

# Prokaryotic biomass and density database

Tanja Stratmann

August 22, 2021

#ProkaBIO database ## Loading benthic prokaryote biomass dataset

```
library(tidyr)
library(ggplot2)
library(scales)
library(openxlsx)

setwd("C:/Users/Mama/Desktop/paper 5_Role of benthos in the global C
cycle/Prokaryotes dataset/Microbial biomass")
prokaryotic_biomass_data <- read.xlsx("Prokaryotic biomass database.xlsx") #
read xlsx file

prokaryotic_biomass_data <- prokaryotic_biomass_data[c(2:4, 6:7, 23:25)]
cols <- c("Ocean", "Latitude", "Longitude", "Depth", "Depth_range", "Biomass",
"Unit", "Method")
colnames(prokaryotic_biomass_data) <- cols

prokaryotic_biomass_corrected <- prokaryotic_biomass_data %>%
drop_na("Biomass")
head(prokaryotic_biomass_corrected)
```

##		Ocean	Latitude	Longitude	Depth	Depth_range
## 1	Mediterranean Sea	35.3559	25.1	40	near-shore (0-50m)	
## 2	Mediterranean Sea	35.3559	25.1	40	near-shore (0-50m)	
## 3	Mediterranean Sea	35.3833	25.1	100	continental shelf (>50-200m)	
## 4	Mediterranean Sea	35.3833	25.1	100	continental shelf (>50-200m)	
## 5	Mediterranean Sea	35.4236	25.1	200	continental shelf (>50-200m)	
## 6	Mediterranean Sea	35.4236	25.1	200	continental shelf (>50-200m)	
##		Biomass			Unit	
## 1	0.0001007	g C cm wet sediment-3				
## 2	0.0001193	g C cm wet sediment-3				
## 3	0.0000423	g C cm wet sediment-3				
## 4	0.0000733	g C cm wet sediment-3				
## 5	0.0000343	g C cm wet sediment-3				
## 6	0.0000464	g C cm wet sediment-3				
##						
##		Method				
## 1	PD measured by epifluorescence microscopy, PD converted to PB using conversion factors					
## 2	PD measured by epifluorescence microscopy, PD converted to PB using conversion factors					
## 3	PD measured by epifluorescence microscopy, PD converted to PB using					

```

conversion factors
## 4 PD measured by epifluorescence microscopy, PD converted to PB using
conversion factors
## 5 PD measured by epifluorescence microscopy, PD converted to PB using
conversion factors
## 6 PD measured by epifluorescence microscopy, PD converted to PB using
conversion factors

```

## Preparing figure

```
knitr::opts_chunk$set(fig.width=13, fig.height=6.5)
```

```
#along a latitudinal gradient
```

```
lab1 <- c(expression(g~C~cm^-3~wet~sediment),
            expression(g~C~g~dry~sediment^-1),
            expression(g~C~g~wet~sediment^-1),
            expression(g~C~m^-2))
```

```
Fig1 <- ggplot(data = prokaryotic_biomass_corrected, 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("Prokaryotic
biomass") +
  theme(axis.text.y = element_text(vjust=0.5, size=15)) +
  theme(text = element_text(size=20)) + geom_hline(yintercept = 0,
linetype="dashed") + theme(legend.position = "bottom", legend.title =
element_blank()) + guides(col = guide_legend(nrow=1)) +
theme(plot.margin=unit(c(0.5,0,0,0.5), "cm")) +
  scale_colour_manual(labels = lab1, values = c('red','orange', 'black',
'gray75')) +
  scale_x_log10(breaks = trans_breaks("log10", function(x) 10^x), labels =
trans_format("log10", math_format(10^.x)), position = "bottom", limits =
c(1e-4,1e4)) + annotation_logticks(sides = "b")
```

```
ggsave(file="prokaryotic biomass vs latitude.png", width=7,height=6.5)
```

```
## Warning: Removed 444 rows containing missing values (geom_point).
```

```
#along a depth gradient
```

```
lab1 <- c(expression(g~C~cm^-3~wet~sediment),
            expression(g~C~g~dry~sediment^-1),
            expression(g~C~g~wet~sediment^-1),
            expression(g~C~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))
}
```

```

Fig2 <- ggplot(data = prokaryotic_biomass_corrected, 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("Prokaryotic biomass")
+
  theme(axis.text.y = element_text(vjust=0.5, size=15)) +
  annotation_logticks(sides = "tl") + geom_hline(yintercept = 0.1,
linetype="dashed", col="white", alpha=0) +
  theme(text = element_text(size=20)) + guides(fill=guide_legend(nrow=1)) +
  guides(col = guide_legend(nrow=2)) + theme(legend.position = "bottom",
legend.title = element_blank()) + theme(plot.margin=unit(c(0.5,0,0,0.5),
"cm")) +
  scale_x_log10(breaks = trans_breaks("log10", function(x) 10^x),
labels = trans_format("log10", math_format(10^.x)), limits =
c(1e-4,1e4), position = "top") + scale_colour_manual(labels = lab1, values =
c('red','orange','black','gray75'))
ggsave(file="prokaryotic biomass vs depth.png", width=7,height=6.5)

## Warning: Removed 460 rows containing missing values (geom_point).

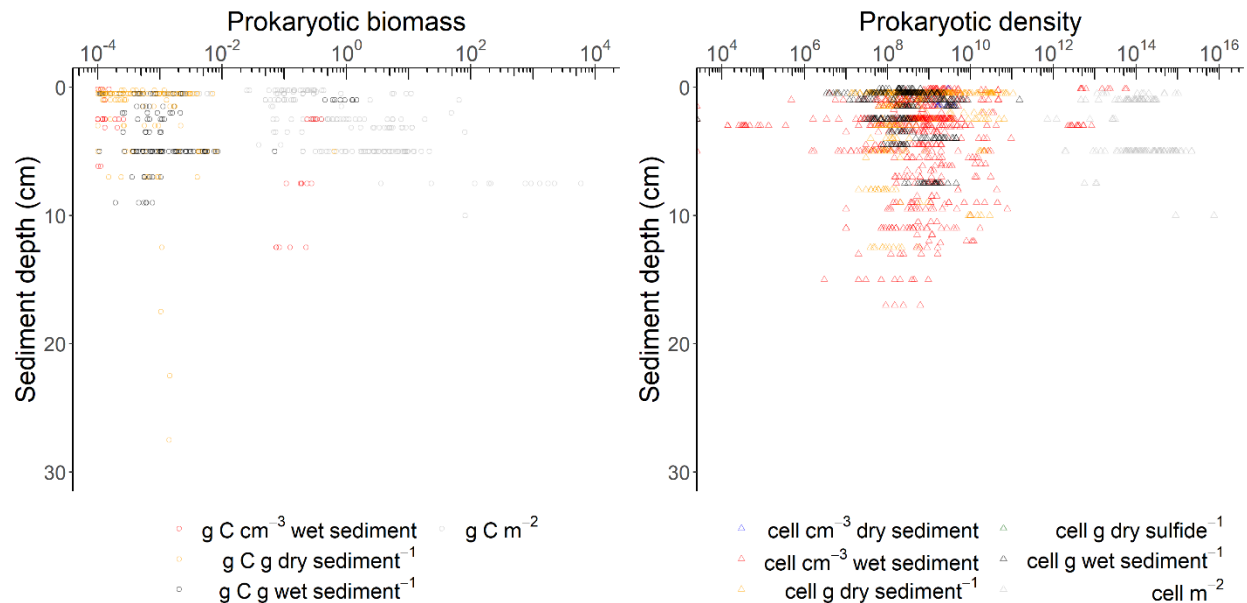
ggpubr::ggarrange(Fig1, Fig2, common.legend = TRUE, legend = "bottom")

## Warning: Removed 444 rows containing missing values (geom_point).

## Warning: Removed 444 rows containing missing values (geom_point).

## Warning: Removed 460 rows containing missing values (geom_point).

```



```

setwd("C:/Users/Mama/Desktop/paper 5_Role of benthos in the global C
cycle/Prokaryotes dataset")
ggsave(file="prokaryotic biomass.png", width=13,height=6.5)

```

## Loading benthic prokaryote density dataset

```
library(tidyr)
library(ggplot2)
library(openxlsx)
library(dplyr)

##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##   filter, lag

## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union

setwd("C:/Users/Mama/Desktop/paper 5_Role of benthos in the global C
cycle/Prokaryotes dataset/Microbial density")
prokaryotic_density_data <- read.xlsx("Prokaryotic density database.xlsx") #
read xlsx file

prokaryotic_density_data <- prokaryotic_density_data[c(2:4, 6:7, 14, 17:18,
23)]
cols <- c("Ocean", "Latitude", "Longitude", "Depth", "Depth_range", "Type",
"Density", "Unit", "Method")
colnames(prokaryotic_density_data) <- cols

prokaryotic_density_corrected <- prokaryotic_density_data %>%
drop_na("Density")
head(prokaryotic_density_corrected)

##           Ocean  Latitude Longitude Depth
## 1 Atlantic Ocean -5.799683  9.708005  3160
## 2 Atlantic Ocean -5.799500  9.708035  3160
## 3 Atlantic Ocean -5.797983  9.711407  3160
## 4 Atlantic Ocean -5.797883  9.711400  3160
## 5 Atlantic Ocean -5.797750  9.711590  3160
## 6 Atlantic Ocean -5.797717  9.711548  3160
##                                     Depth_range      Type Density      Unit
## Method
## 1 abyssal plain/ continental rise (>2000m) Prokaryote 1.4e+14 cell m-2
1.4e+10
## 2 abyssal plain/ continental rise (>2000m) Prokaryote 1.0e+14 cell m-2
1.0e+10
## 3 abyssal plain/ continental rise (>2000m) Prokaryote 9.0e+13 cell m-2
9.0e+09
## 4 abyssal plain/ continental rise (>2000m) Prokaryote 1.0e+14 cell m-2
1.0e+10
## 5 abyssal plain/ continental rise (>2000m) Prokaryote 1.6e+14 cell m-2
```

```
1.6e+10
## 6 abyssal plain/ continental rise (>2000m) Prokaryote 2.7e+14 cell m-2
2.7e+10
```

##Divide datasets in Prokaryote, Bacteria, Archaea

```
Prokaryote_data <- prokaryotic_density_corrected %>% filter(Type ==
"Prokaryote")
head(Prokaryote_data)
```

```
##           Ocean Latitude Longitude Depth
## 1 Atlantic Ocean -5.799683  9.708005  3160
## 2 Atlantic Ocean -5.799500  9.708035  3160
## 3 Atlantic Ocean -5.797983  9.711407  3160
## 4 Atlantic Ocean -5.797883  9.711400  3160
## 5 Atlantic Ocean -5.797750  9.711590  3160
## 6 Atlantic Ocean -5.797717  9.711548  3160
##           Depth_range      Type Density      Unit
Method
## 1 abyssal plain/ continental rise (>2000m) Prokaryote 1.4e+14 cell m-2
1.4e+10
## 2 abyssal plain/ continental rise (>2000m) Prokaryote 1.0e+14 cell m-2
1.0e+10
## 3 abyssal plain/ continental rise (>2000m) Prokaryote 9.0e+13 cell m-2
9.0e+09
## 4 abyssal plain/ continental rise (>2000m) Prokaryote 1.0e+14 cell m-2
1.0e+10
## 5 abyssal plain/ continental rise (>2000m) Prokaryote 1.6e+14 cell m-2
1.6e+10
## 6 abyssal plain/ continental rise (>2000m) Prokaryote 2.7e+14 cell m-2
2.7e+10
```

```
Bacteria_data <- prokaryotic_density_corrected %>% filter(Type == "Bacteria")
head(Bacteria_data)
```

```
##           Ocean Latitude Longitude Depth
## 1 Mediterranean Sea 32.11233  28.17250  3024
## 2 Mediterranean Sea 32.11233  28.17250  3024
## 3 Mediterranean Sea 31.96983  30.13705   507
## 4 Mediterranean Sea 32.11233  28.17252  3022
## 5 Mediterranean Sea 32.11234  28.17248  3024
## 6 Mediterranean Sea 32.36130  31.38895   991
##           Depth_range      Type Density
## 1 abyssal plain/ continental rise (>2000m) Bacteria 4.70e+08
## 2 abyssal plain/ continental rise (>2000m) Bacteria 7.80e+08
## 3 continental slope (>200-2000m) Bacteria 2.08e+09
## 4 abyssal plain/ continental rise (>2000m) Bacteria 4.70e+08
## 5 abyssal plain/ continental rise (>2000m) Bacteria 7.70e+08
## 6 continental slope (>200-2000m) Bacteria 1.65e+09
##           Unit      Method
## 1 cell cm-3 wet sediment 2.08e+09
```

```
## 2 cell cm-3 wet sediment 4.17e+09
## 3 cell cm-3 wet sediment 4.68e+09
## 4 cell cm-3 wet sediment 1.09e+09
## 5 cell cm-3 wet sediment 2.02e+09
## 6 cell cm-3 wet sediment 3.24e+09

Archaea_data <- prokaryotic_density_corrected %>% filter(Type == "Archaea")
head(Archaea_data)

##           Ocean Latitude Longitude Depth
## 1 Mediterranean Sea 32.11233  28.17250  3024
## 2 Mediterranean Sea 32.11233  28.17250  3024
## 3 Mediterranean Sea 31.96983  30.13705   507
## 4 Mediterranean Sea 32.11233  28.17252  3022
## 5 Mediterranean Sea 32.11234  28.17248  3024
## 6 Mediterranean Sea 32.36130  31.38895   991
##           Depth_range      Type Density
## 1 abyssal plain/ continental rise (>2000m) Archaea 1.4e+08
## 2 abyssal plain/ continental rise (>2000m) Archaea 3.0e+07
## 3           continental slope (>200-2000m) Archaea 1.1e+08
## 4 abyssal plain/ continental rise (>2000m) Archaea 6.0e+07
## 5 abyssal plain/ continental rise (>2000m) Archaea 2.0e+07
## 6           continental slope (>200-2000m) Archaea 2.6e+08
##           Unit      Method
## 1 cell cm-3 wet sediment 1.01e+09
## 2 cell cm-3 wet sediment 2.30e+09
## 3 cell cm-3 wet sediment 2.40e+08
## 4 cell cm-3 wet sediment 2.00e+08
## 5 cell cm-3 wet sediment 6.30e+08
## 6 cell cm-3 wet sediment 4.20e+08
```

## Preparing figure: Microbial densities along a latitudinal gradient

*#Plot for prokaryotic density*

```
lab1 <- c(expression(cell~cm-3~dry~sediment),
           expression(cell~cm-3~wet~sediment),
           expression(cell~g~dry~sediment-1),
           expression(cell~g~dry~sulfide-1),
           expression(cell~g~wet~sediment-1),
           expression(cell~m-2))
```

```
Fig3 <- ggplot(data = Prokaryote_data, aes(x = Density, 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)) +
  theme(text = element_text(size=20)) + geom_hline(yintercept = 0,
linetype="dashed") +
  scale_x_log10(breaks = trans_breaks("log10", function(x) 10x),
labels = trans_format("log10", math_format(10^.x)), limits =
c(1e4,1e16)) + theme(legend.position = "bottom", legend.title =
```

```

element_blank()) + guides(col = guide_legend(nrow=3)) +
theme(plot.margin=unit(c(0.5,0,0,0.5), "cm")) +
  scale_colour_manual(labels = lab1, values = c('blue', 'red', 'orange',
'darkgreen', 'black', 'gray75')) + annotate(geom="text", x=1e14, y=100,
label="Prokaryotes", color="black", size=6) + annotation_logticks(sides =
"b")

```

```

ggsave(file="prokaryotic density vs latitude.png", width=6.5,height=6.5)

```

```

## Warning: Transformation introduced infinite values in continuous x-axis

```

```

#Plot for Bacteria density

```

```

lab1 <- c(expression(cell~cm^-3~dry~sediment),
  expression(cell~cm^-3~wet~sediment),
  expression(cell~g~dry~sediment^-1),
  expression(cell~g~dry~sulfide^-1),
  expression(cell~g~wet~sediment^-1),
  expression(cell~m^-2))

```

```

Fig4 <- ggplot(data = Bacteria_data, aes(x = Density, 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)) +
  theme(text = element_text(size=20)) + geom_hline(yintercept = 0,
linetype="dashed") +
  scale_x_log10(breaks = trans_breaks("log10", function(x) 10^x),
  labels = trans_format("log10", math_format(10^.x)), limits =
c(1e4,1e16)) + theme(legend.position = "bottom", legend.title =
element_blank()) + guides(col = guide_legend(nrow=3)) +
theme(plot.margin=unit(c(0.5,0,0,0.5), "cm")) +
  scale_colour_manual(labels = lab1, values = c('blue', 'red', 'orange',
'darkgreen', 'black', 'gray75')) + annotate(geom="text", x=1e14, y=100,
label="Bacteria", color="black", size=6) + annotation_logticks(sides = "b")

```

```

ggsave(file="Bacteria density vs latitude.png", width=6.5,height=6.5)

```

```

## Warning: Transformation introduced infinite values in continuous x-axis

```

```

#Plot for Archaea density

```

```

lab1 <- c(expression(cell~cm^-3~dry~sediment),
  expression(cell~cm^-3~wet~sediment),
  expression(cell~g~dry~sediment^-1),
  expression(cell~g~dry~sulfide^-1),
  expression(cell~g~wet~sediment^-1),
  expression(cell~m^-2))

```

```

Fig5 <- ggplot(data = Archaea_data, aes(x = Density, 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)) +
  theme(text = element_text(size=20)) + geom_hline(yintercept = 0,
linetype="dashed") +
  scale_x_log10(breaks = trans_breaks("log10", function(x) 10^x),
                labels = trans_format("log10", math_format(10^.x)), limits =
c(1e4,1e16)) + theme(legend.position = "bottom", legend.title =
element_blank()) + guides(col = guide_legend(nrow=3)) +
theme(plot.margin=unit(c(0.5,0,0,0.5), "cm")) +
  scale_colour_manual(labels = lab1, values = c('blue', 'red', 'orange',
'darkgreen', 'black', 'gray75')) + annotate(geom="text", x=1e14, y=100,
label="Archaea", color="black", size=6) + annotation_logticks(sides = "b")

ggsave(file="Archaea density vs latitude.png", width=6.5,height=6.5)

## Warning: Transformation introduced infinite values in continuous x-axis

ggpubr::ggarrange(Fig3, Fig4, Fig5, nrow=3, common.legend = TRUE, legend =
"bottom")

## Warning: Transformation introduced infinite values in continuous x-axis

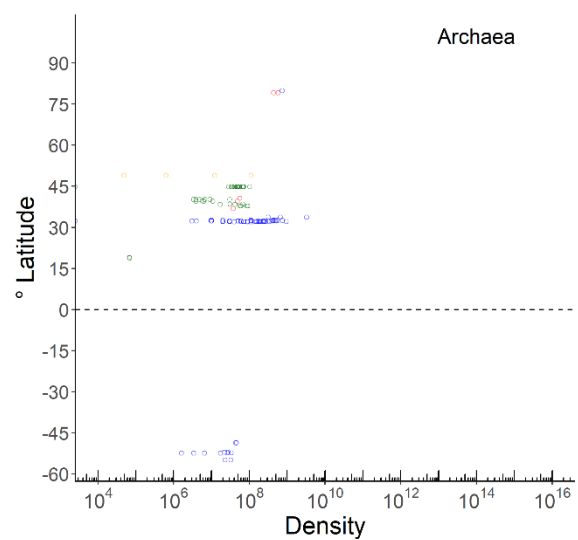
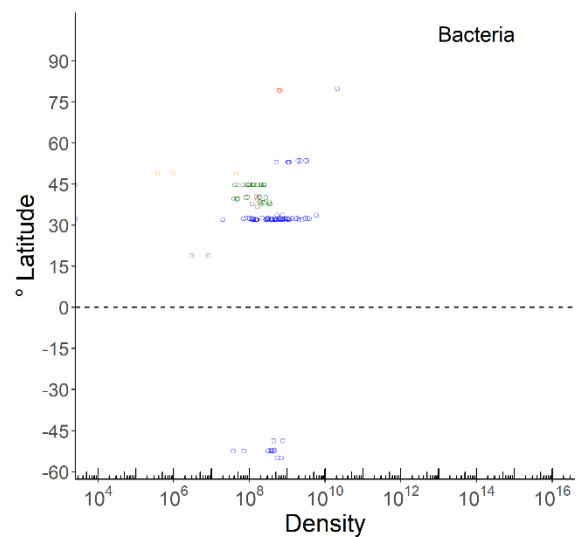
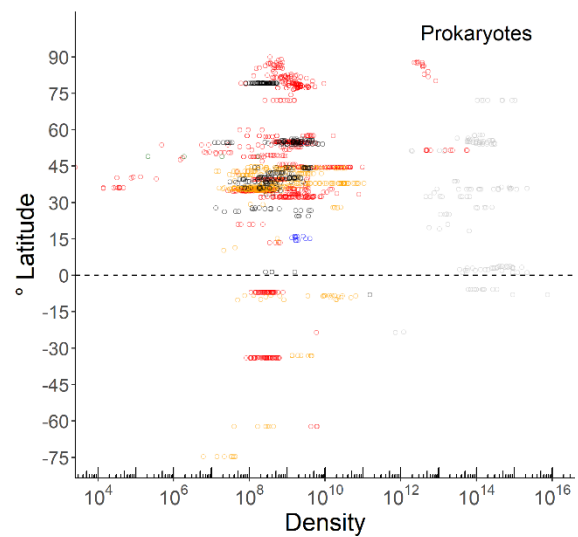
## Warning: Transformation introduced infinite values in continuous x-axis

## Warning: Transformation introduced infinite values in continuous x-axis

## Warning: Transformation introduced infinite values in continuous x-axis

```





- cell  $\text{cm}^{-3}$  dry sediment
- cell  $\text{cm}^{-3}$  wet sediment
- cell  $\text{g dry sediment}^{-1}$
- cell  $\text{g dry sulfide}^{-1}$
- cell  $\text{g wet sediment}^{-1}$
- cell  $\text{m}^{-2}$

```
setwd("C:/Users/Mama/Desktop/paper 5_Role of benthos in the global C
cycle/Prokaryotes dataset")
ggsave(file="microbial density vs latitude.png", width=6.5,height=19.5)
```

## Preparing figure: Microbial densities along a latitudinal gradient

```
library(ggplot2)
library(openxlsx)
```

```
#Plot for prokaryotic density
```

```
lab1 <- c(expression(cell~cm-3~dry~sediment),
           expression(cell~cm-3~wet~sediment),
           expression(cell~g~dry~sediment-1),
           expression(cell~g~dry~sulfide-1),
           expression(cell~g~wet~sediment-1),
           expression(cell~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))
}
```

```
Fig6 <- ggplot(data = Prokaryote_data, aes(x = Density, 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("Density") + theme(axis.text.y =
element_text(vjust=0.5, size=15)) + annotation_logticks(sides = "t1") +
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(col = guide_legend(nrow=3)) +
scale_x_log10(breaks = trans_breaks("log10", function(x) 10x), labels =
trans_format("log10", math_format(10x)), position = "top", limits =
c(1e4,1e16)) + theme(legend.position = "bottom", legend.title =
element_blank()) + theme(plot.margin=unit(c(0.5,0,0,0.5), "cm")) +
annotate(geom="text", x=1e14, y=0.2, label="Prokaryotes", color="black",
size=6) + scale_colour_manual(labels = lab1, values = c('blue',
'red', 'orange', 'darkgreen', 'black', 'gray75'))
```

```
ggsave(file="prokaryotic density vs depth.png", width=6.5,height=6.5)
```

```
## Warning: Transformation introduced infinite values in continuous x-axis
```

```
## Warning: Removed 33 rows containing missing values (geom_point).
```

```
#Plot for Bacteria density
```

```
Fig7 <- ggplot(data = Bacteria_data, aes(x = Density, 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("Density") + 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(col = guide_legend(nrow=3)) +
scale_x_log10(breaks = trans_breaks("log10", function(x) 10^x), labels =
trans_format("log10", math_format(10^.x)), position = "top", limits =
c(1e4, 1e16)) + theme(legend.position = "bottom", legend.title =
element_blank()) + theme(plot.margin=unit(c(0.5,0,0,0.5), "cm")) +
annotate(geom="text", x=1e14, y=0.2, label="Bacteria", color="black", size=6)
+ scale_colour_manual(labels = lab1, values = c('blue', 'red', 'orange',
'darkgreen', 'black', 'gray75'))

```

```

ggsave(file="Bacteria density vs depth.png", width=6.5,height=6.5)

```

```

## Warning: Transformation introduced infinite values in continuous x-axis

```

```

#Plot for Archaea density

```

```

Fig8 <- ggplot(data = Archaea_data, aes(x = Density, 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("Density") + 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(col = guide_legend(nrow=3)) +
scale_x_log10(breaks = trans_breaks("log10", function(x) 10^x), labels =
trans_format("log10", math_format(10^.x)), position = "top", limits =
c(1e4, 1e16)) + theme(legend.position = "bottom", legend.title =
element_blank()) + theme(plot.margin=unit(c(0.5,0,0,0.5), "cm")) +
annotate(geom="text", x=1e14, y=0.2, label="Archaea", color="black", size=6)
+ scale_colour_manual(labels = lab1, values = c('blue', 'red', 'orange',
'darkgreen', 'black', 'gray75'))

```

```

ggsave(file="Archaea density vs depth.png", width=6.5,height=6.5)

```

```

## Warning: Transformation introduced infinite values in continuous x-axis

```

```

ggpubr::ggarrange(Fig6, Fig7, Fig8, nrow=3, common.legend = TRUE)

```

```

## Warning: Transformation introduced infinite values in continuous x-axis

```

```

## Warning: Removed 33 rows containing missing values (geom_point).

```

```

## Warning: Transformation introduced infinite values in continuous x-axis

```

```

## Warning: Removed 33 rows containing missing values (geom_point).

```

```

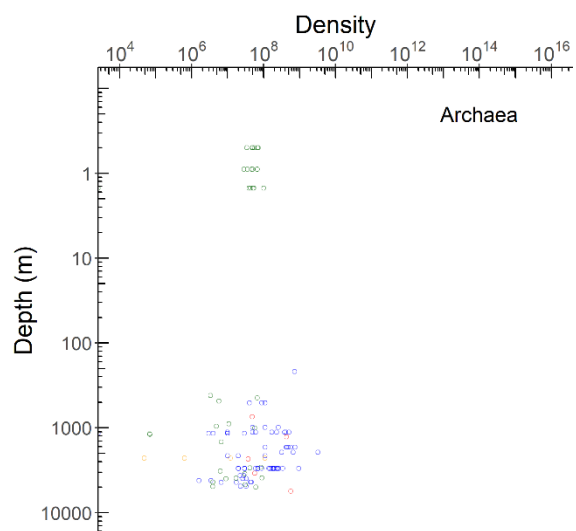
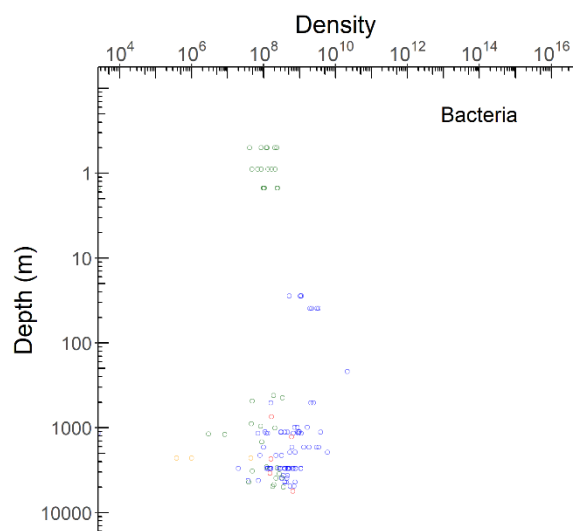
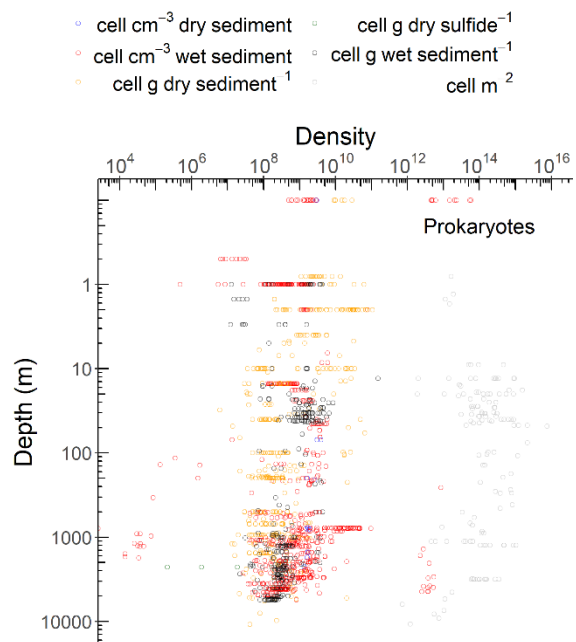
## Warning: Transformation introduced infinite values in continuous x-axis

```

```

## Warning: Transformation introduced infinite values in continuous x-axis

```



```
setwd("C:/Users/Mama/Desktop/paper 5_Role of benthos in the global C
cycle/Prokaryotes dataset")
ggsave(file="microbial density vs depth.png", width=6.5,height=19.5)
```

## Preparing figure: Prokaryotic biomasses & densities in surface sediment vs. integrated sediment cores

```
setwd("C:/Users/Mama/Desktop/paper 5_Role of benthos in the global C
cycle/Prokaryotes dataset/Microbial biomass")
biomass_data <- read.xlsx("Prokaryotic biomass database.xlsx") # read xlsx
file
```

```
biomass_data <- biomass_data[c(6:7, 9, 17:18, 20:21, 23:25)]
cols <- c("Depth", "Depth_range", "mean_sediment", "Biomass", "Unit", "Type",
"int_sediment_layer", "int_Biomass", "int_Unit", "Method")
colnames(biomass_data) <- cols
```

```
biomass_corrected <- biomass_data %>% drop_na("Biomass")
head(biomass_corrected)
```

```
##      Depth      Depth_range mean_sediment    Biomass
## 1    2.5      near-shore (0-50m)      0.75 4.520e-06
## 2    2.5      near-shore (0-50m)      0.75 3.640e-05
## 3    2.5      near-shore (0-50m)      0.75 6.100e-05
## 4   40.0      near-shore (0-50m)      0.15 1.007e-04
## 5   40.0      near-shore (0-50m)      0.15 1.193e-04
## 6 100.0 continental shelf (>50-200m) 0.15 4.230e-05
##              Unit              Type int_sediment_layer int_Biomass
## 1 g C cm wet sediment-3          <NA>              NA          NA
## 2 g C cm wet sediment-3          <NA>              NA          NA
## 3 g C cm wet sediment-3          <NA>              NA          NA
## 4 g C cm wet sediment-3 surface sediment      0.15    0.0001007
## 5 g C cm wet sediment-3 surface sediment      0.15    0.0001193
## 6 g C cm wet sediment-3 surface sediment      0.15    0.0000423
##              int_Unit
## 1              <NA>
## 2              <NA>
## 3              <NA>
## 4 g C cm wet sediment-3
## 5 g C cm wet sediment-3
## 6 g C cm wet sediment-3
##
Method
## 1 PD measured by epifluorescence microscopy, PD converted to PB using
conversion factors
## 2 PD measured by epifluorescence microscopy, PD converted to PB using
conversion factors
## 3 PD measured by epifluorescence microscopy, PD converted to PB using
conversion factors
## 4 PD measured by epifluorescence microscopy, PD converted to PB using
```

```

conversion factors
## 5 PD measured by epifluorescence microscopy, PD converted to PB using
conversion factors
## 6 PD measured by epifluorescence microscopy, PD converted to PB using
conversion factors

setwd("C:/Users/Mama/Desktop/paper 5_Role of benthos in the global C
cycle/Prokaryotes dataset/Microbial density")
density_data <- read.xlsx("Prokaryotic density database.xlsx") # read xlsx
file

density_data <- density_data[c(6:7, 9, 14, 17:18, 20, 22:25)]
cols <- c("Depth", "Depth_range", "mean_sediment", "Microorganisms",
"Density", "Unit", "Type", "int_sediment_layer", "int_Density", "int_Unit",
"Method")
colnames(density_data) <- cols

density_corrected <- density_data %>% drop_na("Density")
head(density_data)

##      Depth              Depth_range mean_sediment
Microorganisms
## 1  3160 abyssal plain/ continental rise (>2000m)          5
Prokaryote
## 2  3160 abyssal plain/ continental rise (>2000m)          5
Prokaryote
## 3  3160 abyssal plain/ continental rise (>2000m)          5
Prokaryote
## 4  3160 abyssal plain/ continental rise (>2000m)          5
Prokaryote
## 5  3160 abyssal plain/ continental rise (>2000m)          5
Prokaryote
## 6  3160 abyssal plain/ continental rise (>2000m)          5
Prokaryote
##      Density      Unit              Type int_sediment_layer int_Density
int_Unit
## 1 1.4e+14 cell m-2 surface sediment          10      1.4e+10 cell m-
2
## 2 1.0e+14 cell m-2 surface sediment          10      1.0e+10 cell m-
2
## 3 9.0e+13 cell m-2 surface sediment          10      9.0e+09 cell m-
2
## 4 1.0e+14 cell m-2 surface sediment          10      1.0e+10 cell m-
2
## 5 1.6e+14 cell m-2 surface sediment          10      1.6e+10 cell m-
2
## 6 2.7e+14 cell m-2 surface sediment          10      2.7e+10 cell m-
2
##
##              Method
## 1 acridine orange epifluorescence microscopy

```

```
## 2 acridine orange epifluorescence microscopy
## 3 acridine orange epifluorescence microscopy
## 4 acridine orange epifluorescence microscopy
## 5 acridine orange epifluorescence microscopy
## 6 acridine orange epifluorescence microscopy
```

### *#Prokaryotic biomass*

```
lab1 <- c(expression(g~C~cm^-3~wet~sediment),
            expression(g~C~g~dry~sediment^-1),
            expression(g~C~g~wet~sediment^-1),
            expression(g~C~m^-2))
```

```
Fig9 <- ggplot(data = biomass_corrected, aes(x = Biomass, y = mean_sediment,
color=Unit)) + geom_point(alpha = 0.5, size=1.5, shape=1) + theme_classic() +
scale_x_log10(breaks = trans_breaks("log10", function(x) 10^x), labels =
trans_format("log10", math_format(10^.x)), position = "top", limits = c(1e-
4,1e4)) + annotation_logticks(sides = "t") + ylab("Sediment depth (cm)") +
xlab("Prokaryotic biomass") + theme(axis.text.y = element_text(vjust=0.5,
size=15)) + annotation_logticks(sides = "t") + geom_hline(yintercept = 0.1,
linetype="dashed", col="white", alpha=0) +
  theme(text = element_text(size=20)) + guides(fill=guide_legend(nrow=1)) +
guides(col = guide_legend(nrow=3)) + theme(legend.position = "bottom",
legend.title = element_blank()) + theme(plot.margin=unit(c(0.5,0,0,0.5),
"cm")) +
  scale_colour_manual(labels = lab1, values = c('red', 'orange', 'black',
'gray75')) + scale_y_reverse(lim=c(30,0))
```

```
ggsave(file="Prokaryotic biomass_upper left.png", width=6.5,height=6.5)
```

```
## Warning: Removed 633 rows containing missing values (geom_point).
```

### *#Prokaryotic density*

```
lab1 <- c(expression(cell~cm^-3~dry~sediment),
            expression(cell~cm^-3~wet~sediment),
            expression(cell~g~dry~sediment^-1),
            expression(cell~g~dry~sulfide^-1),
            expression(cell~g~wet~sediment^-1),
            expression(cell~m^-2))
```

```
Fig10 <- ggplot(data = density_data, aes(x = Density, y = mean_sediment,
color=Unit)) + geom_point(alpha = 0.5, size=1.5, shape=2) + theme_classic() +
scale_x_log10(breaks = trans_breaks("log10", function(x) 10^x), labels =
trans_format("log10", math_format(10^.x)), position = "top", limits =
c(1e4,1e16)) + annotation_logticks(sides = "t") + ylab("Sediment depth (cm)")
+ xlab("Prokaryotic density") + theme(axis.text.y = element_text(vjust=0.5,
size=15)) + annotation_logticks(sides = "t") + geom_hline(yintercept = 0.1,
linetype="dashed", col="white", alpha=0) +
  theme(text = element_text(size=20)) + guides(fill=guide_legend(nrow=1)) +
guides(col = guide_legend(nrow=3)) + theme(legend.position = "bottom",
legend.title = element_blank()) + theme(plot.margin=unit(c(0.5,0,0,0.5),
```



```

"cm")) +
  scale_colour_manual(labels = lab1, values = c('blue', 'red', 'orange',
'darkgreen', 'black', 'gray75')) + scale_y_reverse(lim=c(30,0))

ggsave(file="Prokaryotic density_upper right.png", width=6.5,height=6.5)

## Warning: Transformation introduced infinite values in continuous x-axis
## Warning: Removed 150 rows containing missing values (geom_point).

Fig11 <- ggpubr::ggarrange(Fig9, Fig10, nrow=1, legend = "bottom")

## Warning: Removed 633 rows containing missing values (geom_point).
## Warning: Transformation introduced infinite values in continuous x-axis
## Warning: Removed 150 rows containing missing values (geom_point).

setwd("C:/Users/Mama/Desktop/paper 5_Role of benthos in the global C
cycle/Prokaryotes dataset")
ggsave(file="prokaryotes_upper panel.png", width=13,height=6.5)

```

## Figure to assess difference between surface sediment biomass/ density and vertically integrated biomass/ density

```

library(ggplot2)
library(dplyr)
library(openxlsx)

setwd("C:/Users/Mama/Desktop/paper 5_Role of benthos in the global C
cycle/Prokaryotes dataset/Figures")
sampling_comparison <- read.xlsx("Figure 7_data.xlsx") #read xlsx file

cols <- c("Depth", "Depth_range", "sediment_layer", "surf_parameter",
"log_surf_parameter", "int_sediment_layer", "int_parameter",
"log_int_parameter", "log_log_diff", "unit", "density_biomass",
"times_parameter")
colnames(sampling_comparison)<- cols
head(sampling_comparison)

##   Depth          Depth_range sediment_layer
surf_parameter
## 1    15          near-shore (0-50m)         0-1
2.748503e+08
## 2   1939      continental slope (>200-2000m)     0-2
2.045000e+10
## 3   1939      continental slope (>200-2000m)     0-2
5.960000e+09
## 4   2127 abyssal plain/ continental rise (>2000m) 0-2
1.100000e+08
## 5    15          near-shore (0-50m)         0-1
6.110000e-06

```

```
## 6 1939 continental slope (>200-2000m) 0-2
3.270000e+09
## log_surf_parameter int_sediment_layer int_parameter log_int_parameter
## 1 8.439096 0-05.0 3.143713e+08 8.497443
## 2 10.310693 0-04.0 2.424000e+10 10.384533
## 3 9.775246 0-04.0 7.260000e+09 9.860937
## 4 8.041393 0-04.0 1.400000e+08 8.146128
## 5 -5.213959 0-05.0 7.810000e-06 -5.107349
## 6 9.514548 0-04.0 4.250000e+09 9.628389
## log_log_diff unit density_biomass times_parameter
## 1 0.05834662 cell g dry sediment-1 density 1.143791
## 2 0.07383930 cell cm-3 wet sediment density 1.185330
## 3 0.08569036 cell cm-3 wet sediment density 1.218121
## 4 0.10473535 cell cm-3 wet sediment density 1.272727
## 5 0.10660982 g C g dry sediment-1 biomass 1.278232
## 6 0.11384118 cell cm-3 wet sediment density 1.299694

Biomass_data <- sampling_comparison %>% filter(density_biomass == "biomass")
head(Biomass_data)

## Depth Depth_range sediment_layer surf_parameter
log_surf_parameter
## 1 15.0 near-shore (0-50m) 0-1 6.11e-06 -
5.213959
## 2 0.2 near-shore (0-50m) 0-1 2.71e-03 -
2.567031
## 3 10.0 near-shore (0-50m) 0-1 4.80e-04 -
3.318759
## 4 10.0 near-shore (0-50m) 0-1 1.67e-03 -
2.777284
## 5 15.0 near-shore (0-50m) 0-1 6.60e-06 -
5.180456
## 6 10.0 near-shore (0-50m) 0-1 2.32e-03 -
2.634512
## int_sediment_layer int_parameter log_int_parameter log_log_diff
## 1 0-05.0 7.81e-06 -5.107349 0.1066098
## 2 0-10.0 3.66e-03 -2.436519 0.1305118
## 3 0-03.0 7.31e-04 -3.136083 0.1826761
## 4 0-03.0 2.58e-03 -2.588380 0.1889032
## 5 0-05.0 1.07e-05 -4.970616 0.2098398
## 6 0-03.0 3.77e-03 -2.423659 0.2108534
## unit density_biomass times_parameter
## 1 g C g dry sediment-1 biomass 1.278232
## 2 g C g dry sediment-1 biomass 1.350554
## 3 g C g wet sediment-1 biomass 1.522917
## 4 g C g wet sediment-1 biomass 1.544910
## 5 g C g dry sediment-1 biomass 1.621212
## 6 g C g wet sediment-1 biomass 1.625000
```

```
Density_data <- sampling_comparison %>% filter(density_biomass == "density")
head(Density_data)
```

```
##      Depth                                Depth_range sediment_layer
surf_parameter
## 1      15                                near-shore (0-50m)           0-1
274850299
## 2    1939                                continental slope (>200-2000m)       0-2
20450000000
## 3    1939                                continental slope (>200-2000m)       0-2
5960000000
## 4    2127 abyssal plain/ continental rise (>2000m)           0-2
110000000
## 5    1939                                continental slope (>200-2000m)       0-2
3270000000
## 6      10                                near-shore (0-50m)           0-1
7620000000
##      log_surf_parameter int_sediment_layer int_parameter log_int_parameter
## 1              8.439096              0-05.0      314371257          8.497443
## 2              10.310693              0-04.0     24240000000         10.384533
## 3              9.775246              0-04.0      7260000000          9.860937
## 4              8.041393              0-04.0      140000000          8.146128
## 5              9.514548              0-04.0     4250000000          9.628389
## 6              9.881955              0-03.0     11020000000         10.042182
##      log_log_diff              unit density_biomass times_parameter
## 1    0.05834662    cell g dry sediment-1      density      1.143791
## 2    0.07383930    cell cm-3 wet sediment      density      1.185330
## 3    0.08569036    cell cm-3 wet sediment      density      1.218121
## 4    0.10473535    cell cm-3 wet sediment      density      1.272727
## 5    0.11384118    cell cm-3 wet sediment      density      1.299694
## 6    0.16022662    cell g dry sediment-1      density      1.446194
```

```
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))
}
```

```
Fig12 <- ggplot(data = Biomass_data, aes(y = Depth, x = times_parameter,
color=int_sediment_layer)) + geom_point(alpha = 0.5, size=1.5, shape=19) +
theme_classic() + 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)) + scale_y_continuous(trans=reverselog_trans(10),
breaks = c(1, 10, 100, 1000, 10000)) + annotation_logticks(sides = "l") +
ylab("water depth (m)") +
xlab(bquote(' '*PB[integr.~sed.~layer]/~PB[surf.~sed.~layer]*')) +
theme(legend.position = "bottom") + guides(col = guide_legend(nrow=6,
title="Integrated \nsediment \nprofiles (cm)")) + scale_colour_manual(values
```

```

= c('#194003', '#3b9905', '#5ae609', '#c3fca2', "yellow", '#7915eb',
'#000cad', '#0570fc', '#ff9b7a')) + scale_x_continuous(position = 'top')

ggsave(file="Fig 7_lower part_left.png", width=6.5, height=6.5)

## Warning: Removed 1 rows containing missing values (geom_point).

Fig13 <- ggplot(data = Density_data, aes(y = Depth, x = times_parameter,
color=int_sediment_layer)) + geom_point(alpha = 0.5, size=1.5, shape=19) +
theme_classic() + 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("water depth (m)") +
xlab(bquote('~PB[integr.~sed.~layer]/~PB[surf.~sed.~layer]*')) +
theme(legend.position = "bottom") +
scale_y_continuous(trans=reverselog_trans(10), breaks = c(1, 10, 100, 1000,
10000)) + annotation_logticks(sides = "l") + guides(col =
guide_legend(nrow=6, title="Integrated \nsediment \nprofiles (cm)")) +
scale_colour_manual(values = c('#000000', '#3b9905', '#4ec708',
'#5ae609', '#c3fca2', '#dcfaca', '#f2fab9', '#e9f781', "yellow",
'#7915eb', '#400485', '#000cad',
'#000ed4', '#0011ff', '#0570fc', '#05b2fc', '#7ad7ff')) +
scale_x_continuous(position = 'top')

ggsave(file="Fig 7_lower part_right.png", width=6.5,height=6.5)

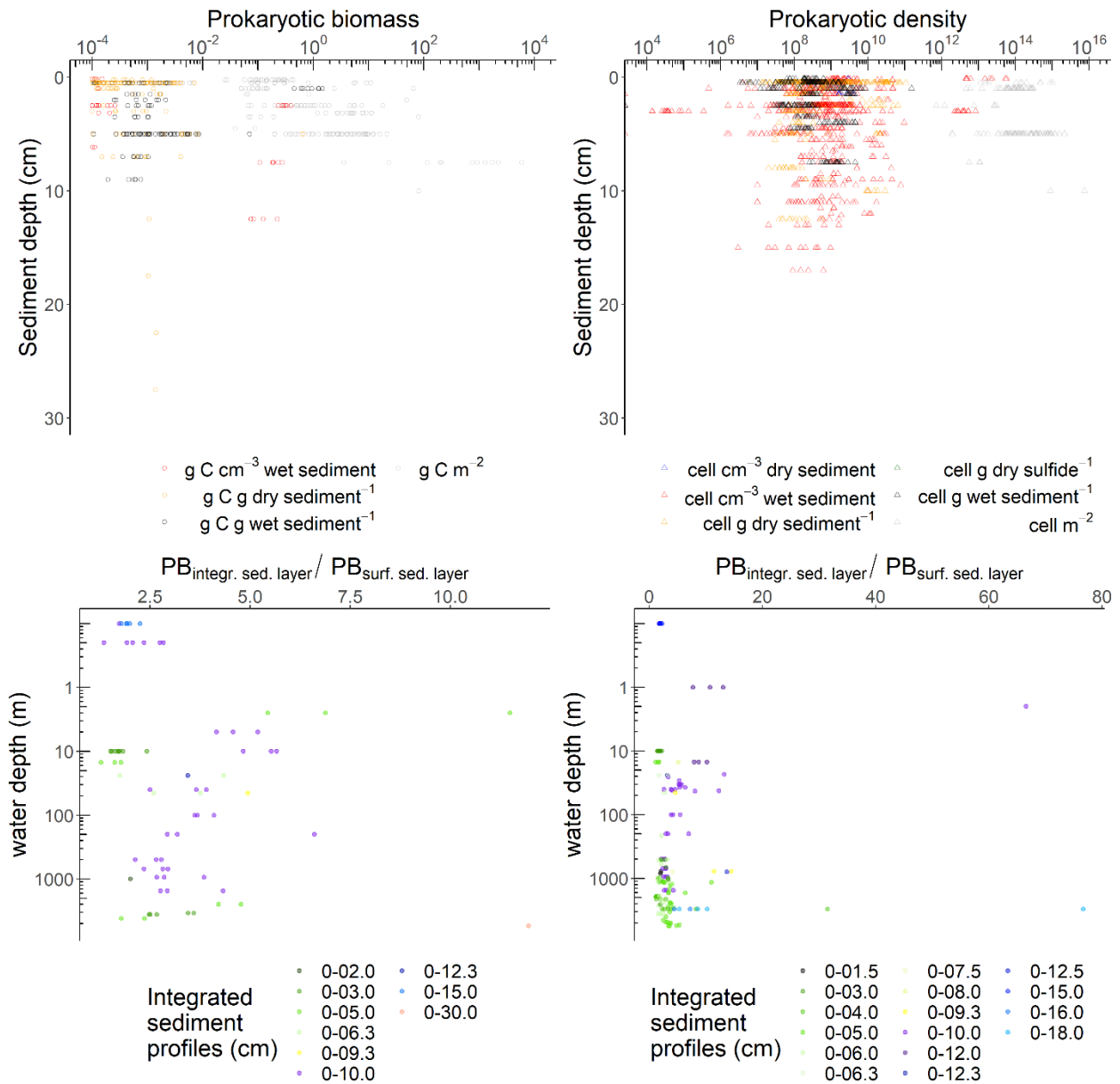
Fig14 <- ggpubr::ggarrange(Fig12, Fig13, nrow=1, legend = "bottom")

## Warning: Removed 1 rows containing missing values (geom_point).

setwd("C:/Users/Mama/Desktop/paper 5_Role of benthos in the global C
cycle/Prokaryotes dataset/Figures")
ggsave(file="Fig 7_lower part.png", width=13,height=6.5)

ggpubr::ggarrange(Fig11, Fig14, nrow=2)

```



```
setwd("C:/Users/Mama/Desktop/paper 5_Role of benthos in the global C
cycle/Prokaryotes dataset/Figures")
ggsave(file="Fig 7.png", width=13,height=13)
```