

JB Baseline - Reefs

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Benthic

```
# import and clean data

rf_benthic <- read_excel(here("jumby_baseline", "data", "JBB_reefs.xlsx"), sheet = "benthic") %>%
  clean_names() %>%
  filter(!is.na(site)) %>% # remove any incomplete rows at the end of the data
  # separate(species_code, c("species_code", "indicator")) %>% # separating variables with an underscore
  mutate(species = to_any_case(species, case = "sentence"), # this makes sure species names are correct
         # site = to_any_case(site, case = "title"),
         # consolidating categories here for graphs:
         cat_c = case_when(category_code %in% c("LC", "SLC") ~ "Hard corals",
                           category_code %in% c("MA") ~ "Macroalgae",
                           category_code %in% c("TA") ~ "Turf algae",
                           category_code %in% c("CCA", "CCA_ND") ~ "CCA",
                           category_code %in% c("OINV", "SPON", "AINV", "CYAN", "PEY") ~ "Other (coral)",
                           category_code %in% c("SAND", "HOLE", "SG", "PAVE") ~ "Other substratum")
  ),
  # adding algal type for graphs about palatability:
  algal_type = case_when(type_code %in% c("BFMA", "GFMA", "RFMA") ~ "Fleshy macroalgae",
                        type_code %in% c("GCMA", "RCMA") ~ "Calcareous macroalgae",
                        type_code %in% c("TA", "TAS", "STA") ~ "Turf algae"),
  # certain substrates are not suitable for coral or algal growth, so should not detract from percent available
  av_sub_yn = if_else(category_code %in% c("SAND", "HOLE", "SG", "PAVE"), "no", "yes")
) %>%
  filter(!is.na(cat_c) & !is.na(species)) # need GRB to fix some data errors, but using this for now
```

Percent cover

```
# "expand" dataframe so that it contains all benthic categories per site/transect/meter -> join full data
rf_pc_cat_m <- rf_benthic %>%
  filter(av_sub_yn == "yes") %>% # percent cover is relative to available substrate
  expand(nesting(site, transect, meter), cat_c) %>%
  # this is where we add in our actual data to this expanded template:
  left_join(rf_benthic %>%
    filter(av_sub_yn == "yes") %>% # only looking at what is considered available substrate (yes/no)
    group_by(site, transect, meter) %>%
    mutate(n_pts = n()) %>% # showing total number of points per meter that are considered available
    ungroup() %>%
```

```

      group_by(site, transect, meter, n_pts, cat_c) %>%
      summarize(pc_m = 100*n()/n_pts) %>% # n() counts the number of entries within a given group
      ungroup() %>%
      distinct() %>%
      select(-n_pts),
      by = c("site", "transect", "meter", "cat_c")) %>%
mutate(pc_m = if_else(is.na(pc_m), 0, pc_m))

# average these meter-level results within transect, then within sites
rf_pc_cat_site <- rf_pc_cat_m %>%
  group_by(site, transect, cat_c) %>%
  summarize(pc_t = mean(pc_m)) %>%
  ungroup() %>%
  group_by(site, cat_c) %>%
  summarize(n_test = n(),
            pc_mean = mean(pc_t),
            pc_se = sd(pc_t)/sqrt(n())
            ) %>%
  filter(cat_c != "Other substratum") %>%
  mutate(cat_c = factor(cat_c, levels = c("Hard corals", "CCA", "Macroalgae", "Turf algae", "Other compo

# quick check to make sure everything adds up to 100% at the meter and site level
test1 <- rf_pc_cat_m %>%
  group_by(site, transect, meter) %>%
  summarize(total = sum(pc_m))
test2 <- rf_pc_cat_site %>%
  group_by(site) %>%
  summarize(total = sum(pc_mean))

```

```

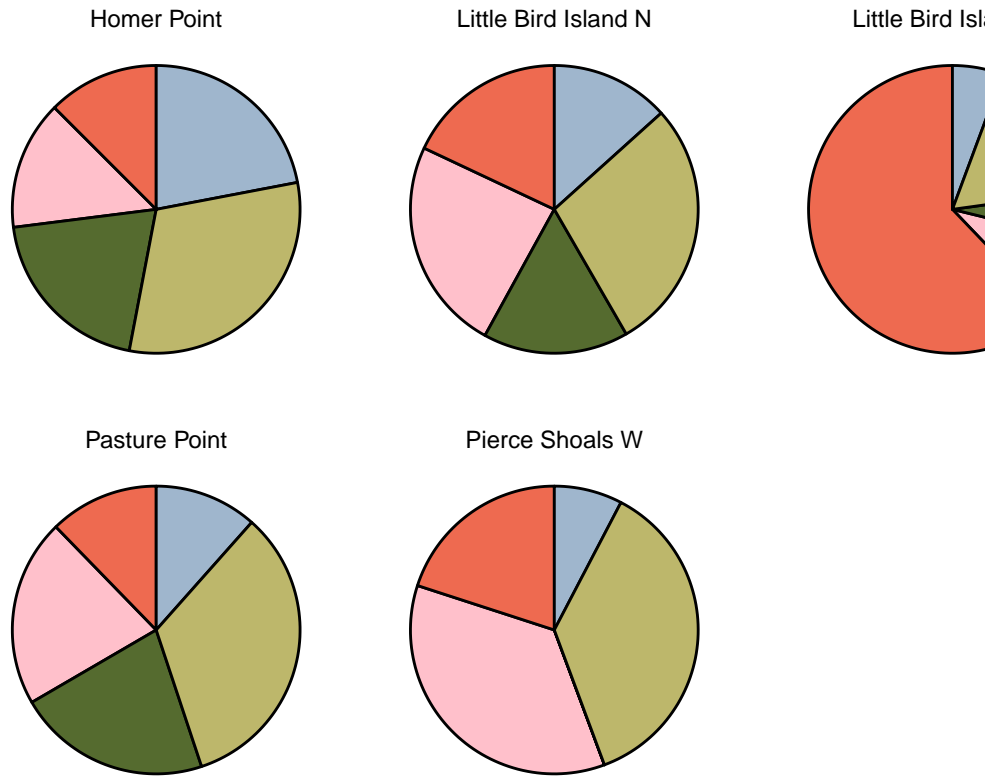
cat_palette <- c("coral2", "pink", "darkolivegreen", "darkkhaki", "slategray3")
ggplot(rf_pc_cat_site,
      aes(x = cat_c, y = pc_mean, fill = cat_c)) +
  geom_col(color = "black", alpha = 0.9) +
  geom_errorbar(aes(ymin = pc_mean - pc_se, ymax = pc_mean + pc_se), width = .2,
                position = position_dodge(.9)) +
  scale_fill_manual(values = cat_palette) +
  facet_wrap(. ~ site, ncol = 2) +
  labs(y = "Mean percent cover", x = "", fill = "") +
  theme_bw() +
  theme(axis.text.x = element_text(angle = 45, h = 1, face = "italic"))

```

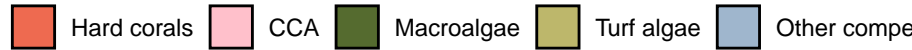
```

cat_palette <- c("coral2", "pink", "darkolivegreen", "darkkhaki", "slategray3")
ggplot(rf_pc_cat_site,
      aes(x = "cat_c", y = pc_mean, fill = cat_c)) +
  geom_bar(width = 1, stat = "identity", color = "black") +
  coord_polar("y", start=0) +
  scale_fill_manual(values = cat_palette) +
  facet_wrap(vars(site), nrow = 2) +
  theme_void() +
  theme(legend.position = "bottom",
        legend.title = element_blank(),
        panel.spacing = unit(1, "lines"))

```



Percent cover by site and category



```
kable(rf_pc_cat_site %>% select(site, category = cat_c, pc_mean, pc_se))
```

site	category	pc_mean	pc_se
Homer Point	CCA	14.500000	3.5000000
Homer Point	Hard corals	12.500000	7.5000000
Homer Point	Macroalgae	20.000000	15.0000000
Homer Point	Other competitors	22.000000	7.0000000
Homer Point	Turf algae	31.000000	4.0000000
Little Bird Island N	CCA	24.000000	5.1316014
Little Bird Island N	Hard corals	18.000000	2.0816660
Little Bird Island N	Macroalgae	16.333333	4.0551750
Little Bird Island N	Other competitors	13.333333	0.6666667
Little Bird Island N	Turf algae	28.333333	4.9103066
Little Bird Island W	CCA	9.037037	1.7642230
Little Bird Island W	Hard corals	62.148148	7.9572762
Little Bird Island W	Macroalgae	6.000000	4.5825757
Little Bird Island W	Other competitors	5.666667	1.2018504
Little Bird Island W	Turf algae	17.148148	5.0537577
Pasture Point	CCA	21.111111	5.8888889
Pasture Point	Hard corals	12.277778	1.2777778
Pasture Point	Macroalgae	21.722222	3.7222222
Pasture Point	Other competitors	11.555556	3.4444444
Pasture Point	Turf algae	33.333333	4.3333333
Pierce Shoals W	CCA	35.666667	8.0897741
Pierce Shoals W	Hard corals	20.000000	7.8102497

site	category	pc_mean	pc_se
Pierce Shoals W	Macroalgae	0.000000	0.000000
Pierce Shoals W	Other competitors	7.666667	2.4037009
Pierce Shoals W	Turf algae	36.666667	3.1797973

Percent cover by species

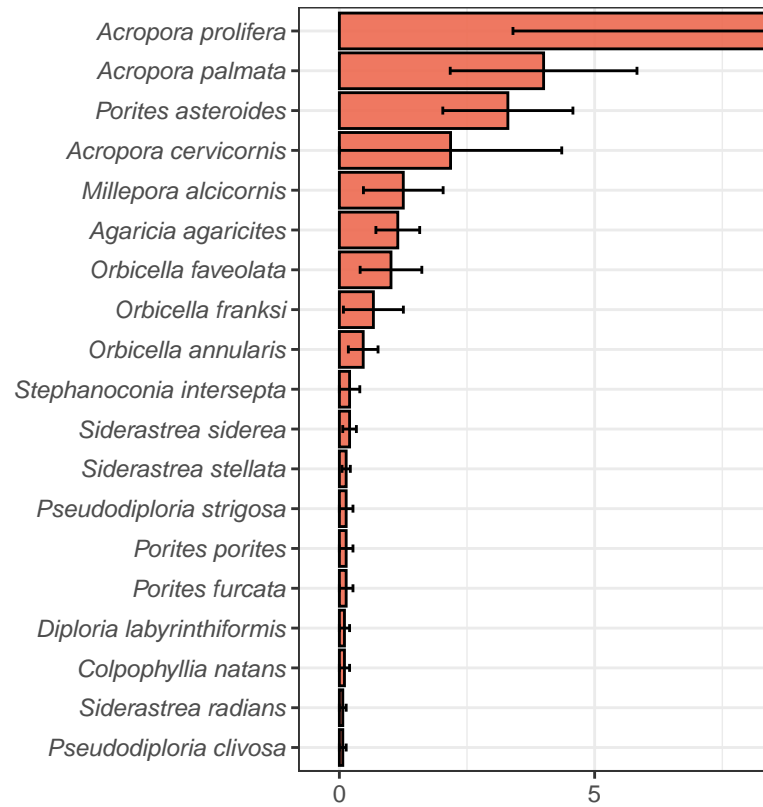
```
# calculating percent cover by species at each meter
rf_pc_spp_m <- rf_benthic %>%
  filter(av_sub_yn == "yes") %>%
  expand(nesting(site, transect, meter), nesting(species, cat_c)) %>%
  left_join(rf_benthic %>%
    filter(av_sub_yn == "yes") %>%
    group_by(site, transect, meter) %>%
    mutate(n_pts = n()) %>%
    ungroup() %>%
    group_by(site, transect, meter, n_pts, species, cat_c) %>%
    summarize(pc_m = 100*n()/n_pts) %>%
    ungroup() %>%
    distinct() %>%
    select(-n_pts),
    by = c("site", "transect", "meter", "species", "cat_c")) %>%
  mutate(pc_m = if_else(is.na(pc_m), 0, pc_m))

# calculating mean percent cover by transect -> site
rf_pc_spp_site <- rf_pc_spp_m %>%
  group_by(site, transect, species, cat_c) %>%
  summarize(pc_t = mean(pc_m)) %>%
  ungroup() %>%
  group_by(site, species, cat_c) %>%
  summarize(pc_mean = mean(pc_t),
    pc_se = sd(pc_t)/sqrt(n())
  ) %>%
  ungroup() %>%
  distinct()

# calculating mean percent cover by species across all sites
rf_pc_spp <- rf_pc_spp_site %>%
  group_by(species, cat_c) %>%
  summarize(pc = mean(pc_mean),
    pc_se = sd(pc_mean)/sqrt(n())) %>%
  rename(pc_mean = pc)

# testing that total percent cover per transect and site add up to 100
test1 <- rf_pc_spp_m %>%
  group_by(site, transect, meter) %>%
  summarize(total = sum(pc_m))
test2 <- rf_pc_spp_site %>%
  group_by(site) %>%
  summarize(total = sum(pc_mean))
test3 <- sum(rf_pc_spp$pc_mean)
```

```
ggplot(rf_pc_spp %>%
  filter(cat_c == "Hard corals"),
  aes(x = reorder(species, pc_mean), y = pc_mean)) +
  geom_col(fill = "coral2", color = "black", alpha = 0.9) +
  geom_errorbar(aes(ymin = pc_mean - pc_se, ymax = pc_mean + pc_se), width = .2,
    position = position_dodge(.9)) +
  coord_flip() +
  labs(y = "Mean percent cover", x = "", fill = "") +
  theme_bw() +
  theme(axis.text.y = element_text(face = "italic"))
```



Stony coral - percent cover by species across all sites

```
kable(rf_pc_spp %>% filter(cat_c == "Hard corals") %>% select(species, pc_mean, pc_se))
```

species	pc_mean	pc_se
<i>Acropora cervicornis</i>	2.1777778	2.1777778
<i>Acropora palmata</i>	4.0000000	1.8287822
<i>Acropora prolifera</i>	9.7000000	6.3000000
<i>Agaricia agaricites</i>	1.1444444	0.4287507
<i>Colpophyllia natans</i>	0.1000000	0.1000000
<i>Diploria labyrinthiformis</i>	0.1000000	0.1000000
<i>Millepora alcicornis</i>	1.2518519	0.7804539
<i>Orbicella annularis</i>	0.4666667	0.2905933
<i>Orbicella faveolata</i>	1.0111111	0.6041012
<i>Orbicella franksi</i>	0.6666667	0.5868939
<i>Porites asteroides</i>	3.3000000	1.2741010

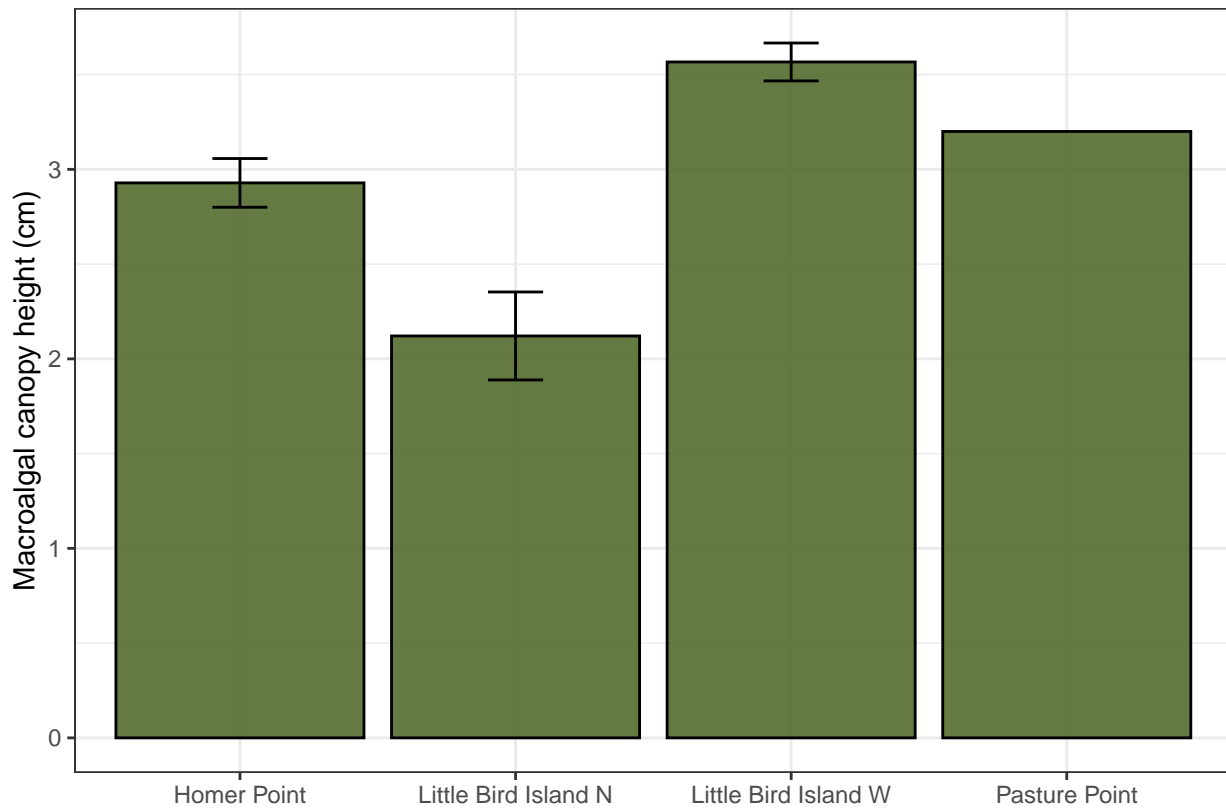
species	pc_mean	pc_se
Porites furcata	0.1333333	0.1333333
Porites porites	0.1333333	0.1333333
Pseudodiploria clivosa	0.0666667	0.0666667
Pseudodiploria strigosa	0.1333333	0.1333333
Siderastrea radians	0.0666667	0.0666667
Siderastrea siderea	0.2000000	0.1333333
Siderastrea stellata	0.1333333	0.0816497
Stephanoconia intersepta	0.2000000	0.2000000

Macroalgal canopy heights

- No macroalgae present at Pierce Shoals W
- Macroalgae only present on one transect at Pasture Point, hence no standard error can be calculated

```
ma_height <- rf_benthic %>%
  filter(category_code == "MA") %>%
  group_by(site, transect) %>%
  summarize(height = mean(height)) %>%
  filter(!is.na(height)) %>%
  group_by(site) %>%
  summarize(height_mean = mean(height),
            height_se = sd(height)/sqrt(n()))

ggplot(ma_height, aes(x = site, y = height_mean)) +
  geom_col(fill = "darkolivegreen", color = "black", alpha = 0.9) +
  geom_errorbar(aes(ymin = height_mean - height_se, ymax = height_mean + height_se), width = .2,
               position = position_dodge(.9)) +
  labs(x = "", y = "Macroalgal canopy height (cm)") +
  theme_bw()
```



Need to add:

- recruits
- urchins

Coral recruits

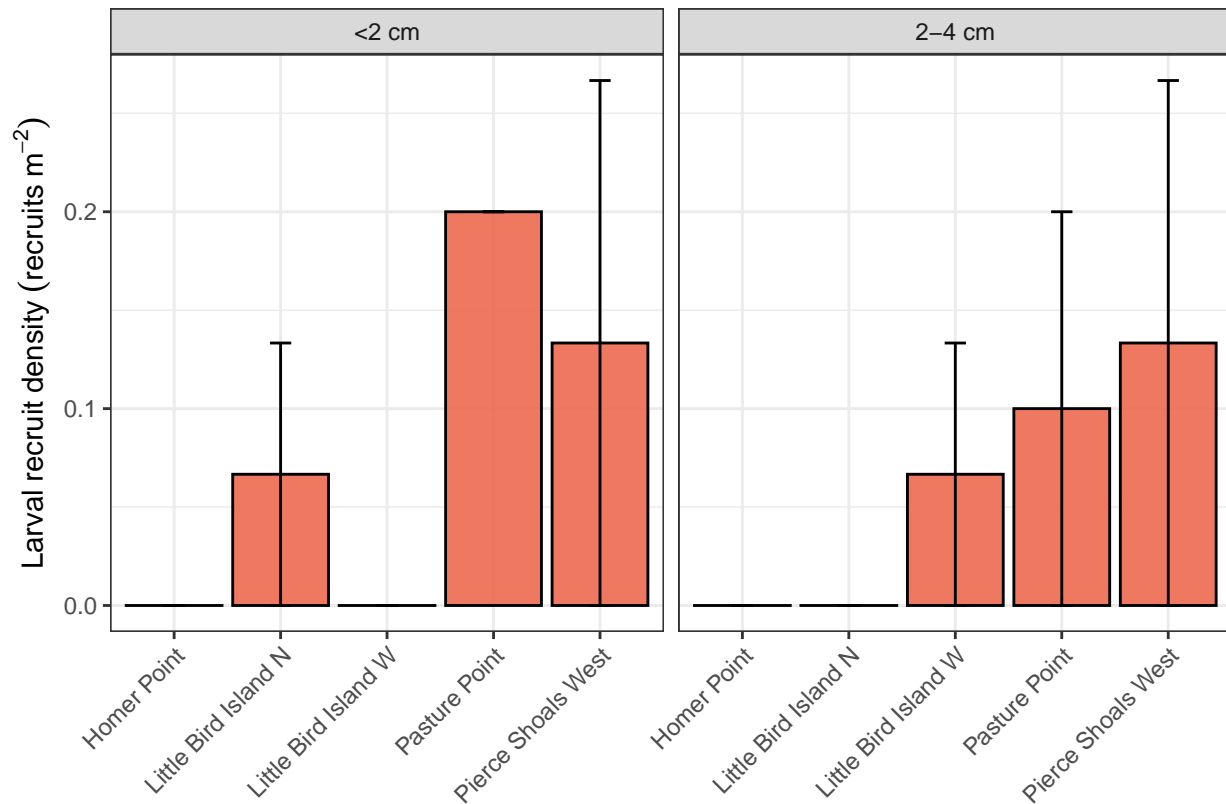
```
rf_recruits <- read_excel(here("jumby_baseline", "data", "JBB_reefs.xlsx"), sheet = "recruits") %>%
  clean_names() %>%
  pivot_longer(cols = starts_with("count"),
               names_to = "size",
               names_pattern = "count_(.*)",
               values_to = "count") %>%
  mutate(size = if_else(size == "0_2cm", "<2 cm", "2-4 cm")) %>%
  select(site, transect, meter, size, code, species, count)
```

Density of coral recruits (all species) by site

- Need to check size of quadrats

```
rf_recruits_tot <- rf_recruits %>%
  group_by(site, transect, size, meter) %>%
  summarize(count = sum(count)) %>%
  group_by(site, transect, size) %>%
  summarize(density = mean(count)) %>% # need to check actual size of quadrat
  group_by(site, size) %>%
  summarize(density_mean = mean(density),
            density_se = sd(density)/sqrt(n())) # se = mean here, which I assume just means there is a
```

```
ggplot(rf_recruits_tot, aes(x = site, y = density_mean)) +
  geom_col(fill = "coral2", color = "black", alpha = 0.9) +
  geom_errorbar(aes(ymin = density_mean - density_se, ymax = density_mean + density_se), width = .2,
    position = position_dodge(.9)) +
  labs(x = "", y = expression(Larval~recruit~density~(recruits~m^-2))) +
  facet_wrap(. ~ size) +
  theme_bw() +
  theme(axis.text.x = element_text(angle = 45, h = 1))
```



```
kable(rf_recruits)
```

site	transect	meter	size	code	species	count
Little Bird Island N	1	1	<2 cm	n/a	#N/A	0
Little Bird Island N	1	1	2-4 cm	n/a	#N/A	0
Little Bird Island N	1	2	<2 cm	n/a	#N/A	0
Little Bird Island N	1	2	2-4 cm	n/a	#N/A	0
Little Bird Island N	1	3	<2 cm	n/a	#N/A	0
Little Bird Island N	1	3	2-4 cm	n/a	#N/A	0
Little Bird Island N	1	4	<2 cm	n/a	#N/A	0
Little Bird Island N	1	4	2-4 cm	n/a	#N/A	0
Little Bird Island N	1	5	<2 cm	n/a	#N/A	0
Little Bird Island N	1	5	2-4 cm	n/a	#N/A	0
Little Bird Island N	2	1	<2 cm	n/a	#N/A	0
Little Bird Island N	2	1	2-4 cm	n/a	#N/A	0
Little Bird Island N	2	2	<2 cm	n/a	#N/A	0
Little Bird Island N	2	2	2-4 cm	n/a	#N/A	0
Little Bird Island N	2	3	<2 cm	PAST	Porites asteroides	1

site	transect	meter	size	code	species	count
Little Bird Island N	2	3	2-4 cm	PAST	Porites asteroides	0
Little Bird Island N	2	4	<2 cm	n/a	#N/A	0
Little Bird Island N	2	4	2-4 cm	n/a	#N/A	0
Little Bird Island N	2	5	<2 cm	n/a	#N/A	0
Little Bird Island N	2	5	2-4 cm	n/a	#N/A	0
Little Bird Island N	3	1	<2 cm	n/a	#N/A	0
Little Bird Island N	3	1	2-4 cm	n/a	#N/A	0
Little Bird Island N	3	2	<2 cm	n/a	#N/A	0
Little Bird Island N	3	2	2-4 cm	n/a	#N/A	0
Little Bird Island N	3	3	<2 cm	n/a	#N/A	0
Little Bird Island N	3	3	2-4 cm	n/a	#N/A	0
Little Bird Island N	3	4	<2 cm	n/a	#N/A	0
Little Bird Island N	3	4	2-4 cm	n/a	#N/A	0
Little Bird Island N	3	5	<2 cm	n/a	#N/A	0
Little Bird Island N	3	5	2-4 cm	n/a	#N/A	0
Homer Point	1	1	<2 cm	n/a	#N/A	0
Homer Point	1	1	2-4 cm	n/a	#N/A	0
Homer Point	1	2	<2 cm	n/a	#N/A	0
Homer Point	1	2	2-4 cm	n/a	#N/A	0
Homer Point	1	3	<2 cm	n/a	#N/A	0
Homer Point	1	3	2-4 cm	n/a	#N/A	0
Homer Point	1	4	<2 cm	n/a	#N/A	0
Homer Point	1	4	2-4 cm	n/a	#N/A	0
Homer Point	1	5	<2 cm	n/a	#N/A	0
Homer Point	1	5	2-4 cm	n/a	#N/A	0
Homer Point	2	1	<2 cm	n/a	#N/A	0
Homer Point	2	1	2-4 cm	n/a	#N/A	0
Homer Point	2	2	<2 cm	n/a	#N/A	0
Homer Point	2	2	2-4 cm	n/a	#N/A	0
Homer Point	2	3	<2 cm	n/a	#N/A	0
Homer Point	2	3	2-4 cm	n/a	#N/A	0
Homer Point	2	4	<2 cm	n/a	#N/A	0
Homer Point	2	4	2-4 cm	n/a	#N/A	0
Homer Point	2	5	<2 cm	n/a	#N/A	0
Homer Point	2	5	2-4 cm	n/a	#N/A	0
Homer Point	3	1	<2 cm	n/a	#N/A	0
Homer Point	3	1	2-4 cm	n/a	#N/A	0
Homer Point	3	2	<2 cm	n/a	#N/A	0
Homer Point	3	2	2-4 cm	n/a	#N/A	0
Homer Point	3	3	<2 cm	n/a	#N/A	0
Homer Point	3	3	2-4 cm	n/a	#N/A	0
Homer Point	3	4	<2 cm	n/a	#N/A	0
Homer Point	3	4	2-4 cm	n/a	#N/A	0
Homer Point	3	5	<2 cm	n/a	#N/A	0
Homer Point	3	5	2-4 cm	n/a	#N/A	0
Pasture Point	1	1	<2 cm	n/a	#N/A	0
Pasture Point	1	1	2-4 cm	n/a	#N/A	0
Pasture Point	1	2	<2 cm	n/a	#N/A	0
Pasture Point	1	2	2-4 cm	n/a	#N/A	0
Pasture Point	1	3	<2 cm	n/a	#N/A	0
Pasture Point	1	3	2-4 cm	n/a	#N/A	0
Pasture Point	1	4	<2 cm	n/a	#N/A	0

site	transect	meter	size	code	species	count
Pasture Point	1	4	2-4 cm	n/a	#N/A	0
Pasture Point	1	5	<2 cm	PAST	Porites asteroides	1
Pasture Point	1	5	2-4 cm	PAST	Porites asteroides	0
Pasture Point	2	1	<2 cm	n/a	#N/A	0
Pasture Point	2	1	2-4 cm	n/a	#N/A	0
Pasture Point	2	2	<2 cm	n/a	#N/A	0
Pasture Point	2	2	2-4 cm	n/a	#N/A	0
Pasture Point	2	3	<2 cm	AAGA	Agaricia agaricites	0
Pasture Point	2	3	2-4 cm	AAGA	Agaricia agaricites	1
Pasture Point	2	4	<2 cm	PAST	Porites asteroides	1
Pasture Point	2	4	2-4 cm	PAST	Porites asteroides	0
Pasture Point	2	5	<2 cm	n/a	#N/A	0
Pasture Point	2	5	2-4 cm	n/a	#N/A	0
Pierce Shoals West	1	1	<2 cm	n/a	#N/A	0
Pierce Shoals West	1	1	2-4 cm	n/a	#N/A	0
Pierce Shoals West	1	2	<2 cm	n/a	#N/A	0
Pierce Shoals West	1	2	2-4 cm	n/a	#N/A	0
Pierce Shoals West	1	3	<2 cm	n/a	#N/A	0
Pierce Shoals West	1	3	2-4 cm	n/a	#N/A	0
Pierce Shoals West	1	4	<2 cm	n/a	#N/A	0
Pierce Shoals West	1	4	2-4 cm	n/a	#N/A	0
Pierce Shoals West	1	5	<2 cm	n/a	#N/A	0
Pierce Shoals West	1	5	2-4 cm	n/a	#N/A	0
Pierce Shoals West	2	1	<2 cm	n/a	#N/A	0
Pierce Shoals West	2	1	2-4 cm	n/a	#N/A	0
Pierce Shoals West	2	2	<2 cm	n/a	#N/A	0
Pierce Shoals West	2	2	2-4 cm	n/a	#N/A	0
Pierce Shoals West	2	3	<2 cm	n/a	#N/A	0
Pierce Shoals West	2	3	2-4 cm	n/a	#N/A	0
Pierce Shoals West	2	4	<2 cm	n/a	#N/A	0
Pierce Shoals West	2	4	2-4 cm	n/a	#N/A	0
Pierce Shoals West	2	5	<2 cm	n/a	#N/A	0
Pierce Shoals West	2	5	2-4 cm	n/a	#N/A	0
Pierce Shoals West	3	1	<2 cm	n/a	#N/A	0
Pierce Shoals West	3	1	2-4 cm	n/a	#N/A	0
Pierce Shoals West	3	2	<2 cm	AAGA	Agaricia agaricites	1
Pierce Shoals West	3	2	2-4 cm	AAGA	Agaricia agaricites	0
Pierce Shoals West	3	3	<2 cm	n/a	#N/A	0
Pierce Shoals West	3	3	2-4 cm	n/a	#N/A	0
Pierce Shoals West	3	4	<2 cm	AAGA	Agaricia agaricites	0
Pierce Shoals West	3	4	2-4 cm	AAGA	Agaricia agaricites	2
Pierce Shoals West	3	5	<2 cm	PAST	Porites asteroides	1
Pierce Shoals West	3	5	2-4 cm	PAST	Porites asteroides	0
Little Bird Island W	1	1	<2 cm	n/a	#N/A	0
Little Bird Island W	1	1	2-4 cm	n/a	#N/A	0
Little Bird Island W	1	2	<2 cm	n/a	#N/A	0
Little Bird Island W	1	2	2-4 cm	n/a	#N/A	0
Little Bird Island W	1	3	<2 cm	n/a	#N/A	0
Little Bird Island W	1	3	2-4 cm	n/a	#N/A	0
Little Bird Island W	1	4	<2 cm	n/a	#N/A	0
Little Bird Island W	1	4	2-4 cm	n/a	#N/A	0
Little Bird Island W	1	5	<2 cm	n/a	#N/A	0

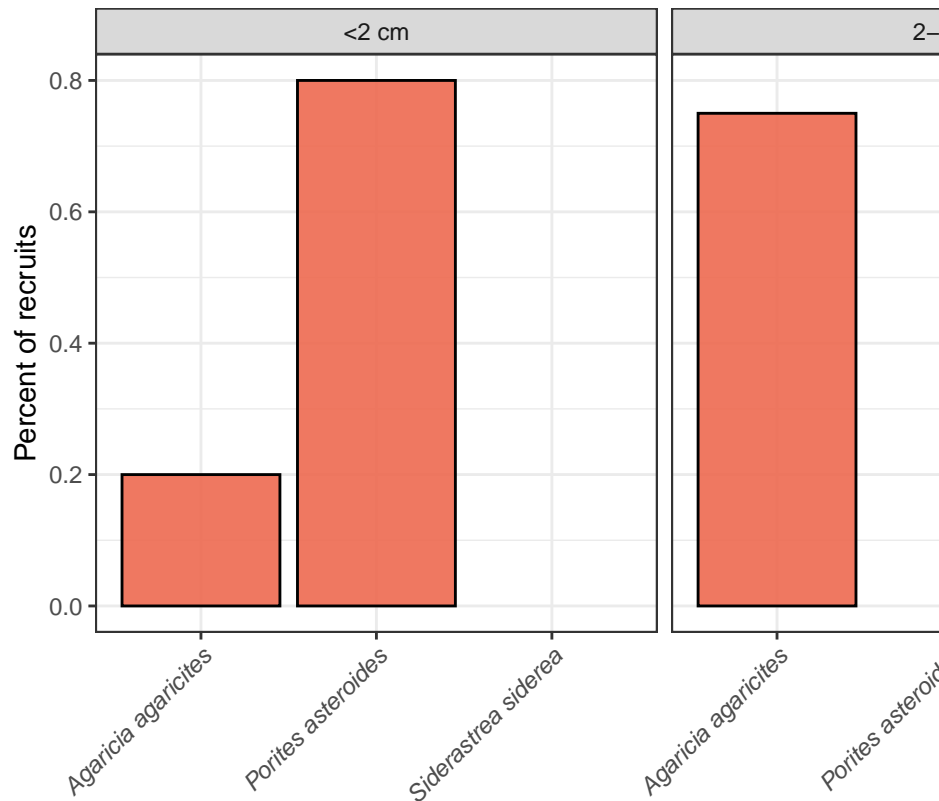
site	transect	meter	size	code	species	count
Little Bird Island W	1	5	2-4 cm	n/a	#N/A	0
Little Bird Island W	2	1	<2 cm	n/a	#N/A	0
Little Bird Island W	2	1	2-4 cm	n/a	#N/A	0
Little Bird Island W	2	2	<2 cm	n/a	#N/A	0
Little Bird Island W	2	2	2-4 cm	n/a	#N/A	0
Little Bird Island W	2	3	<2 cm	n/a	#N/A	0
Little Bird Island W	2	3	2-4 cm	n/a	#N/A	0
Little Bird Island W	2	4	<2 cm	n/a	#N/A	0
Little Bird Island W	2	4	2-4 cm	n/a	#N/A	0
Little Bird Island W	2	5	<2 cm	n/a	#N/A	0
Little Bird Island W	2	5	2-4 cm	n/a	#N/A	0
Little Bird Island W	3	1	<2 cm	n/a	#N/A	0
Little Bird Island W	3	1	2-4 cm	n/a	#N/A	0
Little Bird Island W	3	2	<2 cm	n/a	#N/A	0
Little Bird Island W	3	2	2-4 cm	n/a	#N/A	0
Little Bird Island W	3	3	<2 cm	SSID	Siderastrea siderea	0
Little Bird Island W	3	3	2-4 cm	SSID	Siderastrea siderea	1
Little Bird Island W	3	4	<2 cm	n/a	#N/A	0
Little Bird Island W	3	4	2-4 cm	n/a	#N/A	0
Little Bird Island W	3	5	<2 cm	n/a	#N/A	0
Little Bird Island W	3	5	2-4 cm	n/a	#N/A	0

```

rf_recruits_spp <- rf_recruits %>%
  filter(count > 0) %>%
  uncount(count) %>%
  group_by(size, species) %>%
  summarize(n = n()) %>%
  mutate(freq = n / sum(n))

ggplot(rf_recruits_spp, aes(x = species, y = freq)) +
  geom_col(fill = "coral2", color = "black", alpha = 0.9) +
  facet_wrap(. ~ size) +
  labs(x = "", y = "Percent of recruits") +
  theme_bw() +
  theme(axis.text.x = element_text(angle = 45, h = 1, face = "italic"))

```



Proportion of coral recruits by species

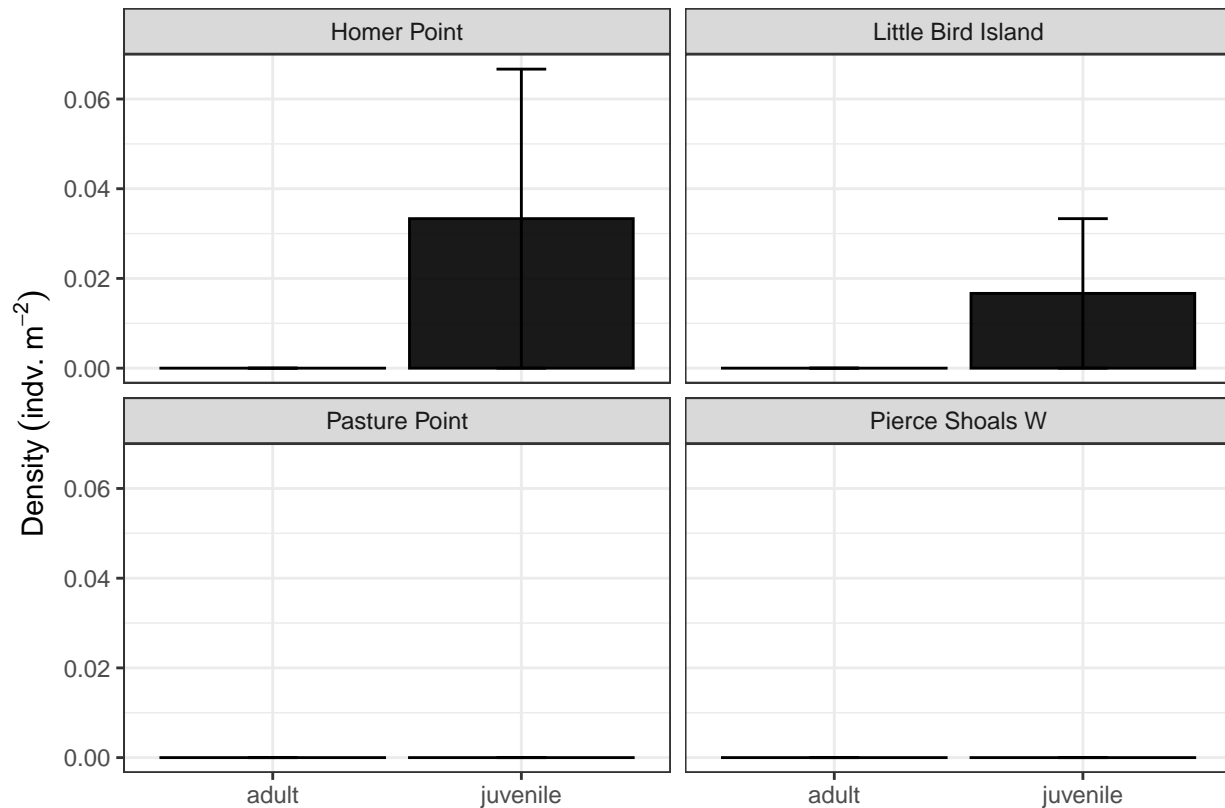
Diadema

Density of Diadema by site and phase

- Need to convert to density when I check belt width with GRB

```
diadema <- rf_recruits <- read_excel(here("jumby_baseline", "data", "JBB_reefs.xlsx"), sheet = "inverts")
clean_names() %>%
select(site, transect, diadema_adult, diadema_juvenile) %>%
pivot_longer(cols = starts_with("diadema"),
              names_to = "phase",
              names_pattern = "diadema_(.*)",
              values_to = "count") %>%
group_by(site, phase) %>%
summarize(density_mean = mean(count/20),
          density_se = sd(count/20)/sqrt(n())) # 2x10m belt?

ggplot(diadema, aes(x = phase, y = density_mean)) +
  geom_col(fill = "black", color = "black", alpha = 0.9) +
  geom_errorbar(aes(ymin = density_mean - density_se, ymax = density_mean + density_se), width = .2,
               position = position_dodge(.9)) +
  facet_wrap(. ~ site) +
  labs(x = "", y = expression(Density~(indv.^m^-2))) +
  theme_bw()
```



Fish

```
# import and clean data

rf_fish <- read_excel(here("jumby_baseline", "data", "JBB_reefs.xlsx"), sheet = "fish") %>%
  clean_names() %>%
  filter(!is.na(site)) %>% # remove any incomplete rows at the end of the data
  mutate(number = if_else(is.na(number), 1, number)) %>% # all entries with no number specified were si
  uncount(number) %>% # expand to replicate rows if multiple fish were recorded to look at length distr
  mutate(biomass = as.numeric(biomass),
         phase_code = tolower(phase),
         phase = case_when(phase == "j" ~ "Juvenile",
                           phase == "i" ~ "Initial",
                           phase == "t" ~ "Terminal"),
         family_c = if_else(family %in% c("Scaridae", "Acanthuridae", "Haemulidae", "Serranidae", "Lutj
         ) # consolidating the number of families
```

Fish biomass

Total biomass at each site

- Regional averages are taken from Karr et al. 2015

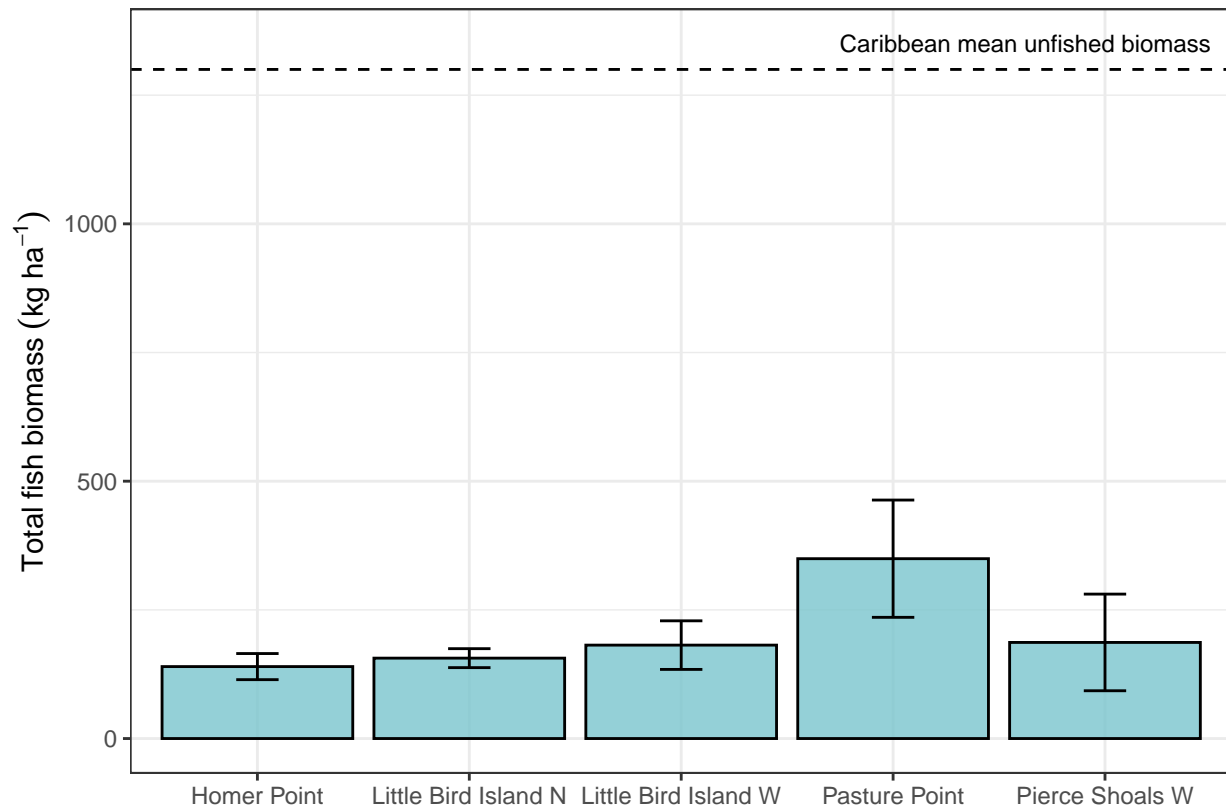
```
# calculating total biomass in each transect (sum) -> mean at each site
rf_fish_site <- rf_fish %>%
  group_by(site, transect) %>%
  summarize(bm_tot = sum(biomass)/1000/120*10000) %>% #kg/ha
  group_by(site) %>%
```

```

summarize(bm_mean = mean(bm_tot),
          bm_se = sd(bm_tot)/sqrt(n()))

# graph
ggplot(rf_fish_site, aes(x = site, y = bm_mean)) +
  geom_col(fill = "cadetblue3", color = "black", alpha = 0.8) +
  geom_errorbar(aes(ymin = bm_mean - bm_se, ymax = bm_mean + bm_se), width = .2,
               position = position_dodge(.9)) +
  geom_hline(yintercept = 1300, linetype = "dashed", color = "black") +
  annotate("text", x = 5.5, y = 1350, size = 3, hjust = 1, label=c('Caribbean mean unfished biomass')) +
  labs(x = "", y = expression(Total~fish~biomass~(kg~ha^-1))) +
  theme_bw()

```



```
kable(rf_fish_site %>% select(site, bm_mean, bm_se))
```

site	bm_mean	bm_se
Homer Point	139.7707	25.35147
Little Bird Island N	156.1916	18.40841
Little Bird Island W	181.4903	47.19336
Pasture Point	349.4497	113.93810
Pierce Shoals W	186.7296	93.87824

Biomass by site and family

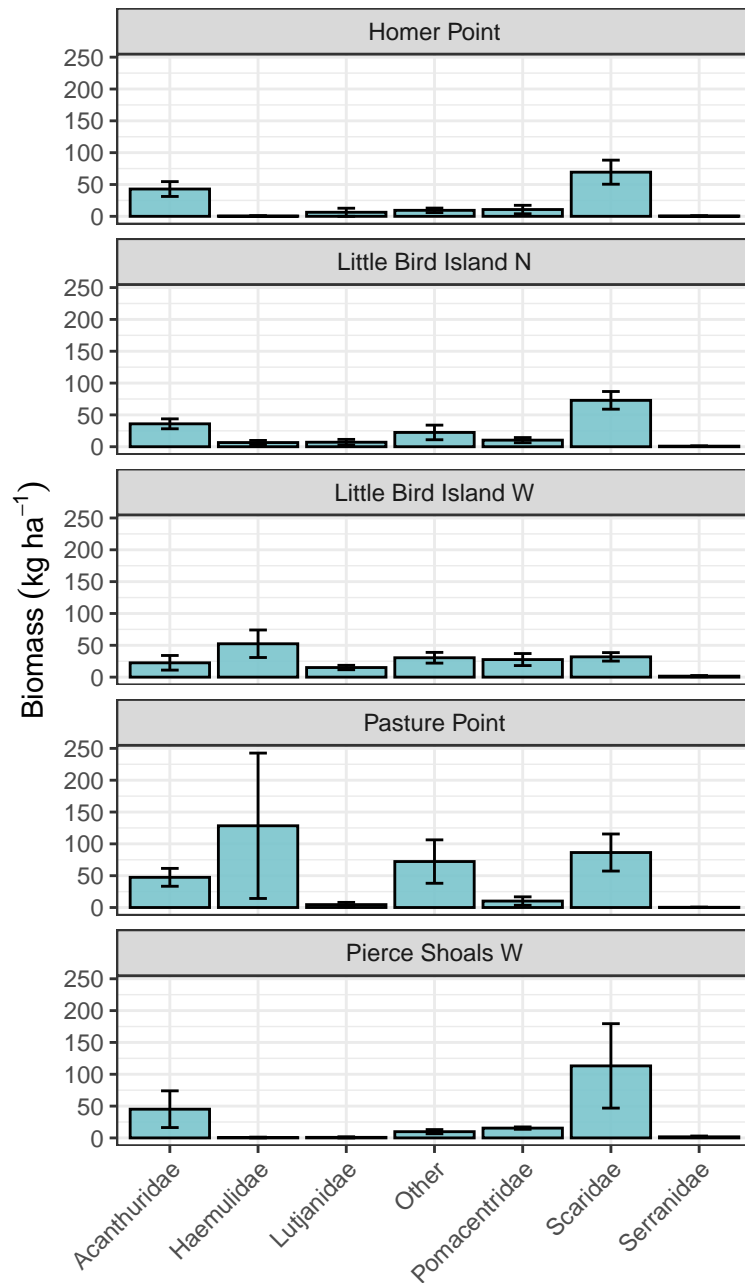
- Need to reorder to put “other” last
- Are these good for families to feature?
- Should I switch to common family names, or both?

```

rf_fish_fam_site <- rf_fish %>%
  expand(nesting(site, transect), family_c) %>%
  left_join(rf_fish %>%
    select(site, transect, family_c, length, biomass)) %>%
  mutate(biomass = if_else(is.na(biomass), 0, biomass)) %>%
  group_by(site, transect, family_c) %>%
  summarize(bm_tot = sum(biomass)/1000/120*10000) %>% #kg/ha
  group_by(site, family_c) %>%
  summarize(bm_mean = mean(bm_tot),
    bm_se = sd(bm_tot)/sqrt(n()))

# graph
ggplot(rf_fish_fam_site, aes(x = family_c, y = bm_mean)) +
  geom_col(fill = "cadetblue3", color = "black", alpha = 0.9) +
  geom_errorbar(aes(ymin = bm_mean - bm_se, ymax = bm_mean + bm_se), width = .2,
    position = position_dodge(.9)) +
  facet_wrap(. ~ site, ncol = 1) +
  labs(x = "", y = expression(Biomass~(kg~ha^-1))) +
  theme_bw() +
  theme(axis.text.x = element_text(angle = 45, h = 1))

```



```
kable(rf_fish_fam_site %>% select(site, family = family_c, bm_mean, bm_se))
```

site	family	bm_mean	bm_se
Homer Point	Acanthuridae	42.8908481	11.6572714
Homer Point	Haemulidae	0.5201659	0.5201659
Homer Point	Lutjanidae	6.3694441	6.3694441
Homer Point	Other	9.4074782	3.5483896
Homer Point	Pomacentridae	10.6749561	6.6431279
Homer Point	Scaridae	69.3588909	18.8969026
Homer Point	Serranidae	0.5488902	0.3430707
Little Bird Island N	Acanthuridae	35.9727390	7.7919239
Little Bird Island N	Haemulidae	6.5774270	3.3044487

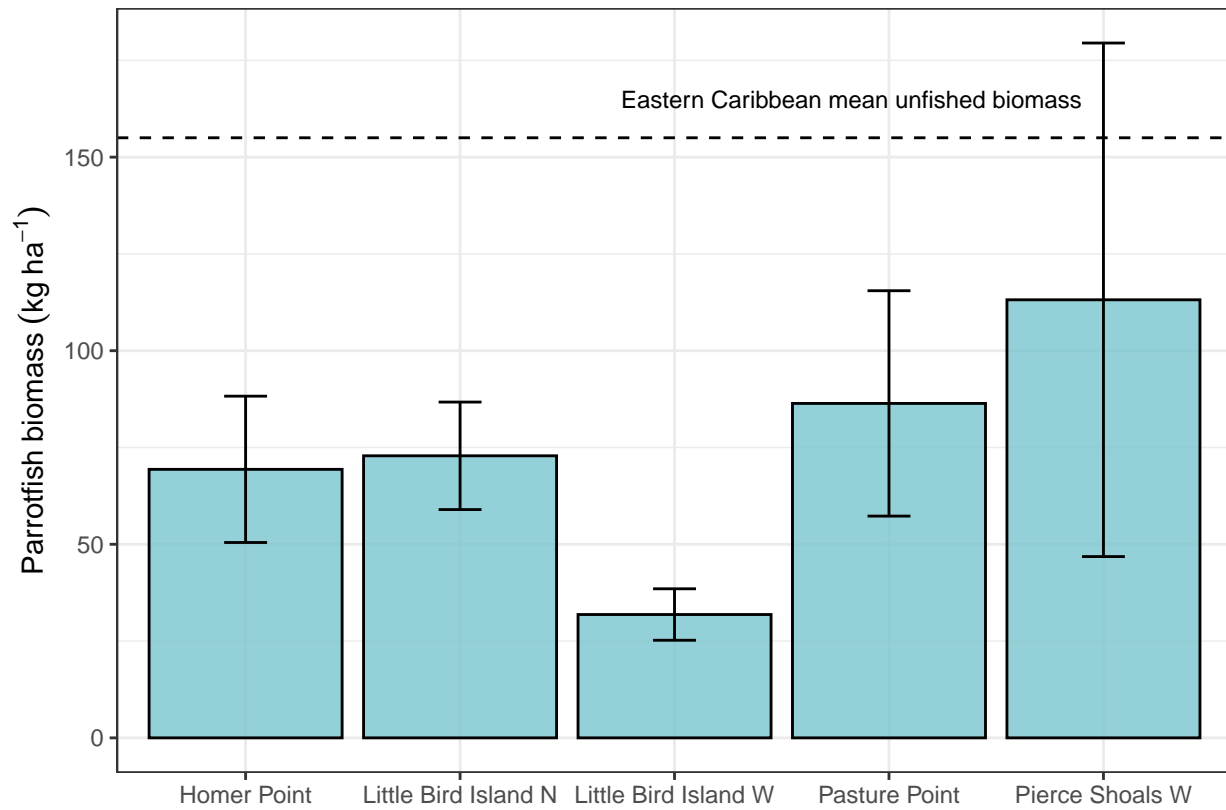
site	family	bm_mean	bm_se
Little Bird Island N	Lutjanidae	7.0848874	4.4216375
Little Bird Island N	Other	22.4505850	11.4622906
Little Bird Island N	Pomacentridae	10.3283883	4.0580768
Little Bird Island N	Scaridae	72.8543359	13.8844571
Little Bird Island N	Serranidae	0.9232343	0.4318075
Little Bird Island W	Acanthuridae	22.5085015	11.4739516
Little Bird Island W	Haemulidae	52.4258652	21.6198819
Little Bird Island W	Lutjanidae	15.0842021	3.4445261
Little Bird Island W	Other	30.4447117	8.4163357
Little Bird Island W	Pomacentridae	27.6073611	9.4573849
Little Bird Island W	Scaridae	31.8587441	6.6490737
Little Bird Island W	Serranidae	1.5608830	0.9406703
Pasture Point	Acanthuridae	47.4353959	14.0426872
Pasture Point	Haemulidae	128.4105447	114.2115388
Pasture Point	Lutjanidae	4.5480098	3.4988036
Pasture Point	Other	72.2111801	34.0993803
Pasture Point	Pomacentridae	10.1399444	6.6488481
Pasture Point	Scaridae	86.3867183	29.1056015
Pasture Point	Serranidae	0.3178841	0.3178841
Pierce Shoals W	Acanthuridae	45.1250994	28.8079159
Pierce Shoals W	Haemulidae	0.6092317	0.6092317
Pierce Shoals W	Lutjanidae	0.8799941	0.8799941
Pierce Shoals W	Other	9.8218799	3.2814828
Pierce Shoals W	Pomacentridae	15.4244093	1.8436711
Pierce Shoals W	Scaridae	113.1501279	66.3227768
Pierce Shoals W	Serranidae	1.7188308	1.2574469

Herbivore biomasses

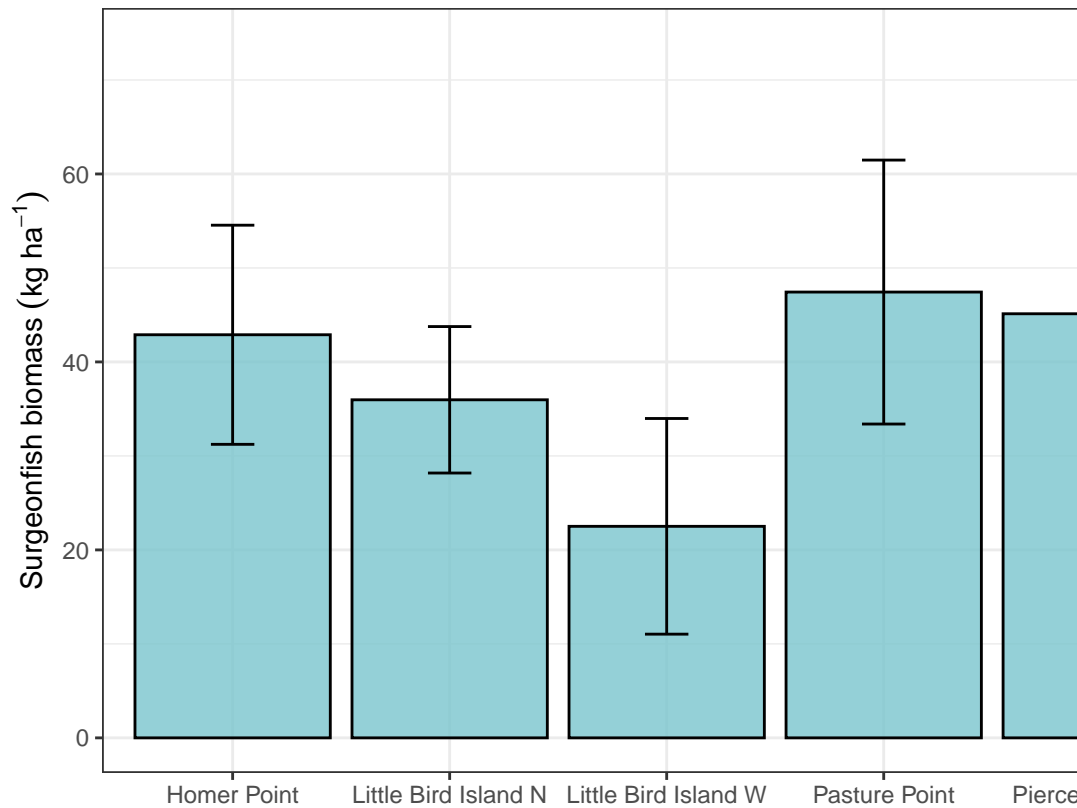
Scarid biomass by site

- Eastern Caribbean average parrotfish biomass for NTRs from Steneck et al. 2018 was ~ 1550 g/100m2, or 155 kg/ha. Note that this is potentially misleading because I'm sure a lot of these NTRs do experience some fishing. But mean fished parrotfish biomasses for the same region was ~ 750 g/100m2

```
ggplot(rf_fish_fam_site %>%
  filter(family_c == "Scaridae"),
  aes(x = site, y = bm_mean)) +
  geom_col(color = "black", fill = "cadetblue3", alpha = 0.8, stat = "identity", position = position_dodge(.9)) +
  geom_errorbar(aes(ymin = bm_mean - bm_se, ymax = bm_mean + bm_se), width = .2,
    position = position_dodge(.9)) +
  geom_hline(yintercept = 155, linetype = "dashed", color = "black") +
  annotate("text", x = 4.9, y = 165, size = 3, hjust = 1, label=c('Eastern Caribbean mean unfished biomass')) +
  labs(x = "", y = expression(Parrotfish~biomass~(kg~ha^-1))) +
  theme_bw()
```



```
ggplot(rf_fish_fam_site %>%
  filter(family_c == "Acanthuridae"),
  aes(x = site, y = bm_mean)) +
  geom_col(color = "black", fill = "cadetblue3", alpha = 0.8, stat = "identity", position = position_dodge(.9)) +
  geom_errorbar(aes(ymin = bm_mean - bm_se, ymax = bm_mean + bm_se), width = .2,
    position = position_dodge(.9)) +
  labs(x = "", y = expression(Surgeonfish~biomass~(kg~ha^-1))) +
  theme_bw()
```



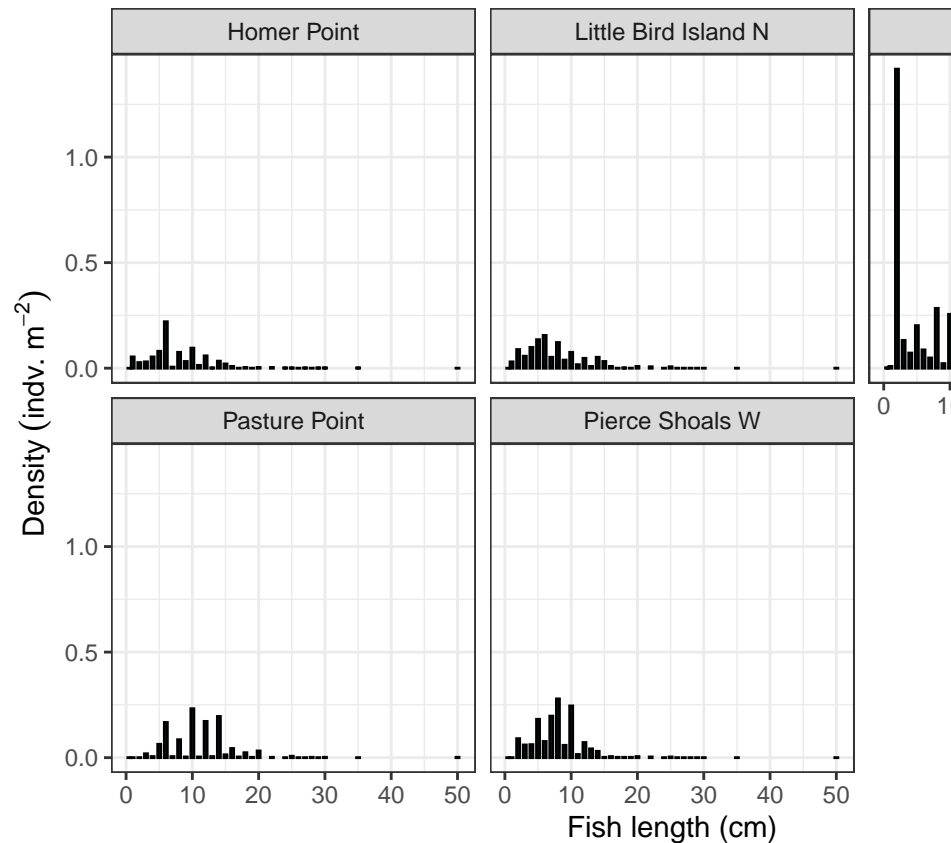
Acanthurid biomass by site

Fish lengths

- These were calculated by taking the mean density of fish of each size at each size (averaged across transects). Because we have distribution data within each transect, we can't make density plots/violin plots straight from the raw data (i.e., some sites could have more transects)
- Open to any suggestions about how we want to communicate size data!

```
rf_fish_length <- rf_fish %>%
  expand(nesting(site, transect), length) %>%
  left_join(rf_fish %>%
    group_by(site, transect, length) %>%
    summarize(count = n())) %>%
  mutate(count = as.numeric(count),
         count = if_else(is.na(count), 0, count),
         density = count/120) %>% # indiv./m2
  group_by(site, length) %>%
  summarize(density_mean = mean(density),
           density_se = sd(density)/sqrt(n()))

ggplot(rf_fish_length, aes(x = length, y = density_mean)) +
  geom_col(fill = "deepskyblue4", alpha = 0.9, color = "black") +
  facet_wrap(. ~ site) +
  labs(x = "Fish length (cm)", y = expression(Density~(indv.~m^-2))) +
  theme_bw()
```



Length distributions of all fish by site

```
rf_fish_length_scarids <- rf_fish %>%
  expand(nesting(site, transect), length) %>%
  left_join(rf_fish %>%
    filter(family == "Scaridae") %>%
    group_by(site, transect, length) %>%
    summarize(count = n())) %>%
  mutate(count = as.numeric(count),
         count = if_else(is.na(count), 0, count),
         density = count/120) %>% # indv/m2
  group_by(site, length) %>%
  summarize(density_mean = mean(density),
           density_se = sd(density)/sqrt(n()))

ggplot(rf_fish_length_scarids, aes(x = length, y = density_mean)) +
  geom_col(fill = "deepskyblue4", alpha = 0.9, color = "black") +
  facet_wrap(. ~ site) +
  labs(x = "Fish length (cm)", y = expression(Scarid~density~(indv.~m^-2))) +
  theme_bw()
```

Length distributions of scarids at each site

