Prokaryotic biomass and density database

Tanja Stratmann

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#ProkaBIO database ## Loading benthic prokaryote biomass dataset

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

setwd("C:/Users/Mama/Desktop/manuscript revised/Figures")
prokaryotic_biomass_data <- read.xlsx("ProkaBio database.xlsx")  # read xlsx
file
head(prokaryotic_biomass_data)

##        Region         Ocean Latitude.(N) Longitude.(E)      Location
Depth.(m)
## 1 North Sea Atlantic Ocean          53           3.9 exact location
24
## 2 North Sea Atlantic Ocean          53           3.9 exact location
24
## 3 North Sea Atlantic Ocean          53           3.9 exact location
24
## 4 North Sea Atlantic Ocean          53           3.9 exact location
24
## 5 North Sea Atlantic Ocean          53           3.9 exact location
24
## 6 North Sea Atlantic Ocean          53           3.9 exact location
24
##         Depth.range upper.-.lower.sediment.layers.(cm)
## 1 near-shore (0-50m)                            0.0-0.3
## 2 near-shore (0-50m)                            0.0-0.3
## 3 near-shore (0-50m)                            0.0-0.3
## 4 near-shore (0-50m)                          12.0-12.3
## 5 near-shore (0-50m)                            3.0-3.3
## 6 near-shore (0-50m)                            3.0-3.3
##   middle.depth.of.sampled.sediment.layer.(cm) sediment.type
## 1                                        0.15       <2% mud
## 2                                        0.15       <2% mud
## 3                                        0.15       <2% mud
## 4                                       12.20       <2% mud
## 5                                        3.15       <2% mud
## 6                                        3.15       <2% mud
##   median.sediment.grain.size.(µm) sediment.density.(g.cm-3) porosity
## 1                             225                        NA      <NA>
```

```
## 2                                                225            NA        <NA>
## 3                                                225            NA        <NA>
## 4                                                225            NA        <NA>
## 5                                                225            NA        <NA>
## 6                                                225            NA        <NA>
##    type.of.microorganisms
## 1           Prokaryote
## 2           Prokaryote
## 3           Prokaryote
## 4           Prokaryote
## 5           Prokaryote
## 6           Prokaryote
##
mean/.median.density.per.sediment.layer.as.presented.in.the.original.publicat
ion
## 1
54
## 2
52
## 3
32
## 4
50
## 5
21
## 6
29
##    unit.of.mean/.median.as.presented.in.original.publication
## 1                                 µg C cm-3 wet sediment
## 2                                 µg C cm-3 wet sediment
## 3                                 µg C cm-3 wet sediment
## 4                                 µg C cm-3 wet sediment
## 5                                 µg C cm-3 wet sediment
## 6                                 µg C cm-3 wet sediment
##    error.term.as.presented.in.original.publication
## 1                                           NA
## 2                                           NA
## 3                                           NA
## 4                                           NA
## 5                                           NA
## 6                                           NA
##    type.of.error.term.as.presented.in.the.original.publication
## 1                                                       <NA>
## 2                                                       <NA>
## 3                                                       <NA>
## 4                                                       <NA>
## 5                                                       <NA>
## 6                                                       <NA>
##    standardized.biomass.per.sediment.layer     standardized.unit
## 1                             5.4e-05 g C cm-3 wet sediment
```

```
## 2                                 5.2e-05 g C cm-3 wet sediment
## 3                                 3.2e-05 g C cm-3 wet sediment
## 4                                 5.0e-05 g C cm-3 wet sediment
## 5                                 2.1e-05 g C cm-3 wet sediment
## 6                                 2.9e-05 g C cm-3 wet sediment
##    conversion.factor.to.convert.PD.to.PB/.ATP.to.PB
## 1                2.2*10^(-11) g C μm-3 biovolume
## 2                2.2*10^(-11) g C μm-3 biovolume
## 3                2.2*10^(-11) g C μm-3 biovolume
## 4                2.2*10^(-11) g C μm-3 biovolume
## 5                2.2*10^(-11) g C μm-3 biovolume
## 6                2.2*10^(-11) g C μm-3 biovolume
##
reference.for.conversion.factor
## 1 Bratbak, G., & Dundas, I. (1984). Bacterial dry matter content and
biomass estimations. Applied and Environmental Microbiology, 48(4), 755–757.
https://doi.org/10.1128/aem.48.4.755-757.1984
## 2 Bratbak, G., & Dundas, I. (1984). Bacterial dry matter content and
biomass estimations. Applied and Environmental Microbiology, 48(4), 755–757.
https://doi.org/10.1128/aem.48.4.755-757.1984
## 3 Bratbak, G., & Dundas, I. (1984). Bacterial dry matter content and
biomass estimations. Applied and Environmental Microbiology, 48(4), 755–757.
https://doi.org/10.1128/aem.48.4.755-757.1984
## 4 Bratbak, G., & Dundas, I. (1984). Bacterial dry matter content and
biomass estimations. Applied and Environmental Microbiology, 48(4), 755–757.
https://doi.org/10.1128/aem.48.4.755-757.1984
## 5 Bratbak, G., & Dundas, I. (1984). Bacterial dry matter content and
biomass estimations. Applied and Environmental Microbiology, 48(4), 755–757.
https://doi.org/10.1128/aem.48.4.755-757.1984
## 6 Bratbak, G., & Dundas, I. (1984). Bacterial dry matter content and
biomass estimations. Applied and Environmental Microbiology, 48(4), 755–757.
https://doi.org/10.1128/aem.48.4.755-757.1984
##    integrated.sediment.layers.(lower.-.upper;.cm)
## 1                                 0.0-12.3
## 2                                  0.0-6.3
## 3                                  0.0-6.3
## 4                                     <NA>
## 5                                     <NA>
## 6                                     <NA>
##    integrated.sediment.layer/.surface.sediment.layer
## 1                            integrated sediment
## 2                            integrated sediment
## 3                            integrated sediment
## 4                                         <NA>
## 5                                         <NA>
## 6                                         <NA>
##    integrated.sediment.depth.(cm)
## 1                            12.3
## 2                             6.3
## 3                             6.3
```

```
## 4                                       NA
## 5                                       NA
## 6                                       NA
##   integrated.standardized.biomass.per.station/.sampling.event
## 1                                              0.000186
## 2                                              0.000091
## 3                                              0.000139
## 4                                                    NA
## 5                                                    NA
## 6                                                    NA
##   integrated.standardized.unit
## 1        g C cm-3 wet sediment
## 2        g C cm-3 wet sediment
## 3        g C cm-3 wet sediment
## 4                        <NA>
## 5                        <NA>
## 6                        <NA>
##
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
##   substrate.type
## 1        sediment
## 2        sediment
## 3        sediment
## 4        sediment
## 5        sediment
## 6        sediment
##
Reference
## 1 Osinga, R., Kop, A. J., Duineveld, G. C. A., Prins, R. A., & Van Duyl,
F. C. (1996). Benthic mineralization rates at two locations in the southern
North Sea. Journal of Sea Research, 36(3-4), 181-191.
https://doi.org/10.1016/S1385-1101(96)90788-1
## 2 Osinga, R., Kop, A. J., Duineveld, G. C. A., Prins, R. A., & Van Duyl,
F. C. (1996). Benthic mineralization rates at two locations in the southern
North Sea. Journal of Sea Research, 36(3-4), 181-191.
https://doi.org/10.1016/S1385-1101(96)90788-1
## 3 Osinga, R., Kop, A. J., Duineveld, G. C. A., Prins, R. A., & Van Duyl,
F. C. (1996). Benthic mineralization rates at two locations in the southern
```

North Sea. Journal of Sea Research, 36(3–4), 181–191.
https://doi.org/10.1016/S1385-1101(96)90788-1
4 Osinga, R., Kop, A. J., Duineveld, G. C. A., Prins, R. A., & Van Duyl,
F. C. (1996). Benthic mineralization rates at two locations in the southern
North Sea. Journal of Sea Research, 36(3–4), 181–191.
https://doi.org/10.1016/S1385-1101(96)90788-1
5 Osinga, R., Kop, A. J., Duineveld, G. C. A., Prins, R. A., & Van Duyl,
F. C. (1996). Benthic mineralization rates at two locations in the southern
North Sea. Journal of Sea Research, 36(3–4), 181–191.
https://doi.org/10.1016/S1385-1101(96)90788-1
6 Osinga, R., Kop, A. J., Duineveld, G. C. A., Prins, R. A., & Van Duyl,
F. C. (1996). Benthic mineralization rates at two locations in the southern
North Sea. Journal of Sea Research, 36(3–4), 181–191.
https://doi.org/10.1016/S1385-1101(96)90788-1

```r
prokaryotic_biomass_data <- prokaryotic_biomass_data[c(2:4, 6:7, 19:20, 28)]
cols <- c("Ocean","Latitude", "Longitude", "Depth", "Depth_range", "Biomass",
"Unit", "Method")
colnames(prokaryotic_biomass_data) <- cols

prokaryotic_biomass_corrected <-
prokaryotic_biomass_data[complete.cases(prokaryotic_biomass_data$Biomass), ]
#prokaryotic_biomass_corrected <- prokaryotic_biomass_data %>%
drop_na("Biomass")
head(prokaryotic_biomass_corrected)
```

```
##              Ocean Latitude Longitude Depth    Depth_range Biomass
## 1 Atlantic Ocean         53       3.9    24 near-shore (0-50m) 5.4e-05
## 2 Atlantic Ocean         53       3.9    24 near-shore (0-50m) 5.2e-05
## 3 Atlantic Ocean         53       3.9    24 near-shore (0-50m) 3.2e-05
## 4 Atlantic Ocean         53       3.9    24 near-shore (0-50m) 5.0e-05
## 5 Atlantic Ocean         53       3.9    24 near-shore (0-50m) 2.1e-05
## 6 Atlantic Ocean         53       3.9    24 near-shore (0-50m) 2.9e-05
##                    Unit
## 1 g C cm-3 wet sediment
## 2 g C cm-3 wet sediment
## 3 g C cm-3 wet sediment
## 4 g C cm-3 wet sediment
## 5 g C cm-3 wet sediment
## 6 g C cm-3 wet sediment
##
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 = 0.3, size=2.5, shape=16) +
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',
'blue')) +
    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 612 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 = 0.3, size=2.5, shape=16) +
```

```r
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', 'blue'))
ggsave(file="prokaryotic biomass vs depth.png", width=7,height=6.5)

## Warning: Removed 629 rows containing missing values (geom_point).

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

## Warning: Removed 612 rows containing missing values (geom_point).
## Removed 612 rows containing missing values (geom_point).

## Warning: Removed 629 rows containing missing values (geom_point).
```
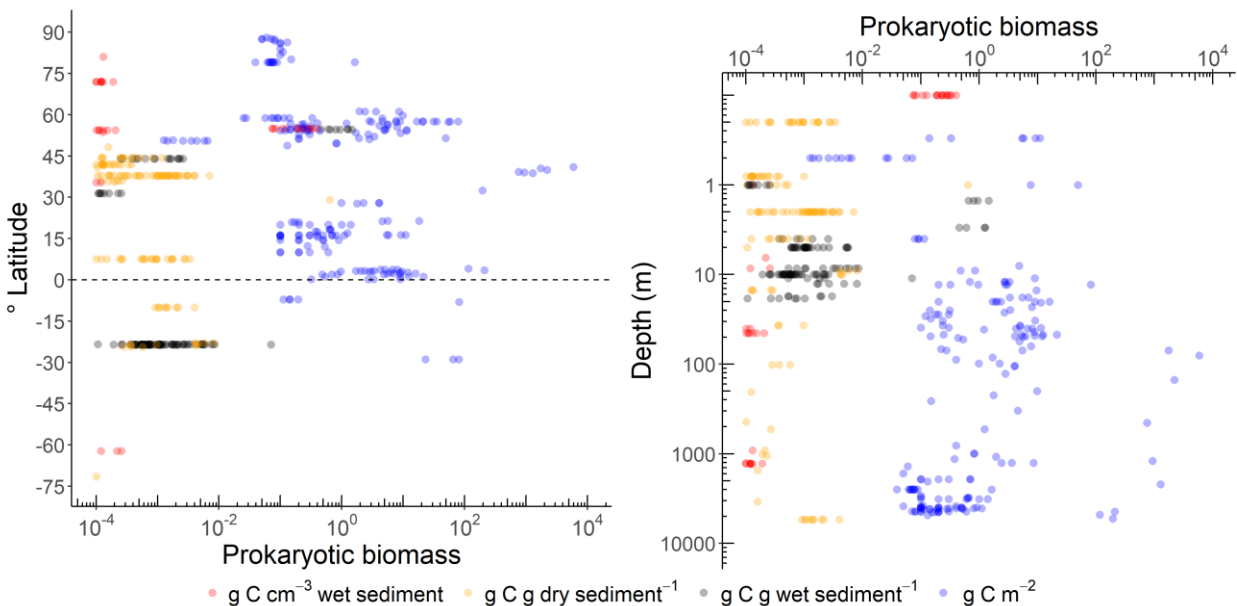


```r
setwd("C:/Users/Mama/Desktop/manuscript revised/Figures")
ggsave(file="prokaryotic biomass.png", width=13,height=6.5)
```

Loading benthic prokaryote density dataset
```r
library(tidyr)
library(ggplot2)
```

```
library(openxlsx)
library(dplyr)

##
## Attache Paket: 'dplyr'

## Die folgenden Objekte sind maskiert von 'package:stats':
##
##     filter, lag

## Die folgenden Objekte sind maskiert von 'package:base':
##
##     intersect, setdiff, setequal, union

setwd("C:/Users/Mama/Desktop/manuscript revised/Figures")
prokaryotic_density_data <- read.xlsx("ProkaDen database.xlsx")  # read xlsx
file
head(prokaryotic_density_data)

##           Region                Ocean Latitude.(N) Longitude.(E)      Location
## 1 Adriatic Sea Mediterranean Sea       42.866       15.095 exact location
## 2 Adriatic Sea Mediterranean Sea       42.874       15.092 exact location
## 3 Adriatic Sea Mediterranean Sea       42.903       15.069 exact location
## 4 Adriatic Sea Mediterranean Sea       42.907       15.072 exact location
## 5 Adriatic Sea Mediterranean Sea       42.911       15.062 exact location
## 6 Adriatic Sea Mediterranean Sea       43.600       13.500 exact location
##   Depth.(m)              Depth.range upper.-
.lower.sediment.layers.(cm)
## 1       189 continental shelf (>50-200m)                          0.0-
1.0
## 2       194 continental shelf (>50-200m)                          0.0-
1.0
## 3       190 continental shelf (>50-200m)                          0.0-
1.0
## 4       190 continental shelf (>50-200m)                          0.0-
1.0
## 5       197 continental shelf (>50-200m)                          0.0-
1.0
## 6         5          near-shore (0-50m)                           0.0-
1.0
##   middle.depth.of.sampled.sediment.layer.(cm) sediment.type
## 1                                         0.5           <NA>
## 2                                         0.5           <NA>
## 3                                         0.5           <NA>
## 4                                         0.5           <NA>
## 5                                         0.5           <NA>
## 6                                         0.5           <NA>
##   median.sediment.grain.size.(µm) sediment.density.(g.cm-3) porosity
## 1                              NA                        NA       NA
## 2                              NA                        NA       NA
## 3                              NA                        NA       NA
```

```
## 4                                    NA                        NA       NA
## 5                                    NA                        NA       NA
## 6                                    NA                        NA       NA
##   type.of.microorganisms
## 1           Prokaryote
## 2           Prokaryote
## 3           Prokaryote
## 4           Prokaryote
## 5           Prokaryote
## 6           Prokaryote
##
mean/.median.density.per.sediment.layer.as.presented.in.the.original.publicat
ion
## 1
3.35e+08
## 2
3.38e+08
## 3
1.18e+08
## 4
2.31e+08
## 5
1.43e+08
## 6
5.20e+08
##   unit.of.mean/.median.as.presented.in.original.publication
## 1                                 cell g-1 dry sediment
## 2                                 cell g-1 dry sediment
## 3                                 cell g-1 dry sediment
## 4                                 cell g-1 dry sediment
## 5                                 cell g-1 dry sediment
## 6                                 cell g-1 dry sediment
##   error.term.as.presented.in.original.publication
## 1                               61674009
## 2                               10572687
## 3                               31718062
## 4                               33480176
## 5                               12334802
## 6                                     NA
##   type.of.error.term.as.presented.in.the.original.publication
## 1                                   standard deviation
## 2                                   standard deviation
## 3                                   standard deviation
## 4                                   standard deviation
## 5                                   standard deviation
## 6                                              <NA>
##   standardized.density.per.sediment.layer     standardized.unit
## 1                          3.35e+08 cell g-1 dry sediment
## 2                          3.38e+08 cell g-1 dry sediment
## 3                          1.18e+08 cell g-1 dry sediment
```

```
## 4                                        2.31e+08 cell g-1 dry sediment
## 5                                        1.43e+08 cell g-1 dry sediment
## 6                                        5.20e+08 cell g-1 dry sediment
##   integrated.sediment.layers.(lower.-.upper;.cm)
## 1                                            0.0-1.0
## 2                                            0.0-1.0
## 3                                            0.0-1.0
## 4                                            0.0-1.0
## 5                                            0.0-1.0
## 6                                            0.0-1.0
##   integrated.sediment.layer/.surface.sediment.layer
## 1                                   surface sediment
## 2                                   surface sediment
## 3                                   surface sediment
## 4                                   surface sediment
## 5                                   surface sediment
## 6                                   surface sediment
##   integrated.sediment.depth.(cm)
## 1                                1
## 2                                1
## 3                                1
## 4                                1
## 5                                1
## 6                                1
##   integrated.standardized.density.per.station/.sampling.event
## 1                                                     3.35e+08
## 2                                                     3.38e+08
## 3                                                     1.18e+08
## 4                                                     2.31e+08
## 5                                                     1.43e+08
## 6                                                     5.20e+08
##   integrated.standardized.unit
## 1         cell g-1 dry sediment
## 2         cell g-1 dry sediment
## 3         cell g-1 dry sediment
## 4         cell g-1 dry sediment
## 5         cell g-1 dry sediment
## 6         cell g-1 dry sediment
##                                                 method substrate.type
## 1 epifluorescence microscopy (stain: acridine orange)       sediment
## 2 epifluorescence microscopy (stain: acridine orange)       sediment
## 3 epifluorescence microscopy (stain: acridine orange)       sediment
## 4 epifluorescence microscopy (stain: acridine orange)       sediment
## 5 epifluorescence microscopy (stain: acridine orange)       sediment
## 6 epifluorescence microscopy (stain: acridine orange)       sediment
##
Reference
## 1       Giovannelli, D., D'Errico, G., Fiorentino, F., Fattorini, D.,
Regoli, F., Angeletti, L., et al. (2016). Diversity and distribution of
prokaryotes within a shallow-water pockmark field. Frontiers in Microbiology,
```

7, 941. https://doi.org/10.3389/fmicb.2016.00941
2   Giovannelli, D., D'Errico, G., Fiorentino, F., Fattorini, D.,
Regoli, F., Angeletti, L., et al. (2016). Diversity and distribution of
prokaryotes within a shallow-water pockmark field. Frontiers in Microbiology,
7, 941. https://doi.org/10.3389/fmicb.2016.00941
3   Giovannelli, D., D'Errico, G., Fiorentino, F., Fattorini, D.,
Regoli, F., Angeletti, L., et al. (2016). Diversity and distribution of
prokaryotes within a shallow-water pockmark field. Frontiers in Microbiology,
7, 941. https://doi.org/10.3389/fmicb.2016.00941
4   Giovannelli, D., D'Errico, G., Fiorentino, F., Fattorini, D.,
Regoli, F., Angeletti, L., et al. (2016). Diversity and distribution of
prokaryotes within a shallow-water pockmark field. Frontiers in Microbiology,
7, 941. https://doi.org/10.3389/fmicb.2016.00941
5   Giovannelli, D., D'Errico, G., Fiorentino, F., Fattorini, D.,
Regoli, F., Angeletti, L., et al. (2016). Diversity and distribution of
prokaryotes within a shallow-water pockmark field. Frontiers in Microbiology,
7, 941. https://doi.org/10.3389/fmicb.2016.00941
6 Danovaro, R., Armeni, M., Dell'Anno, A., Fabiano, M., Manini, E.,
Marrale, D., et al. (2001). Small-scale distribution of bacteria, enzymatic
activities, and organic matter in coastal sediments. Microbial Ecology,
42(2), 177–185. https://doi.org/10.1007/s002480000109

```
prokaryotic_density_data <- prokaryotic_density_data[c(2:4, 6:7, 14, 19:20,
26)]
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                Depth_range
## 1 Mediterranean Sea   42.866    15.095    189 continental shelf (>50-200m)
## 2 Mediterranean Sea   42.874    15.092    194 continental shelf (>50-200m)
## 3 Mediterranean Sea   42.903    15.069    190 continental shelf (>50-200m)
## 4 Mediterranean Sea   42.907    15.072    190 continental shelf (>50-200m)
## 5 Mediterranean Sea   42.911    15.062    197 continental shelf (>50-200m)
## 6 Mediterranean Sea   43.600    13.500      5          near-shore (0-50m)
##        Type  Density                 Unit
## 1 Prokaryote 3.35e+08 cell g-1 dry sediment
## 2 Prokaryote 3.38e+08 cell g-1 dry sediment
## 3 Prokaryote 1.18e+08 cell g-1 dry sediment
## 4 Prokaryote 2.31e+08 cell g-1 dry sediment
## 5 Prokaryote 1.43e+08 cell g-1 dry sediment
## 6 Prokaryote 5.20e+08 cell g-1 dry sediment
##                                            Method
## 1 epifluorescence microscopy (stain: acridine orange)
## 2 epifluorescence microscopy (stain: acridine orange)
## 3 epifluorescence microscopy (stain: acridine orange)
```

```
## 4 epifluorescence microscopy (stain: acridine orange)
## 5 epifluorescence microscopy (stain: acridine orange)
## 6 epifluorescence microscopy (stain: acridine orange)
```

##Divide datasets in Prokaryote, Bacteria, Archaea

```
Prokaryote_data <- prokaryotic_density_corrected %>% filter(Type ==
"Prokaryote")
Pro_data <- Prokaryote_data[!(Prokaryote_data$Density==0),]
head(Pro_data)

##                 Ocean Latitude Longitude Depth                Depth_range
## 1 Mediterranean Sea   42.866    15.095    189 continental shelf (>50-200m)
## 2 Mediterranean Sea   42.874    15.092    194 continental shelf (>50-200m)
## 3 Mediterranean Sea   42.903    15.069    190 continental shelf (>50-200m)
## 4 Mediterranean Sea   42.907    15.072    190 continental shelf (>50-200m)
## 5 Mediterranean Sea   42.911    15.062    197 continental shelf (>50-200m)
## 6 Mediterranean Sea   43.600    13.500      5       near-shore (0-50m)
##        Type  Density                 Unit
## 1 Prokaryote 3.35e+08 cell g-1 dry sediment
## 2 Prokaryote 3.38e+08 cell g-1 dry sediment
## 3 Prokaryote 1.18e+08 cell g-1 dry sediment
## 4 Prokaryote 2.31e+08 cell g-1 dry sediment
## 5 Prokaryote 1.43e+08 cell g-1 dry sediment
## 6 Prokaryote 5.20e+08 cell g-1 dry sediment
##                                        Method
## 1 epifluorescence microscopy (stain: acridine orange)
## 2 epifluorescence microscopy (stain: acridine orange)
## 3 epifluorescence microscopy (stain: acridine orange)
## 4 epifluorescence microscopy (stain: acridine orange)
## 5 epifluorescence microscopy (stain: acridine orange)
## 6 epifluorescence microscopy (stain: acridine orange)

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

##                 Ocean Latitude Longitude Depth
Depth_range
## 1 Mediterranean Sea   32.368    31.704   1158 continental slope (>200-
2000m)
## 2 Mediterranean Sea   32.369    31.711   1122 continental slope (>200-
2000m)
## 3 Mediterranean Sea   32.369    31.711   1122 continental slope (>200-
2000m)
## 4 Mediterranean Sea   32.368    31.704   1158 continental slope (>200-
2000m)
## 5 Mediterranean Sea   32.368    31.704   1158 continental slope (>200-
2000m)
## 6 Mediterranean Sea   32.369    31.711   1122 continental slope (>200-
2000m)
##       Type  Density                 Unit                        Method
```

```
## 1 Bacteria 1.12e+09 cell cm-3 wet sediment CARD-FISH (probe: EUB338I-III)
## 2 Bacteria 3.87e+09 cell cm-3 wet sediment CARD-FISH (probe: EUB338I-III)
## 3 Bacteria 8.90e+08 cell cm-3 wet sediment CARD-FISH (probe: EUB338I-III)
## 4 Bacteria 9.40e+08 cell cm-3 wet sediment CARD-FISH (probe: EUB338I-III)
## 5 Bacteria 7.00e+07 cell cm-3 wet sediment CARD-FISH (probe: EUB338I-III)
## 6 Bacteria 3.10e+08 cell cm-3 wet sediment CARD-FISH (probe: EUB338I-III)

Bac_data <- Bacteria_data[!(Bacteria_data$Density==0),]
head(Bac_data)

##                Ocean Latitude Longitude Depth
Depth_range
## 1 Mediterranean Sea   32.368    31.704  1158 continental slope (>200-
2000m)
## 2 Mediterranean Sea   32.369    31.711  1122 continental slope (>200-
2000m)
## 3 Mediterranean Sea   32.369    31.711  1122 continental slope (>200-
2000m)
## 4 Mediterranean Sea   32.368    31.704  1158 continental slope (>200-
2000m)
## 5 Mediterranean Sea   32.368    31.704  1158 continental slope (>200-
2000m)
## 6 Mediterranean Sea   32.369    31.711  1122 continental slope (>200-
2000m)
##       Type Density              Unit                        Method
## 1 Bacteria 1.12e+09 cell cm-3 wet sediment CARD-FISH (probe: EUB338I-III)
## 2 Bacteria 3.87e+09 cell cm-3 wet sediment CARD-FISH (probe: EUB338I-III)
## 3 Bacteria 8.90e+08 cell cm-3 wet sediment CARD-FISH (probe: EUB338I-III)
## 4 Bacteria 9.40e+08 cell cm-3 wet sediment CARD-FISH (probe: EUB338I-III)
## 5 Bacteria 7.00e+07 cell cm-3 wet sediment CARD-FISH (probe: EUB338I-III)
## 6 Bacteria 3.10e+08 cell cm-3 wet sediment CARD-FISH (probe: EUB338I-III)

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

##                Ocean Latitude Longitude Depth
Depth_range
## 1 Mediterranean Sea   32.369    31.710  1120 continental slope (>200-
2000m)
## 2 Mediterranean Sea   32.368    31.704  1158 continental slope (>200-
2000m)
## 3 Mediterranean Sea   32.369    31.711  1122 continental slope (>200-
2000m)
## 4 Mediterranean Sea   32.368    31.704  1158 continental slope (>200-
2000m)
## 5 Mediterranean Sea   32.369    31.710  1120 continental slope (>200-
2000m)
## 6 Mediterranean Sea   32.368    31.704  1158 continental slope (>200-
2000m)
##      Type Density              Unit                        Method
## 1 Archaea 5.0e+07 cell cm-3 wet sediment CARD-FISH (probe: ARCH915)
```

```
## 2 Archaea 4.0e+06 cell cm-3 wet sediment CARD-FISH (probe: ARCH915)
## 3 Archaea 5.1e+08 cell cm-3 wet sediment CARD-FISH (probe: ARCH915)
## 4 Archaea 0.0e+00 cell cm-3 wet sediment CARD-FISH (probe: ARCH915)
## 5 Archaea 1.0e+07 cell cm-3 wet sediment CARD-FISH (probe: ARCH915)
## 6 Archaea 3.0e+06 cell cm-3 wet sediment CARD-FISH (probe: ARCH915)

Arc_data <- Archaea_data[!(Archaea_data$Density==0),]
head(Arc_data)

##                 Ocean Latitude Longitude Depth
Depth_range
## 1 Mediterranean Sea    32.369    31.710  1120 continental slope (>200-
2000m)
## 2 Mediterranean Sea    32.368    31.704  1158 continental slope (>200-
2000m)
## 3 Mediterranean Sea    32.369    31.711  1122 continental slope (>200-
2000m)
## 5 Mediterranean Sea    32.369    31.710  1120 continental slope (>200-
2000m)
## 6 Mediterranean Sea    32.368    31.704  1158 continental slope (>200-
2000m)
## 7 Mediterranean Sea    32.369    31.711  1122 continental slope (>200-
2000m)
##      Type Density                  Unit                   Method
## 1 Archaea 5.0e+07 cell cm-3 wet sediment CARD-FISH (probe: ARCH915)
## 2 Archaea 4.0e+06 cell cm-3 wet sediment CARD-FISH (probe: ARCH915)
## 3 Archaea 5.1e+08 cell cm-3 wet sediment CARD-FISH (probe: ARCH915)
## 5 Archaea 1.0e+07 cell cm-3 wet sediment CARD-FISH (probe: ARCH915)
## 6 Archaea 3.0e+06 cell cm-3 wet sediment CARD-FISH (probe: ARCH915)
## 7 Archaea 1.7e+08 cell cm-3 wet sediment CARD-FISH (probe: ARCH915)
```

Preparing figure: Microbial densities along a latitudinal gradient

```r
#Plot for prokaryotic density
lab1 <- c(expression(cell~cm^-3~dry~sediment),
          expression(cell~cm^-3~wet~sediment),
          expression(cell~g^-1~dry~sediment),
          expression(cell~g^-1~dry~sulfide),
          expression(cell~g^-1~vent~precipitate),
          expression(cell~g^-1~wet~sediment),
          expression(cell~m^-2))

Fig3 <- ggplot(data = Pro_data, aes(x = Density, y = Latitude, color=Unit)) +
geom_point(alpha = 0.3, size=2.5, shape=16) + 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=4)) +
theme(plot.margin=unit(c(0.5,0,0,0.5), "cm")) +
   scale_colour_manual(labels = lab1, values = c('blue', 'red','orange',
'black', '#8918FA', '1CF339', '#1CD7F3')) + 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)

#Plot for Bacteria density
lab1 <- c(expression(cell~cm^-3~dry~sediment),
        expression(cell~cm^-3~wet~sediment),
        expression(cell~g^-1~dry~sediment),
        expression(cell~g^-1~dry~sulfide),
        expression(cell~g^-1~vent~precipitate),
        expression(cell~g^-1~wet~sediment),
        expression(cell~m^-2))

Fig4 <- ggplot(data = Bac_data, aes(x = Density, y = Latitude, color=Unit)) +
geom_point(alpha = 0.3, size=2.5, shape=16) + 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=4)) +
theme(plot.margin=unit(c(0.5,0,0,0.5), "cm")) +
   scale_colour_manual(labels = lab1, values = c('blue', 'red','orange',
'black', '#8918FA', '1CF339', '#1CD7F3')) + 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)

#Plot for Archaea density
lab1 <- c(expression(cell~cm^-3~dry~sediment),
        expression(cell~cm^-3~wet~sediment),
        expression(cell~g^-1~dry~sediment),
        expression(cell~g^-1~dry~sulfide),
        expression(cell~g^-1~vent~precipitate),
        expression(cell~g^-1~wet~sediment),
        expression(cell~m^-2))

Fig5 <- ggplot(data = Arc_data, aes(x = Density, y = Latitude, color=Unit)) +
geom_point(alpha = 0.3, size=2.5, shape=16) + theme_classic() +
scale_y_continuous(breaks = c(-90, -75, -60, -45, -30, -15, 0, 15, 30, 45,
```

```r
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=4)) +
theme(plot.margin=unit(c(0.5,0,0,0.5), "cm")) +
    scale_colour_manual(labels = lab1, values = c('blue', 'red','orange',
'black', '#8918FA', '1CF339', '#1CD7F3')) + 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)

ggpubr::ggarrange(Fig3, Fig4, Fig5, ncol=1, common.legend = TRUE, legend =
"bottom")
```

Prokaryotes

Bacteria

Archaea
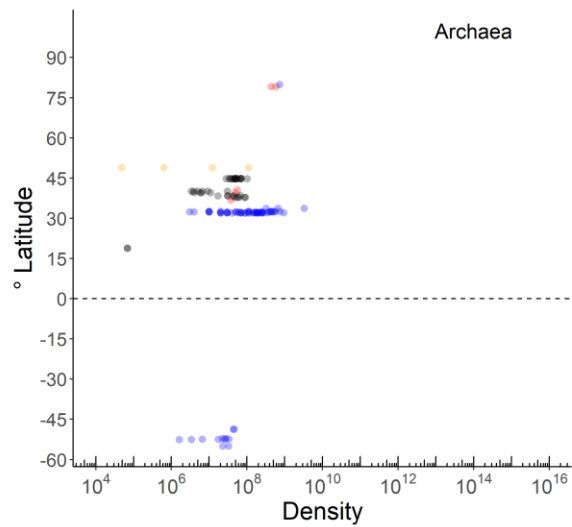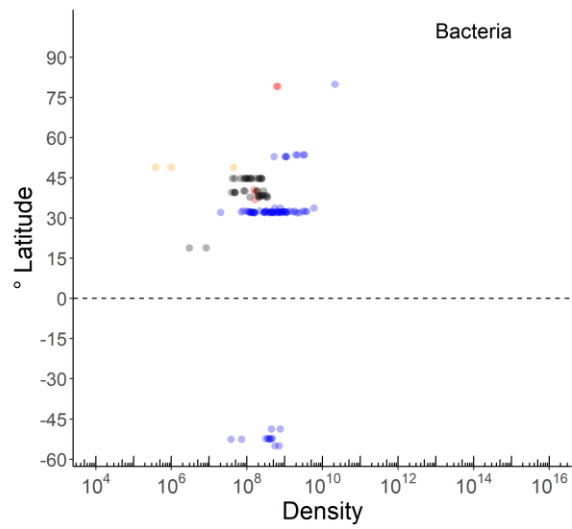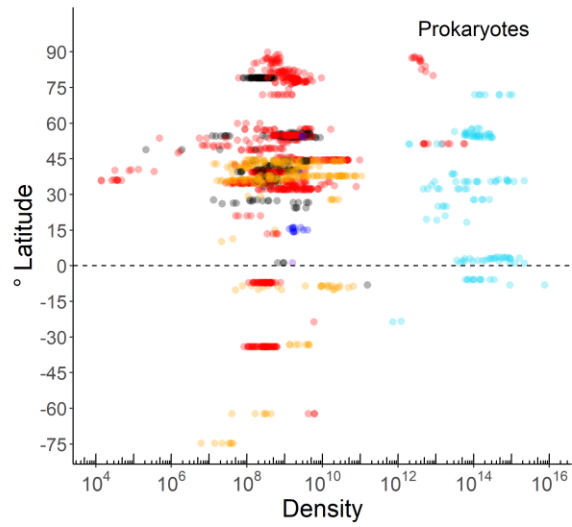
- cell cm^{-3} dry sediment
- cell cm^{-3} wet sediment
- cell g^{-1} dry sediment
- cell g^{-1} dry sulfide
- cell g^{-1} vent precipitate
- cell g^{-1} wet sediment
- cell m^{-2}

```
setwd("C:/Users/Mama/Desktop/manuscript revised/Figures")
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 = Pro_data, aes(x = Density, y = Depth, color=Unit)) +
geom_point(alpha = 0.3, size=2.5, shape=16) + 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="Prokaryotes", color="black",
size=6) + scale_colour_manual(labels = lab1, values = c('blue',
'red','orange', 'black', '#8918FA', '1CF339', '#1CD7F3'))

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

## 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 = 0.3, size=2.5, shape=16) + 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',
'black', '#8918FA', '1CF339', '#1CD7F3'))

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 = 0.3, size=2.5, shape=16) + 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',
'black', '#8918FA', '1CF339', '#1CD7F3'))

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, legend =
"bottom")

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

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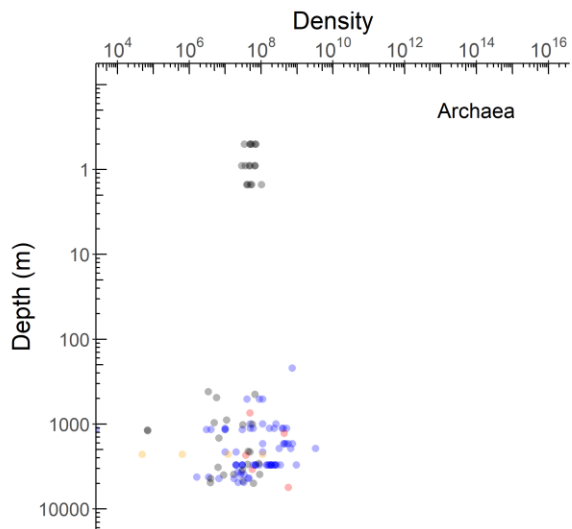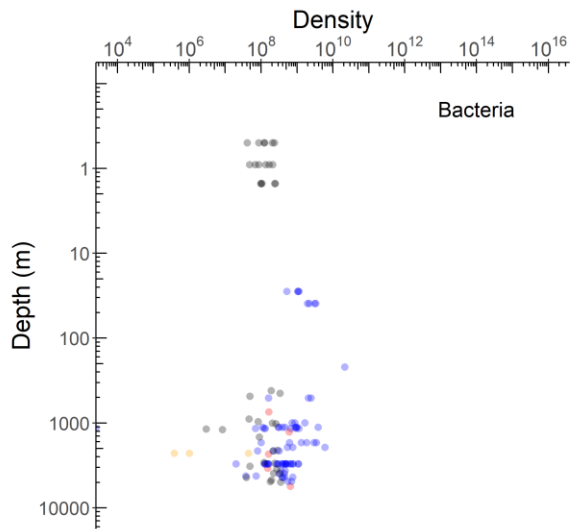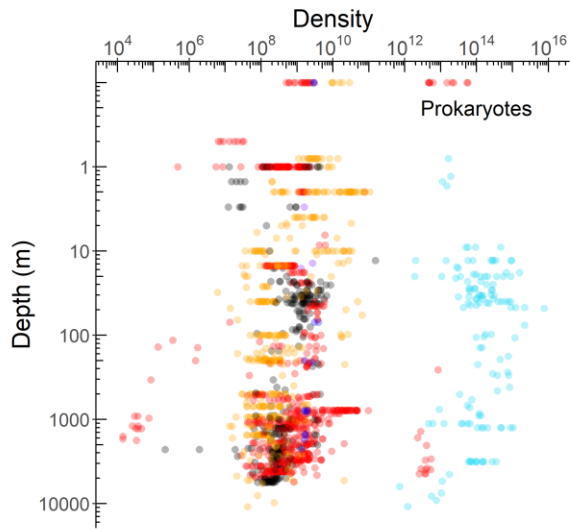
Density

Prokaryotes

10^4 10^6 10^8 10^{10} 10^{12} 10^{14} 10^{16}

Depth (m)

1
10
100
1000
10000

Density

Bacteria

10^4 10^6 10^8 10^{10} 10^{12} 10^{14} 10^{16}

Depth (m)

1
10
100
1000
10000

Density

Archaea

10^4 10^6 10^8 10^{10} 10^{12} 10^{14} 10^{16}

Depth (m)

1
10
100
1000
10000

cell cm^{-3} dry sediment   cell g dry sulfide^{-1}

cell cm^{-3} wet sediment   cell g wet sediment^{-1}

cell g dry sediment^{-1} cell m^{-2}

```r
setwd("C:/Users/Mama/Desktop/manuscript revised/Figures")
ggsave(file="microbial density vs depth.png", width=6.5,height=19.5)
```