UVC datasets - exploring monitoring structure and herbivore assemblages

Seychelles

- Seychelles data are 7m radius point counts conducted at 21 reef sites in 1994, 2005, 2008, 2011, 2014, 2017.
- Sites were stratified according to habitat (granite = 7, patch = 7, carbonate = 7) and management status (12 = fished, 9 = MPAs)
- Reefs are the inhabited Seychelles islands, Mahe and Praslin
- Useful papers describing dataset methods: Graham et al. 2015 (Predicting climate-driven regime shifts..., Nature)

Across all surveys, 37 herbivore species were recorded, which are composed of:

```
##                 FG species
## 1 Herbivore Browser       5
## 2  Herbivore Grazer      15
## 3 Herbivore Scraper      17
```

Scrapers dominated herbivore assemblages on both fished and protected reefs, and browser biomass was slightly higher than grazer biomass after 1994 (i.e. after bleaching). High variability in browser biomass suggests that strong spatial variation in browser presence. This was less true for scrapers, for which biomass may be high at all reef sites. There was a weak protection effect apparent, with slightly higher biomass of all feeding groups in protected sites.
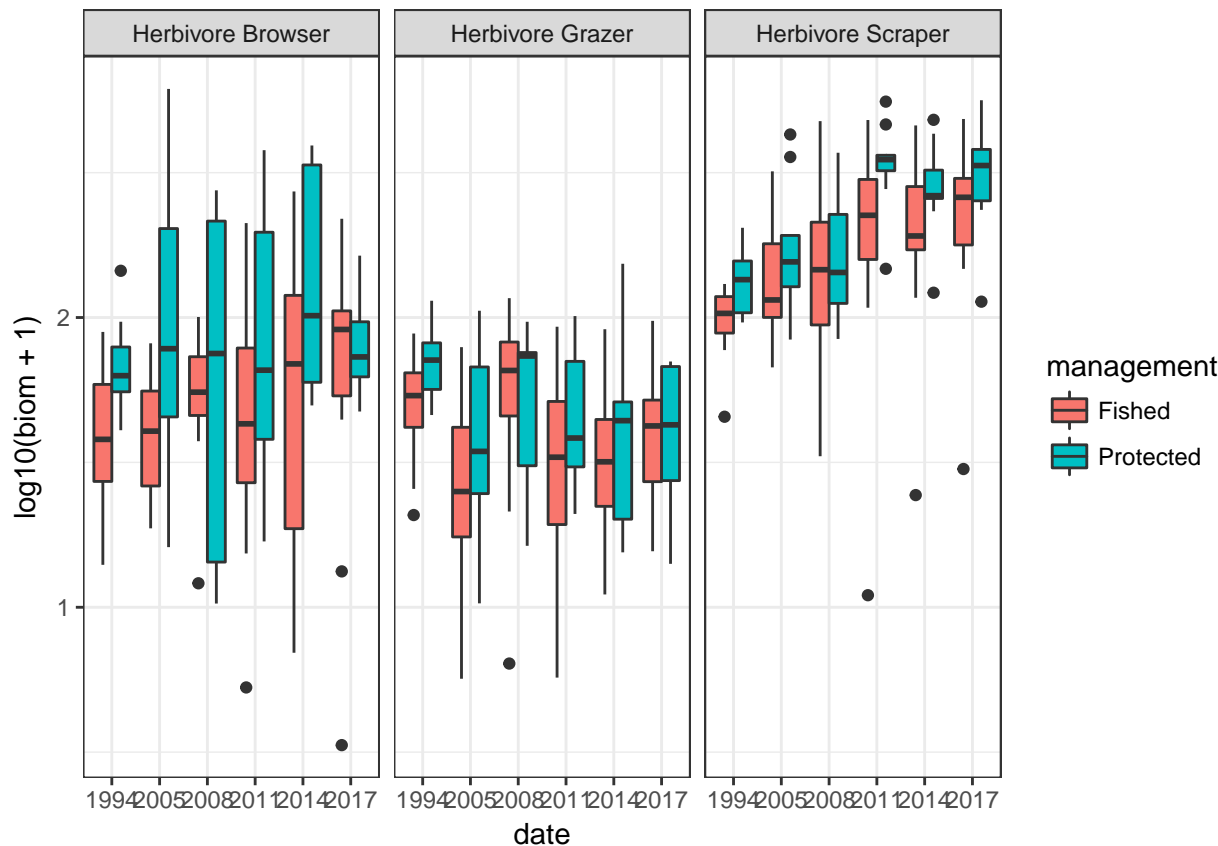
Grazer size distributions indicated high abundance of small-bodied individuals. Scraper and browser sizes were
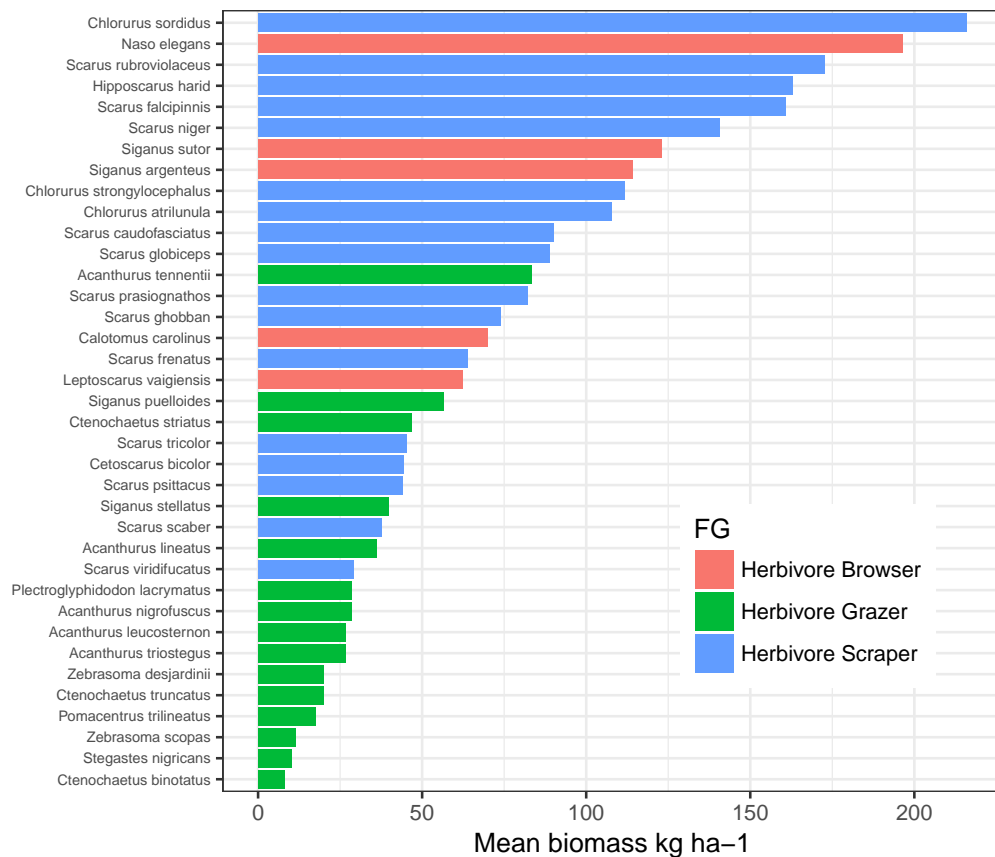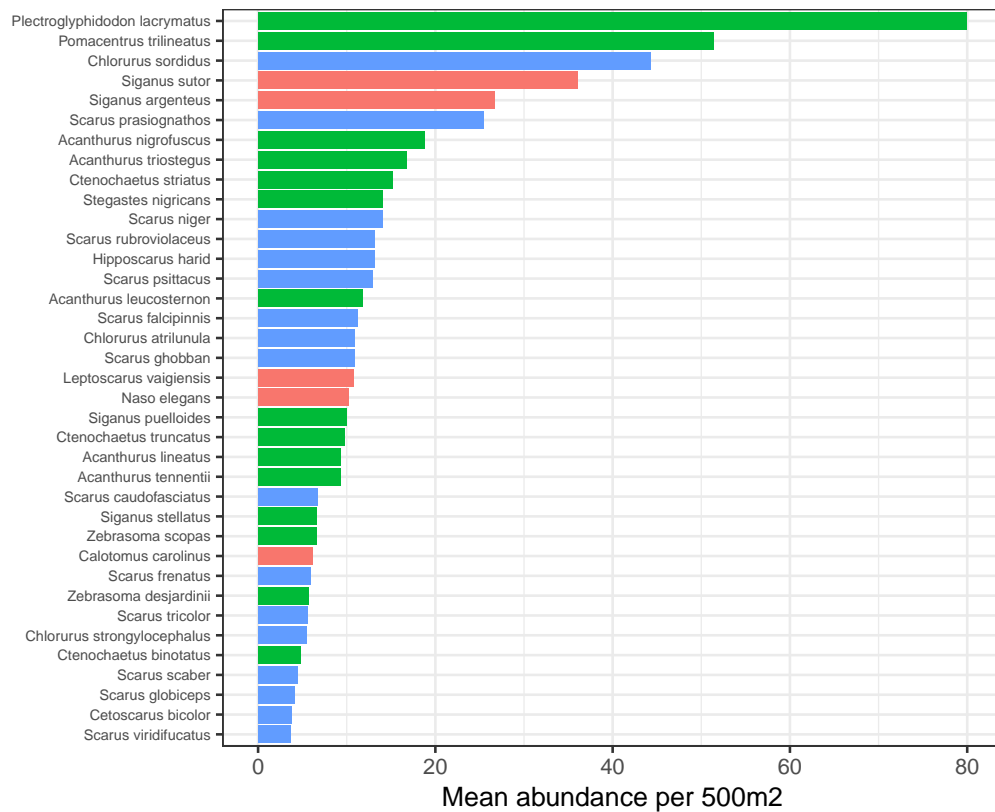
more equitably distributed across the size range. Scrapers had the largest body sizes, with some individuals between 0.5-2 kg.
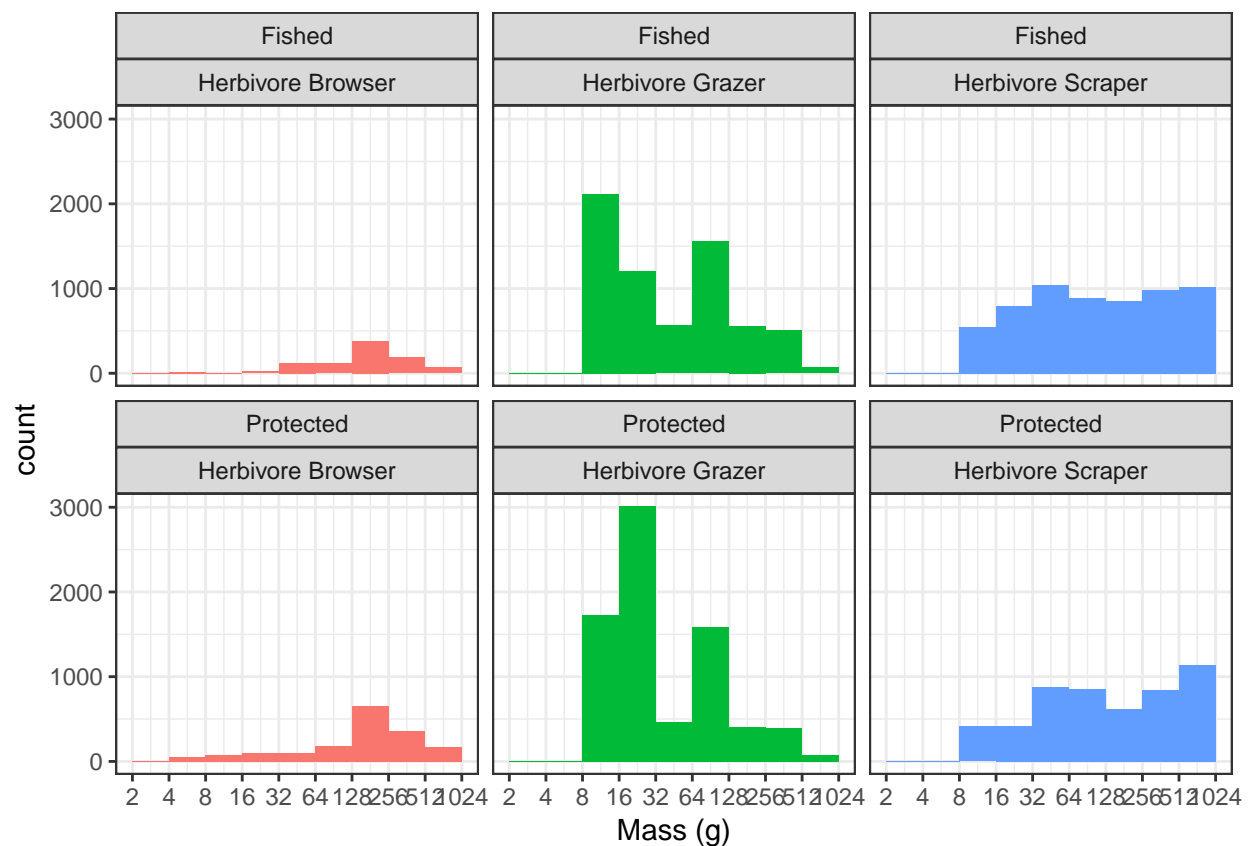
Common herbivore species

Considering common species as those that are high in abundance or biomass (i.e. mean biomass across UVC replicates at each site).

Seychelles: abundance/biomass distributions

Maldives

GBR

Chagos

```
#Load data and filter for chagos
load("data/wio_gbr_herb_master.Rdata")
str(herb) ## check structure of data frame
```

```
## 'data.frame':    53533 obs. of  18 variables:
## $ date          : chr  NA NA NA NA ...
## $ dataset       : chr  "Chagos" "Chagos" "Chagos" "Chagos" ...
## $ reef          : chr  "Great Chagos Bank" "Great Chagos Bank" "Great Chagos Bank" "Great Chagos Ba
## $ site          : chr  "Middle Brother" "Eagle" "Eagle" "Eagle" ...
## $ site.number   : chr  "3" "3" "3" "1" ...
## $ management    : chr  "Unfished" "Unfished" "Unfished" "Unfished" ...
## $ habitat       : chr  "Exposed" "Sheltered" "Sheltered" "Sheltered" ...
## $ unique.id     : chr  "GreatChagosBank.MiddleBrother.4" "GreatChagosBank.Eagle.4" "GreatChagosBank
## $ depth         : num  9 9 9 9 9 9 9 9 9 9 ...
## $ transect      : int  4 4 4 3 3 4 4 4 2 2 ...
## $ transect.area : int  250 250 250 250 250 250 250 250 250 250 ...
## $ family        : Factor w/ 51 levels "Acanthuridae",..: 1 1 1 1 1 1 1 1 1 1 ...
## $ species       : chr  "Acanthurus auranticavus" "Acanthurus blochii" "Acanthurus blochii" "Acanthu
## $ FG            : chr  "Herbivore Grazer" "Herbivore Grazer" "Herbivore Grazer" "Herbivore Grazer"
## $ length.cm     : num  17 29 29 19 20 30 30 34 32 34 ...
## $ mass.g        : num  137 705 705 192 224 ...
## $ biomass.kgha  : num  5.49 28.2 28.2 7.69 8.97 ...
## $ abundance.500m2: num  2 2 2 2 2 2 2 2 2 2 ...
```

```
unique(herb$dataset) ## check regions in herb
```

```
## [1] "Chagos"     "GBR"        "Seychelles" "Maldives"
```

```
chagos <- herb[herb$dataset == 'Chagos',]
write.csv(chagos, file = 'data/chagos_master.csv')
chagos$FG <- as.factor(chagos$FG)
levels(chagos$FG)
```

```
## [1] "Herbivore Browser" "Herbivore Grazer"  "Herbivore Scraper"
```

```
#Load packages
library(tidyverse)
library (ggplot2)
library(gridExtra)
```

Exploring the data

```
#Get some descriptive info on survey data
summary(chagos) #5729 records
```

```
##      date               dataset              reef
## Length:5729         Length:5729         Length:5729
## Class :character    Class :character    Class :character
## Mode  :character    Mode  :character    Mode  :character
##
##
```

4

```
## 
## 
##      site            site.number         management       
##  Length:5729        Length:5729        Length:5729        
##  Class :character   Class :character   Class :character   
##  Mode  :character   Mode  :character   Mode  :character   
## 
## 
## 
## 
##    habitat            unique.id             depth          transect    
##  Length:5729        Length:5729        Min.   :3.000   Min.   :1.000  
##  Class :character   Class :character   1st Qu.:3.000   1st Qu.:1.000  
##  Mode  :character   Mode  :character   Median :9.000   Median :3.000  
##                                        Mean   :6.228   Mean   :2.559  
##                                        3rd Qu.:9.000   3rd Qu.:4.000  
##                                        Max.   :9.000   Max.   :4.000  
## 
##   transect.area             family        species         
##  Min.   :100.0   Acanthuridae :2534   Length:5729        
##  1st Qu.:250.0   Scaridae     :2150   Class :character   
##  Median :250.0   Pomacentridae: 656   Mode  :character   
##  Mean   :230.8   Balistidae   : 192                      
##  3rd Qu.:250.0   Kyphosidae   : 152                      
##  Max.   :250.0   pomacentridae:  38                      
##                  (Other)      :   7                      
##                FG          length.cm         mass.g       
##  Herbivore Browser: 339   Min.   : 8.00   Min.   :  12.43  
##  Herbivore Grazer :3239   1st Qu.:13.00   1st Qu.:  51.31  
##  Herbivore Scraper:2151   Median :19.00   Median : 141.79  
##                           Mean   :25.49   Mean   : 830.79  
##                           3rd Qu.:38.00   3rd Qu.:1140.95  
##                           Max.   :82.00   Max.   :8639.94  
## 
##   biomass.kgha      abundance.500m2 
##  Min.   :  0.497   Min.   :2.000   
##  1st Qu.:  2.430   1st Qu.:2.000   
##  Median :  6.032   Median :2.000   
##  Mean   : 33.439   Mean   :2.384   
##  3rd Qu.: 45.638   3rd Qu.:2.000   
##  Max.   :345.598   Max.   :5.000   
## 
```

```r
#Number of sites
chagos$site <- as.factor(chagos$site)
levels(chagos$site) #20 sites
```

```
## [1] "Barton Point"          "Barton Point west"  
## [3] "Cannon Point"          "Cannon Point 2"     
## [5] "Diego Garcia East coast" "Eagle"            
## [7] "Exposed site 1"        "Exposed site 2"     
## [9] "Exposed site 3"        "Ile Anglais"        
## [11] "Ile Fouquet"          "Ile Poule"          
## [13] "Ile Takamaka"         "Middle Brother"     
## [15] "Middle Island"        "North Diamont"      
```

```
## [17] "Sheltered site 2"         "Sheltered site 3"
## [19] "South"                     "South Brother"
```
```r
#Number of reefs
chagos$reef <- as.factor(chagos$reef) #4 reefs
#Number of transects per site
chagos$transect <- as.factor(chagos$transect) #1-4 transects
chagos %>% count(site, transect, sort =TRUE)
```
```
## # A tibble: 80 x 3
##    site            transect     n
##    <fct>           <fct>    <int>
##  1 Ile Anglais     3          379
##  2 Sheltered site 2 1         286
##  3 Ile Anglais     2          267
##  4 Ile Anglais     4          267
##  5 South Brother   4          256
##  6 Eagle           3          250
##  7 Eagle           4          244
##  8 Ile Anglais     1          238
##  9 South Brother   2          204
## 10 Eagle           1          197
## # ... with 70 more rows
```
```r
#Number of sitings of each species
chagos$species <- as.factor(chagos$species)
chagos %>% count(species) # 52 species
```
```
## # A tibble: 52 x 2
##    species                   n
##    <fct>                 <int>
##  1 Acanthurus auranticavus   1
##  2 Acanthurus blochii        2
##  3 Acanthurus leucocheilus  52
##  4 Acanthurus leucosternon 867
##  5 Acanthurus lineatus     234
##  6 Acanthurus nigricauda    51
##  7 Acanthurus nigrofuscus  745
##  8 acanthurus tennenti       4
##  9 Acanthurus tennenti     213
## 10 Acanthurus triostegus    69
## # ... with 42 more rows
```
```r
#From James
# count number of unique species per functional group
aggregate(species ~ FG, chagos, function(x) length(unique(x)))
```
```
##                 FG species
## 1 Herbivore Browser       5
## 2  Herbivore Grazer      22
## 3 Herbivore Scraper      25
```

Total of 52 species, 5729 records, across 20 sites at 4 reefs, with between 1-4 transects at each site

```r
#From James script
# count number of unique species per functional group
aggregate(species ~ FG, chagos, function(x) length(unique(x)))
```

```
##                FG species
## 1 Herbivore Browser        5
## 2  Herbivore Grazer        22
## 3 Herbivore Scraper        25
```

```r
#From James script
## estimate size distribution by functional groups
ggplot(chagos, aes(log(mass.g, 2), fill=FG)) + geom_histogram(breaks=c(1:10)) + facet_wrap(management~FG
```
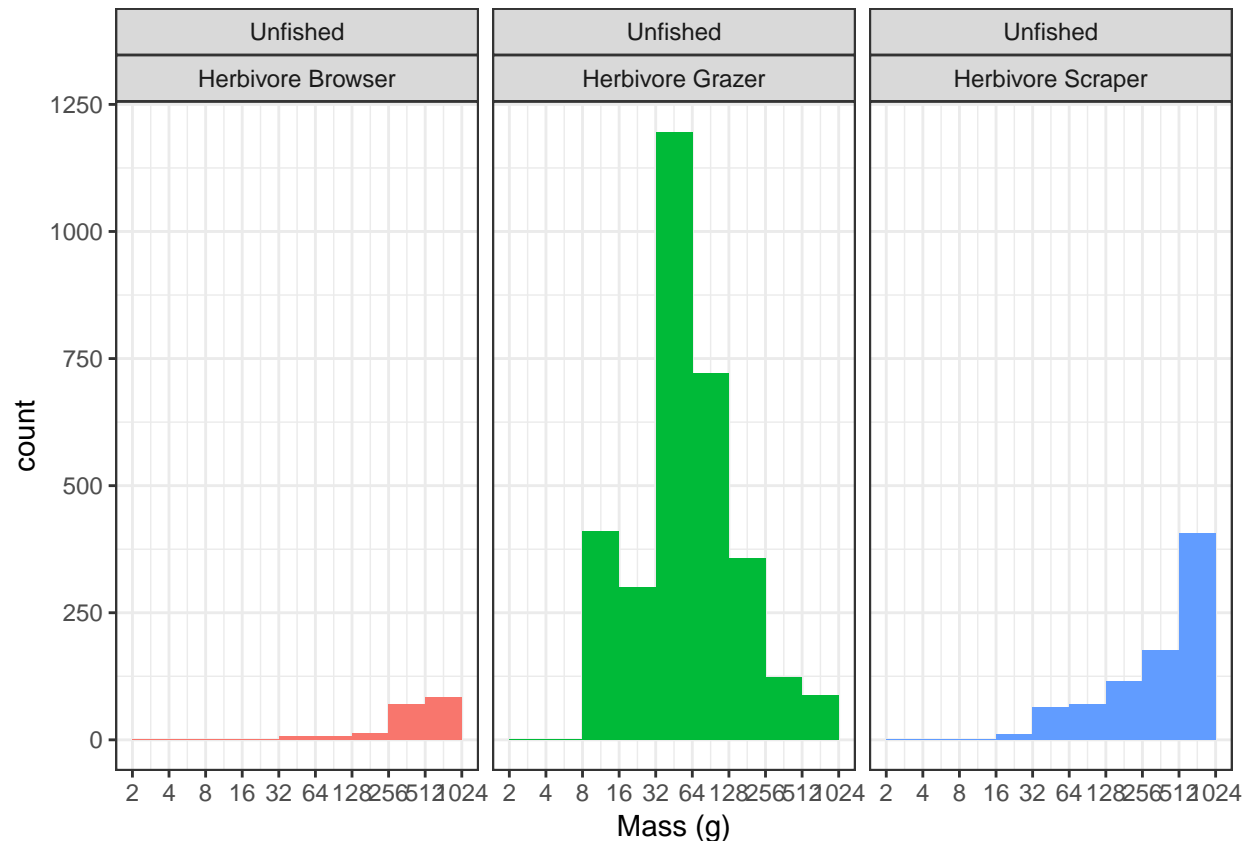

Now need to look at abundance and biomass of species and functional groups across sites. . .

insert graphs on spp and FG abundance and biomass across sites, what are the common species?

From James

```r
## estimate mean abundance at site level, by species
abund <- chagos %>% group_by(unique.id, site, species, FG) %>%
        summarise(abund = sum(abundance.500m2)) %>% ## total abundance per UVC
        group_by(species, FG) %>%
        summarise(abund = mean(abund)) ## mean abundance per site

## estimate mean biomass at site level, by species
biom <- chagos %>% group_by(unique.id, site, species, FG) %>%
```

```
        summarise(biom = sum(biomass.kgha)) %>% ## total biomass per UVC
        group_by(species, FG) %>%
        summarise(biom = mean(biom)) ## mean biomass per site

g2<-ggplot(abund[abund$abund<100,], aes(reorder(species,abund), abund, fill=FG)) +
  geom_bar(stat='identity') +
  labs(y='Mean abundance per 500m2', x='',title='Chagos: abundance/biomass distributions') +
  coord_flip() + theme(legend.position='none', axis.text.y=element_text(size=6))

g3<-ggplot(biom[biom$biom<300,], aes(reorder(species,biom), biom, fill=FG)) +
  geom_bar(stat='identity') +
  labs(y='Mean biomass kg ha-1', x='') +
  coord_flip() + theme(legend.position=c(0.75, 0.25), axis.text.y=element_text(size=6))

grid.arrange(g2, g3)
```
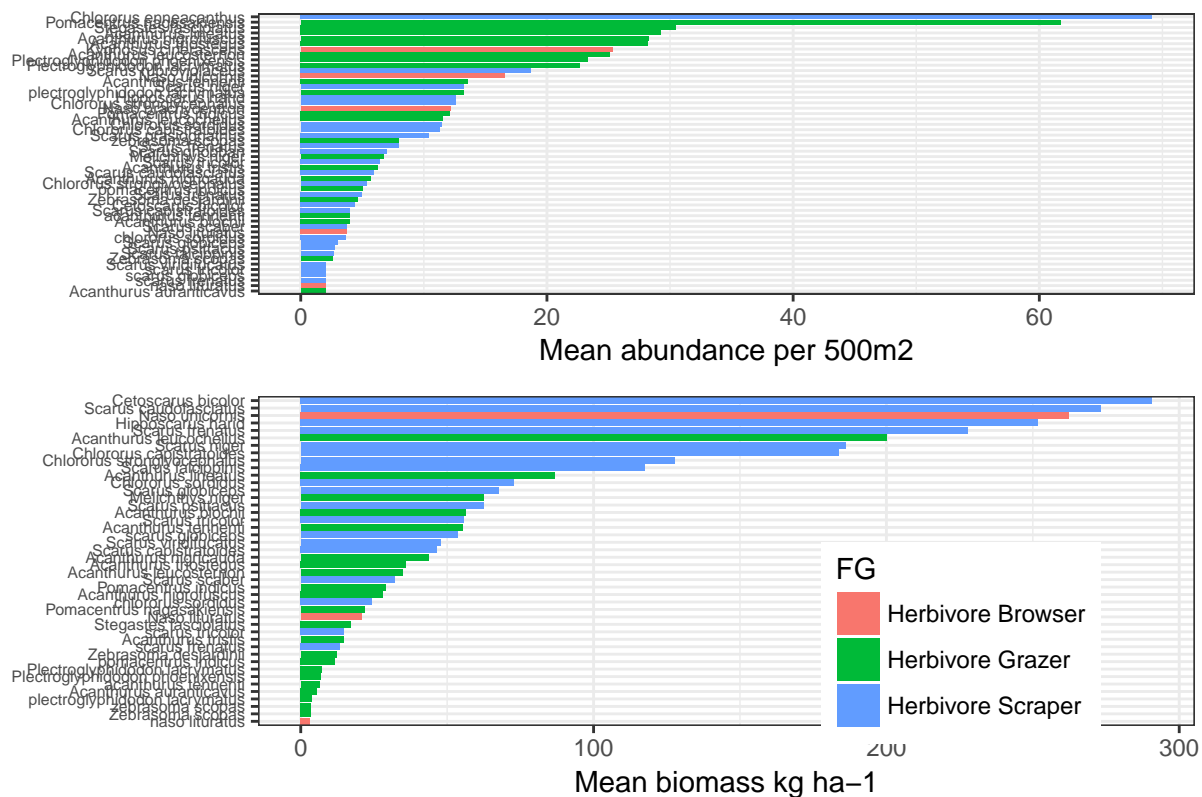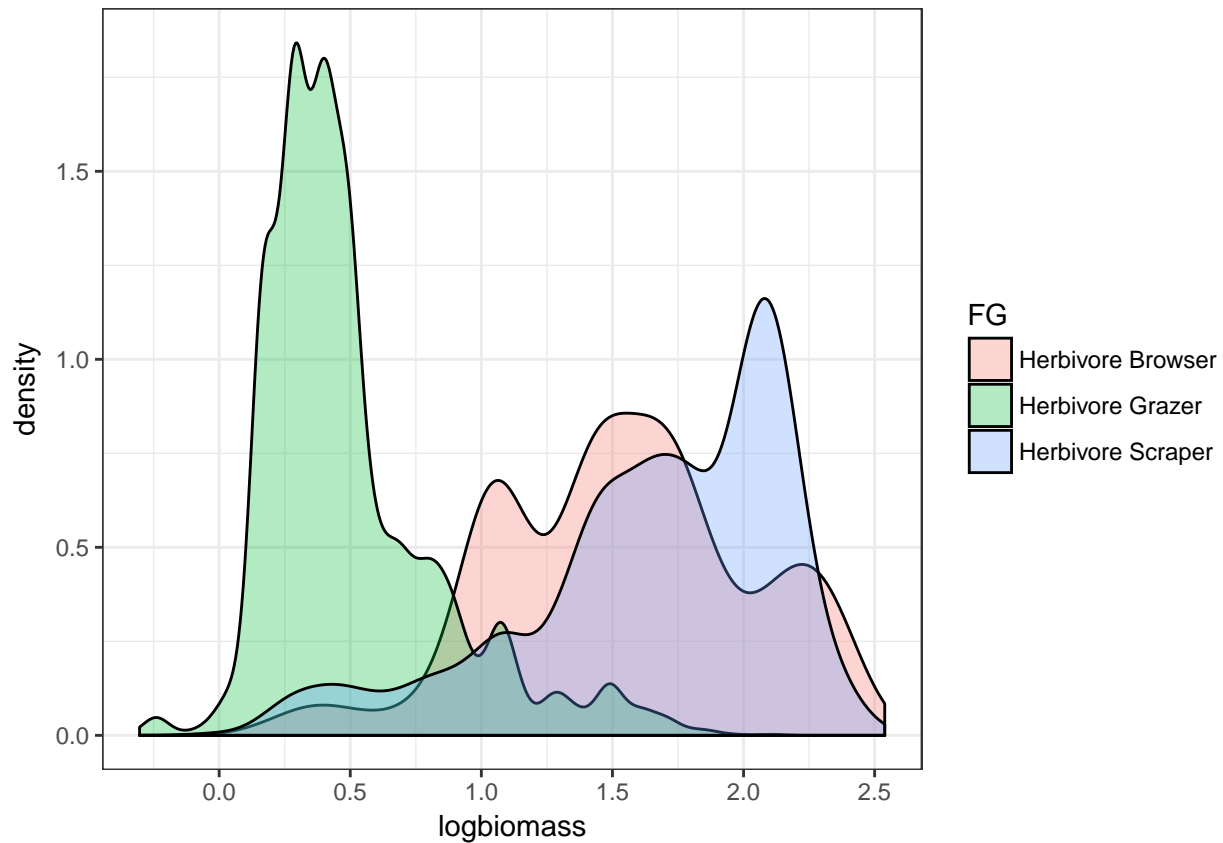

Chagos: abundance/biomass distributions

```
#log scale biomass gradient
chagos$logbiomass <- log10(chagos$biomass.kgha)
ggplot(chagos, aes(x=logbiomass, fill=FG)) + geom_density(alpha=.3)
```

There are no dates recorded for the Chagos dataset, so no time series analyses could be done. Additionally, all of Chagos is "unfished". Therefore, only "depth" and "habitat" gradients were explored further to biomass. If lat long values can be attached to site names, a spatial look at the data can be done as well.

```r
#Comparing sheltered and unsheltered functional groups
#Grouped bar chart showing biomass of each FG at different habitats, blank is unrecorded habitat type
ggplot(chagos, aes(fill=FG, y=biomass.kgha, x=habitat)) +
  geom_bar(position="dodge", stat="identity")
```
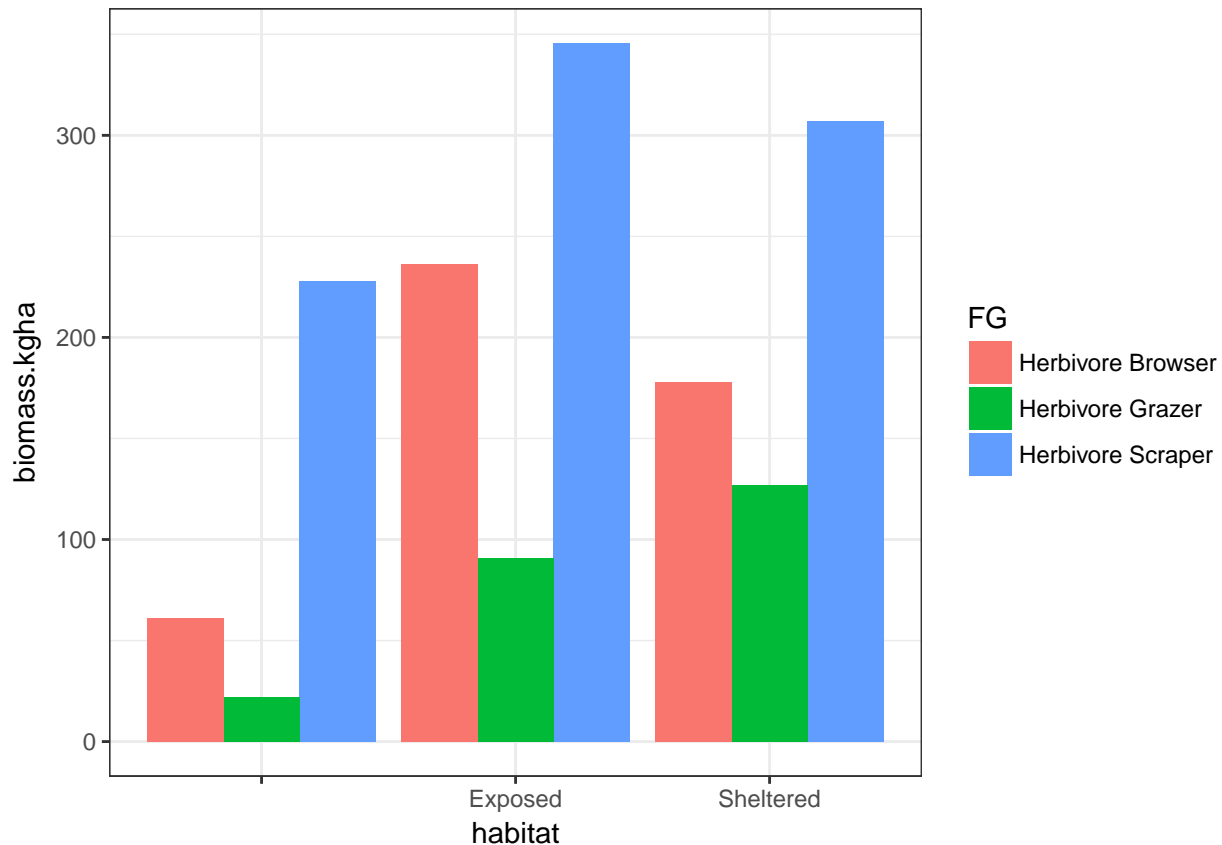
```
#Comaparing depth at 3m and 9m
str(chagos) #change depth from numeric to character for graph
```

```
## 'data.frame':    5729 obs. of  19 variables:
##  $ date          : chr  NA NA NA NA ...
##  $ dataset       : chr  "Chagos" "Chagos" "Chagos" "Chagos" ...
##  $ reef          : Factor w/ 4 levels "Diego Garcia",..: 2 2 2 2 2 2 2 2 2 2 ...
##  $ site          : Factor w/ 20 levels "Barton Point",..: 14 6 6 6 6 6 6 6 6 6 ...
##  $ site.number   : chr  "3" "3" "3" "1" ...
##  $ management    : chr  "Unfished" "Unfished" "Unfished" "Unfished" ...
##  $ habitat       : chr  "Exposed" "Sheltered" "Sheltered" "Sheltered" ...
##  $ unique.id     : chr  "GreatChagosBank.MiddleBrother.4" "GreatChagosBank.Eagle.4" "GreatChagosBan
##  $ depth         : num  9 9 9 9 9 9 9 9 9 9 ...
##  $ transect      : Factor w/ 4 levels "1","2","3","4": 4 4 4 3 3 4 4 4 2 2 ...
##  $ transect.area : int  250 250 250 250 250 250 250 250 250 250 ...
##  $ family        : Factor w/ 51 levels "Acanthuridae",..: 1 1 1 1 1 1 1 1 1 1 1 1 ...
##  $ species       : Factor w/ 52 levels "Acanthurus auranticavus",..: 1 2 2 3 3 3 3 3 3 3 ...
##  $ FG            : Factor w/ 3 levels "Herbivore Browser",..: 2 2 2 2 2 2 2 2 2 2 2 ...
##  $ length.cm     : num  17 29 29 19 20 30 30 34 32 34 ...
##  $ mass.g        : num  137 705 705 192 224 ...
##  $ biomass.kgha  : num  5.49 28.2 28.2 7.69 8.97 ...
##  $ abundance.500m2: num  2 2 2 2 2 2 2 2 2 2 2 ...
##  $ logbiomass    : num  0.74 1.45 1.45 0.886 0.953 ...
```

```
chagos$depth <- as.character(chagos$depth)
#Plot biomass of each FG at 3 and 9 m
ggplot(chagos, aes(fill=FG, y=biomass.kgha, x=depth)) +
  geom_bar(position="dodge", stat="identity")
```