Morro Bay Seine Analyses

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Metadata

Sample Size Breakdown

```r
seine_data <-
  read_csv(here("data", "seine_fish_data.csv")) %>%
  filter(year == 2017 | year == 2018) %>%
  mutate(year = factor(year, levels = c("2017", "2018"), ordered = TRUE)) %>%
  filter(site_name %in% c("Windy Cove", "Colemans")) %>%
  mutate(date = as.Date(date, format = "%m/%d/%Y"),
         spec_binomial = paste(genus, species, sep = " "),
         spec_binomial = dplyr::recode(spec_binomial, "Sebastes NA" = "Sebastes YOY"),
         month = map_chr(date, ~month.name[lubridate::month(.x)]),
         `seagrass/unvegetated` = map_chr(`seagrass/unvegetated`, capitalize)) %>%
  filter(month %in% c("April", "May"))

seine_data %>%
  group_by(`seagrass/unvegetated`, year, site_name) %>%
  summarise(count = length(unique(seine_id))) %>%
  spread(`seagrass/unvegetated`, count) %>%
  knitr::kable()
```

year	site_name	Seagrass	Unvegetated
2017	Colemans	2	2
2017	Windy Cove	3	3
2018	Colemans	2	2
2018	Windy Cove	3	3

Abundance

Bar Chart

```r
seine_count_data <-
  seine_data %>%
  group_by(year, site_name, `seagrass/unvegetated`,
           seine_id, distance_m, spec_binomial) %>%
  summarise(count = n()) %>% ungroup() %>%
  complete(nesting(year, site_name, `seagrass/unvegetated`,
           seine_id, distance_m), spec_binomial, fill = list(count = 0)) %>%
  separate(spec_binomial, c("genus", "species"), sep = " ") %>%
```
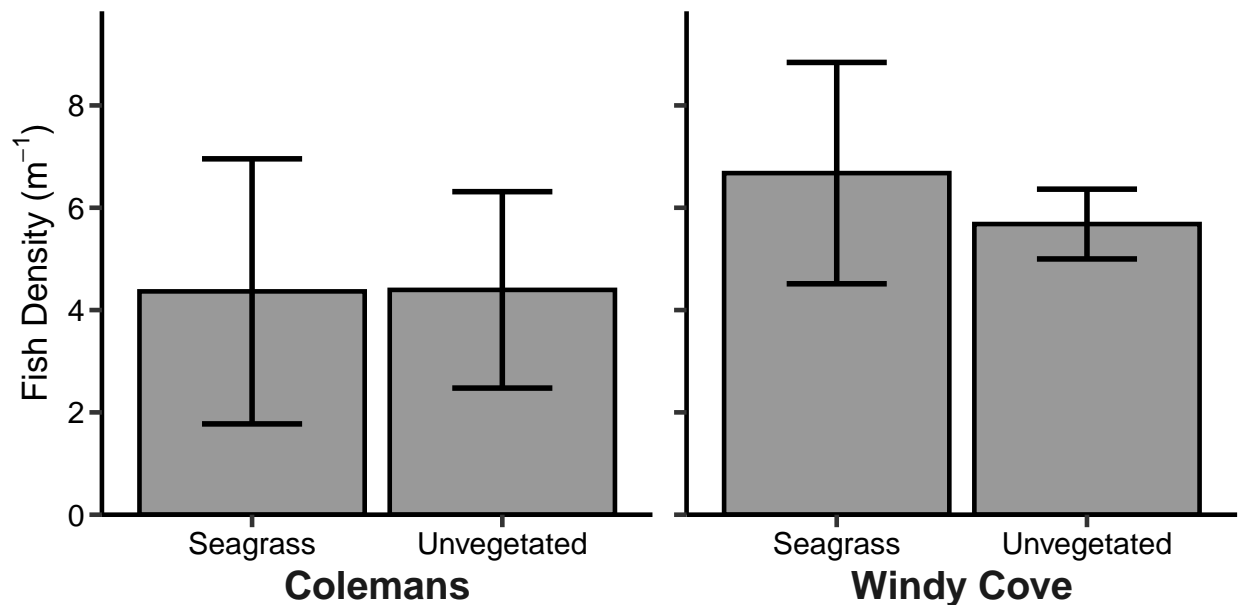
```
  mutate(density = count/distance_m) %>%
  rename(seagrass_unvegetated = `seagrass/unvegetated`)

seine_summary <-
  seine_count_data %>%
  group_by(year, site_name, seagrass_unvegetated, seine_id) %>%
  summarize(density = sum(density)) %>% ungroup() %>%
  group_by(site_name, seagrass_unvegetated) %>%
  summarize(se = sd(density)/sqrt(n()),
            density = mean(density)) %>%
  complete(site_name, seagrass_unvegetated)

seine_summary %>%
  ggplot(aes(seagrass_unvegetated, density)) +
  geom_bar(stat = "identity", position = "dodge", color = "black",
           fill = "grey60", size = 1) +
  geom_errorbar(aes(ymin = density - se, ymax = density + se),
                position = position_dodge(width = 0.8),
                width = 0.4, size = 1.2) +
  scale_y_continuous(expand = c(0,0), breaks = seq(0,12,2),
                     limits = c(0, with(seine_summary, max(density + se + 1, na.rm = TRUE)))) +
  lemon::facet_rep_wrap(~site_name, strip.position = "bottom") +
  ylab(expression(paste("Fish Density (m"^{-1}, ")"))) +
  theme_trawls +
  coord_cartesian(clip = "off") +
  theme(axis.title.x = element_blank(),
        panel.spacing = unit(0, "lines"))
```


Abundance Model

```
seine_count_lm_data <-
  seine_count_data %>%
  group_by(year, site_name, seagrass_unvegetated, seine_id, distance_m) %>%
```

```
  summarize(count = sum(count)) %>%
  ungroup() %>%
  mutate(density = count/distance_m)

seine_count_model <- glm(density ~ site_name*seagrass_unvegetated,
                         data = seine_count_lm_data,
                         family = Gamma(link = "log"))

seine_count_model %>%
  car::Anova(test.statistic = "LR") %>% as.data.frame() %>%
  rownames_to_column("term") %>%
  mutate_if(is.numeric, round, digits = 3) %>%
  knitr::kable()
```

term	LR Chisq	Df	Pr(>Chisq)
site_name	0.855	1	0.355
seagrass_unvegetated	0.070	1	0.791
site_name:seagrass_unvegetated	0.054	1	0.817

Biomass

Bar Chart

```
seine_biomass_lm_data <- seine_data %>%
  filter(!is.na(weight_g)) %>% # 1 bat ray (Myliobatis californica) observation
  group_by(year, site_name, `seagrass/unvegetated`, seine_id, distance_m) %>%
  summarize(biomass = sum(weight_g)) %>%
  ungroup() %>%
  mutate(scaled_biomass = biomass/distance_m) %>%
  rename("seagrass_unvegetated" = `seagrass/unvegetated`)

seine_biomass_summary <-
  seine_biomass_lm_data %>%
  group_by(site_name, seagrass_unvegetated) %>%
  summarize(mean = mean(scaled_biomass),
            se = sd(scaled_biomass)/sqrt(n()),
            lower = mean - se,
            upper = mean + se)

seine_biomass_summary %>%
  ggplot(aes(seagrass_unvegetated, mean)) +
  geom_bar(stat = "identity", position = "dodge", color = "black",
           fill = "grey60", size = 1) +
  geom_errorbar(aes(ymin = lower, ymax = upper),
                position = position_dodge(width = 0.8),
                width = 0.4, size = 1.2) +
  scale_y_continuous(expand = c(0,0), breaks = seq(0,130,20),
                     limits = c(0, max(seine_biomass_summary$upper + 5))) +
  lemon::facet_rep_wrap(~site_name, strip.position = "bottom") +
  ylab(expression(paste("Fish Biomass (g*m"^{-1}, ")"))) +
  theme_trawls +
```

```
theme(axis.title.x = element_blank(),
      panel.spacing = unit(0, "lines"))
```
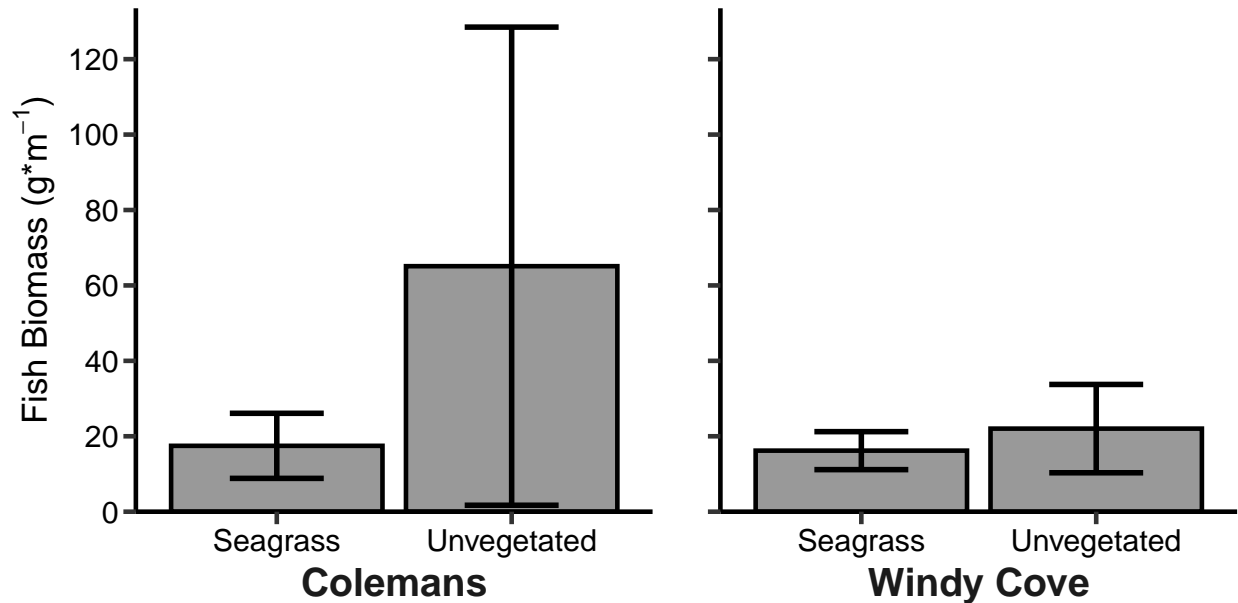

Biomass Model

```
biomass_model <- glm(scaled_biomass ~ site_name*seagrass_unvegetated,
                     data = seine_biomass_lm_data,
                     family = Gamma(link = "log"))

biomass_model %>% car::Anova(test = "LR") %>% as.data.frame() %>%
  rownames_to_column("term") %>%
  mutate_if(is.numeric, round, digits = 3) %>%
  knitr::kable()
```

term	LR Chisq	Df	Pr(>Chisq)
site_name	1.057	1	0.304
seagrass_unvegetated	1.443	1	0.230
site_name:seagrass_unvegetated	0.750	1	0.386

Species Composition

NMDS Plot

```
## Convert data to wide-format species counts
seine_sp_data <- seine_data %>%
  group_by(year, site_name, `seagrass/unvegetated`, seine_id, distance_m, spec_binomial) %>%
  summarise (Count = n()) %>% ungroup() %>%
  mutate(density = Count/distance_m) %>%
  dplyr::select(-Count) %>%
  spread(spec_binomial, density, fill = 0) %>%
  rename(seagrass_unvegetated = `seagrass/unvegetated`)
```

```
## Species matrix
seine_sp_matrix <- as.matrix(seine_sp_data[,6:23])
rownames(seine_sp_matrix) <- with(seine_sp_data, paste(seagrass_unvegetated, site_name))

## Bray-Curtis dissimiliarity matrix
seine_bray <- vegdist(seine_sp_matrix, method = "bray")

## Fit NMDS
seine_mds <- metaMDS(seine_bray, k = 2)

## Format data for plotting
mds_plot_data <- seine_mds$points
mds_rownames <- rownames(mds_plot_data)
mds_plot_data <- as.data.frame(mds_plot_data, row.names =FALSE)
mds_plot_data$seagrass <- mds_rownames
nmds_colors <- RColorBrewer::brewer.pal(6, "Paired")[c(2, 6)]
```
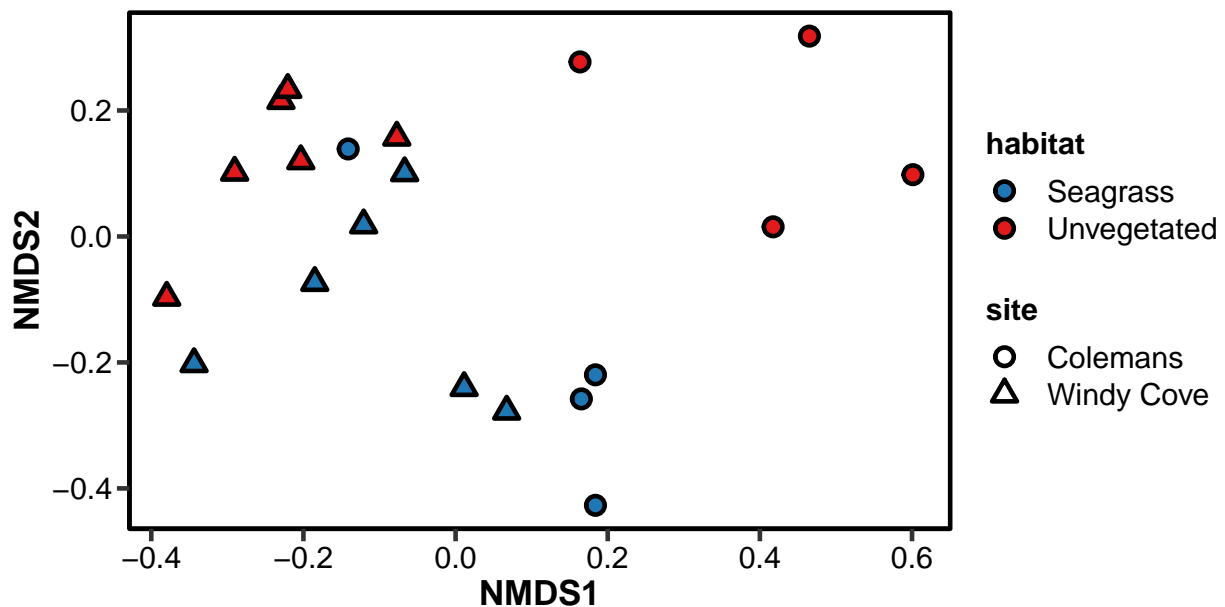
```
mds_plot_data %>%
  separate(seagrass, c("seagrass", "site"), sep = " ", extra = "merge") %>%
  ggplot(aes(MDS1, MDS2, fill = seagrass, pch = site)) +
  geom_point(size = 3, stroke = 1.5) +
  scale_fill_manual(values = nmds_colors) +
  scale_shape_manual(values=c(21, 24)) + theme_bw() +
  labs(x = "NMDS1", y = "NMDS2", fill = "habitat") +
  theme_trawls +
  cowplot::panel_border("black", 1) +
  coord_cartesian(clip = "off") +
  guides(fill=guide_legend(override.aes=list(shape=21)))
```


PERMANOVA

SIMPER