=Unit)) + geom_point(alpha = 0.5, size=1.5, shape=1)+ theme_classic() +
scale_y_continuous(breaks = c(-90, -75, -60, -45, -30, -15, 0, 15, 30, 45,
60, 75, 90)) + ylab("° Latitude") +
  theme(axis.text.y = element_text(vjust=0.5, size=15)) +
annotation_logticks(sides = "b") +
  theme(text = element_text(size=20)) + geom_hline(yintercept = 0,
linetype="dashed") + guides(fill=guide_legend(ncol=2)) + guides(col =
guide_legend(nrow=2)) +
    scale_x_log10(breaks = trans_breaks("log10", function(x) 10^x),
              labels = trans_format("log10", math_format(10^.x)), limits =
c(1e-4,1e6)) + theme(legend.position = "bottom", legend.title =
element_blank()) + theme(plot.margin=unit(c(0.5,0,0,0.5), "cm")) +
  annotate(geom="text", x=1e4, y=100, label="Meiobenthos",
              color="black", size=6) + theme(axis.title.x = element_blank(),
axis.text.x = element_blank()) +
   scale_colour_manual(labels = lab1, values = c('red','orange', 'black',
'grey'))

#Plot for macrobenthos biomass
p2 <- ggplot(data = macrobenthos_data, aes(x = Biomass, y = Latitude,
color=Unit)) + geom_point(alpha = 0.5, size=1.5, shape=1)+ theme_classic() +
scale_y_continuous(breaks = c(-90, -75, -60, -45, -30, -15, 0,
                              15, 30, 45, 60, 75, 90)) + ylab("°
Latitude") +
  theme(axis.text.x = element_text(vjust=0.5, size=15)) +
  theme(axis.text.y = element_text(vjust=0.5, size=15)) +
annotation_logticks(sides = "b") +
  theme(text = element_text(size=20)) + geom_hline(yintercept = 0,
linetype="dashed") + guides(fill=guide_legend(ncol=2)) +
    scale_x_log10(breaks = trans_breaks("log10", function(x) 10^x),
              labels = trans_format("log10", math_format(10^.x)), limits =
c(1e-4,1e6)) + theme(legend.position = "bottom", legend.title =
element_blank()) + theme(plot.margin=unit(c(0.5,0,0,0.5), "cm")) +
scale_color_manual(values=c('red','orange', 'black', 'grey')) +
  annotate(geom="text", x=1e4, y=100, label="Macrobenthos",
              color="black", size=6) + theme(axis.title.x = element_blank(),
axis.text.x = element_blank())

#Plot for megabenthos biomass
p3 <- ggplot(data = megabenthos_data, aes(x = Biomass, y = Latitude,
color=Unit)) + geom_point(alpha = 0.5, size=1.5, shape=1)+ theme_classic() +
```

```
scale_y_continuous(breaks = c(-90, -75, -60, -45, -30, -15, 0,
                                  15, 30, 45, 60, 75, 90)) + ylab("°
Latitude") + xlab("Benthic biomass") +
  theme(axis.text.x = element_text(vjust=0.5, size=15)) +
  theme(axis.text.y = element_text(vjust=0.5, size=15)) +
annotation_logticks(sides = "b") +
  theme(text = element_text(size=20)) + geom_hline(yintercept = 0,
linetype="dashed") + guides(fill=guide_legend(ncol=2)) +
    scale_x_log10(breaks = trans_breaks("log10", function(x) 10^x),
              labels = trans_format("log10", math_format(10^.x)), limits =
c(1e-4,1e6)) + theme(legend.position = "bottom", legend.title =
element_blank()) + theme(plot.margin=unit(c(0.5,0,0,0.5), "cm")) +
scale_color_manual(values=c('orange', 'grey')) +
  annotate(geom="text", x=1e4, y=100, label="Megabenthos",
              color="black", size=6)

ggarrange(p1, p2, p3, ncol=1, nrow=3, common.legend = TRUE, legend="bottom")
```

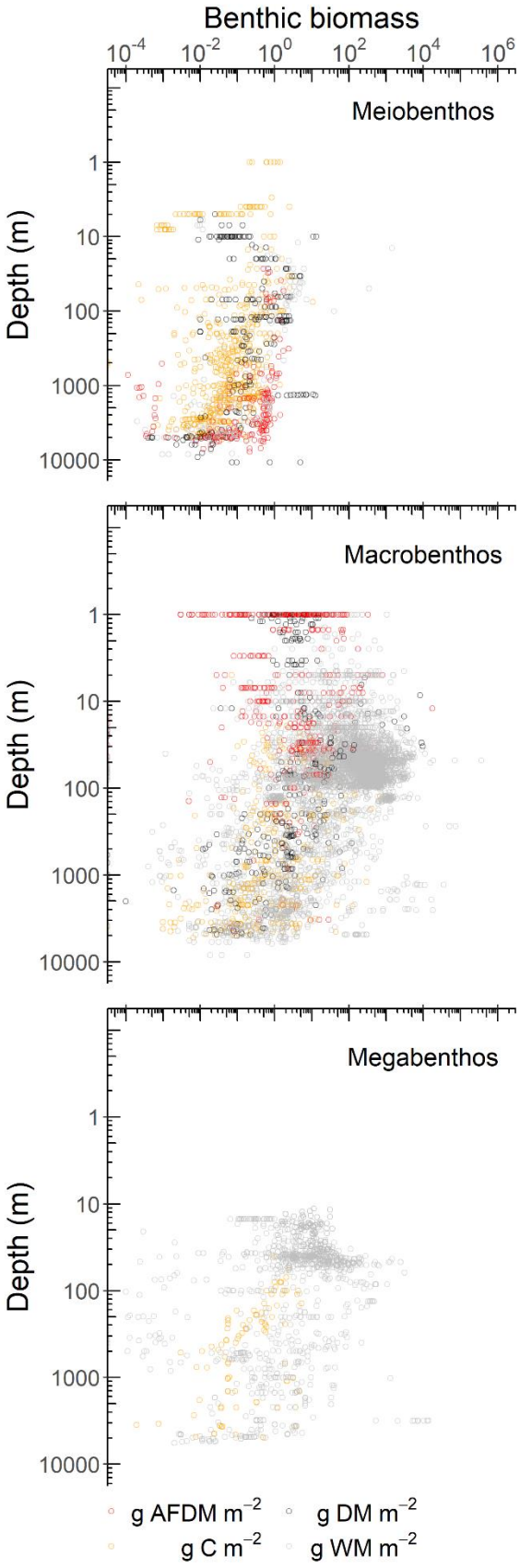

Meiobenthos
Macrobenthos
Megabenthos
° Latitude
90
75
60
45
30
15
0
-15
-30
-45
-60
-75
10^{-4}
10^{-2}
10^{0}
10^{2}
10^{4}
10^{6}
Benthic biomass
g AFDM m^{-2}
g DM m^{-2}
g C m^{-2}
g WM m^{-2}

```
setwd("C:/Users/Mama/Desktop/manuscript version 6")
ggsave(file="benthic biomass vs latitude.png", width=5,height=15)
```

Preparing figure: Benthic biomasses along a depth gradient

```
#Plot for meiobenthic biomass
lab1 <- c(expression(g~AFDM~m^-2),
          expression(g~C~m^-2),
          expression(g~DM~m^-2),
          expression(g~WM~m^-2))

reverselog_trans <- function(base = exp(1)) {
    trans <- function(y) -log(y, base)
    inv <- function(y) base^(-y)
    trans_new(paste0("reverselog-", format(base)), trans, inv,
              log_breaks(base = base),
              domain = c(1e-100, Inf))
}


meiobenthos_data_depth <- subset(meiobenthos_data, Depth!="intertidal")
meiobenthos_data_depth$Depth <- as.numeric(meiobenthos_data_depth$Depth)

p4 <- ggplot(data = meiobenthos_data_depth, aes(x = Biomass, y = Depth,
color=Unit)) + geom_point(alpha = 0.5, size=1.5, shape=1)+ theme_classic() +
scale_y_continuous(trans=reverselog_trans(10), breaks = c(1, 10, 100, 1000,
10000)) + ylab("Depth (m)") + xlab("Benthic biomass") +
  theme(axis.text.y = element_text(vjust=0.5, size=15)) +
annotation_logticks(sides = "tl") + geom_hline(yintercept = 10000,
linetype="dashed", col="white", alpha=0) + geom_hline(yintercept = 0.1,
linetype="dashed", col="white", alpha=0) +
  theme(text = element_text(size=20)) +  guides(fill=guide_legend(ncol=2)) +
guides(col = guide_legend(nrow=2)) +
    scale_x_log10(breaks = trans_breaks("log10", function(x) 10^x),
              labels = trans_format("log10", math_format(10^.x)), limits =
c(1e-4,1e6), position = "top") + theme(legend.position = "bottom",
legend.title = element_blank()) + theme(plot.margin=unit(c(0.5,0,0,0.5),
"cm")) +
  annotate(geom="text", x=1e4, y=0.2, label="Meiobenthos",
              color="black", size=6) +
   scale_colour_manual(labels = lab1, values = c('red','orange', 'black',
'grey'))

#Plot for macrobenthos biomass
macrobenthos_data_depth <- subset(macrobenthos_data, Depth!="intertidal")
macrobenthos_data_depth$Depth <- as.numeric(macrobenthos_data_depth$Depth)

p5 <- ggplot(data = macrobenthos_data_depth, aes(x = Biomass, y = Depth,
color=Unit)) + geom_point(alpha = 0.5, size=1.5, shape=1)+ theme_classic() +
scale_y_continuous(trans=reverselog_trans(10), breaks = c(1, 10, 100, 1000,
```

```
10000)) + ylab("Depth (m)") + xlab("Benthic biomass") +
  theme(axis.text.y = element_text(vjust=0.5, size=15)) +
annotation_logticks(sides = "tl") + geom_hline(yintercept = 10000,
linetype="dashed", col="white", alpha=0) + geom_hline(yintercept = 0.1,
linetype="dashed", col="white", alpha=0) +
  theme(text = element_text(size=20)) +  guides(fill=guide_legend(ncol=2)) +
guides(col = guide_legend(nrow=2)) +
    scale_x_log10(breaks = trans_breaks("log10", function(x) 10^x),
              labels = trans_format("log10", math_format(10^.x)), limits =
c(1e-4,1e6), position = "top") + theme(legend.position = "bottom",
legend.title = element_blank()) + theme(plot.margin=unit(c(0.5,0,0,0.5),
"cm")) +
  annotate(geom="text", x=1e4, y=0.2, label="Macrobenthos",
              color="black", size=6) +
   scale_colour_manual(labels = lab1, values = c('red','orange', 'black',
'grey')) +
  theme(axis.title.x = element_blank(), axis.text.x = element_blank())

#Plot for megabenthos biomass
megabenthos_data_depth <- subset(megabenthos_data, Depth!="intertidal")
megabenthos_data_depth$Depth <- as.numeric(megabenthos_data_depth$Depth)

p6 <- ggplot(data = megabenthos_data_depth, aes(x = Biomass, y = Depth,
color=Unit)) + geom_point(alpha = 0.5, size=1.5, shape=1)+ theme_classic() +
scale_y_continuous(trans=reverselog_trans(10), breaks = c(1, 10, 100, 1000,
10000)) + ylab("Depth (m)") + xlab("Benthic biomass") +
  theme(axis.text.y = element_text(vjust=0.5, size=15)) +
annotation_logticks(sides = "tl") + geom_hline(yintercept = 10000,
linetype="dashed", col="white", alpha=0) + geom_hline(yintercept = 0.1,
linetype="dashed", col="white", alpha=0) +
  theme(text = element_text(size=20)) +  guides(fill=guide_legend(ncol=2)) +
guides(col = guide_legend(nrow=2)) +
    scale_x_log10(breaks = trans_breaks("log10", function(x) 10^x),
              labels = trans_format("log10", math_format(10^.x)), limits =
c(1e-4,1e6), position = "top") + theme(legend.position = "bottom",
legend.title = element_blank()) + theme(plot.margin=unit(c(0.5,0,0,0.5),
"cm")) +
  annotate(geom="text", x=1e4, y=0.2, label="Megabenthos",
              color="black", size=6) +
   scale_colour_manual(labels = lab1, values = c('orange', 'grey'))  +
  theme(axis.title.x = element_blank(), axis.text.x = element_blank())

ggarrange(p4, p5, p6, ncol=1, nrow=3, common.legend = TRUE, legend="bottom")
```


Benthic biomass
10^{-4} 10^{-2} 10^{0} 10^{2} 10^{4} 10^{6}
Meiobenthos
Macrobenthos
Megabenthos
Depth (m)
1
10
100
1000
10000
g AFDM m^{-2}
g DM m^{-2}
g C m^{-2}
g WM m^{-2}

```
setwd("C:/Users/Mama/Desktop/manuscript version 6")
ggsave(file="benthic biomass vs depth.png", width=5,height=15)
```

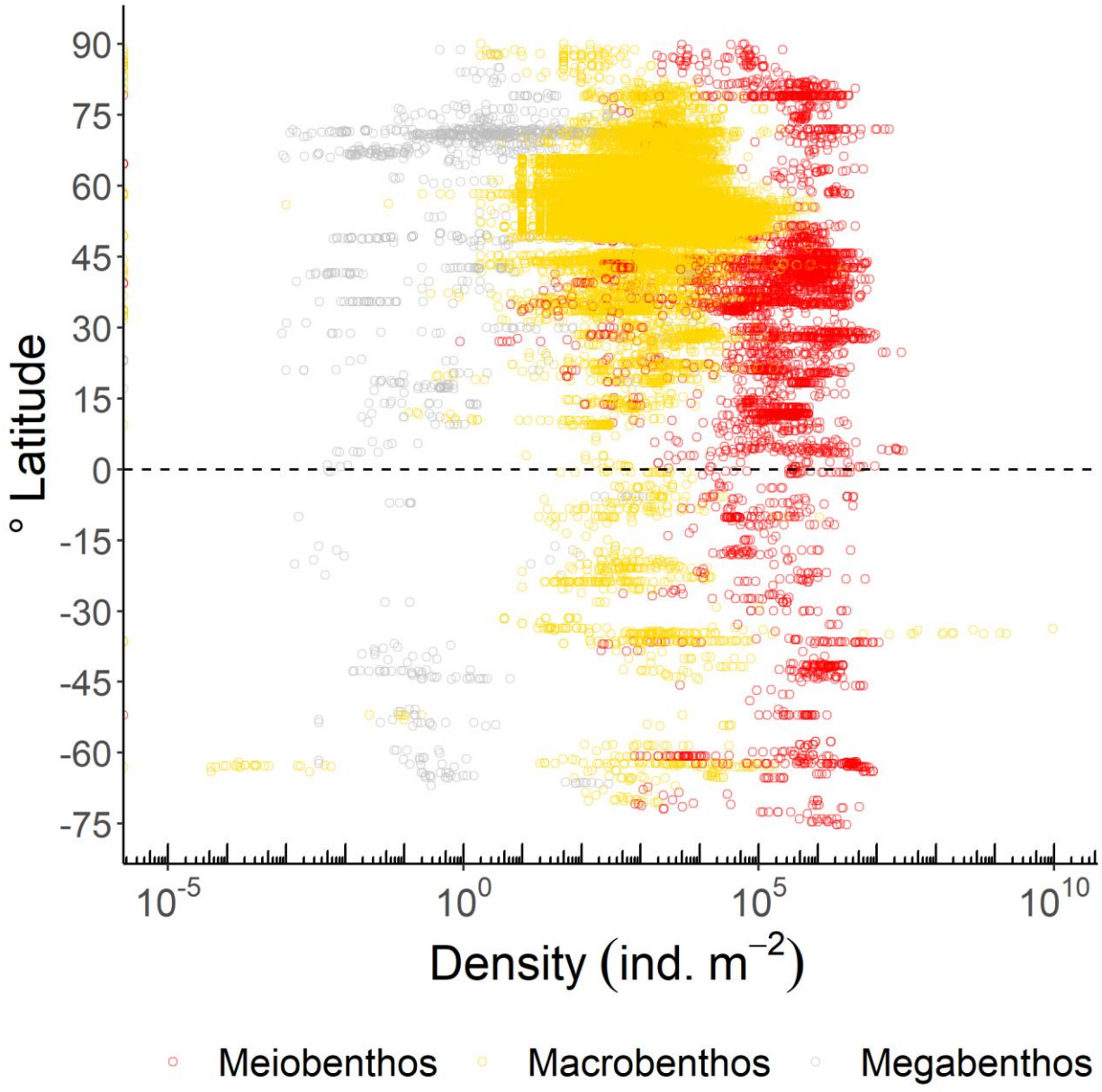
#BenDEN database ## Loading benthic density dataset

```
require(ggplot2)
require(scales)
require(varhandle)
require(psych)
require(tidyverse)
require(gridExtra)
require(grid)
require(ggpubr)
require(openxlsx)

setwd("C:/Users/Mama/Desktop/manuscript version 6/resubmission")
benthic_abundance_data <- read.xlsx("BenDEN database.xlsx")  # read xlsx file

benthic_abundance_data <- benthic_abundance_data[c(2:4, 6, 8:9)]
cols <- c("Ocean","Latitude", "Longitude", "Depth", "Density", "Benthos")
colnames(benthic_abundance_data) <- cols

benthic_abundance_data$Density <- as.numeric(benthic_abundance_data$Density)

head(benthic_abundance_data)

##               Ocean Latitude Longitude Depth Density      Benthos
## 1 Mediterranean Sea  37.2573    9.9235   3.7   190.0 macrobenthos
## 2 Mediterranean Sea  37.2552    9.8667   3.1    12.7 macrobenthos
## 3 Mediterranean Sea  37.2347    9.8359   3.1   127.0 macrobenthos
## 4 Mediterranean Sea  37.2240    9.8576   3.3    72.5 macrobenthos
## 5 Mediterranean Sea  37.2193    9.9035   2.9    56.2 macrobenthos
## 6 Mediterranean Sea  37.2052    9.8011   3.2   362.0 macrobenthos
```

Preparing figure: Benthic density along a latitudinal gradient

```
benthic_abundance_data$Benthos <- factor(benthic_abundance_data$Benthos,
levels = c("meiobenthos", "macrobenthos", "megabenthos"))

ggplot(data = benthic_abundance_data, aes(x = Density, y = Latitude,
color=Benthos)) + geom_point(alpha = 0.5, size=1.5, shape=1)+ theme_classic()
+ scale_y_continuous(breaks = c(-90, -75, -60, -45, -30, -15, 0, 15, 30, 45,
60, 75, 90)) + ylab("° Latitude") +
  theme(axis.text.y = element_text(vjust=0.5, size=15)) +
annotation_logticks(sides = "b") +
  theme(text = element_text(size=20)) +
  theme(text = element_text(size=20)) + geom_hline(yintercept = 0,
linetype="dashed") + guides(fill=guide_legend(ncol=2)) + guides(col =
guide_legend(nrow=2)) + scale_x_log10(breaks = trans_breaks("log10",
function(x) 10^x),
              labels = trans_format("log10", math_format(10^.x)), limits =
```

```
c(1e-5,1e10)) + xlab(bquote(' '*Density~(ind.~m^-2*''))) +
theme(legend.position = "bottom", legend.title = element_blank()) +
theme(plot.margin=unit(c(0.5,0,0,0.5), "cm")) + scale_colour_manual(labels =
c("Meiobenthos", "Macrobenthos", "Megabenthos"), values = c('red', 'gold',
'grey')) + guides(colour = guide_legend(nrow = 1))
```

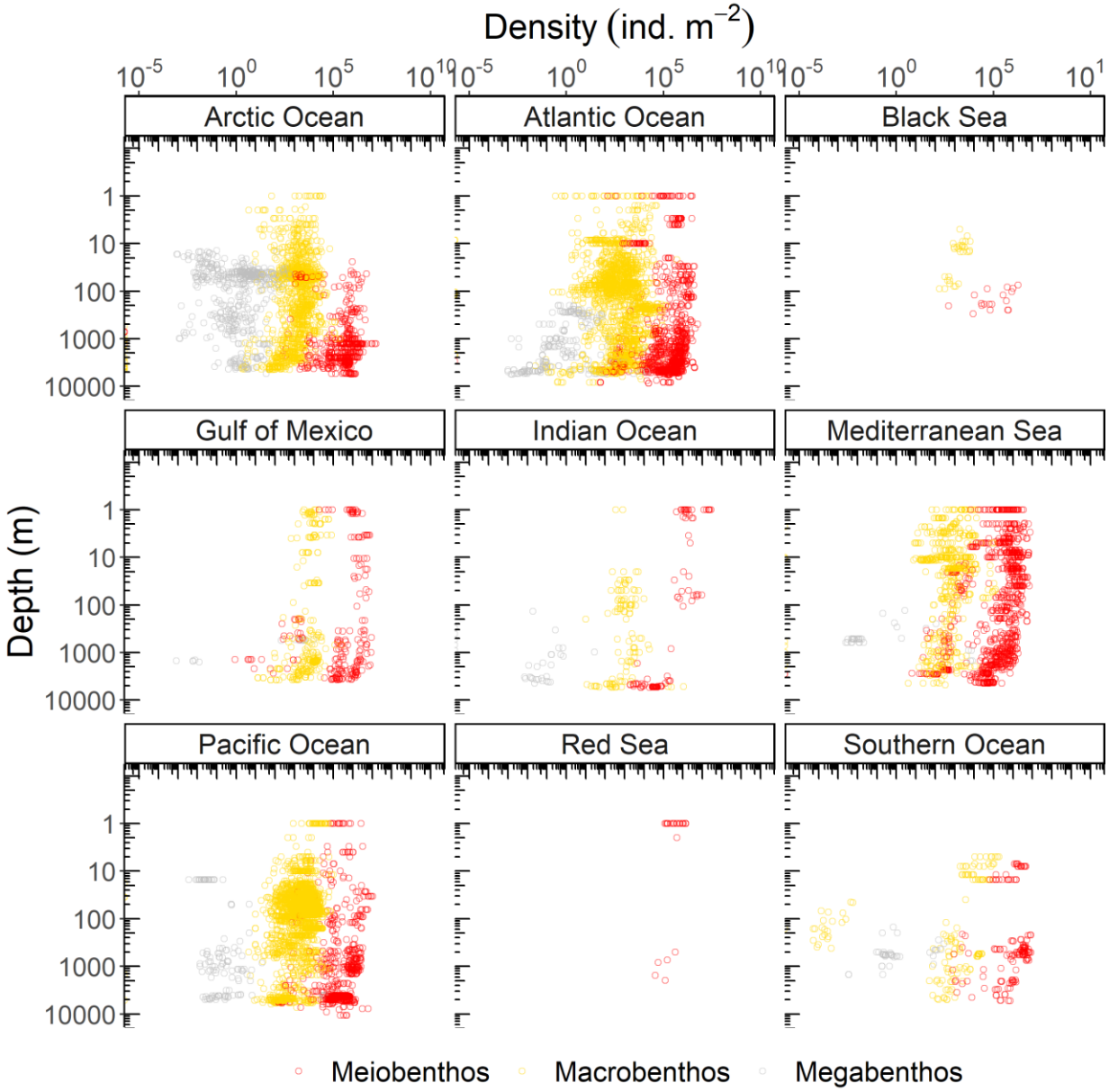



```
setwd("C:/Users/Mama/Desktop/manuscript version 6")
ggsave(file="benthic density vs latitude.png", width=6.5,height=6.5)
```

Preparing figure: Benthic density along a depth gradient

```
benthic_abundance_data$Benthos <- factor(benthic_abundance_data$Benthos,
levels = c("meiobenthos", "macrobenthos", "megabenthos"))
```

```
reverselog_trans <- function(base = exp(1)) {
    trans <- function(y) -log(y, base)
    inv <- function(y) base^(-y)
    trans_new(paste0("reverselog-", format(base)), trans, inv,
              log_breaks(base = base),
              domain = c(1e-100, Inf))
}

benthic_abundance_data_depth <- subset(benthic_abundance_data,
Depth!="intertidal")
benthic_abundance_data_depth$Depth <-
as.numeric(benthic_abundance_data_depth$Depth)

ggplot(data = benthic_abundance_data_depth, aes(x = Density, y = Depth,
color=Benthos)) + geom_point(alpha = 0.5, size=1.5, shape=1)+ theme_classic()
+ scale_y_continuous(trans=reverselog_trans(10), breaks = c(1, 10, 100, 1000,
10000)) + ylab("Depth (m)") + xlab(bquote(' '*Density~(ind.~m^-2*''))) +
  theme(axis.text.y = element_text(vjust=0.5, size=15)) +
annotation_logticks(sides = "tl") + geom_hline(yintercept = 10000,
linetype="dashed", col="white", alpha=0) + geom_hline(yintercept = 0.1,
linetype="dashed", col="white", alpha=0) +
  theme(text = element_text(size=20)) +  guides(fill=guide_legend(ncol=2)) +
guides(col = guide_legend(nrow=2)) +
    scale_x_log10(breaks = trans_breaks("log10", function(x) 10^x),
              labels = trans_format("log10", math_format(10^.x)), limits =
c(1e-5,1e10), position = "top") + theme(legend.position = "bottom",
legend.title = element_blank()) + theme(plot.margin=unit(c(0.5,0,0,0.5),
"cm")) + scale_colour_manual(labels = c("Meiobenthos", "Macrobenthos",
"Megabenthos"), values = c('red', 'gold', 'grey')) + guides(colour =
guide_legend(nrow = 1)) + facet_wrap(~Ocean, ncol=3)
```




```
setwd("C:/Users/Mama/Desktop/manuscript version 6")
ggsave(file="benthic density vs depth.png", width=9,height=9)
```

Loading summary dataset to assess undersampling

```
require(ggplot2)
require(dplyr)
require(tidyverse)
require(openxlsx)

setwd("C:/Users/Mama/Desktop/manuscript version 6")
sampling_effort_data <- read.xlsx("BenBioDen database_statistics.xlsx")  #
```

```
read xlsx file
head(sampling_effort_data)

##                        Seas/.Oceans area.(km2)
## 1                    N Pacific Ocean   64550459
## 2                    S Pacific Ocean   76568076
## 3                       Indian Ocean   57824473
## 4 N Atlantic Ocean & Gulf of Mexico   34265825
## 5                   S Atlantic Ocean   40251619
## 6                     Southern Ocean   20258878
##
Reference
## 1 Costello, M. J., Cheung, A. & De Hauwere, N. Surface area and the seabed
area, volume, depth, slope, and topographic variation for the world's seas,
oceans, and countries. Environ. Sci. Technol. 44, 8821–8828 (2010).
## 2 Costello, M. J., Cheung, A. & De Hauwere, N. Surface area and the seabed
area, volume, depth, slope, and topographic variation for the world's seas,
oceans, and countries. Environ. Sci. Technol. 44, 8821–8828 (2010).
## 3 Costello, M. J., Cheung, A. & De Hauwere, N. Surface area and the seabed
area, volume, depth, slope, and topographic variation for the world's seas,
oceans, and countries. Environ. Sci. Technol. 44, 8821–8828 (2010).
## 4 Costello, M. J., Cheung, A. & De Hauwere, N. Surface area and the seabed
area, volume, depth, slope, and topographic variation for the world's seas,
oceans, and countries. Environ. Sci. Technol. 44, 8821–8828 (2010).
## 5 Costello, M. J., Cheung, A. & De Hauwere, N. Surface area and the seabed
area, volume, depth, slope, and topographic variation for the world's seas,
oceans, and countries. Environ. Sci. Technol. 44, 8821–8828 (2010).
## 6 Costello, M. J., Cheung, A. & De Hauwere, N. Surface area and the seabed
area, volume, depth, slope, and topographic variation for the world's seas,
oceans, and countries. Environ. Sci. Technol. 44, 8821–8828 (2010).
##      %.area total.Meiobenthic.biomass.samples
## 1 27.210688                                144
## 2 32.276610                                131
## 3 24.375407                                 21
## 4 14.444462                                337
## 5 16.967722                                 47
## 6  8.539955                                 38
##   total.Macrobenthic.biomass.samples total.Megabenthic.biomass.samples
## 1                               1168                                256
## 2                                185                                 42
## 3                                121                                  0
## 4                               4643                                194
## 5                                139                                 72
## 6                                137                                  9
##   total.Meiobenthic.abundance.samples total.Macrobenthic.abundance.samples
## 1                                 661                                3162
## 2                                 233                                 190
## 3                                 110                                 146
## 4                                 820                               39008
## 5                                 248                                 336
```

```
## 6                                  148                                  164
##   total.Megabenthic.abundance.samples %.Meiobenthic.biomass.samples
## 1                                  89                      14.501511
## 2                                  54                      13.192346
## 3                                  32                       2.114804
## 4                                 175                      33.937563
## 5                                  48                       4.733132
## 6                                  39                       3.826788
##   %.Macrobenthic.biomass.samples %.Megabenthic.biomass.samples
## 1                      14.827980                     25.6770311
## 2                       2.348610                      4.2126379
## 3                       1.536118                      0.0000000
## 4                      58.943760                     19.4583751
## 5                       1.764631                      7.2216650
## 6                       1.739241                      0.9027081
##   %.Meiobenthic.abundance.samples %.Macrobenthic.abundance.samples
## 1                      11.183780                       7.3714885
## 2                       7.619359                       0.4429421
## 3                       3.597122                       0.3403660
## 4                      26.455199                      91.2297471
## 5                       6.442119                       0.4965614
## 6                       4.087639                       0.3823289
##   %.Megabenthic.abundance.samples
## 1                       9.539121
## 2                       5.787781
## 3                       3.429796
## 4                      18.756699
## 5                       5.144695
## 6                       4.180064
```

```
sampling_effort_data <- sampling_effort_data[c(1, 4, 11:16)]
cols <- c("Ocean","Area", "Biomass_Meiobenthos", "Biomass_Macrobenthos",
"Biomass_Megabenthos", "Density_Meiobenthos", "Density_Macrobenthos",
"Density_Megabenthos")
colnames(sampling_effort_data) <- cols
head(sampling_effort_data)
```

```
##                              Ocean      Area Biomass_Meiobenthos
## 1                  N Pacific Ocean 27.210688           14.501511
## 2                  S Pacific Ocean 32.276610           13.192346
## 3                     Indian Ocean 24.375407            2.114804
## 4 N Atlantic Ocean & Gulf of Mexico 14.444462           33.937563
## 5                  S Atlantic Ocean 16.967722            4.733132
## 6                    Southern Ocean  8.539955            3.826788
##   Biomass_Macrobenthos Biomass_Megabenthos Density_Meiobenthos
## 1            14.827980          25.6770311           11.183780
## 2             2.348610           4.2126379            7.619359
## 3             1.536118           0.0000000            3.597122
## 4            58.943760          19.4583751           26.455199
## 5             1.764631           7.2216650            6.442119
```

```
## 6             1.739241           0.9027081            4.087639
##   Density_Macrobenthos Density_Megabenthos
## 1            7.3714885            9.539121
## 2            0.4429421            5.787781
## 3            0.3403660            3.429796
## 4           91.2297471           18.756699
## 5            0.4965614            5.144695
## 6            0.3823289            4.180064
```

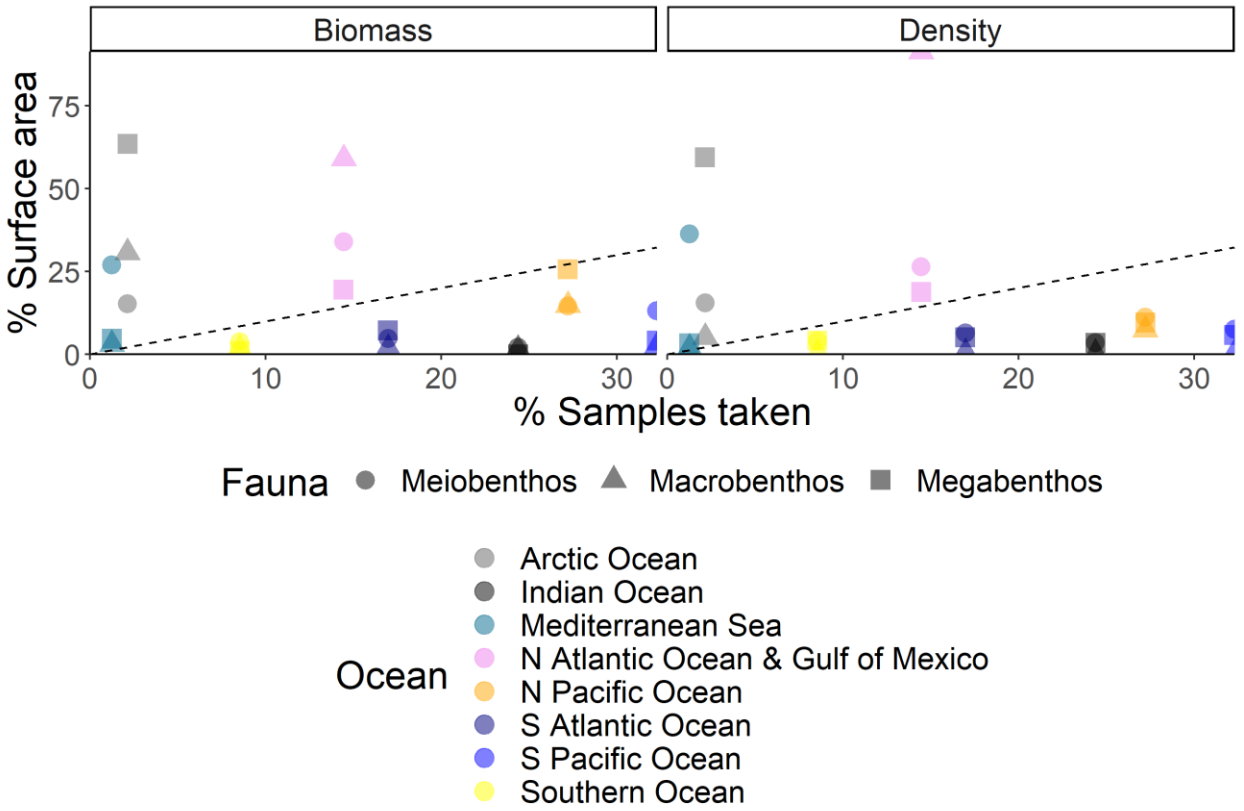
```
sampling_effort<-gather(sampling_effort_data, data, Value,
Biomass_Meiobenthos:Density_Megabenthos)
sampling_effort$Datatype <- str_sub(sampling_effort$data, 1, 7)
sampling_effort$Fauna <- str_sub(sampling_effort$data, 9, 20)
sampling_effort <- sampling_effort[c(1:2, 4:6)]
head(sampling_effort)
```

```
##                               Ocean      Area     Value Datatype
Fauna
## 1                  N Pacific Ocean 27.210688 14.501511  Biomass
Meiobenthos
## 2                  S Pacific Ocean 32.276610 13.192346  Biomass
Meiobenthos
## 3                     Indian Ocean 24.375407  2.114804  Biomass
Meiobenthos
## 4 N Atlantic Ocean & Gulf of Mexico 14.444462 33.937563  Biomass
Meiobenthos
## 5                 S Atlantic Ocean 16.967722  4.733132  Biomass
Meiobenthos
## 6                   Southern Ocean  8.539955  3.826788  Biomass
Meiobenthos
```

Preparing figure: % surface area vs. % samples taken in that specific area

```
sampling_effort$Fauna <- factor(sampling_effort$Fauna, levels =
c("Meiobenthos", "Macrobenthos", "Megabenthos"))

colours <- c("gray39", "black", "deepskyblue4", "violet", "orange", "navy",
"blue", "yellow")

ggplot(data = sampling_effort, aes(x = Area, y = Value, color=Ocean)) +
geom_point(alpha = 0.5, size=4.5, aes(shape=Fauna)) + theme_classic() +
geom_abline(intercept = 0, linetype="dashed") + scale_x_continuous(expand =
c(0, 0)) + expand_limits(x = 0, y = 0) + scale_y_continuous(expand = c(0, 0))
+ theme(axis.text.x = element_text(vjust=0.5, size=15)) +
  theme(axis.text.y = element_text(vjust=0.5, size=15)) +
  theme(text = element_text(size=20)) + ylab("% Surface area") + xlab("%
Samples taken")+ facet_wrap(~Datatype, ncol=2) + theme(legend.position =
"bottom",
          legend.box = "vertical") + guides(shape = guide_legend(order = 1),
```

```
                                                color = guide_legend(order = 1))
+ guides(col = guide_legend(nrow = 8)) + scale_color_manual(values = colours)
```




```
setwd("C:/Users/Mama/Desktop/manuscript version 6")
ggsave(file="sampling effort.png", width=9,height=6)
```