

## ENSO

```
density <- arrow::read_feather(here::here("data", "tidy", "Density.feather")) %>%
  dplyr::filter(!CommonName %in% c(
    "soupfin shark", 'rockfish spp.', "barred sand bass",
    'black croaker', 'broadnose sevengill shark',
    'calico rockfish, juvenile', 'clingfish spp.',
    "copper rockfish, all", "crevice kelpfish",
    'canary rockfish, juvenile', 'cusk eel spp.',
    "finescale triggerfish, adult", "goby spp.",
    "gunnel spp.", "halfbanded rockfish, adult",
    "horn shark", "kelp greenling, adult",
    "kelp greenling, female", "kelp greenling, juvenile",
    "kelp greenling, male", "leopard shark",
    "monkeyface pricklyback", "northern anchovy", "northern ronquil",
    "ocean sunfish", "onespot fringehead", "orangethroat pikeblenny",
    "Pacific bonito", "plain cardinalfish", "plainfin midshipman",
    "pricklyback spp.", "rockfish spp., adult", "rosy rockfish, juvenile",
    "sailfin sculpin", "sanddab spp.", "sarcastic fringehead",
    "    bocaccio, adult", "brown rockfish, juvenile", "California halibut",
    "halfmoon, juvenile", "splitnose rockfish, juvenile", "spotfin sculpin",
    "square-spot rockfish, juvenile", "swallowtail damselfish", "thornback ray",
    "top smelt, juvenile", "walleye surfperch", "white abalone",
    "white seabass", "zebra perch", "sargo", "surfperch spp.",
    "tubenose, juvenile", "wakame, adult", "wakame, juvenile",
    "wolf eel", "zebra goby", "baitfish unidentified",
    "bat ray", "spotted kelpfish", "garibaldi, subadult")) %>%
  dplyr::left_join(oni_yearly)
```

```
## Joining, by = "SurveyYear"
```

```
Results <- density %>%
  dplyr::group_by(CommonName) %>%
  dplyr::summarise(
    generics::tidy(
      stats::lm(Mean_Density ~ SST_Anom)
    ) %>%
  tidy::pivot_wider(names_from = term, values_from = estimate) %>%
  dplyr::mutate(beta_0 = lag(`(Intercept)`, n = 1)) %>%
  tidy::drop_na(SST_Anom, p.value) %>%
  dplyr::filter(p.value <= .05) %>%
  dplyr::arrange(p.value) %>%
  dplyr::mutate(statistic = round(statistic, 3),
    p.value = round(p.value, 3),
    p.value = ifelse(p.value < 0.001, "< 0.001", as.character(p.value)),
    `Predictor Variable` = "SST_Anom") %>%
  dplyr::rename(`Response Variable` = CommonName,
```

```

      beta_1 = SST_An timer) %>%
dplyr::select(`Response Variable`, `Predictor Variable`,
              beta_0, beta_1, std.error, statistic, p.value)

```

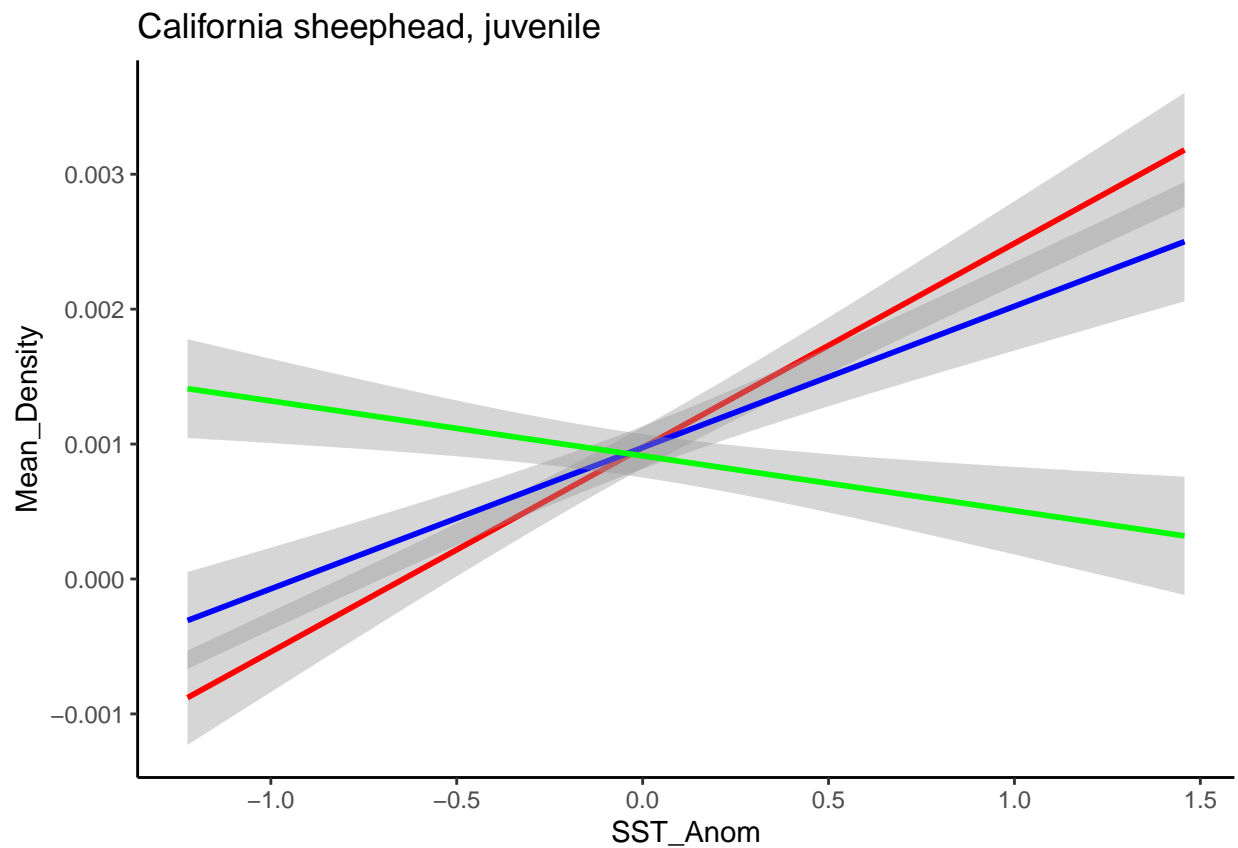
## 'summarise()' has grouped output by 'CommonName'. You can override using the '.groups' argument.

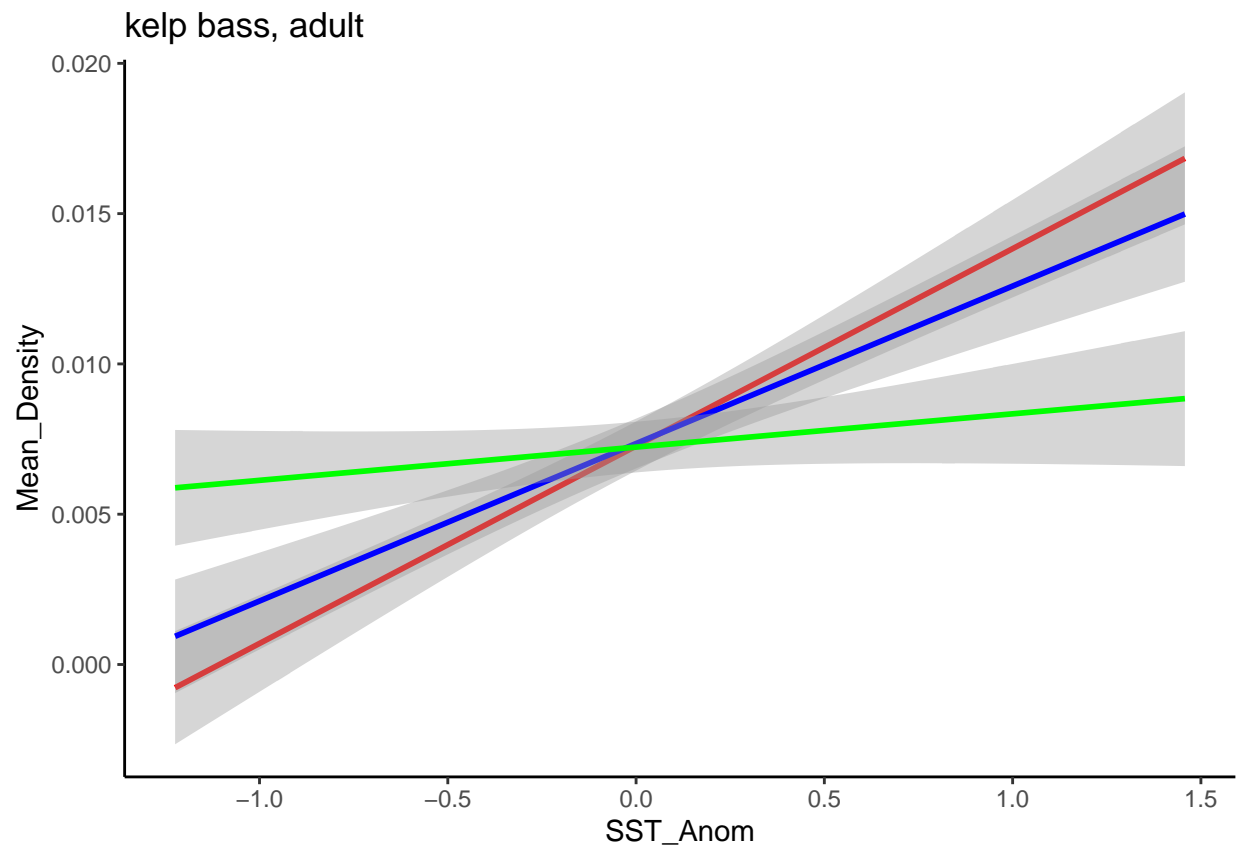
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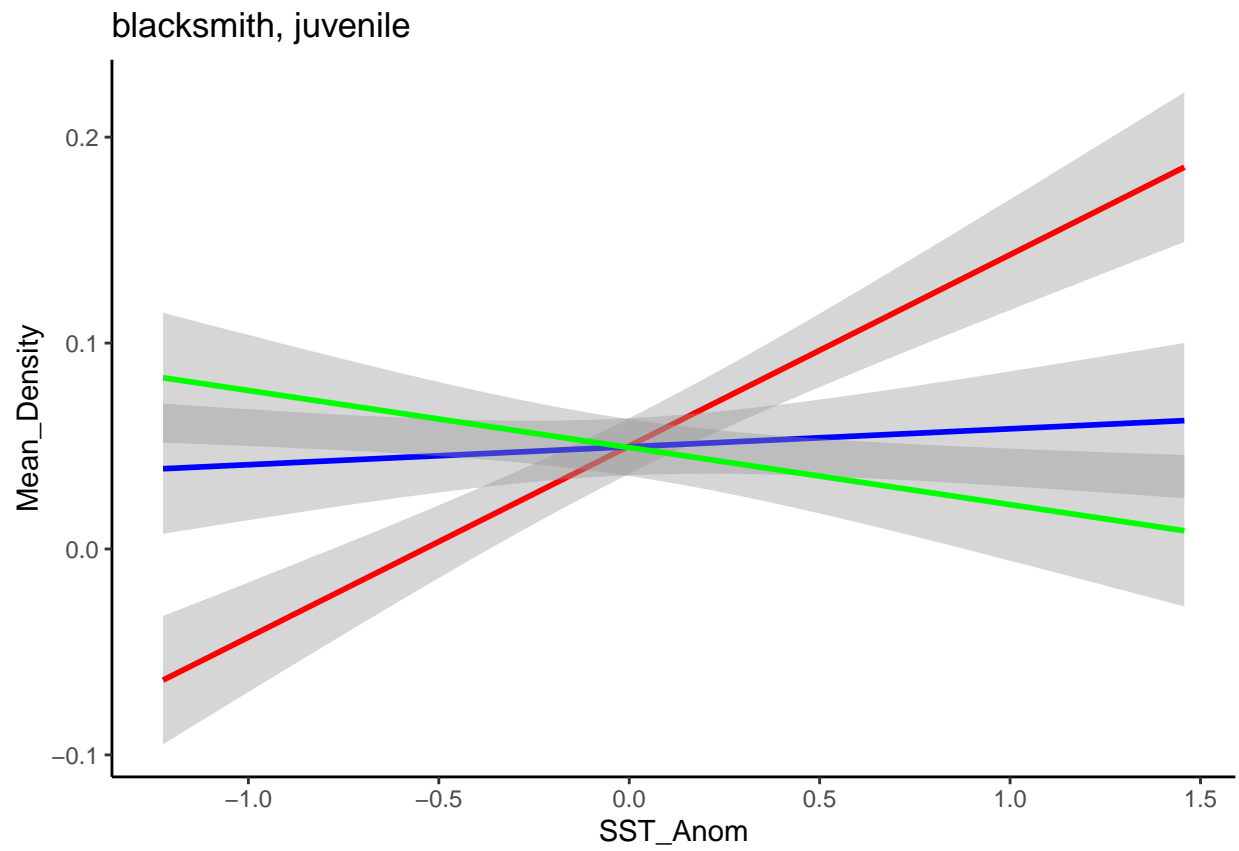
for (sp in unique(Results$`Response Variable`)) {
  p <- density %>%
    filter(CommonName == sp) %>%
    ggplot() +
      # geom_point() +
      geom_smooth(aes(y = Mean_Density, x = SST_An timer), method = lm, formula = "y~x", color = "red") +
      geom_smooth(aes(y = Mean_Density, x = SST_An timer_1), method = lm, formula = "y~x", color = "blue") +
      geom_smooth(aes(y = Mean_Density, x = SST_An timer_2), method = lm, formula = "y~x", color = "green") +
      labs(title = sp) +
      theme_classic()

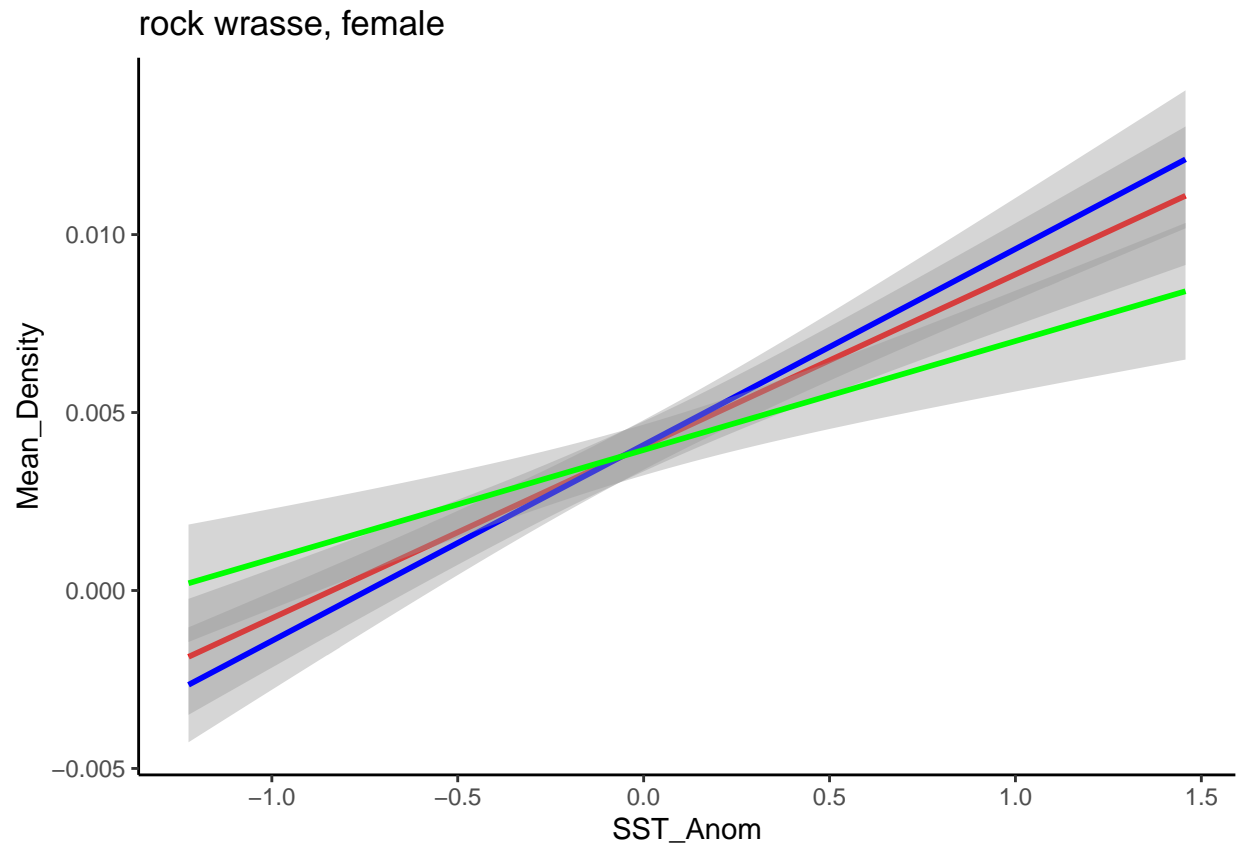
  print(p)
}

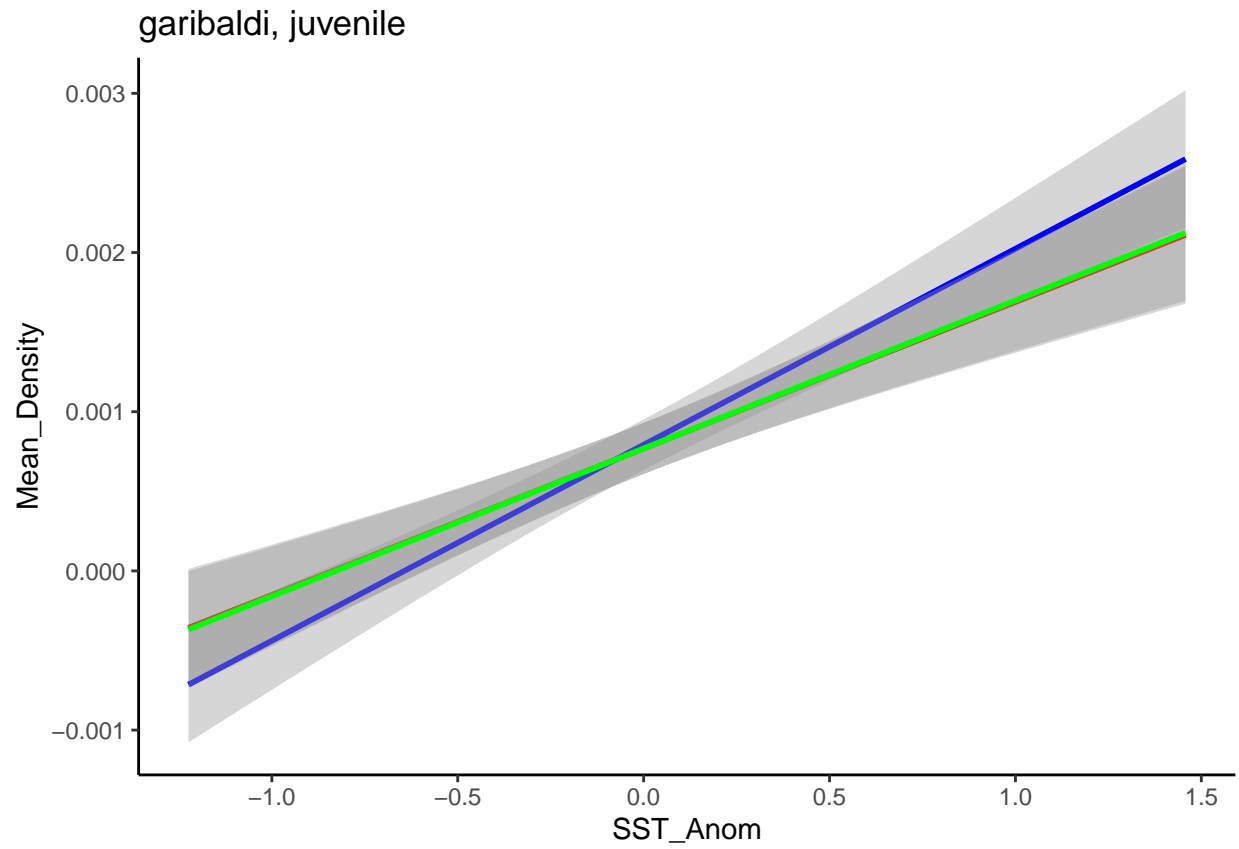
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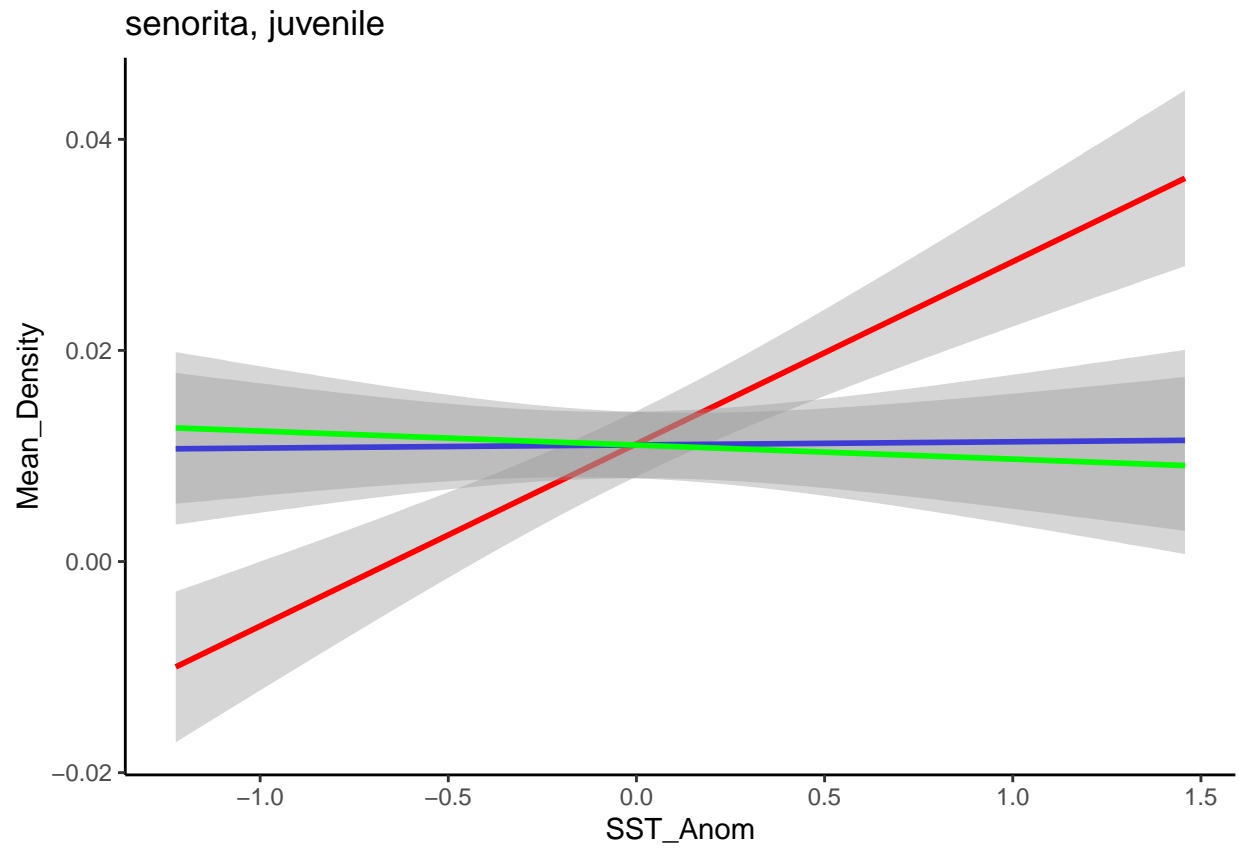


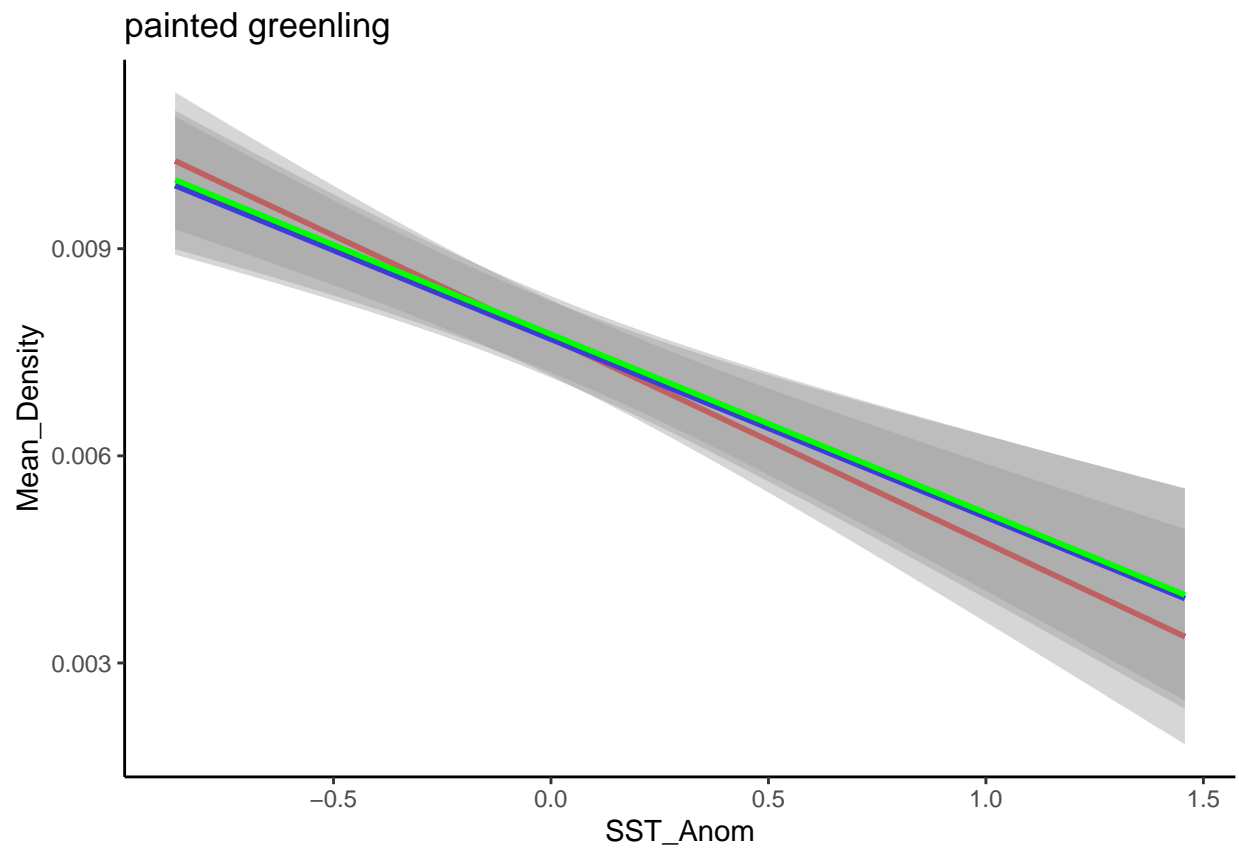




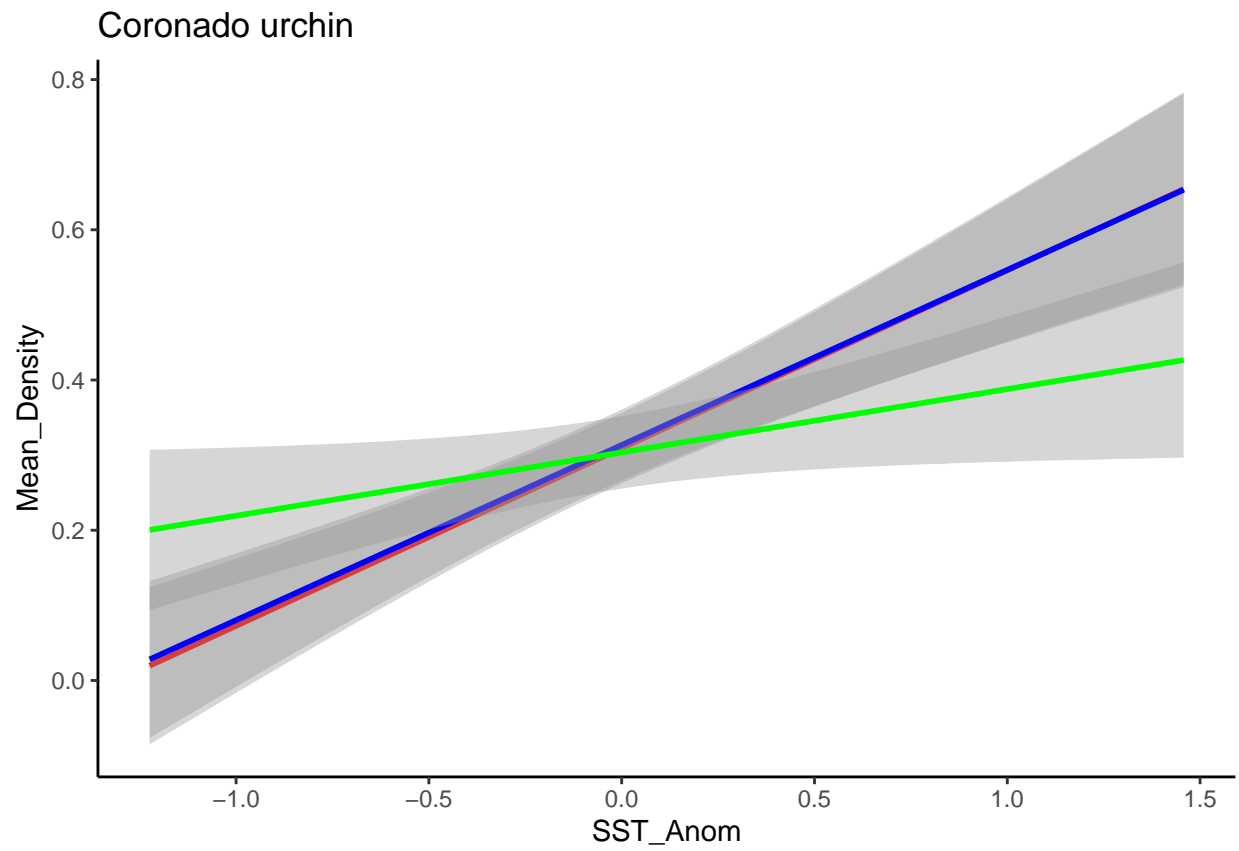


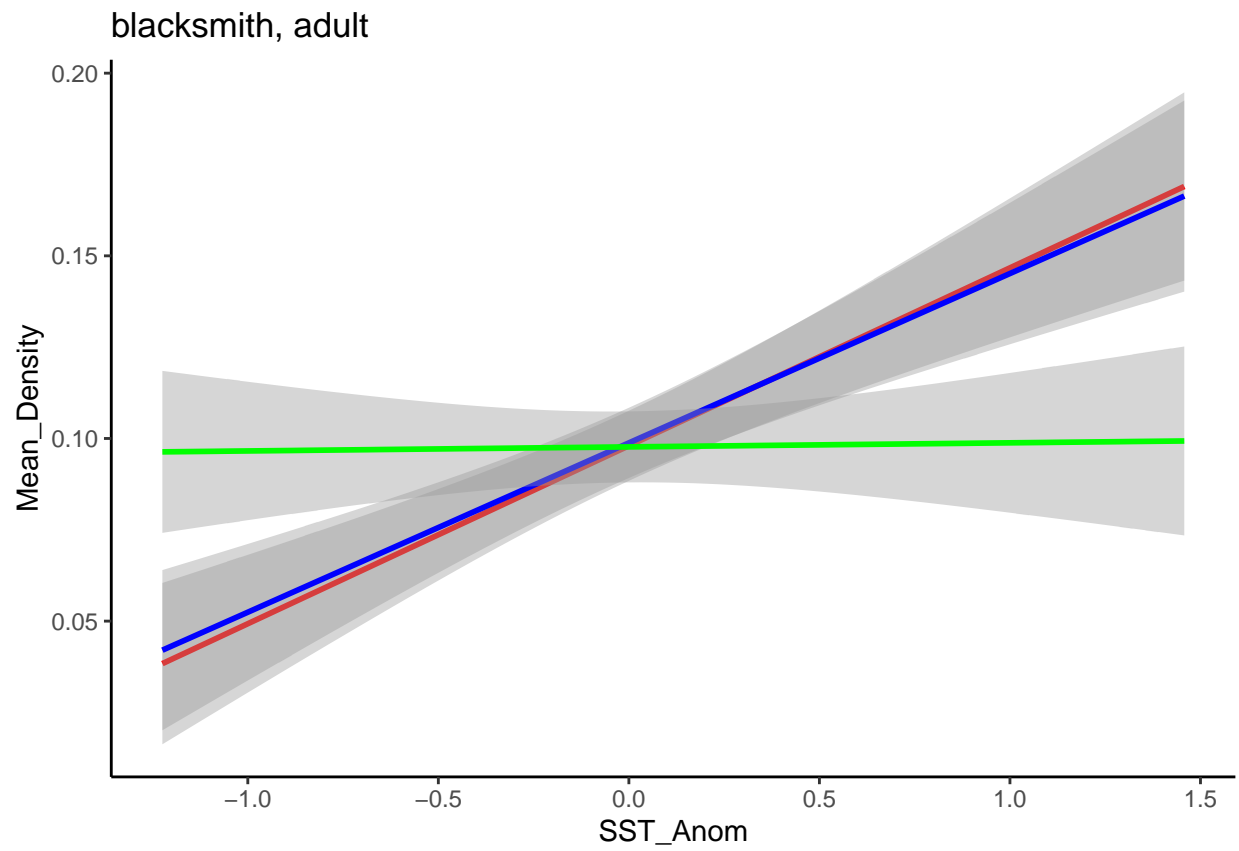


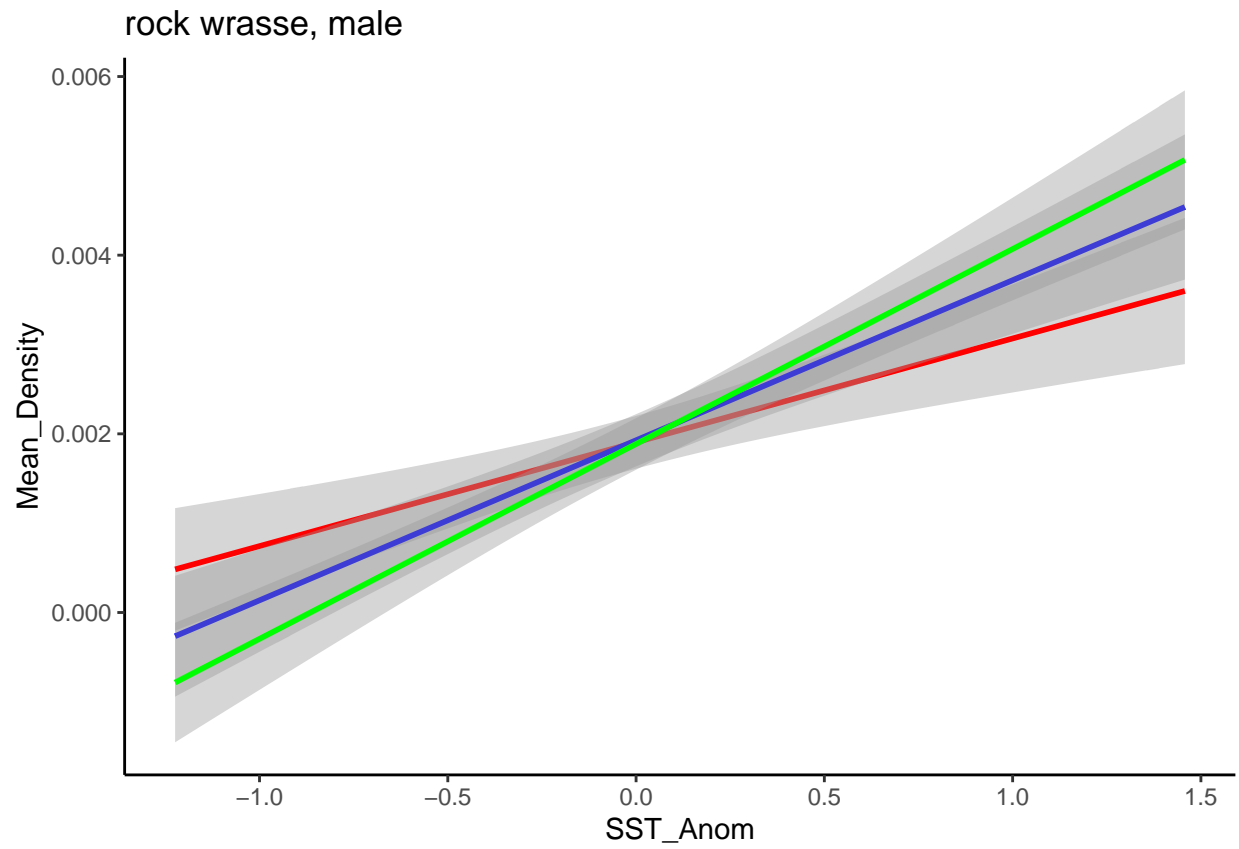


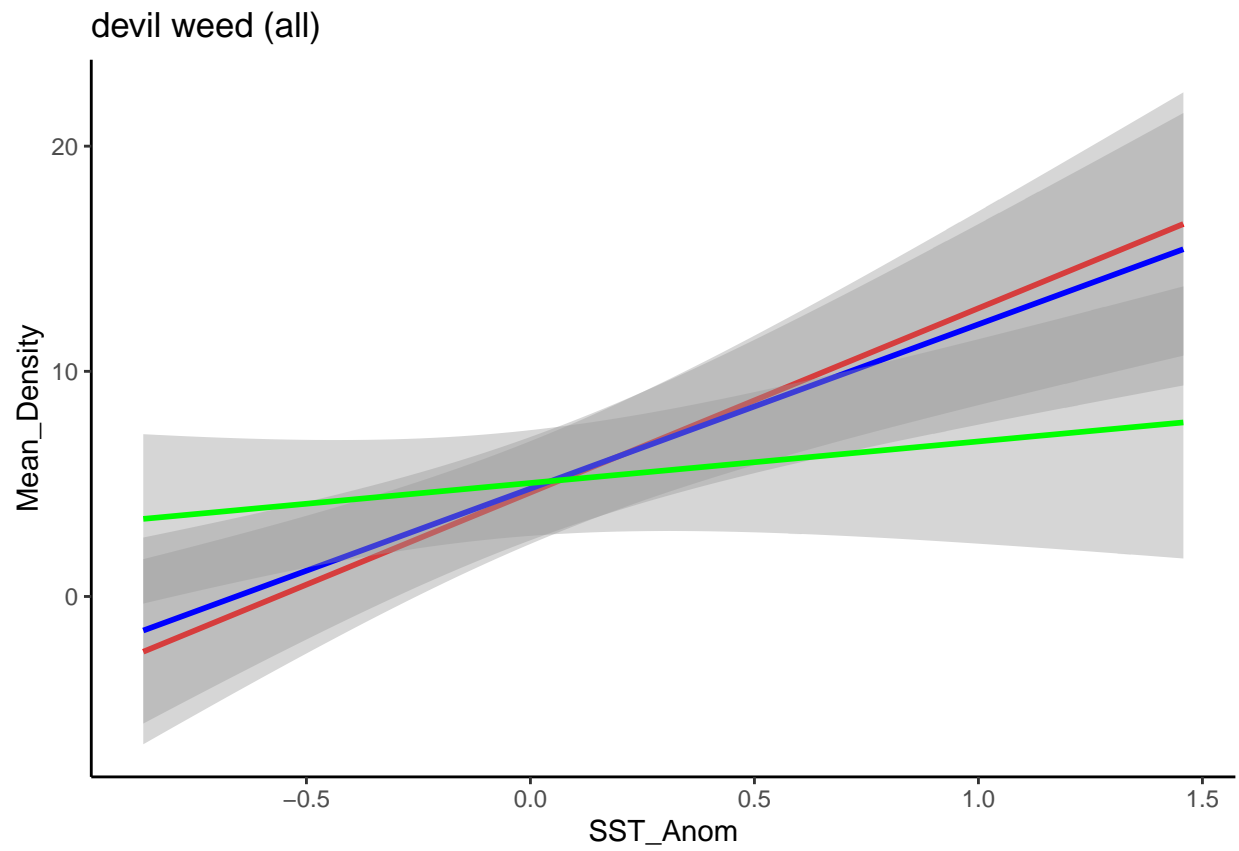


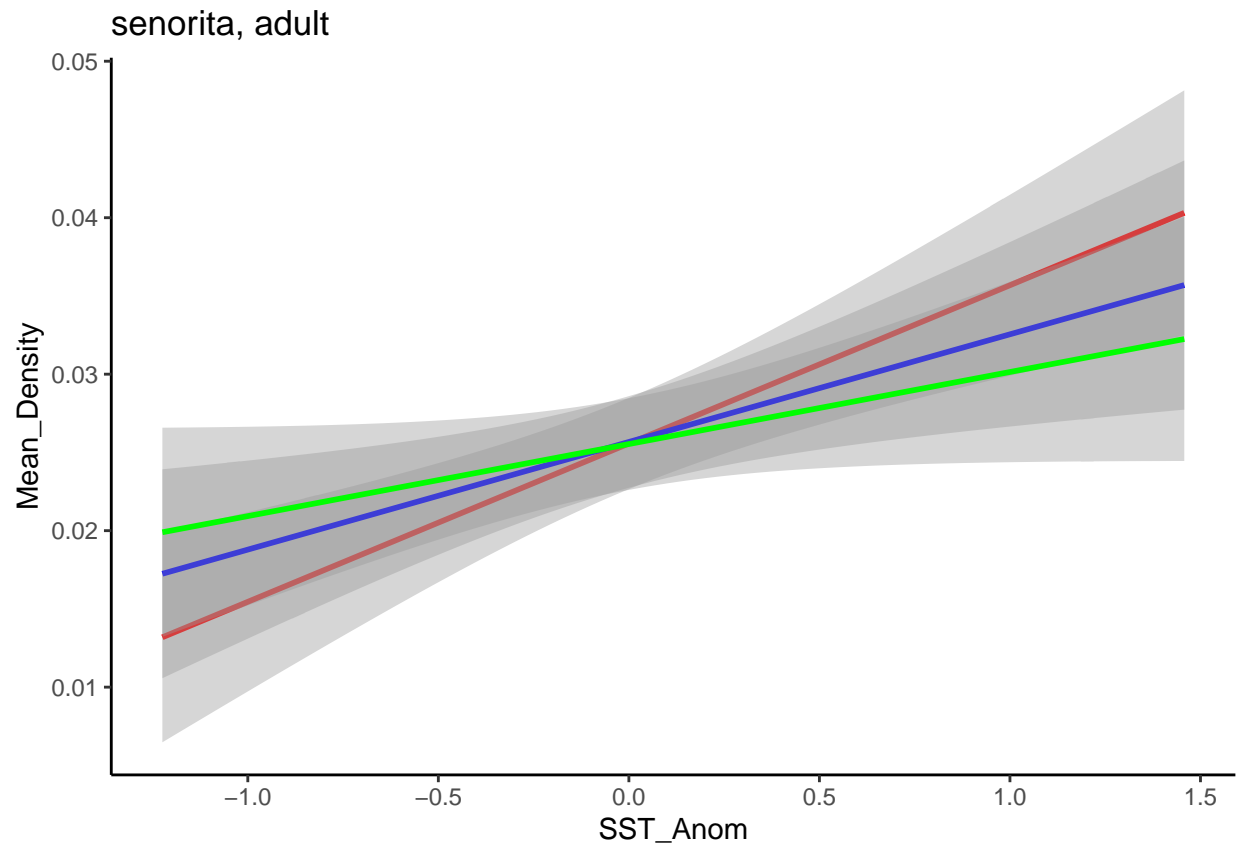


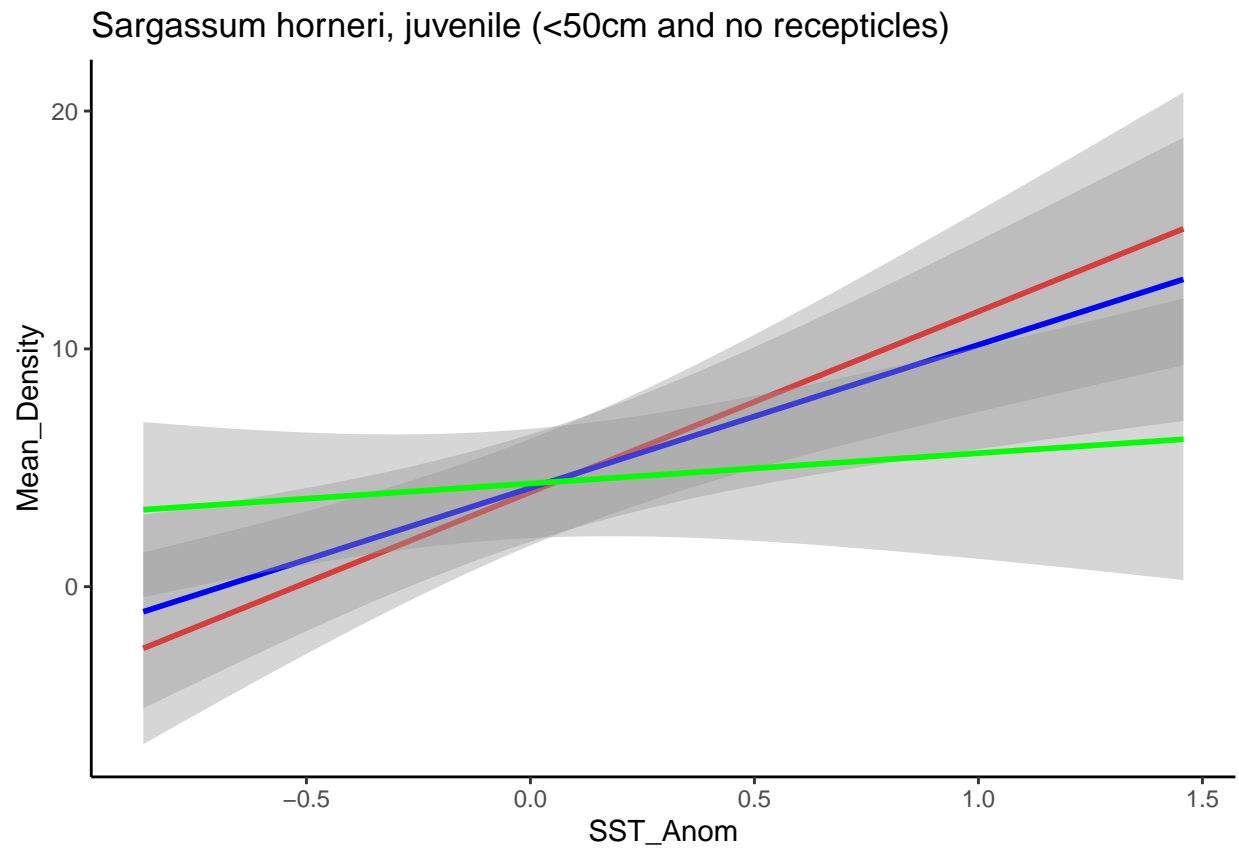


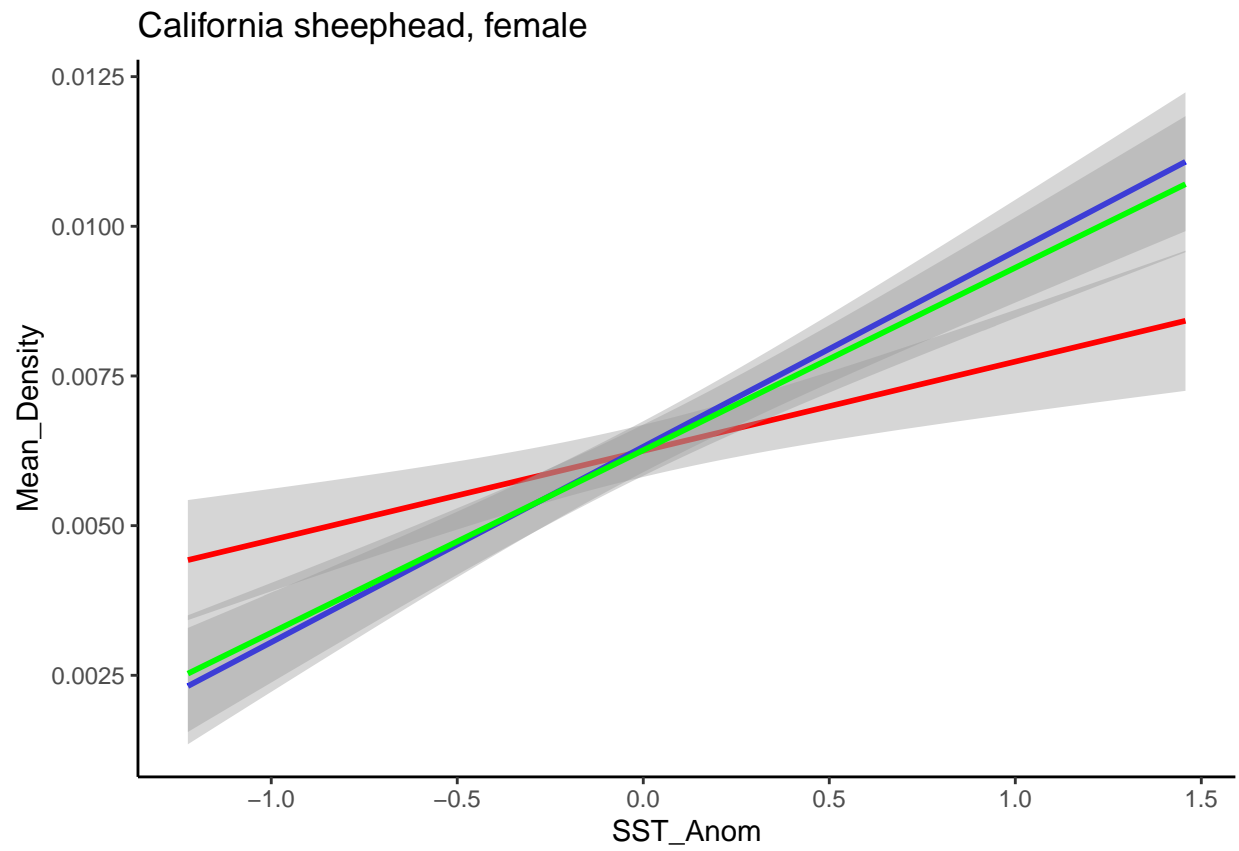


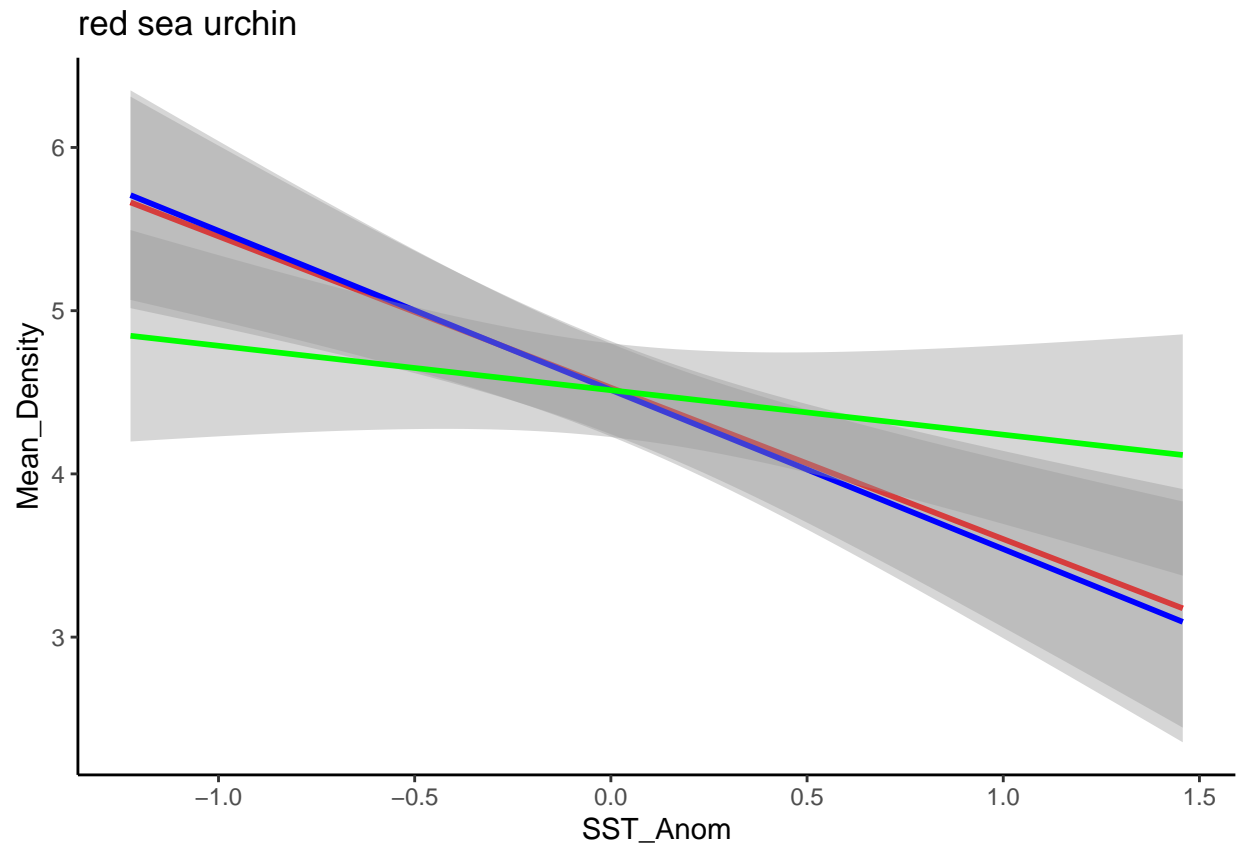




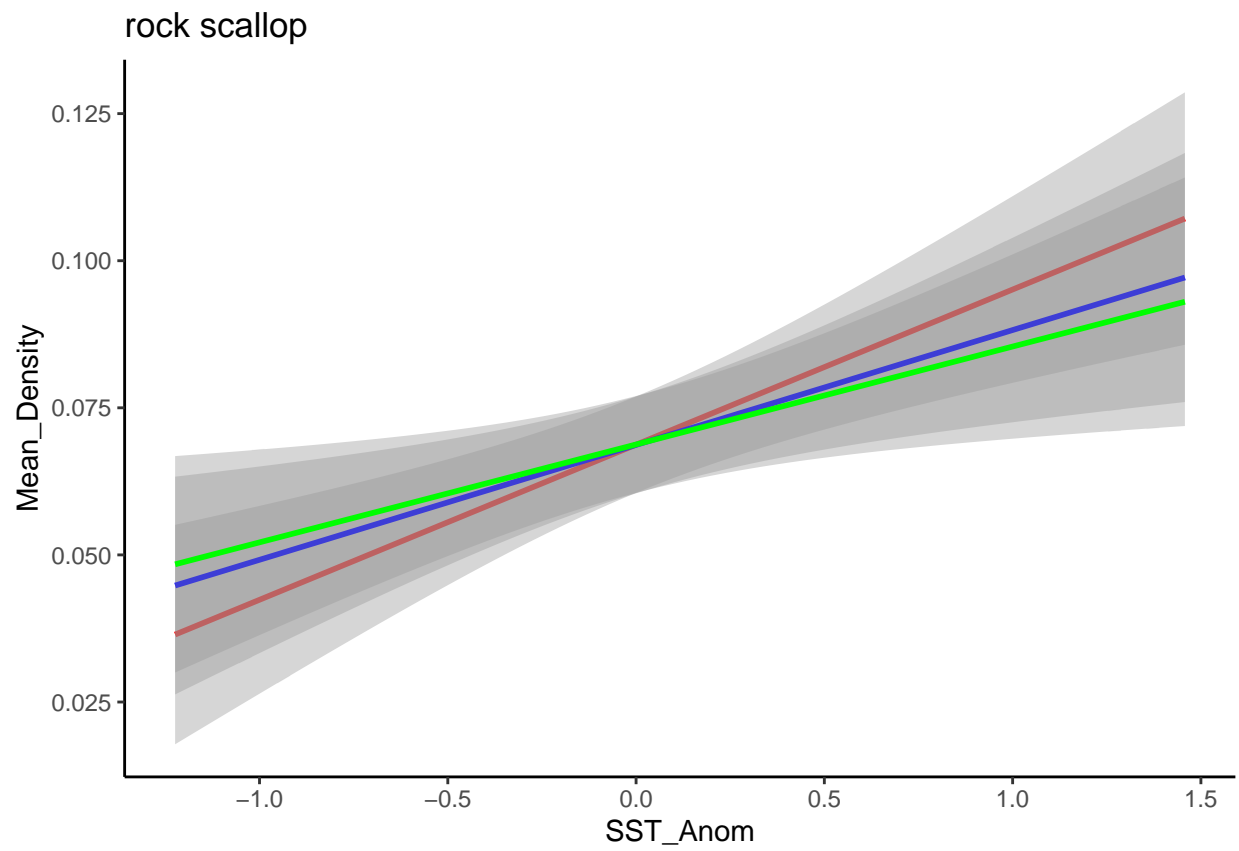


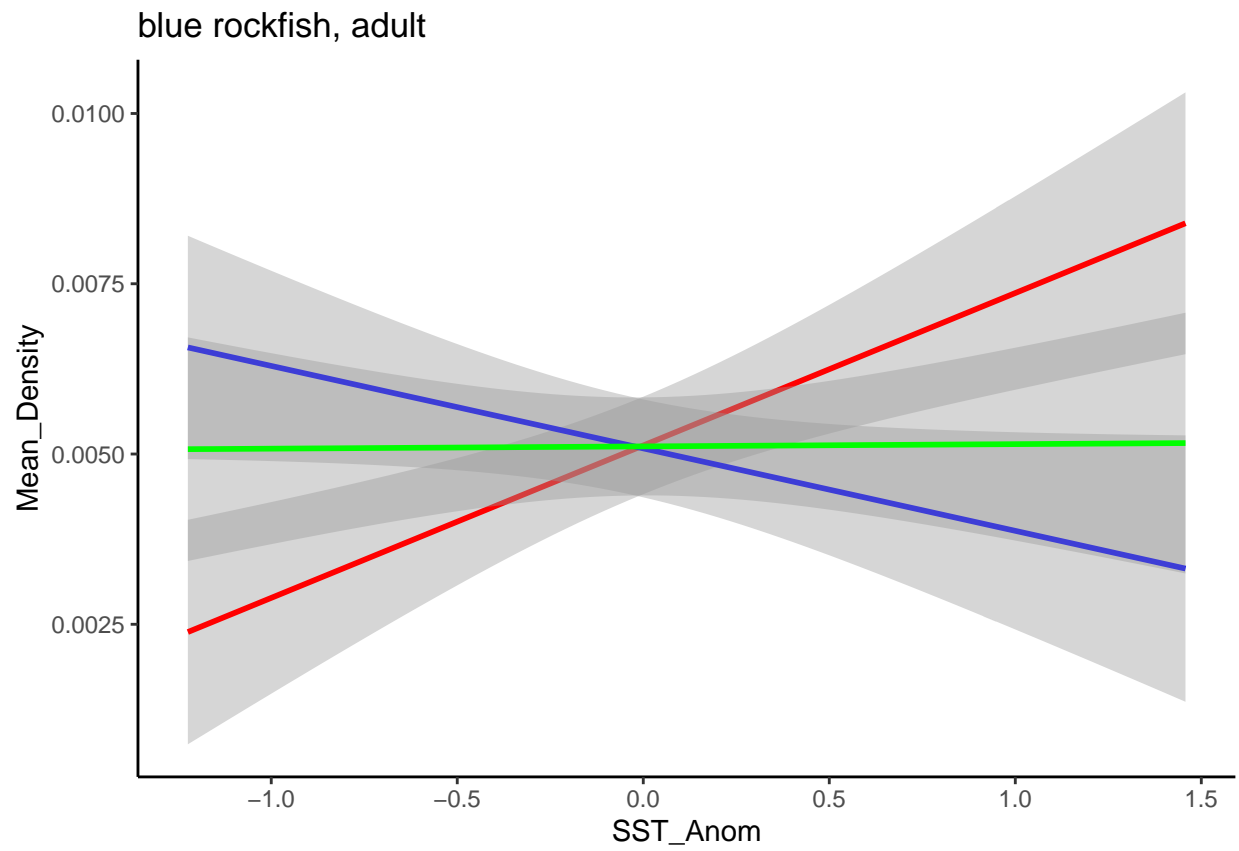


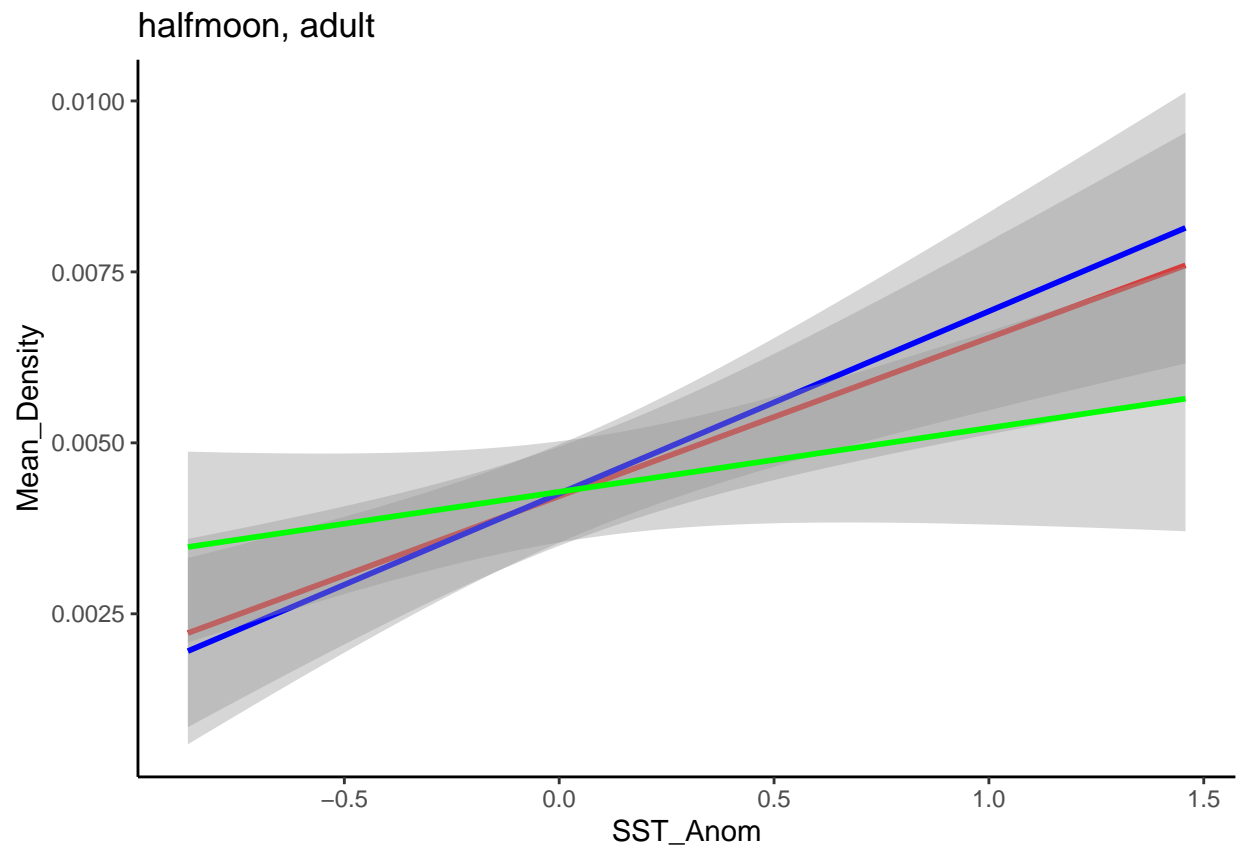


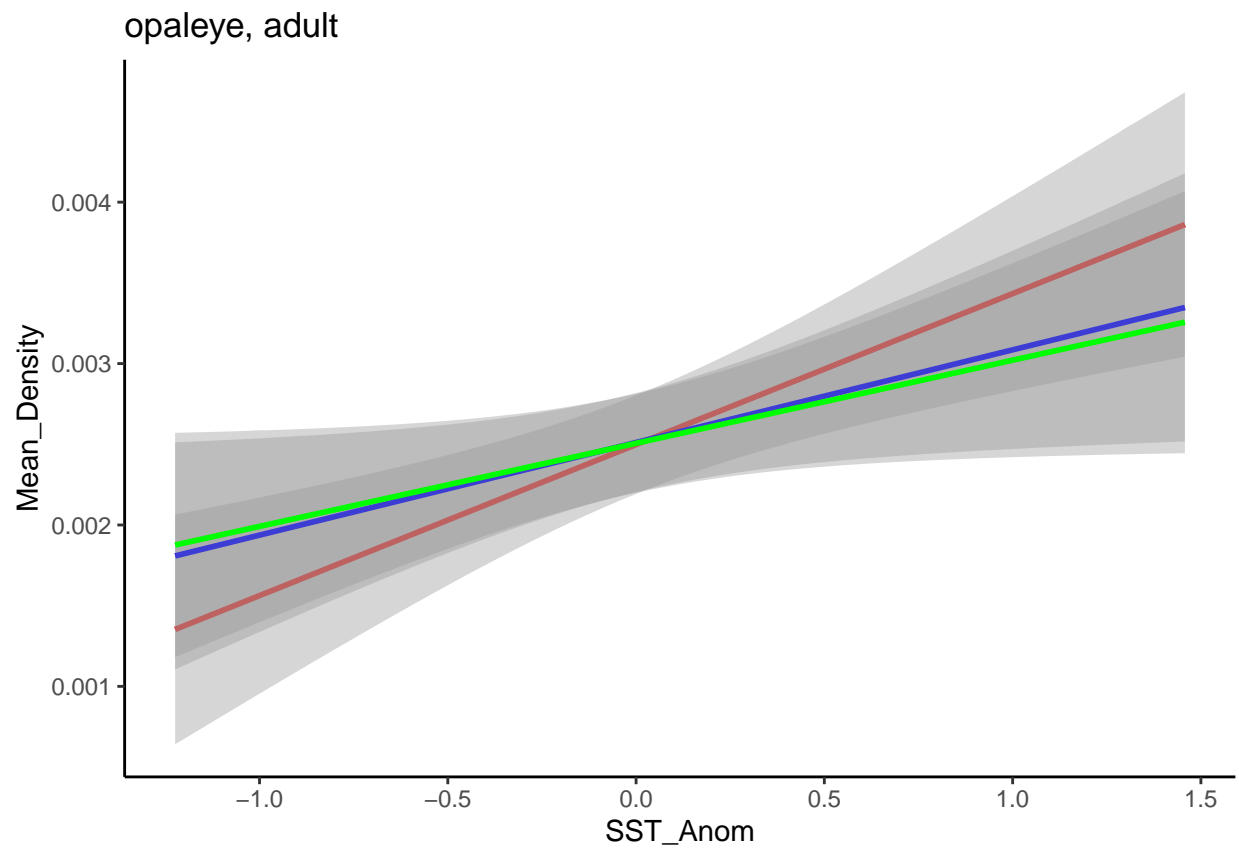


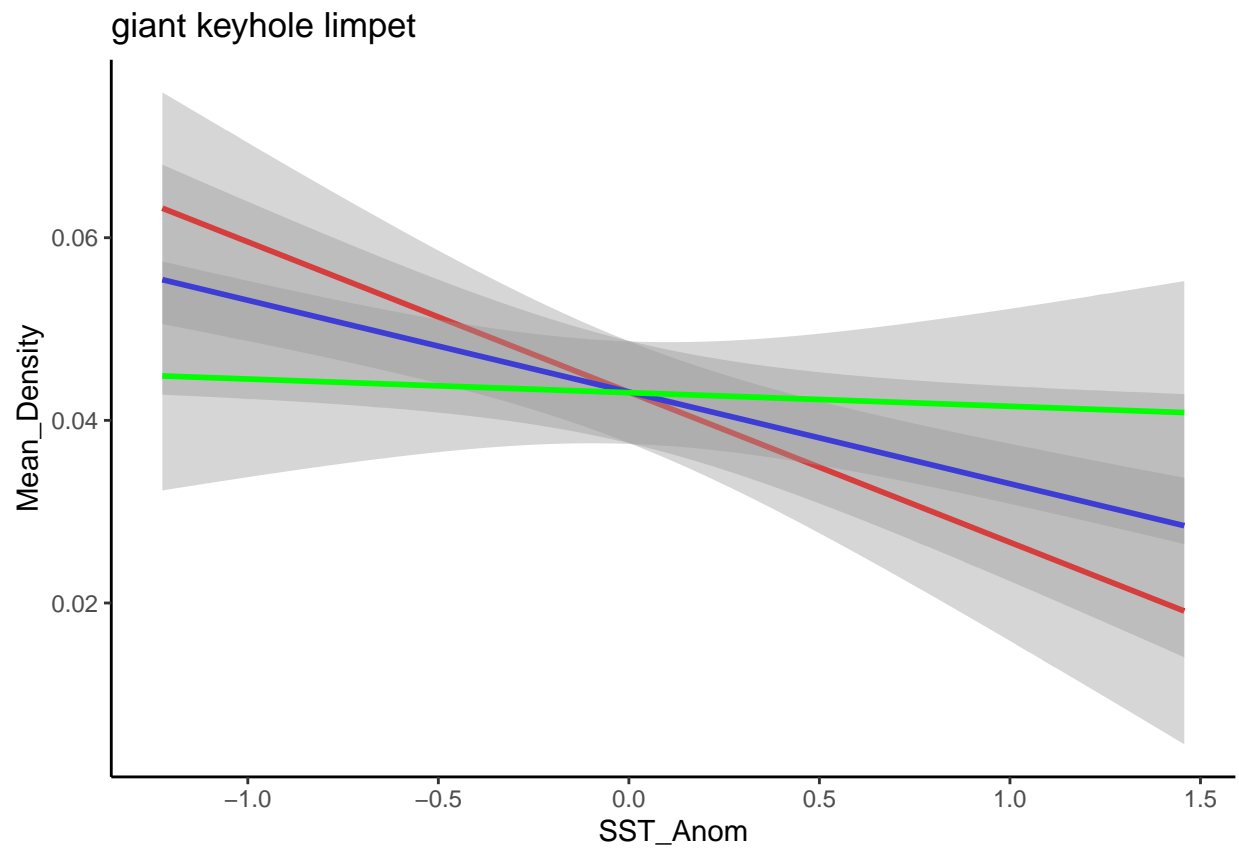


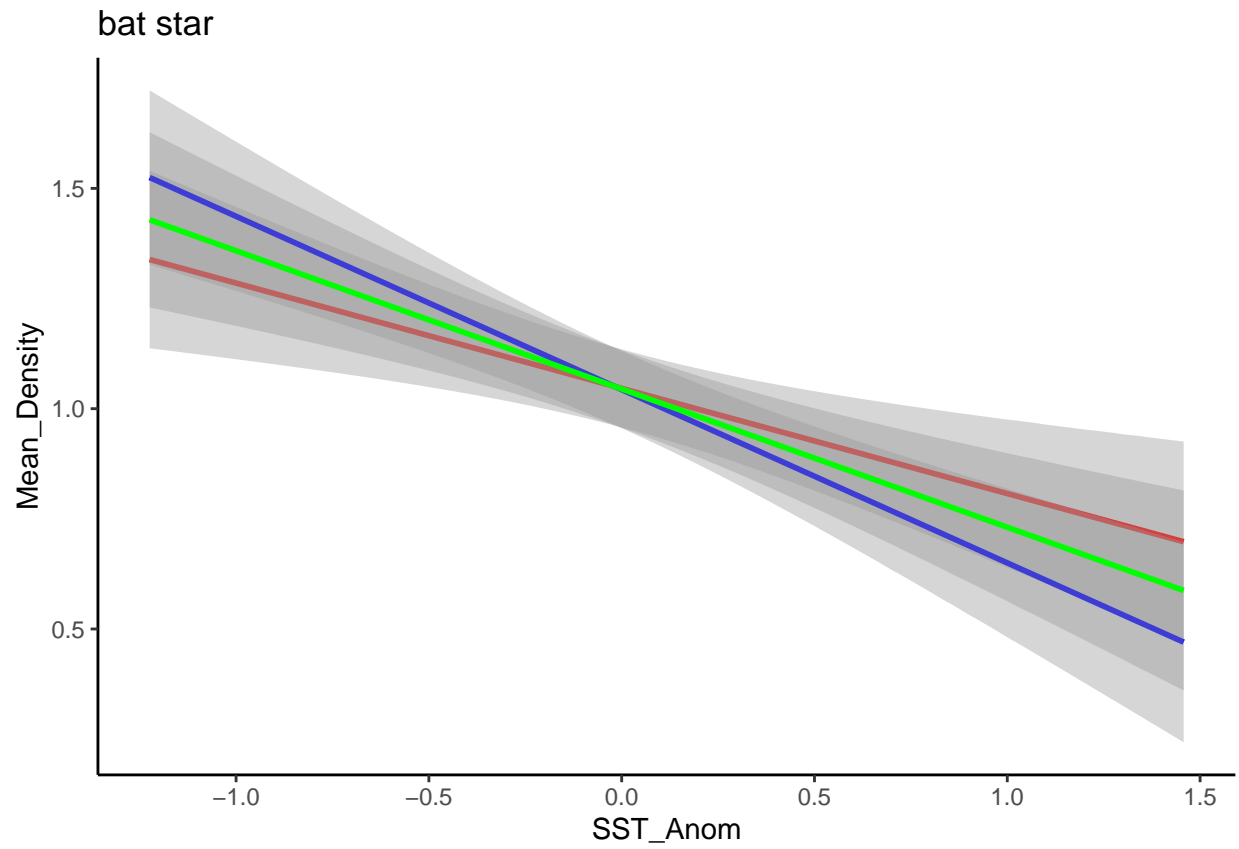


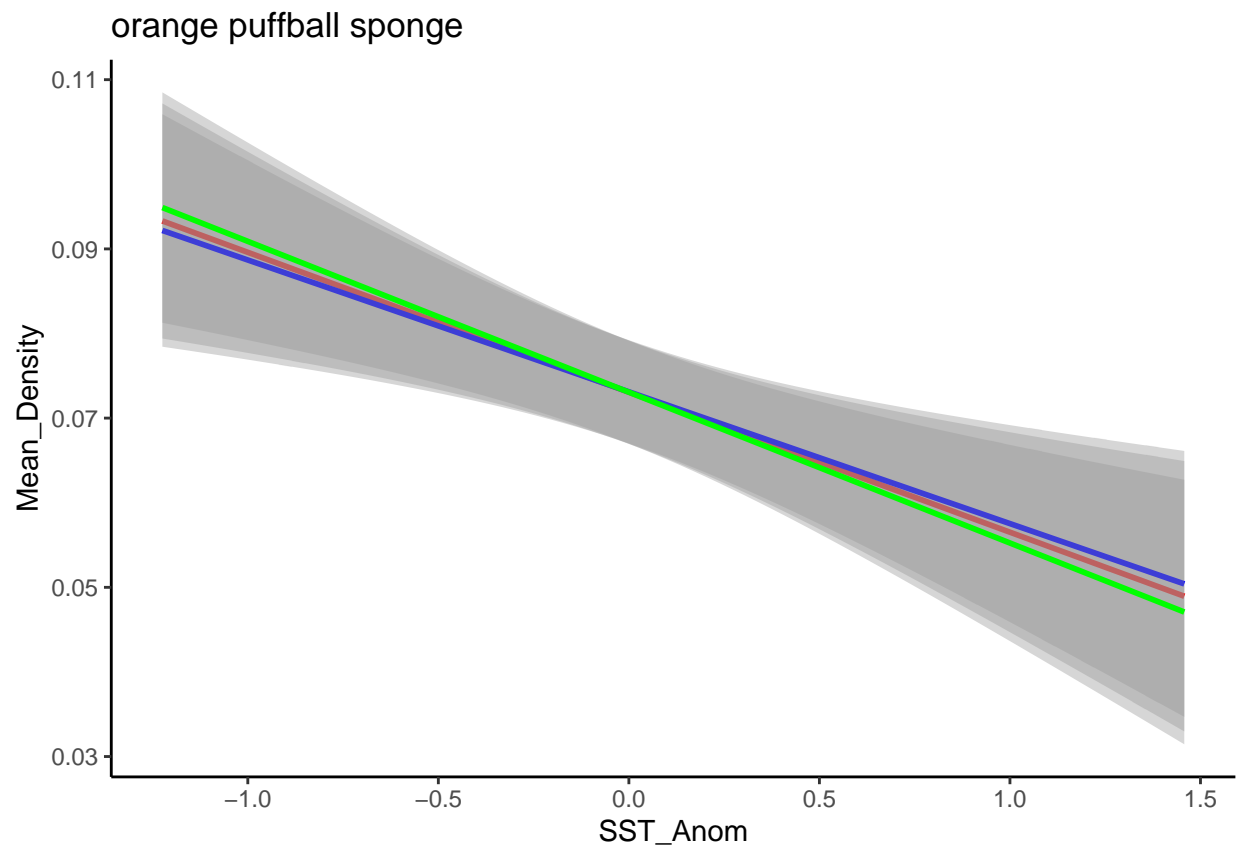


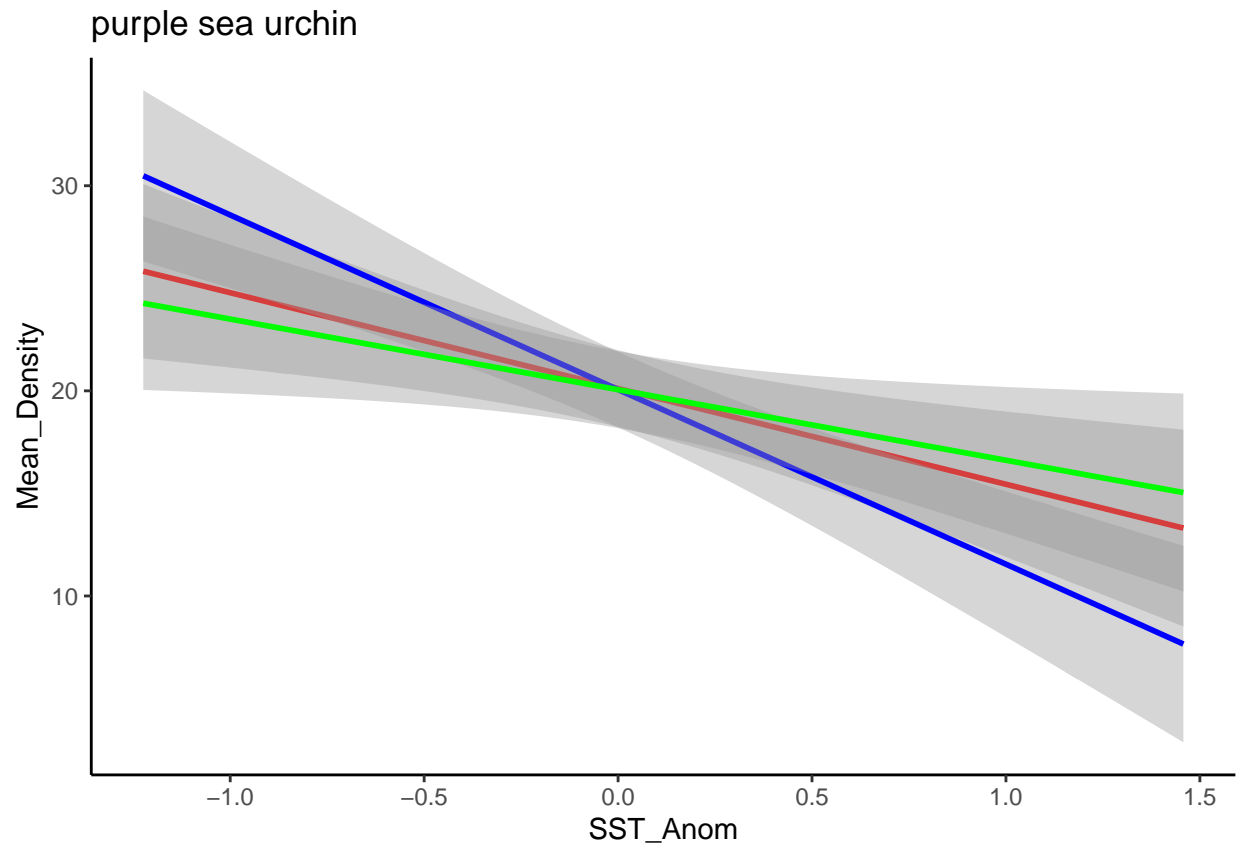




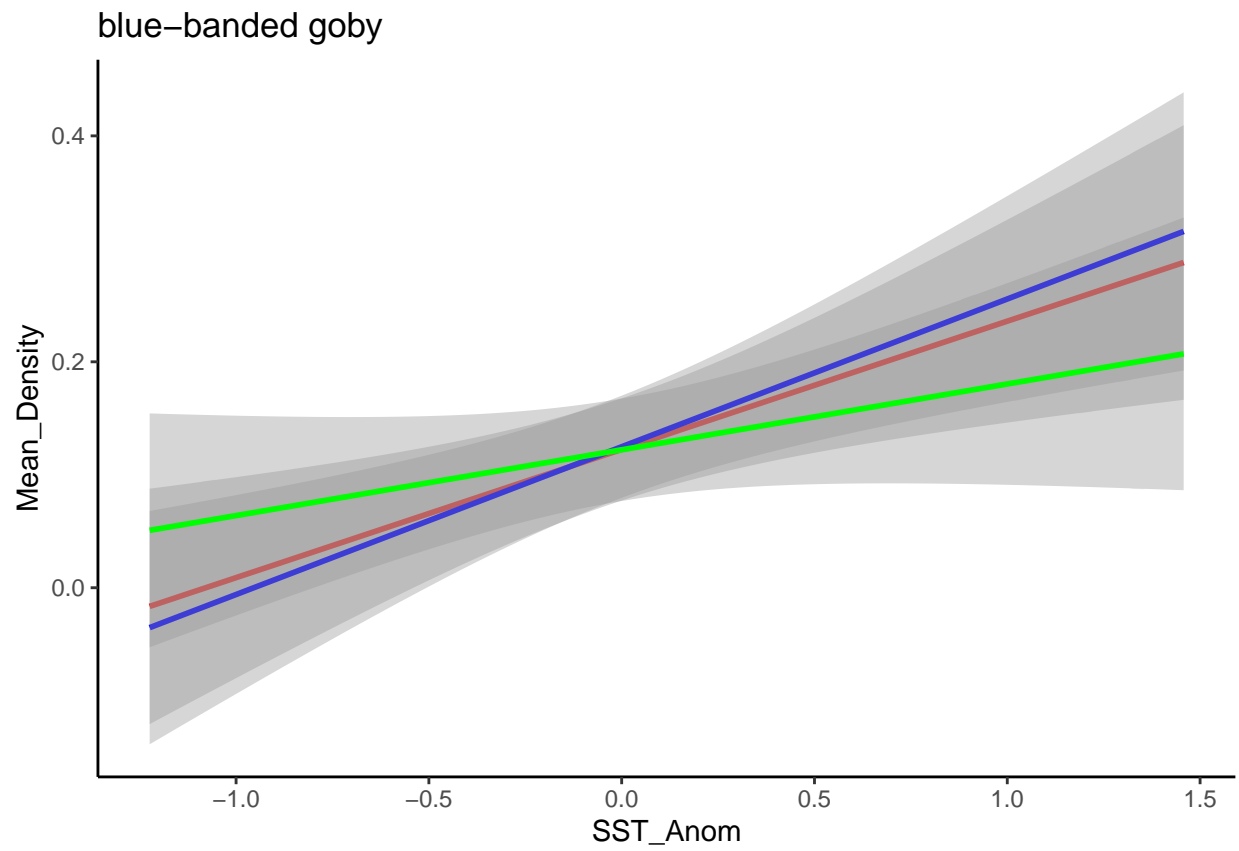


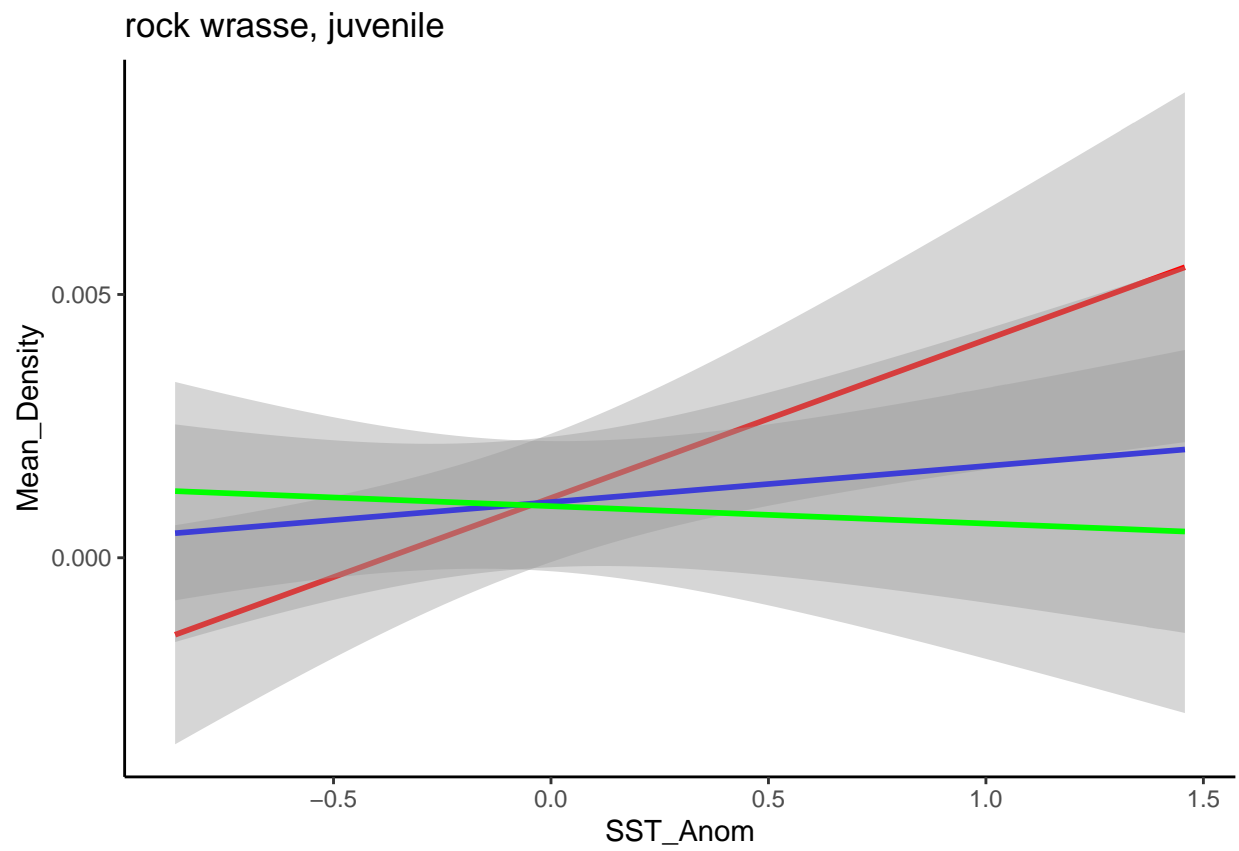


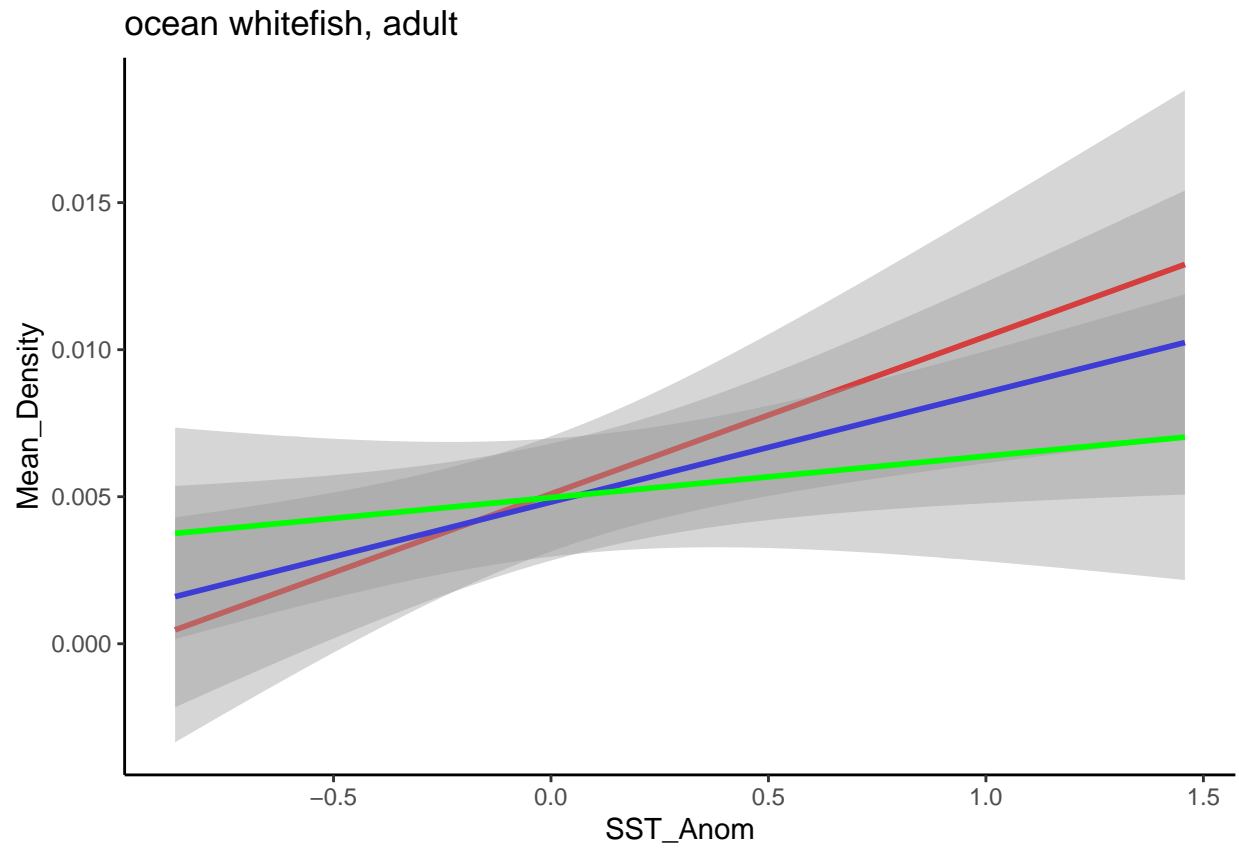


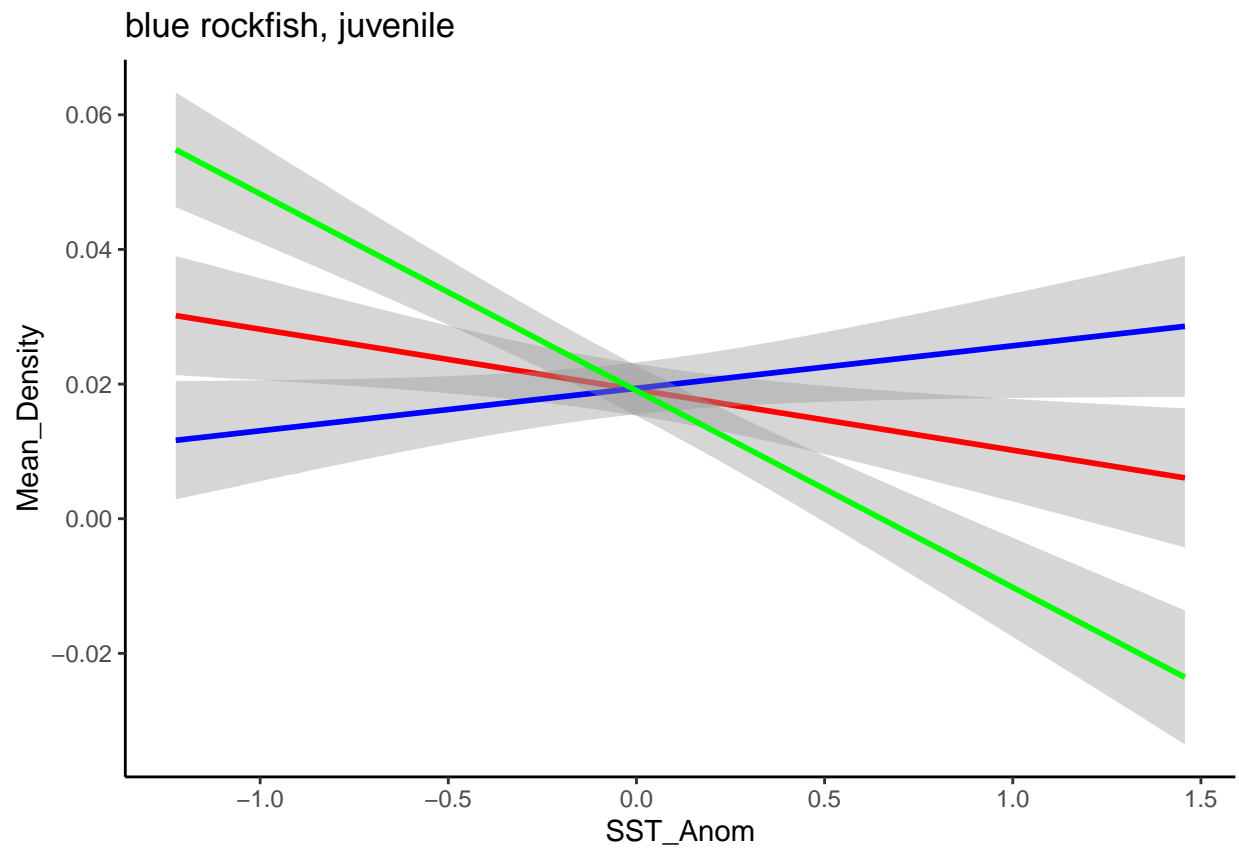


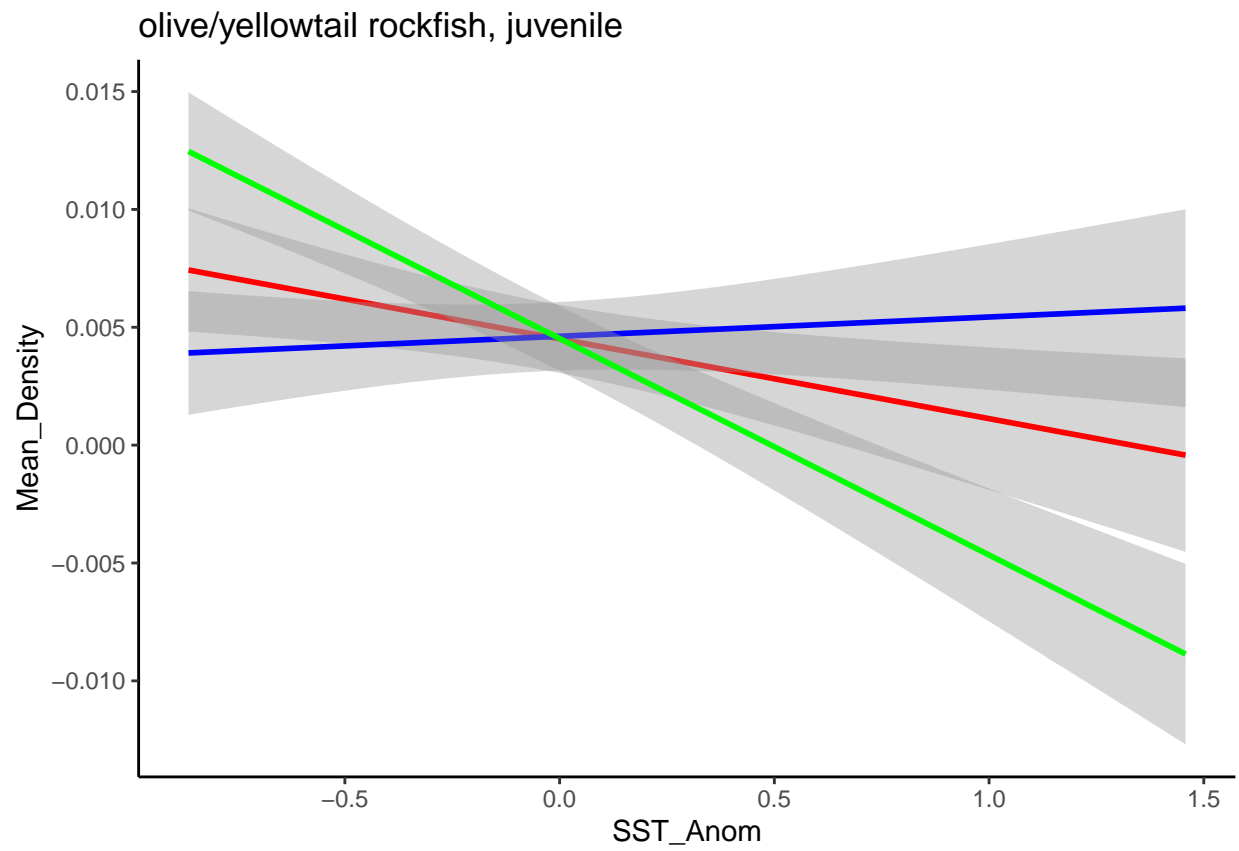


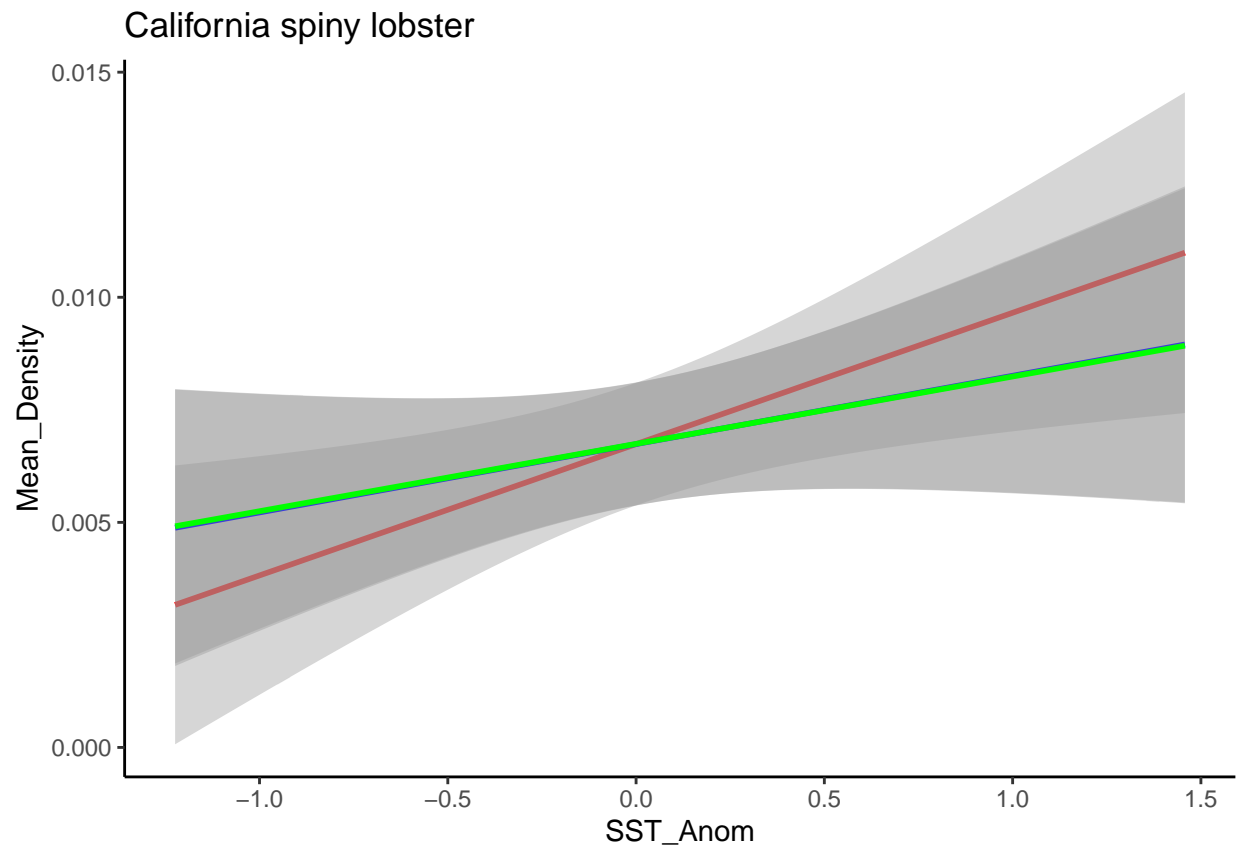


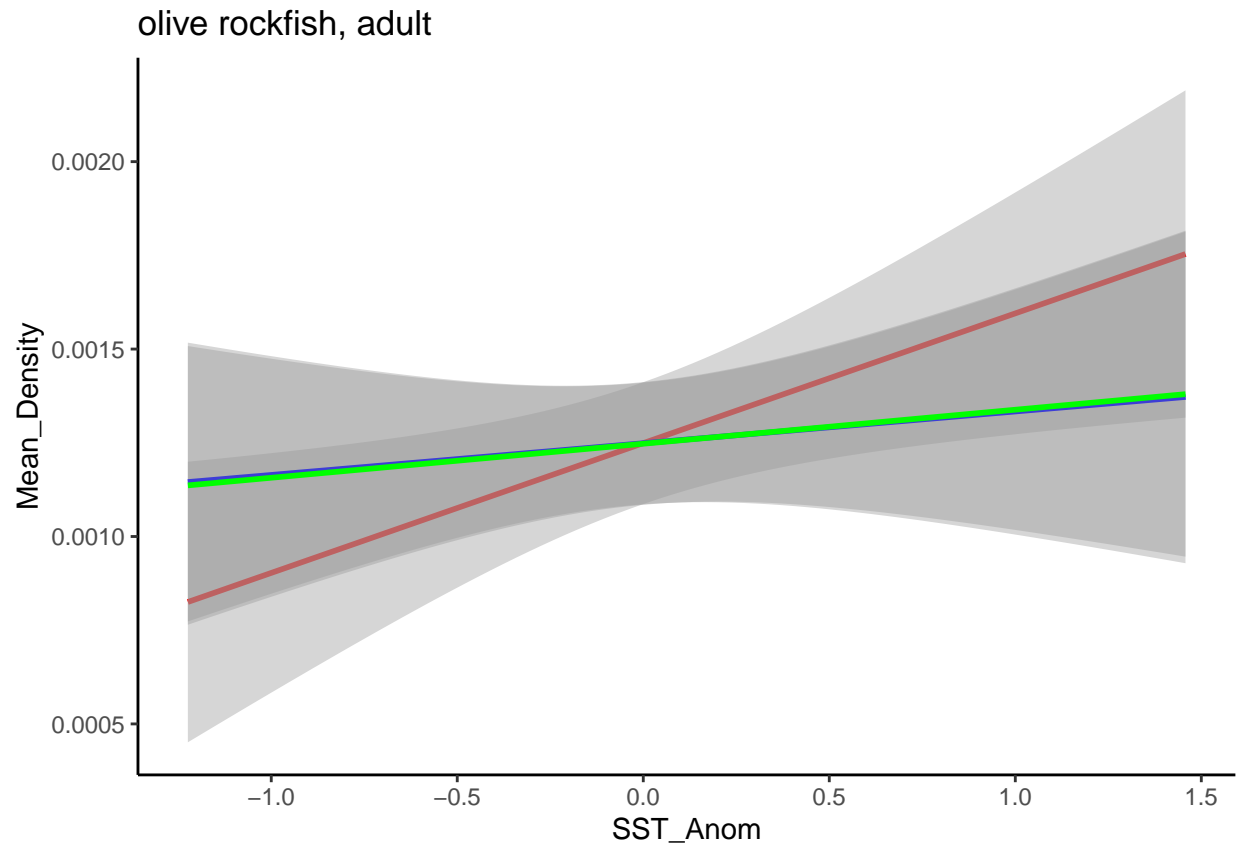


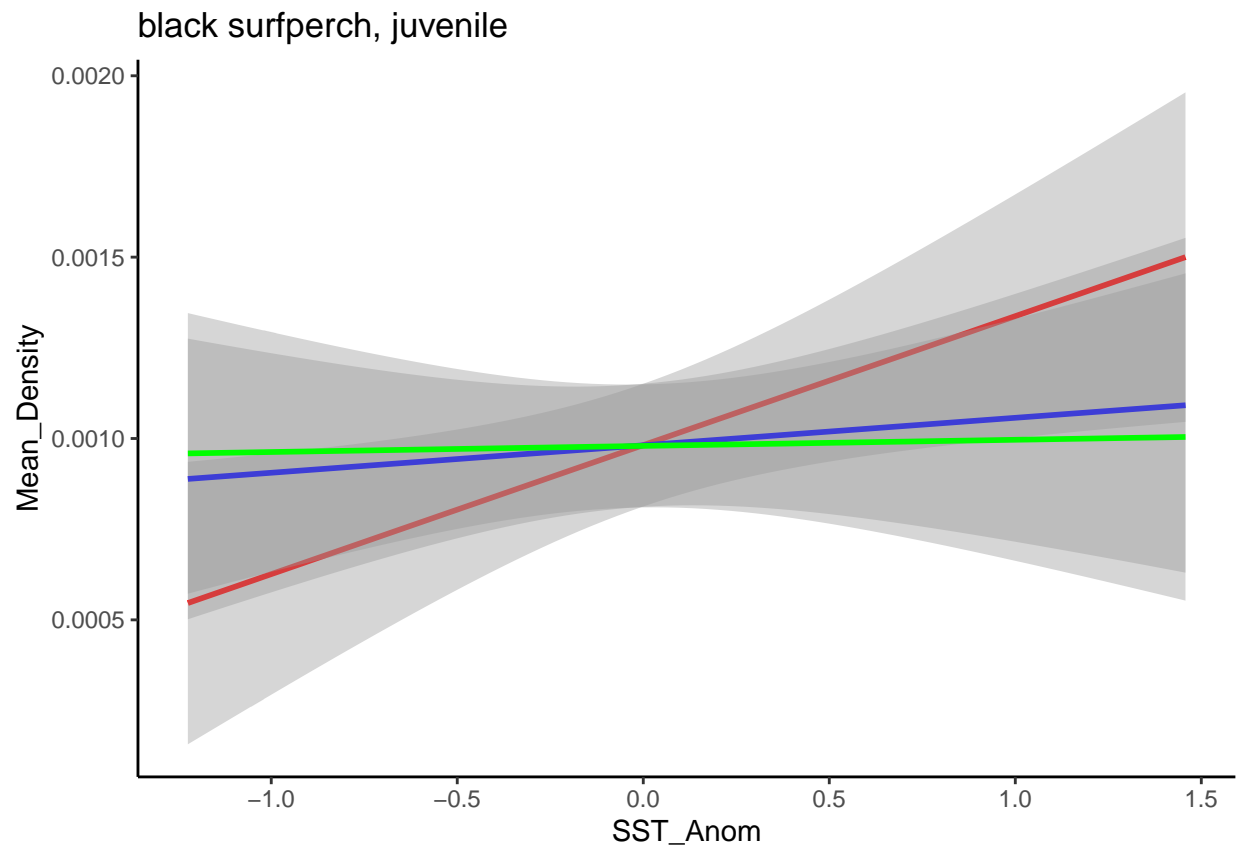




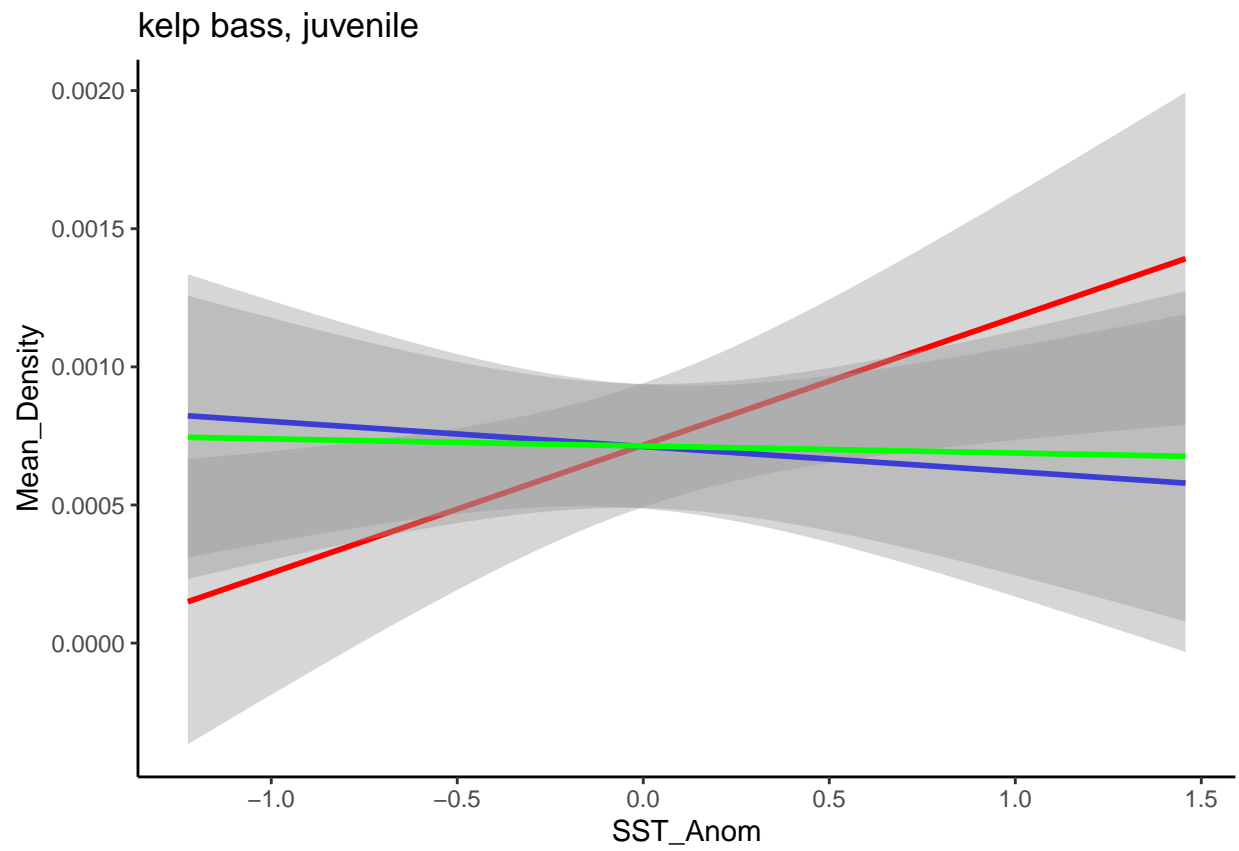


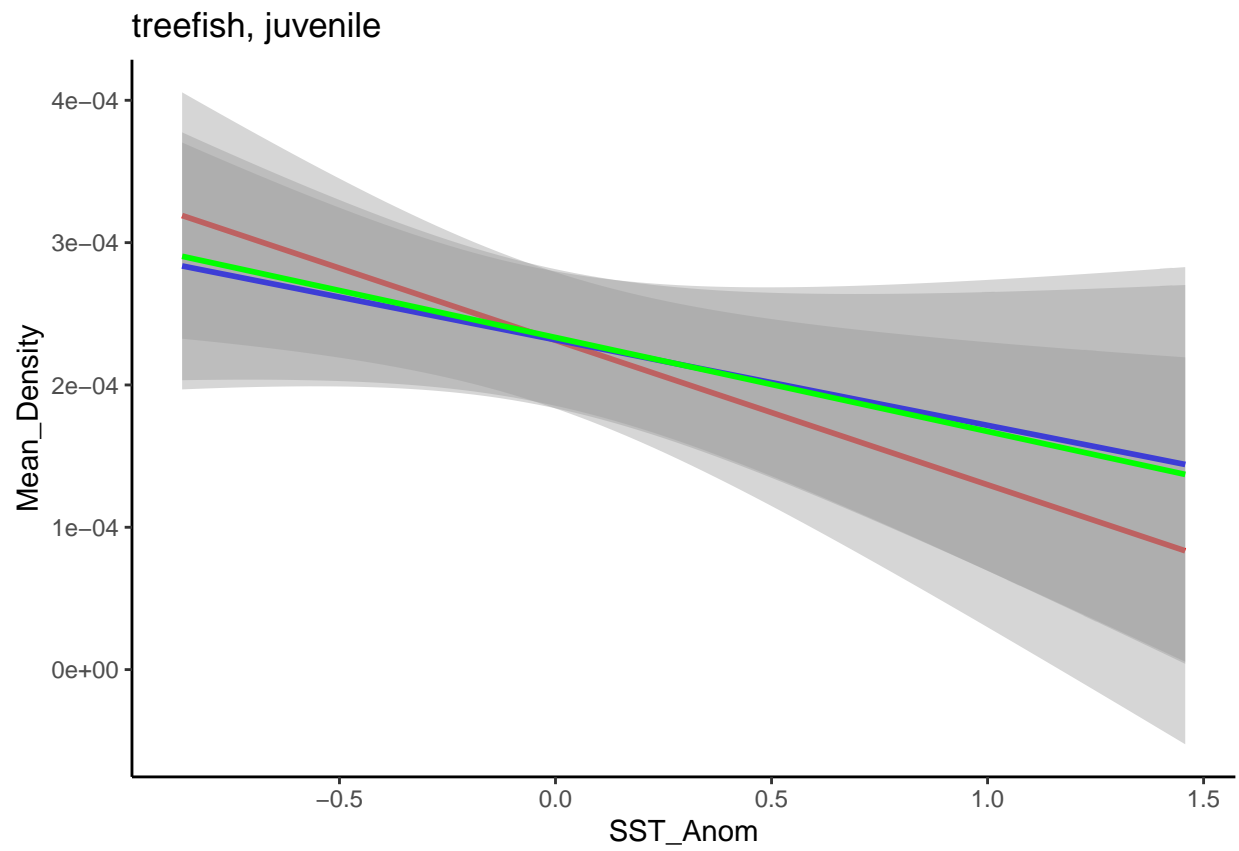


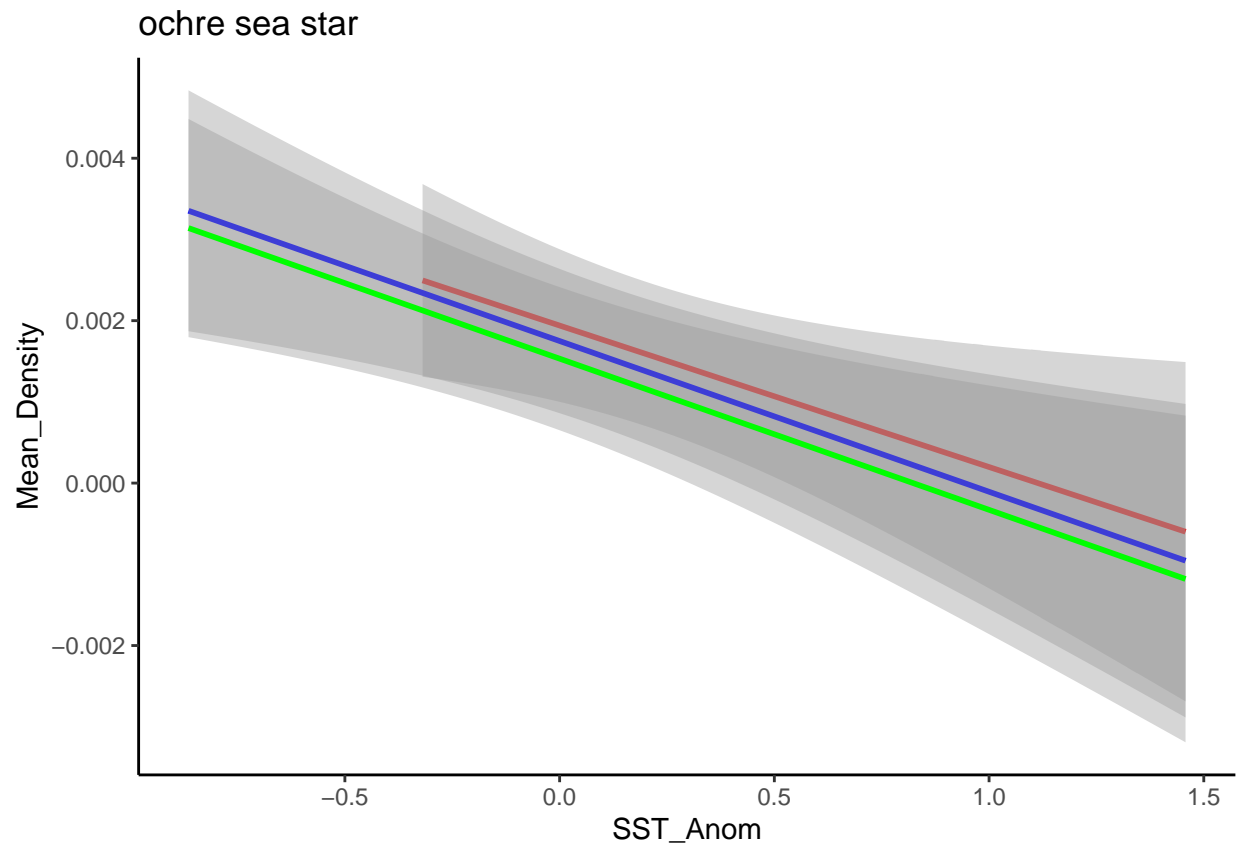


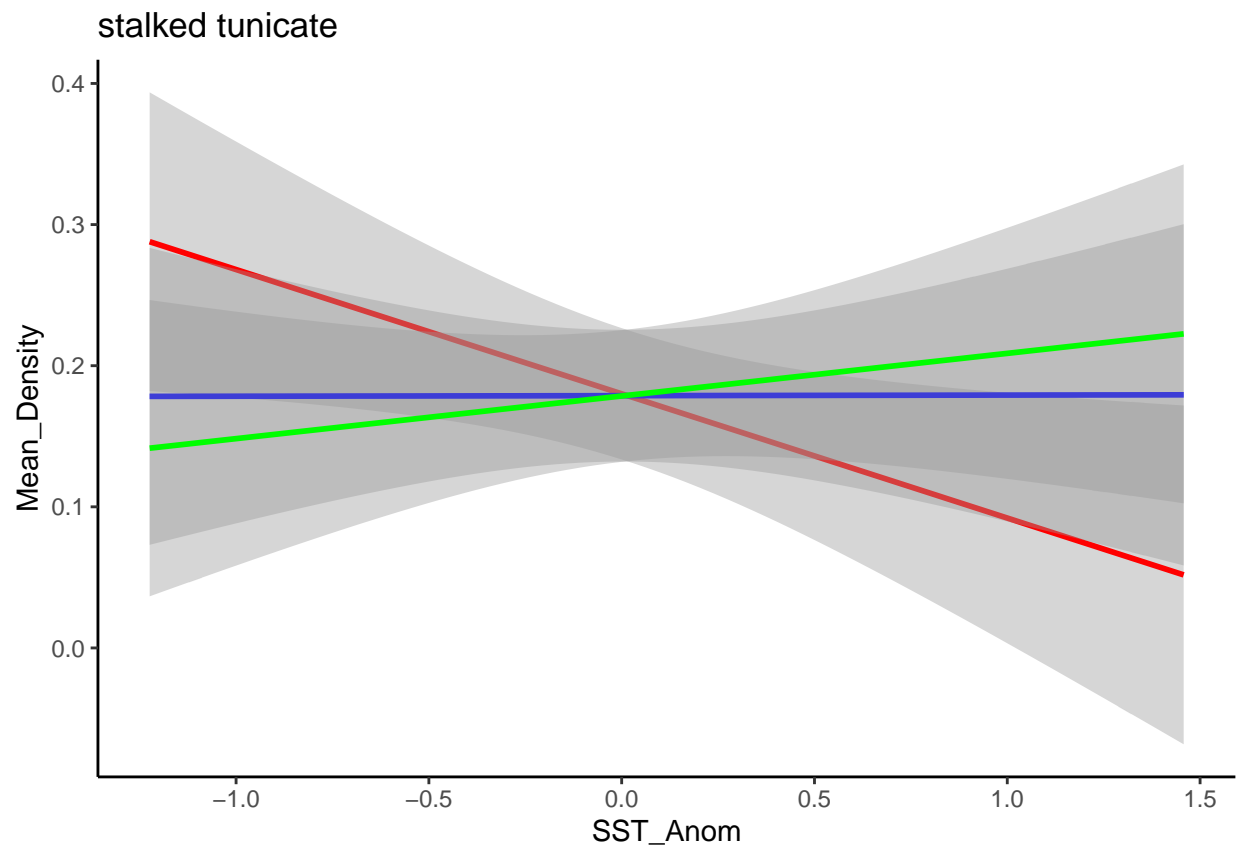




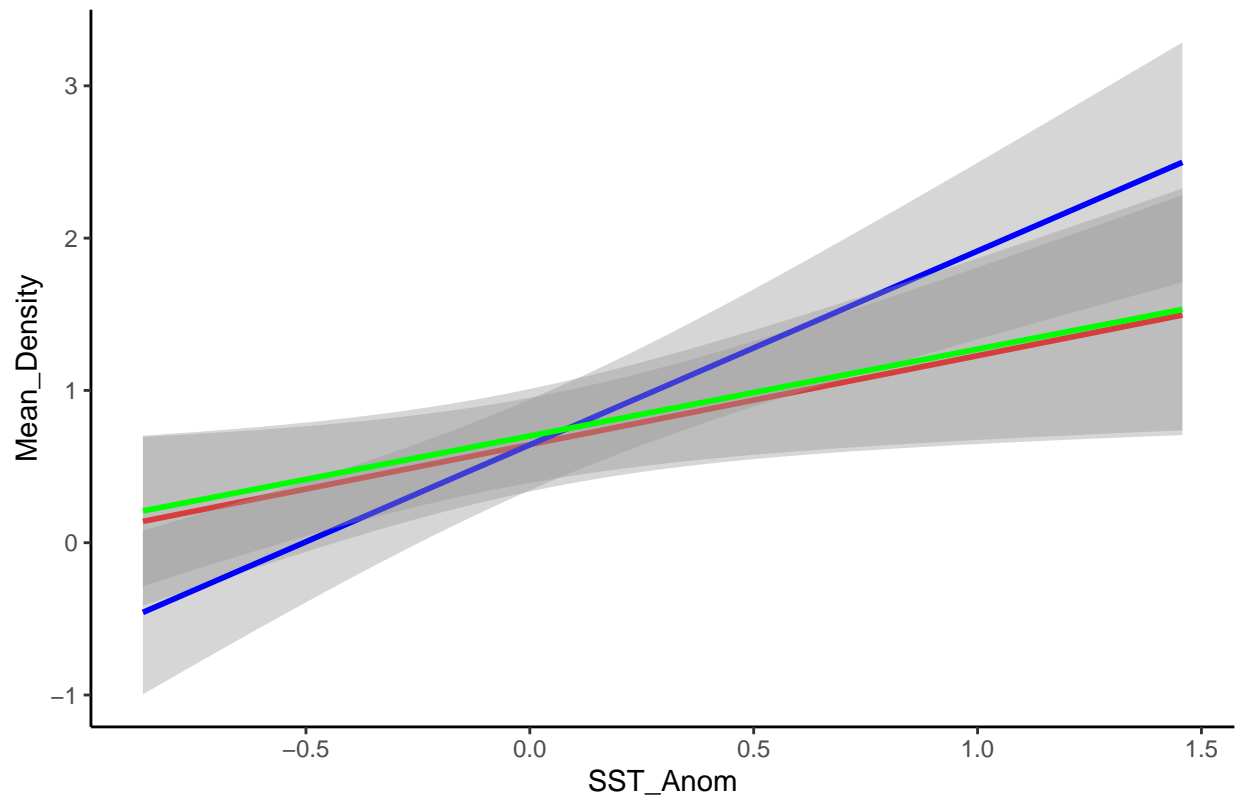


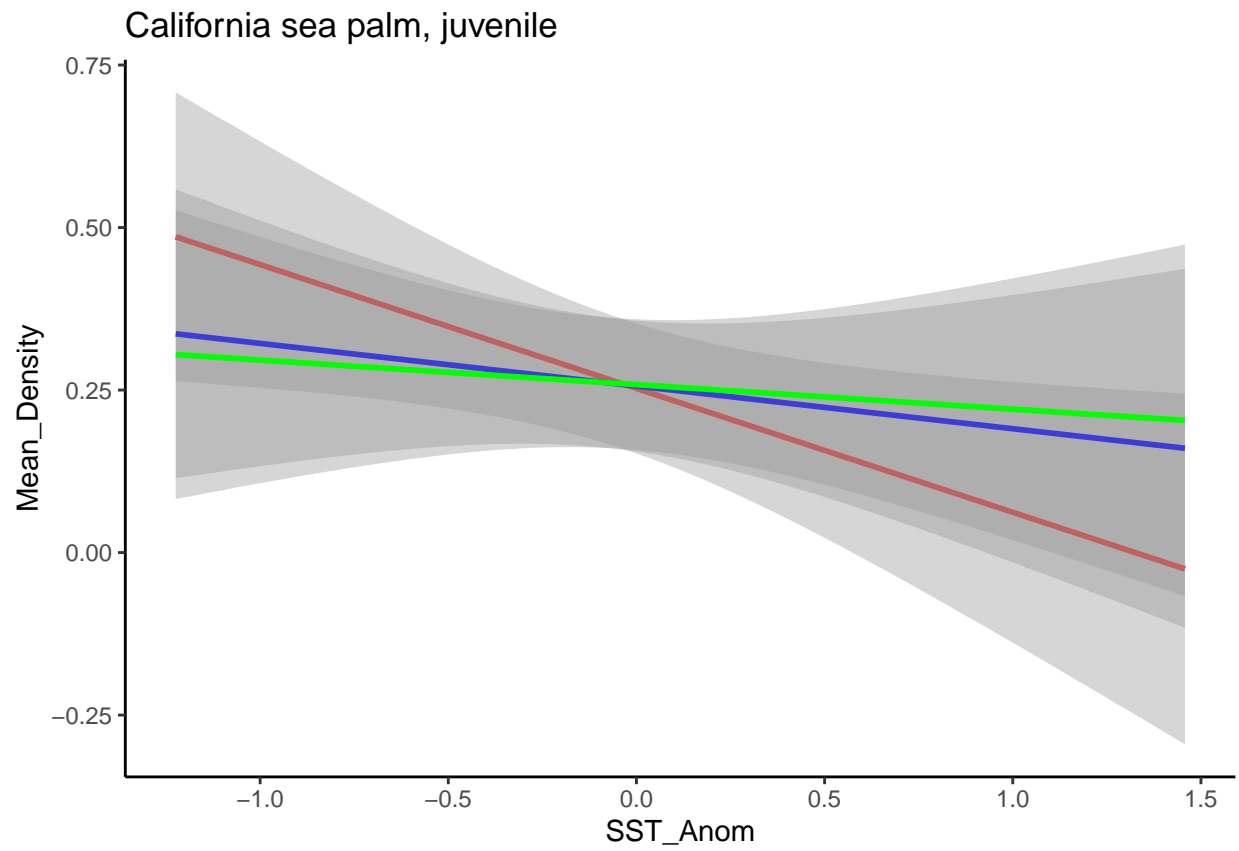


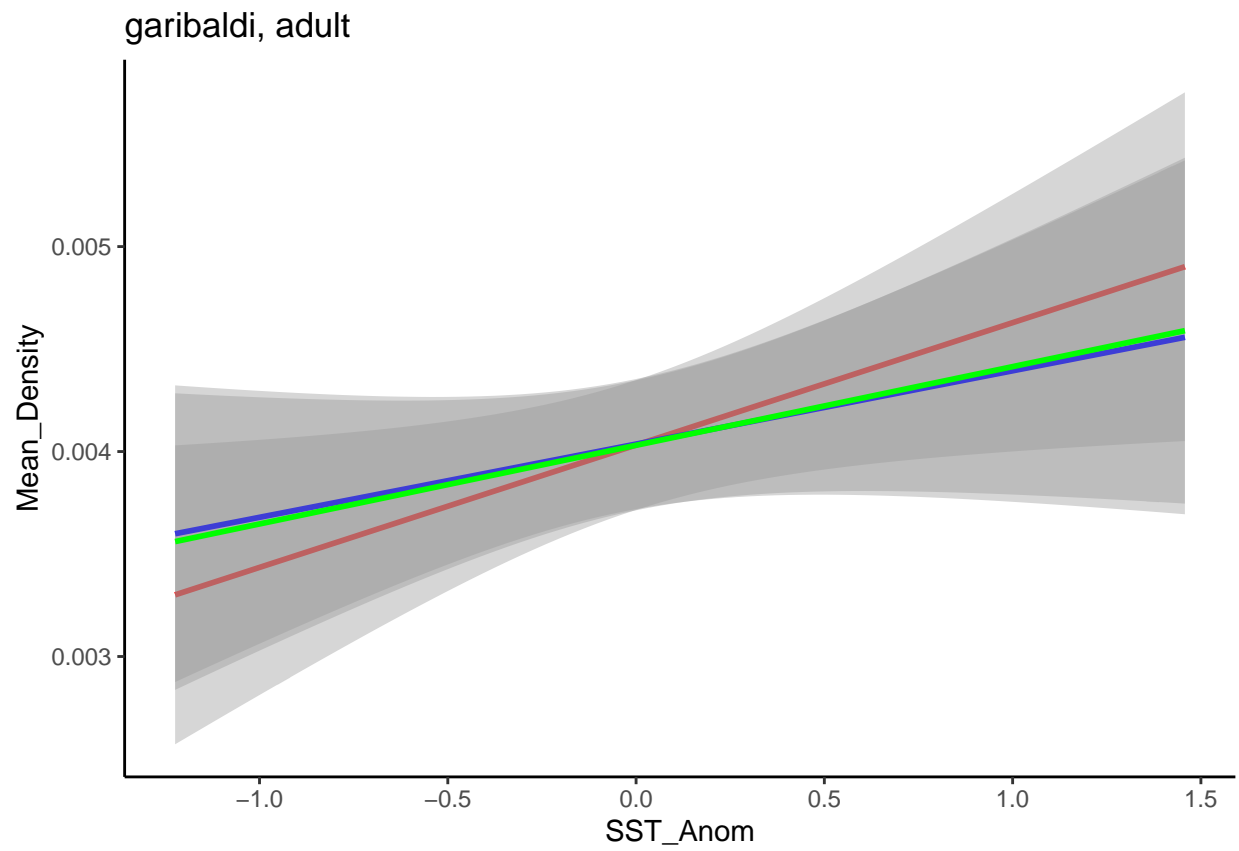


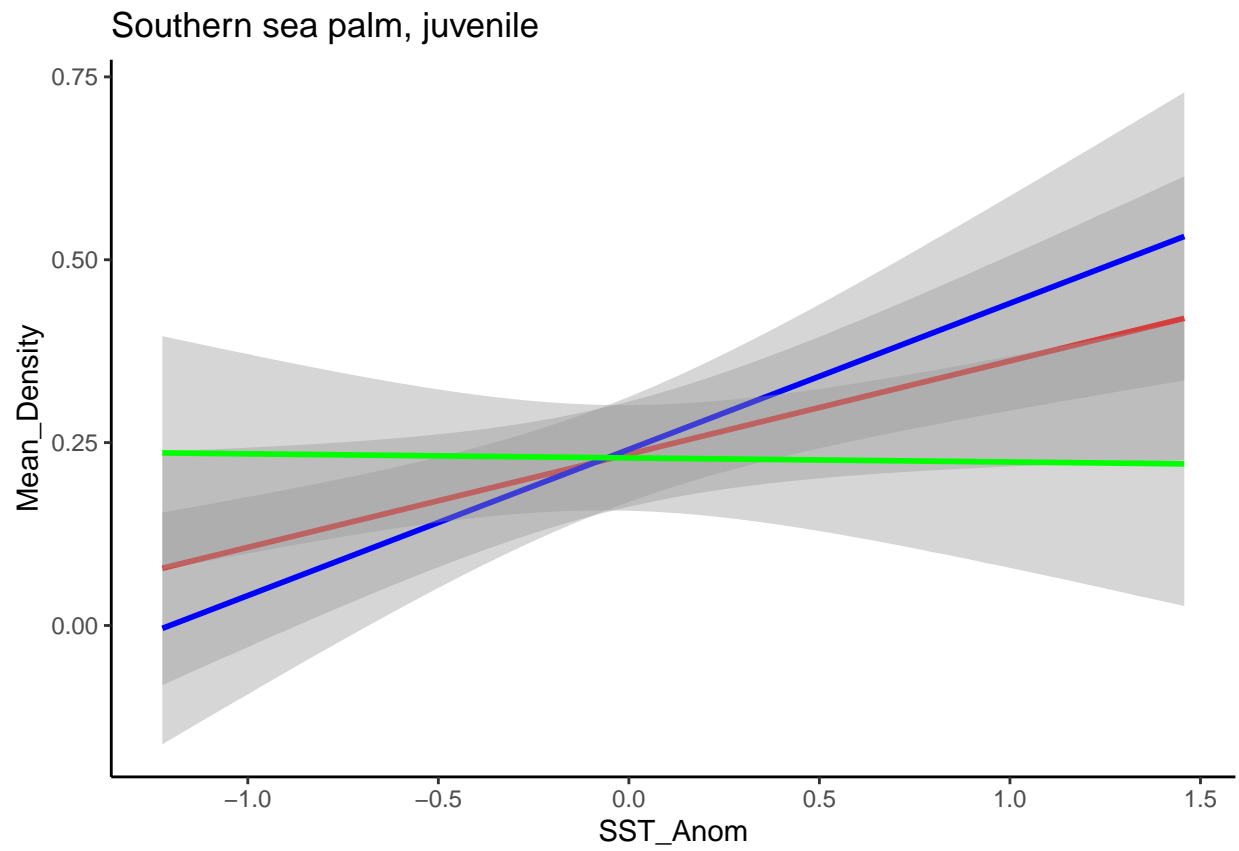


Sargassum horneri, adult (>50cm or receptacles present)

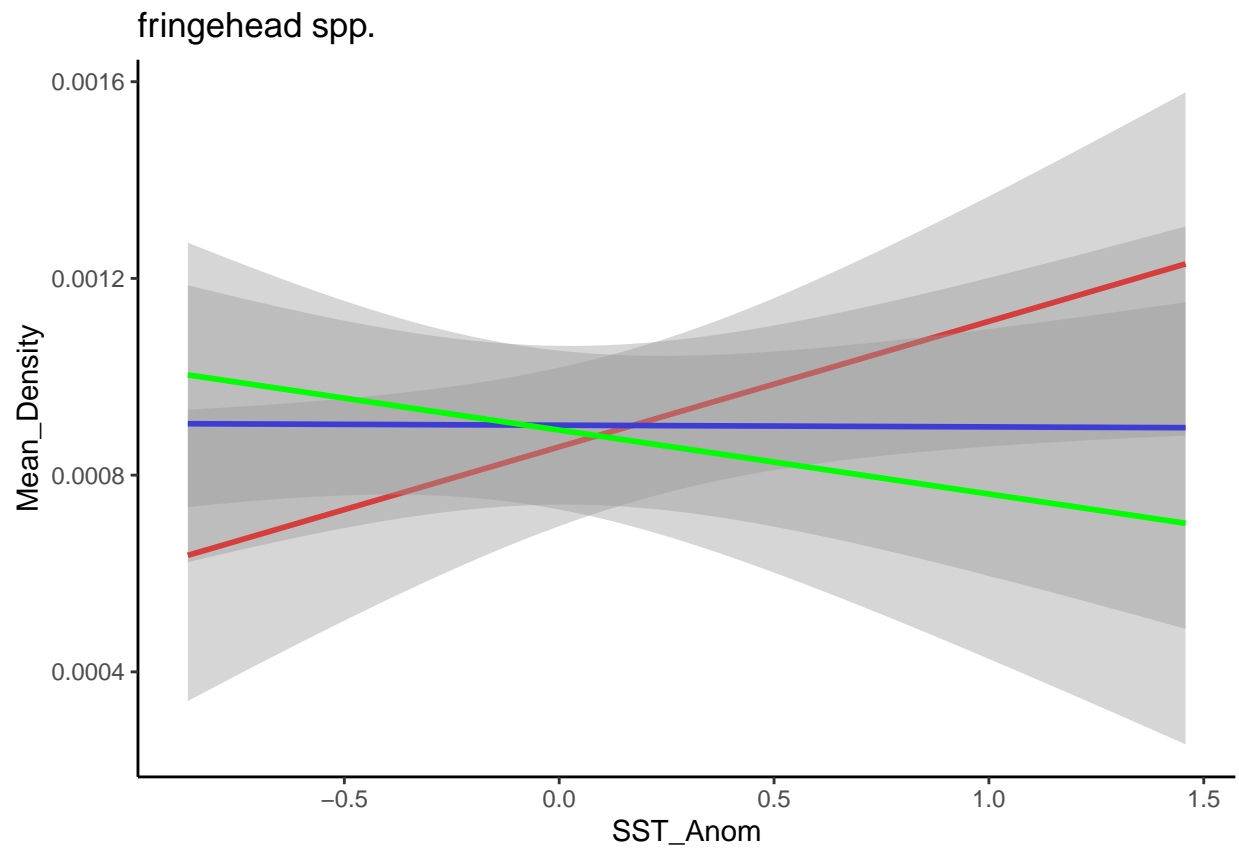


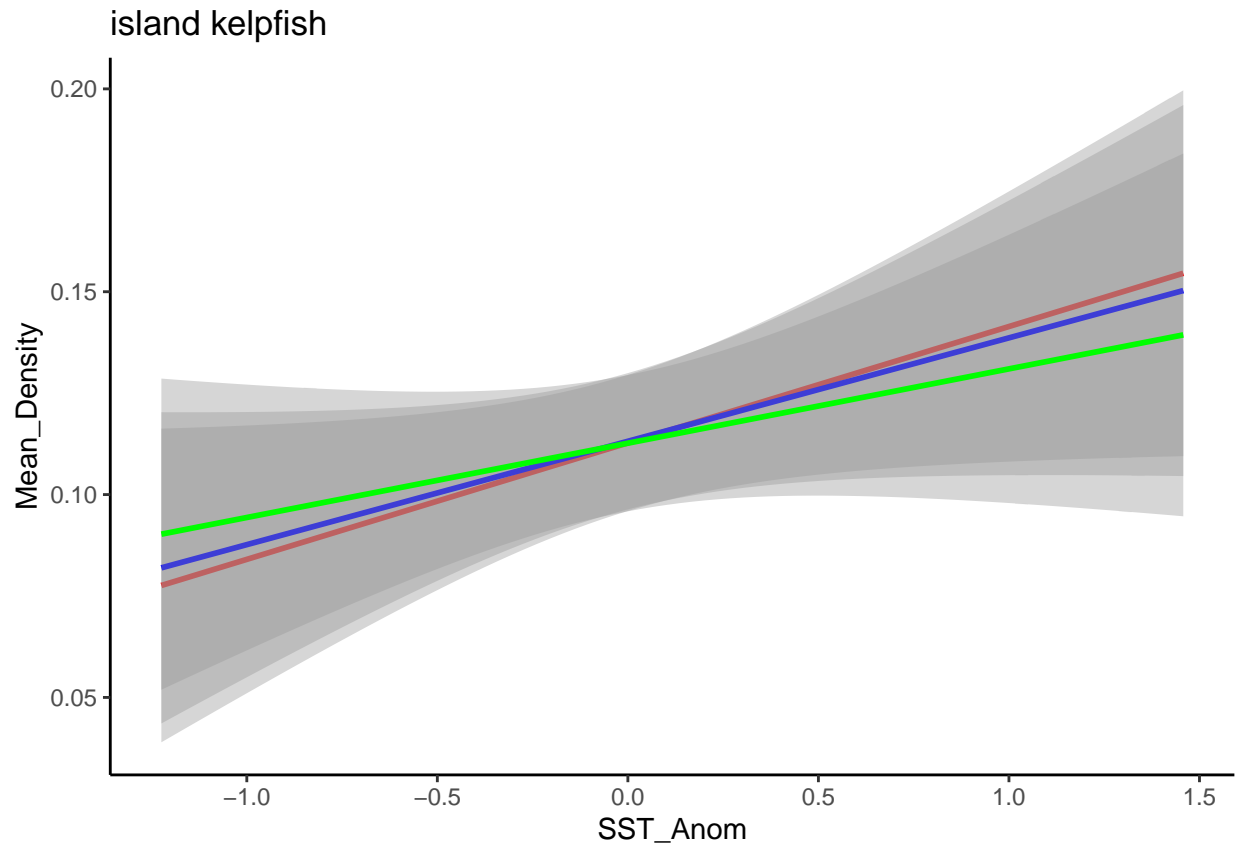












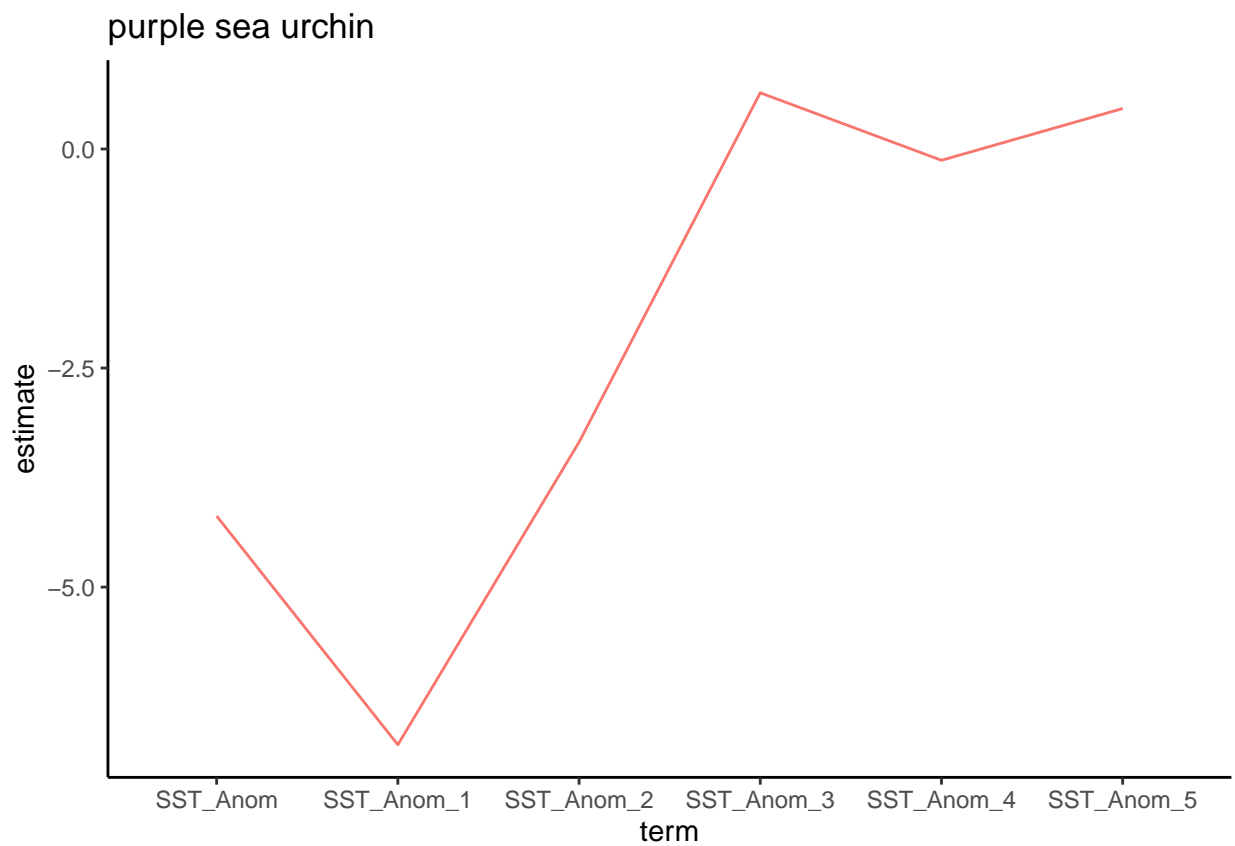
```
Results_lag_5 <- density %>%
  dplyr::group_by(CommonName) %>%
  dplyr::summarise(
    generics::tidy(
      stats::lm(Mean_Density ~ SST_Anom + SST_Anom_1 + SST_Anom_2 + SST_Anom_3 + SST_Anom_4 + SST_Anom_5)
    ) %>%
    tidyr::drop_na(p.value) %>%
    dplyr::filter(p.value <= .05, term != "(Intercept)") %>%
    dplyr::arrange(estimate) %>%
    # dplyr::arrange(p.value) %>%
    dplyr::mutate(statistic = round(statistic, 3),
                  p.value = round(p.value, 3),
                  p.value = ifelse(p.value < 0.001, "< 0.001", as.character(p.value)))
```

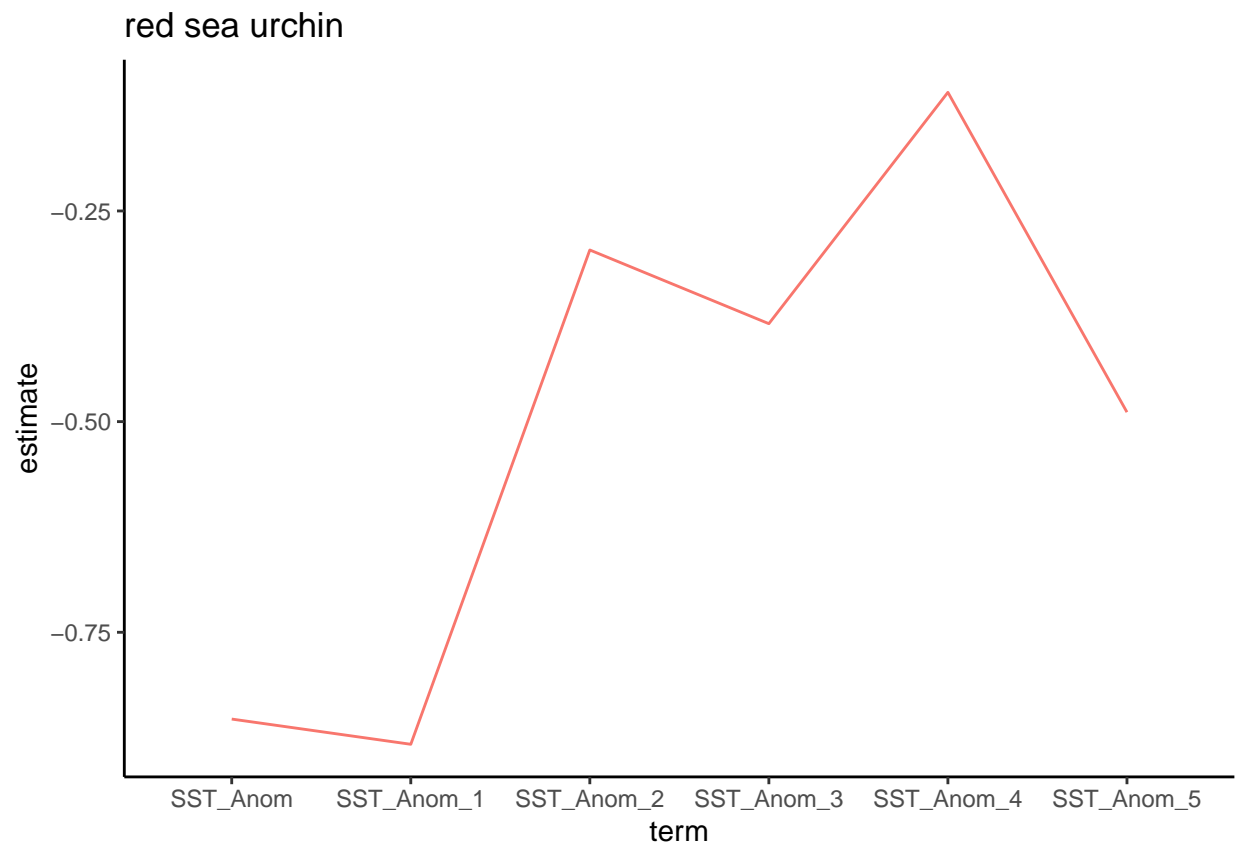
## 'summarise()' has grouped output by 'CommonName'. You can override using the '.groups' argument.

```
Results_lag <- density %>%
  dplyr::group_by(CommonName) %>%
  dplyr::summarise(
    generics::tidy(
      stats::lm(Mean_Density ~ SST_Anom + SST_Anom_1 + SST_Anom_2 + SST_Anom_3 + SST_Anom_4 + SST_Anom_5)
    ) %>%
    tidyr::drop_na(p.value) %>%
    dplyr::filter(term != "(Intercept)")
```

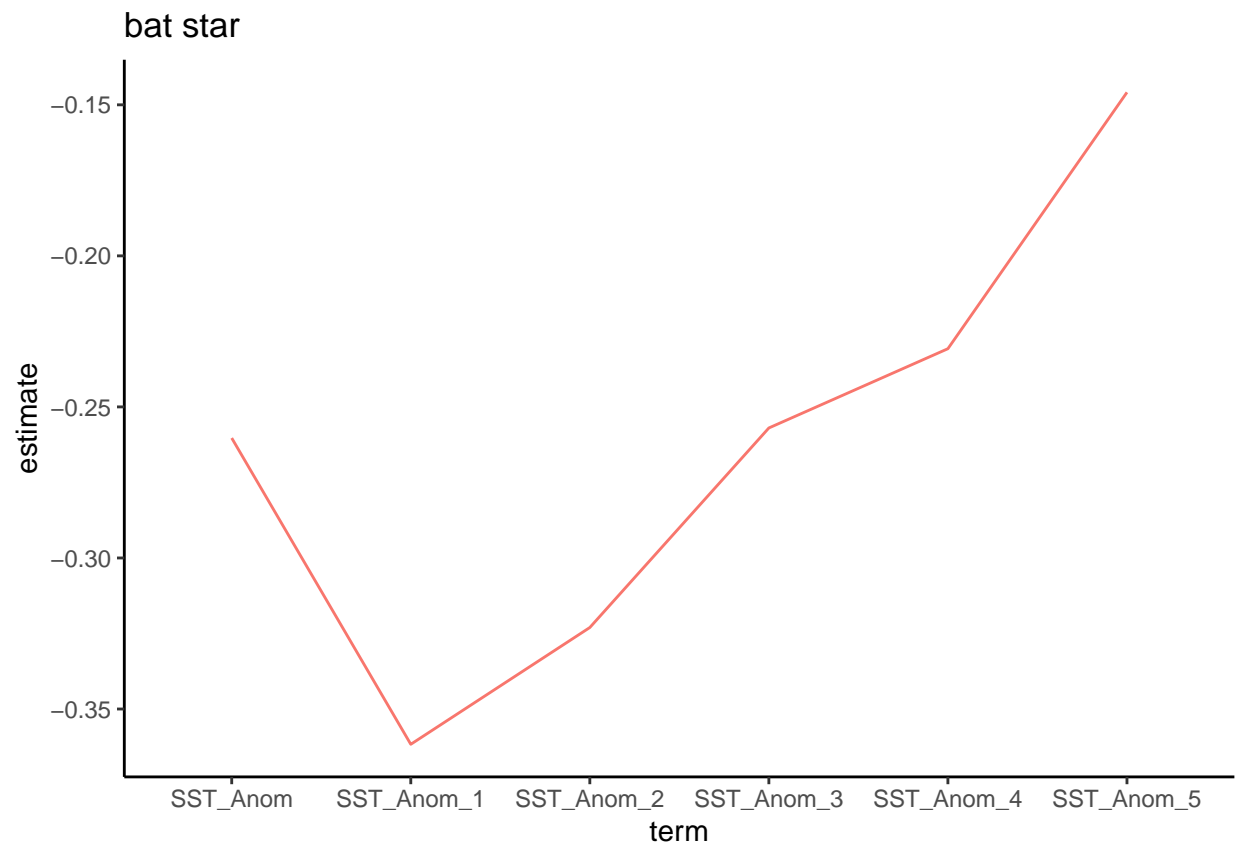
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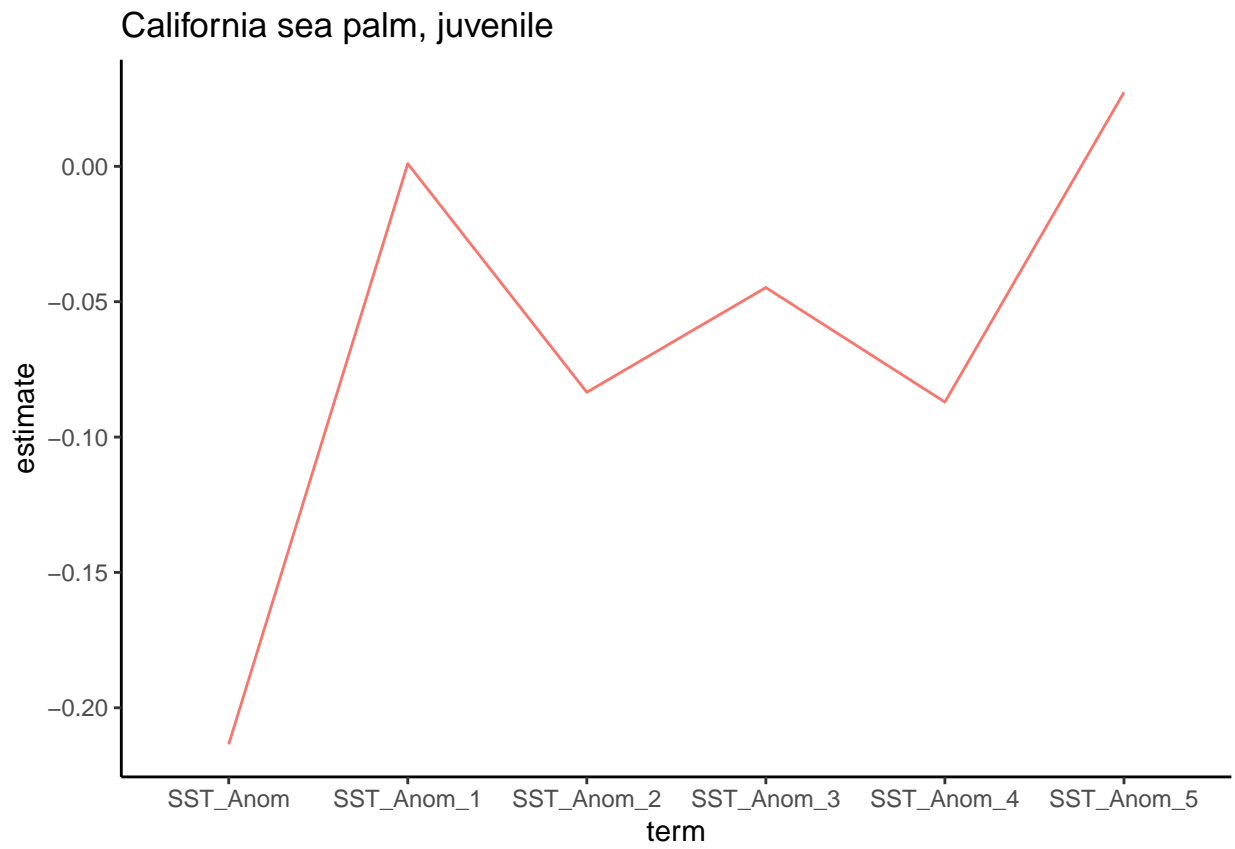
```
for (sp in unique(Results_lag_5$CommonName)) {  
  p <- Results_lag %>%  
    filter(CommonName == sp) %>%  
    ggplot(aes(x = term, y = estimate, color = CommonName, group = CommonName)) +  
    geom_line(show.legend = F) +  
    labs(title = sp) +  
    theme_classic()  
  
  print(p)  
}
```

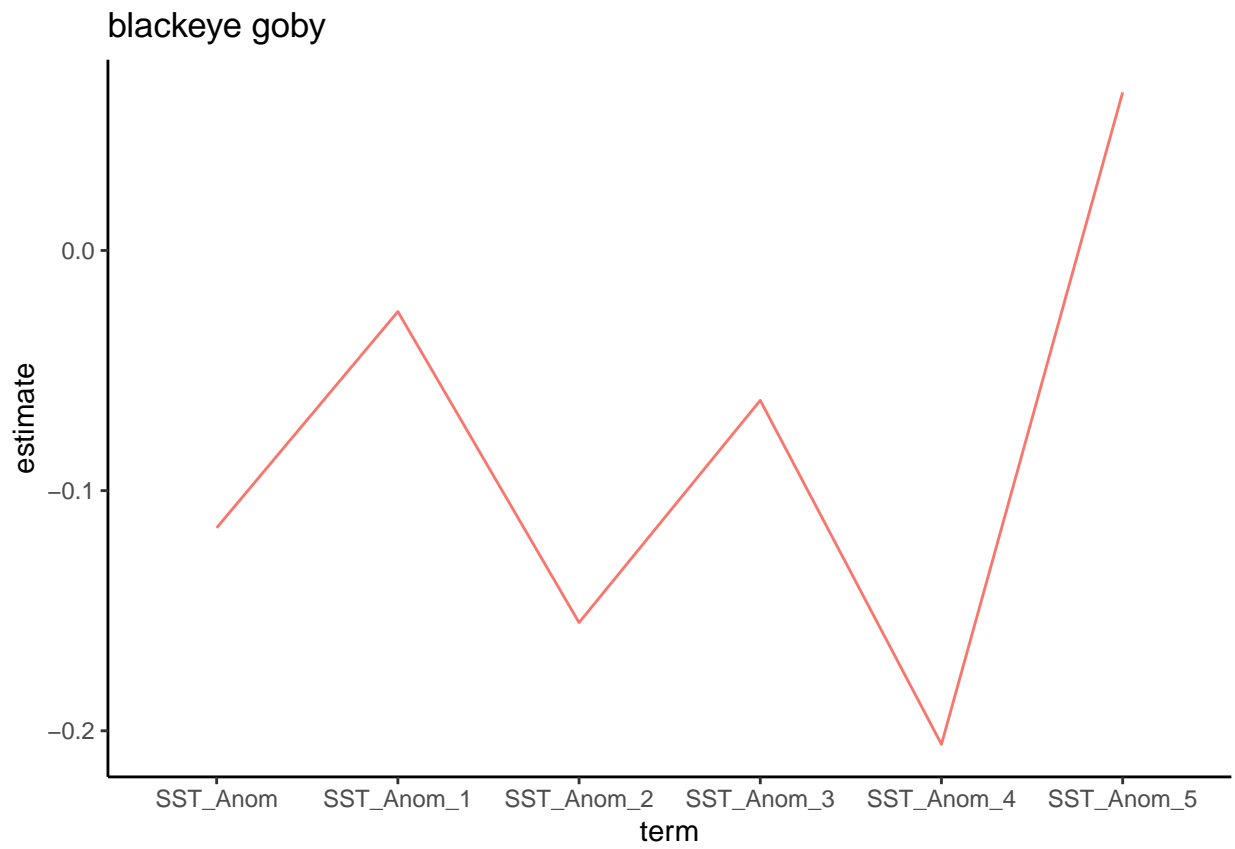




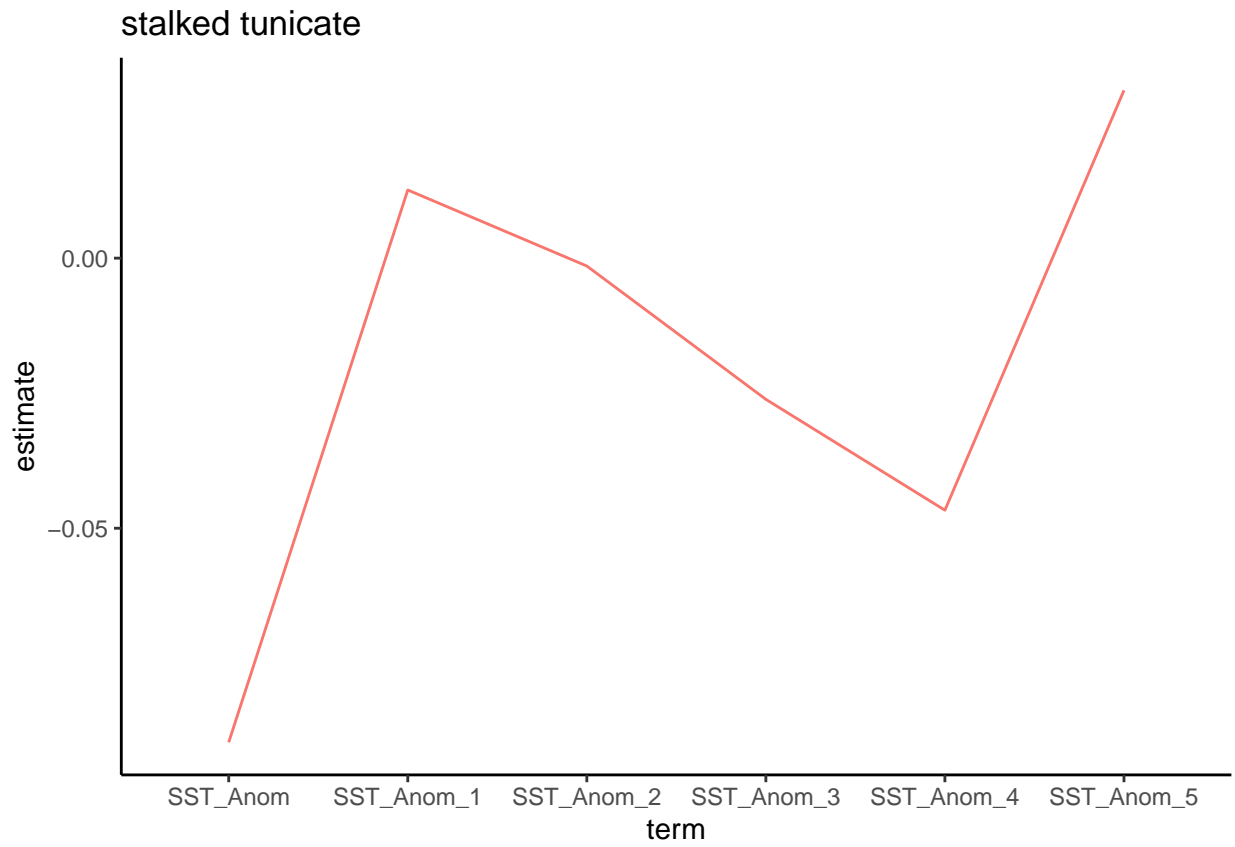


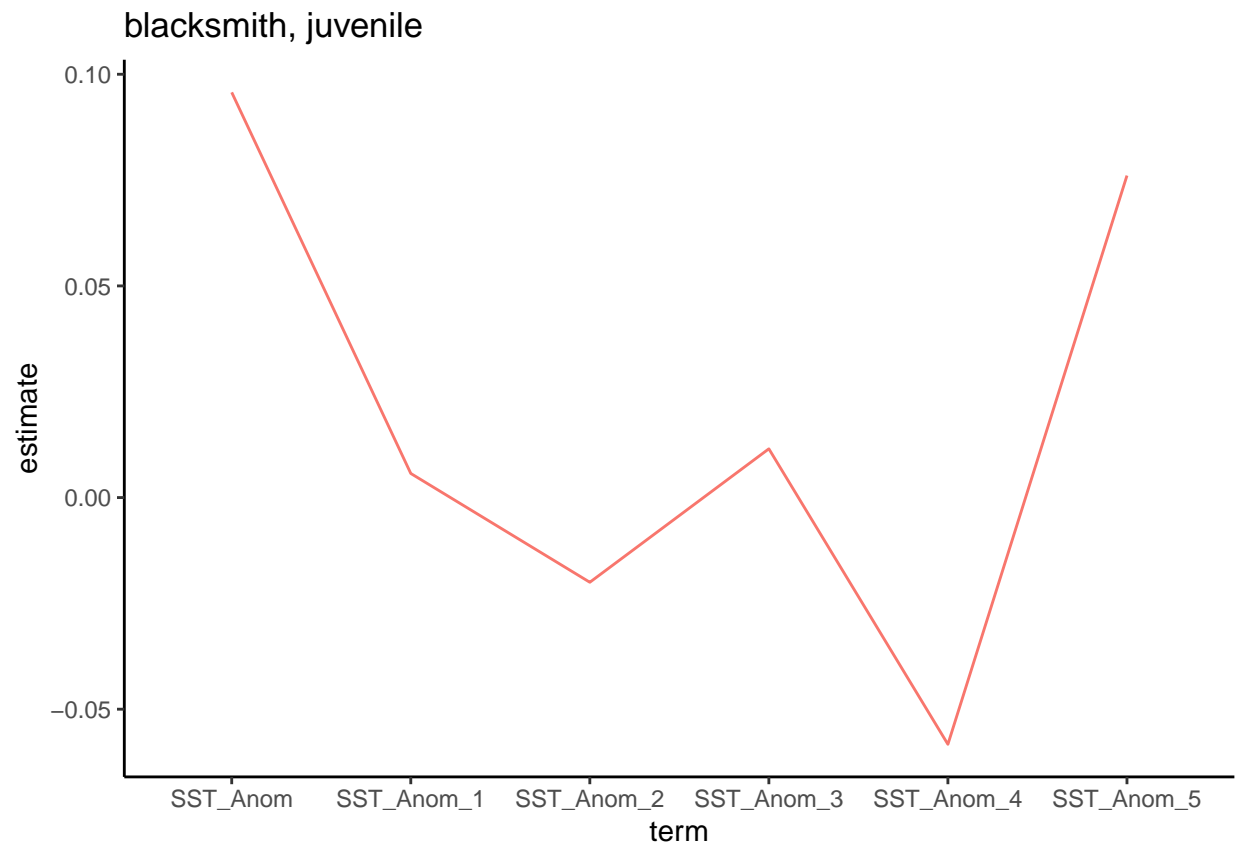


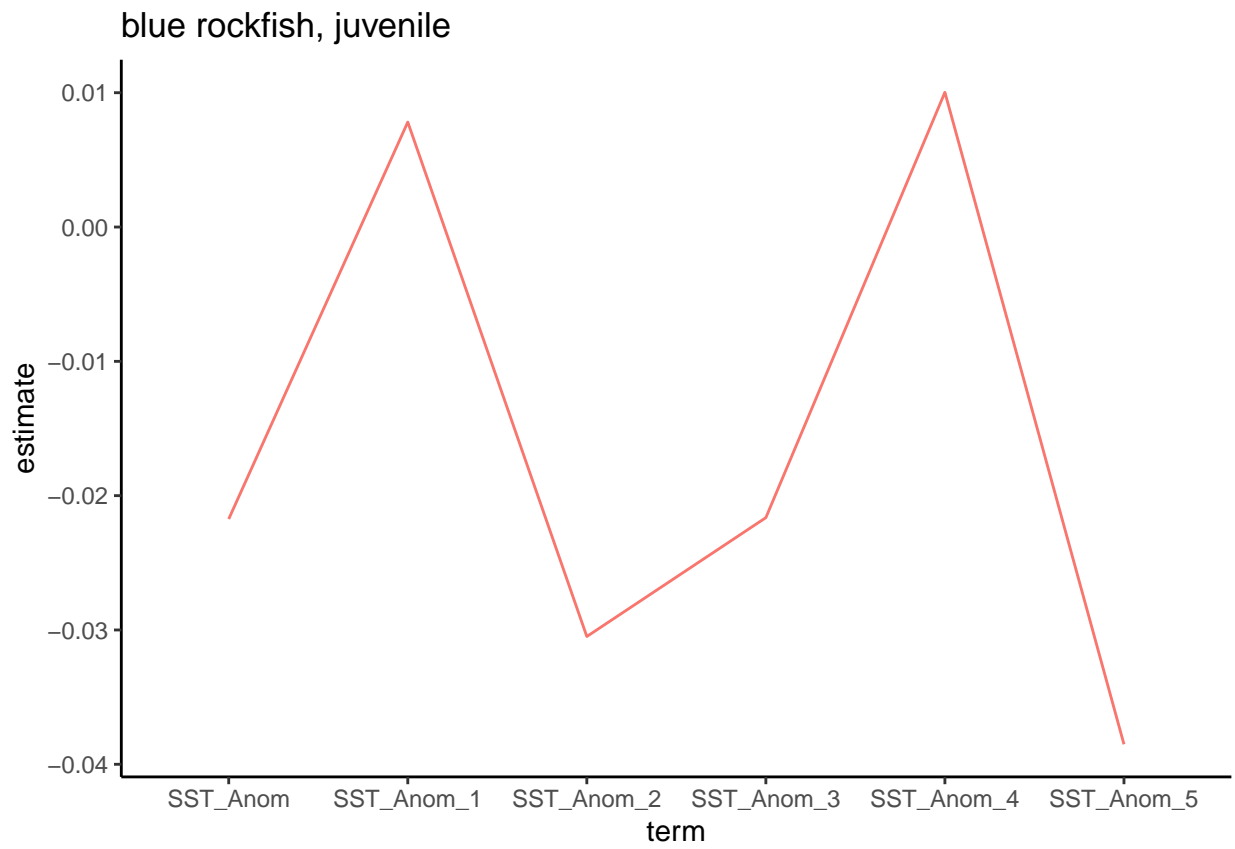


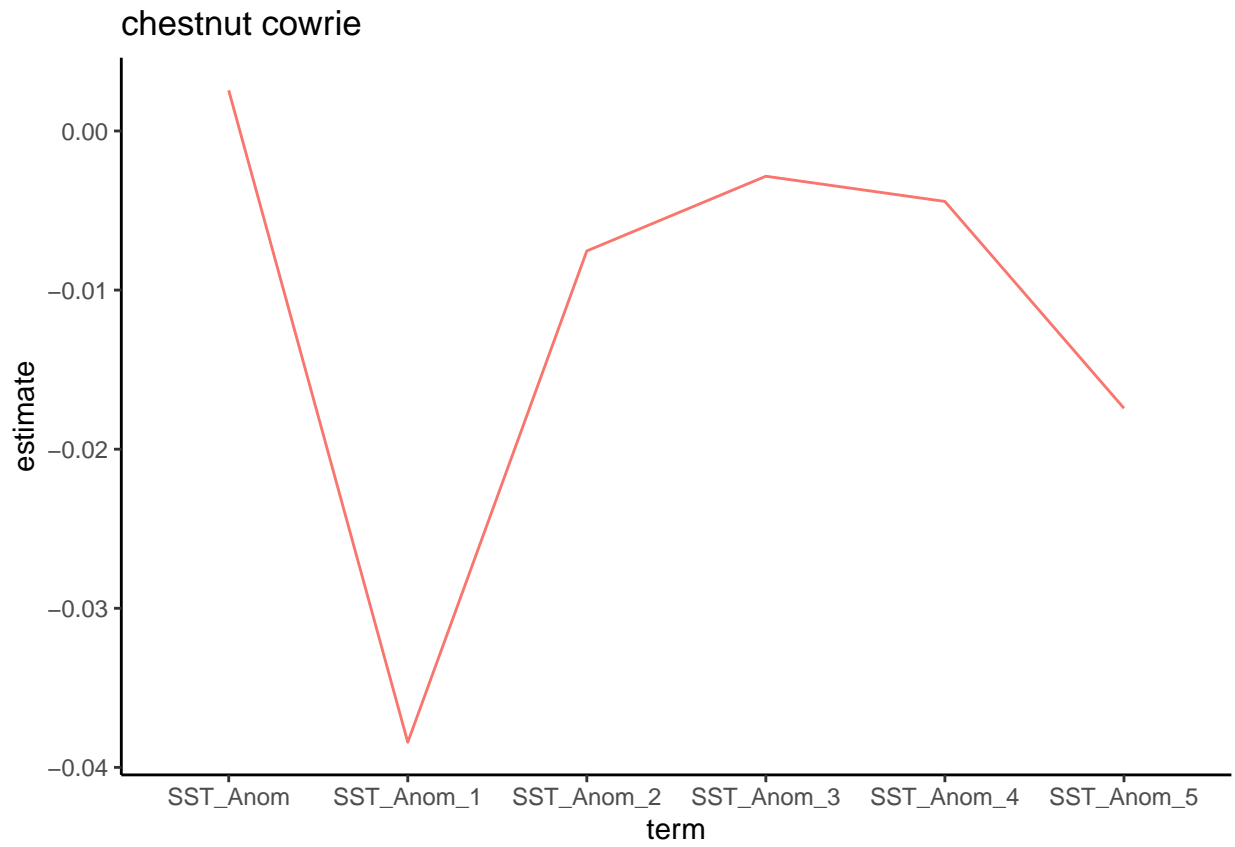


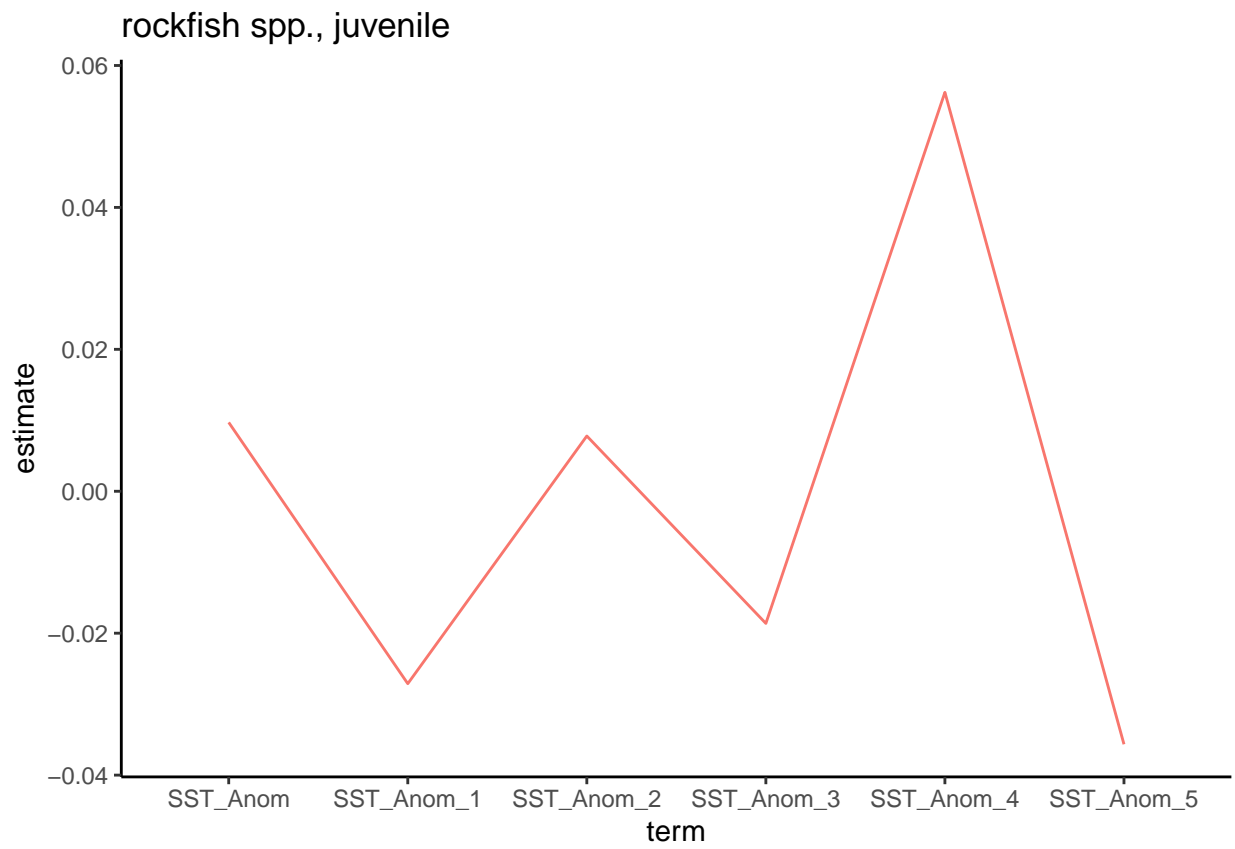


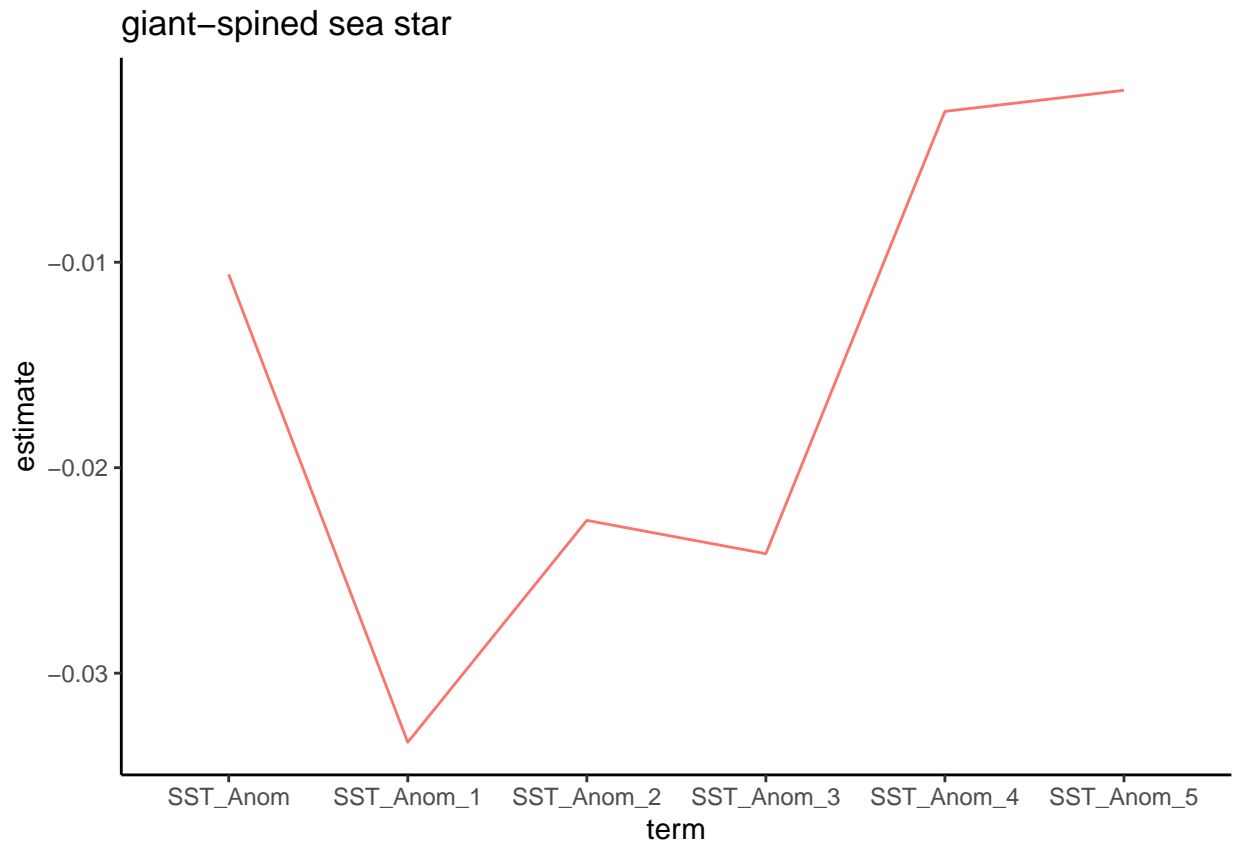


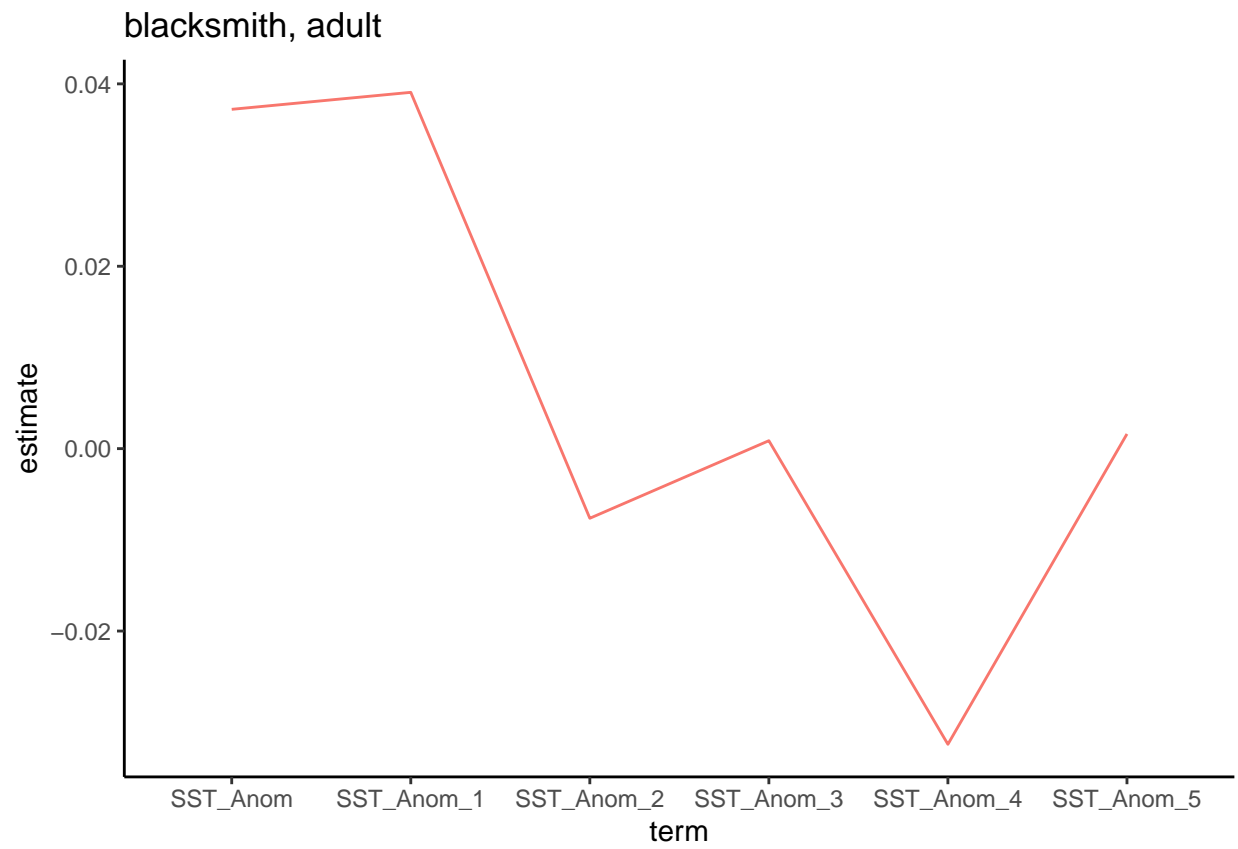


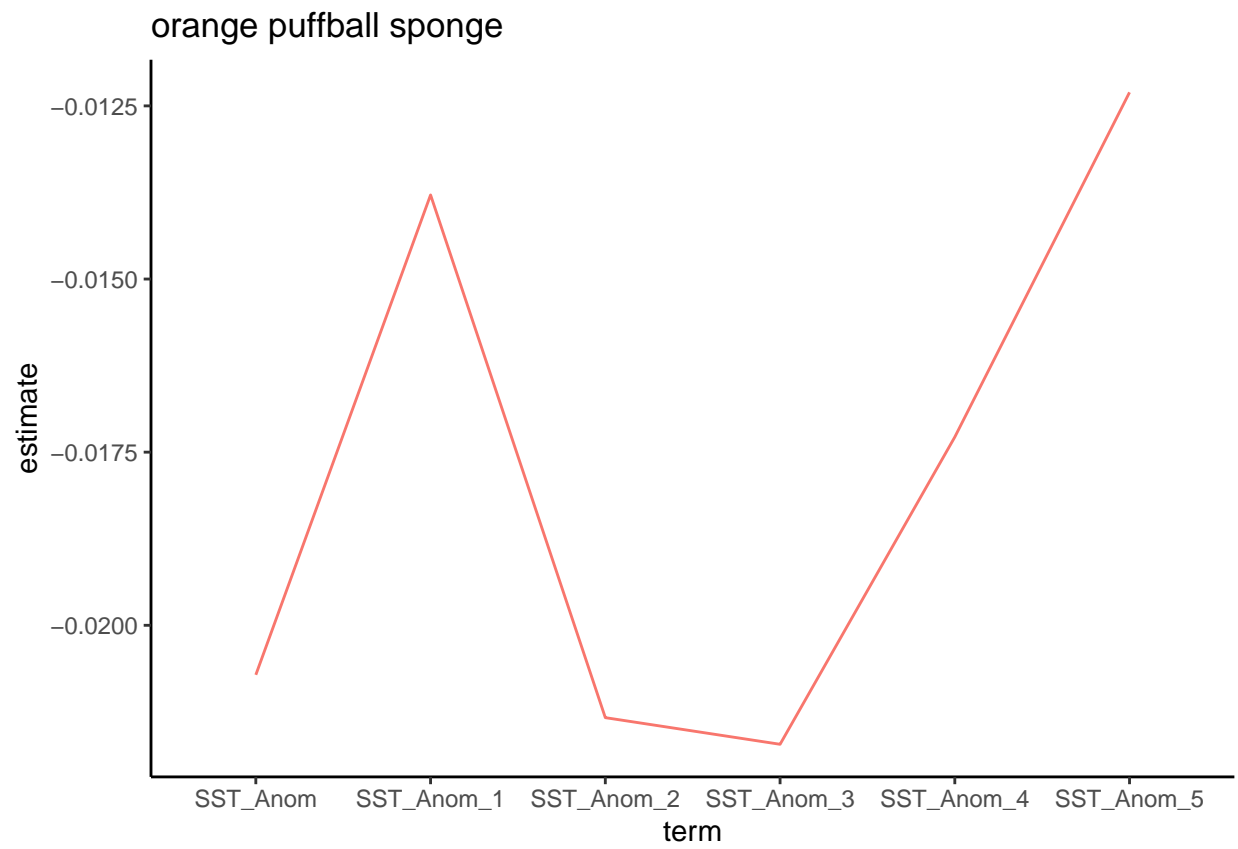




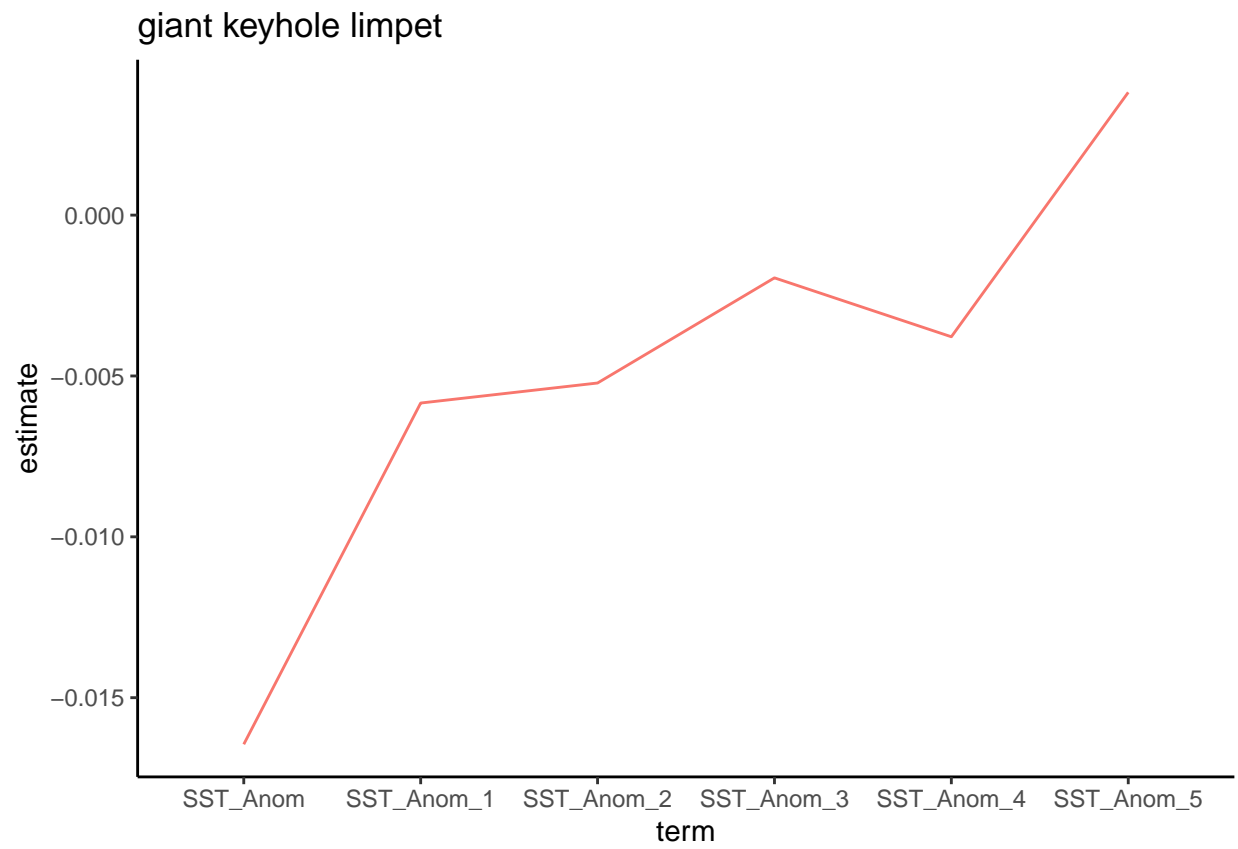


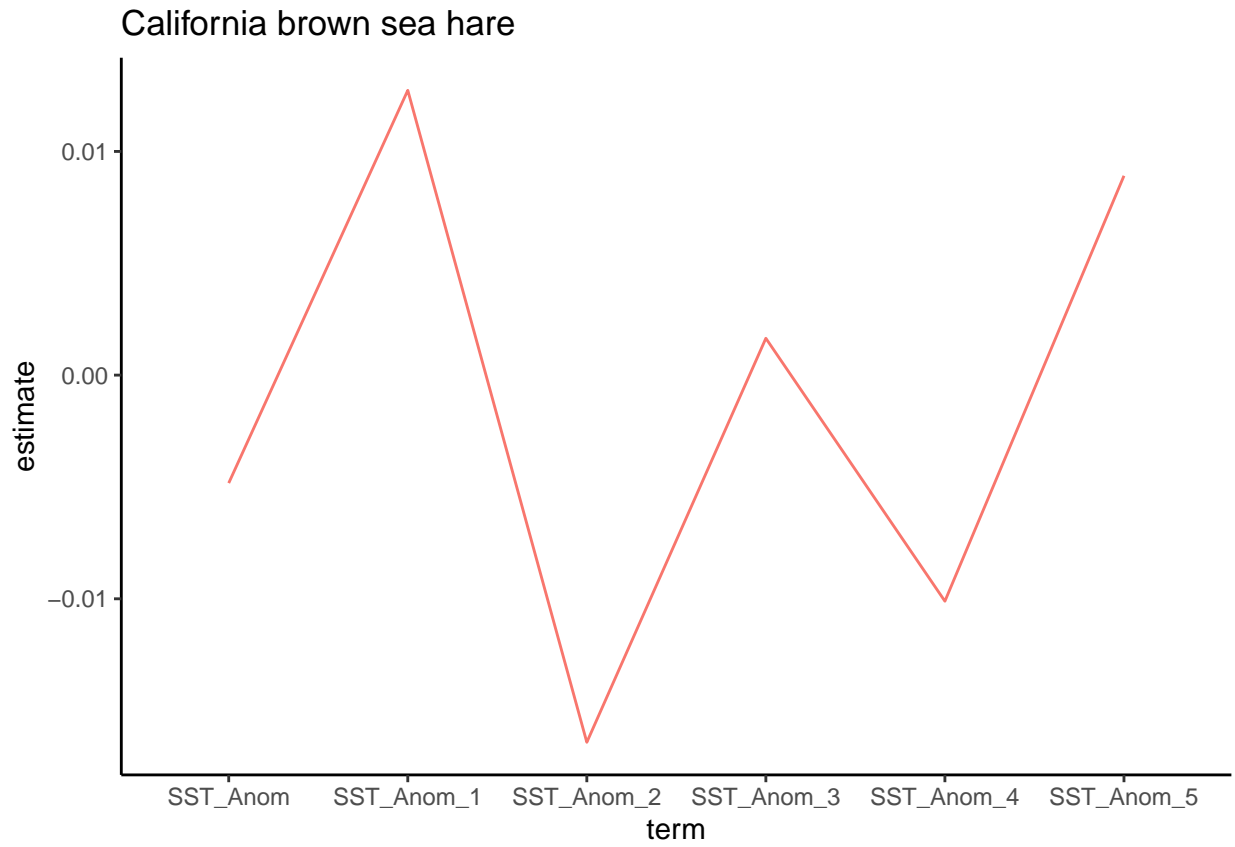


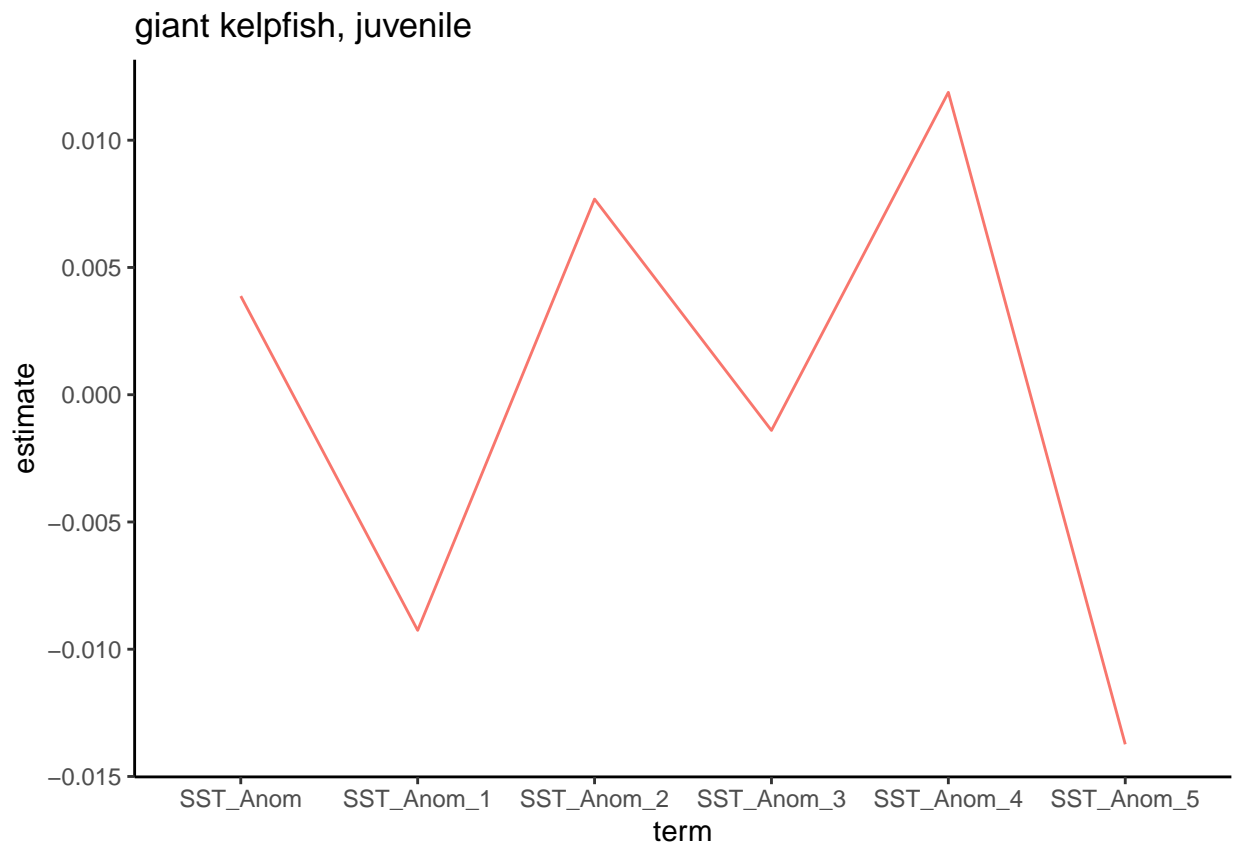


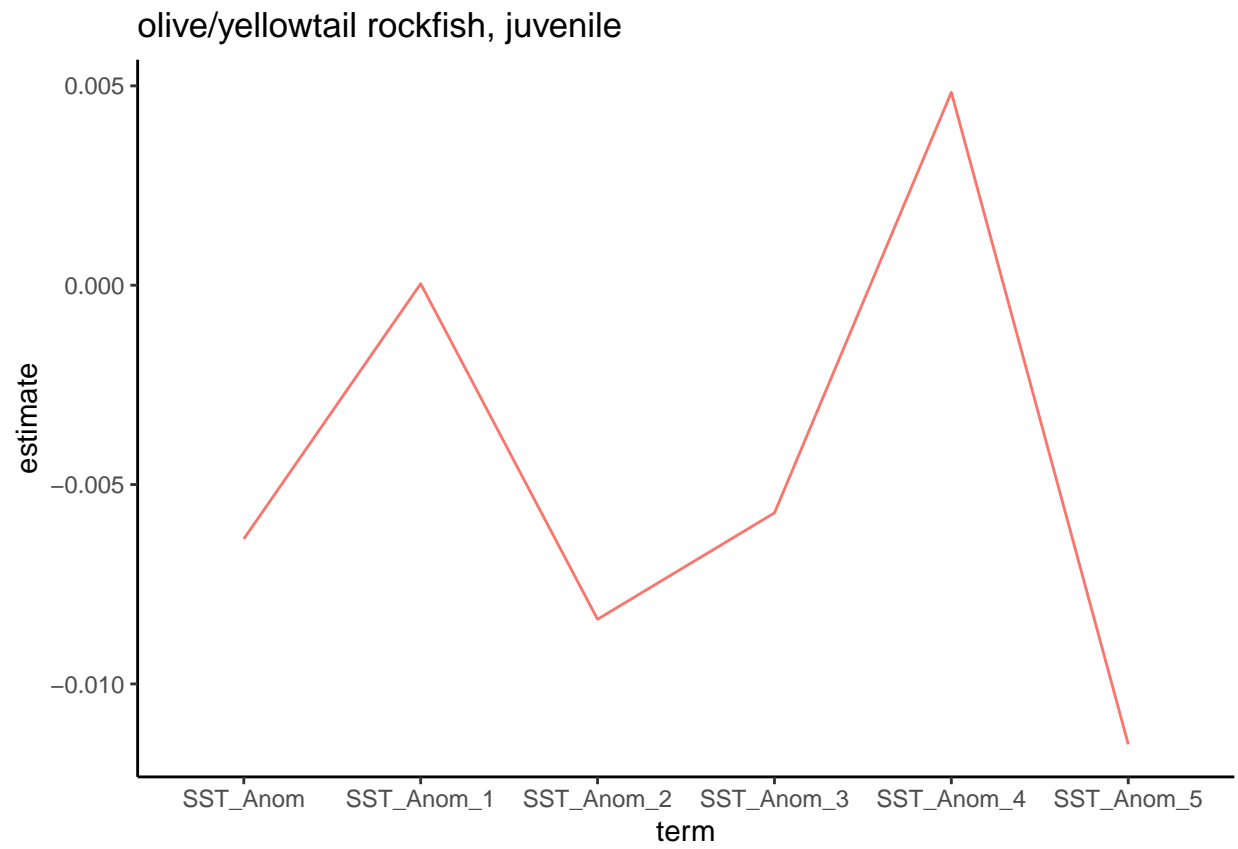


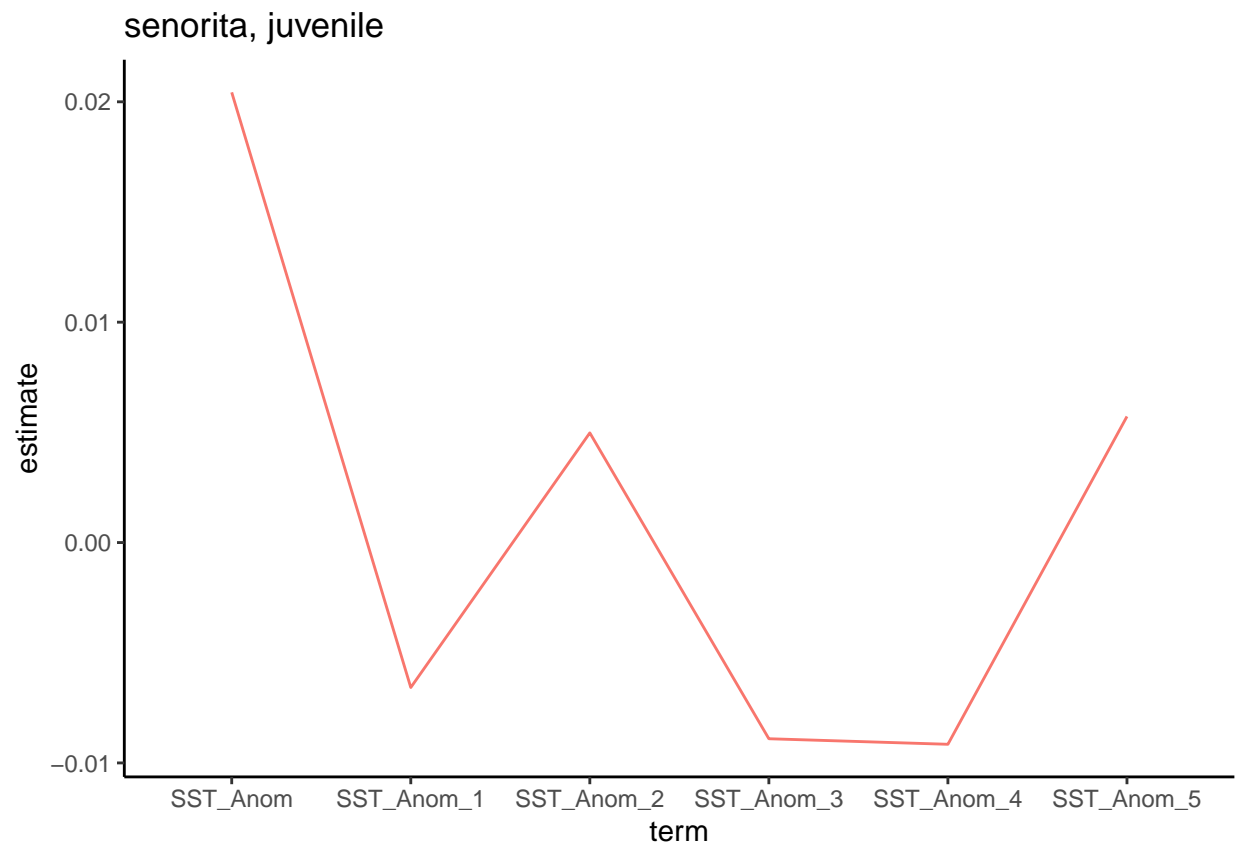


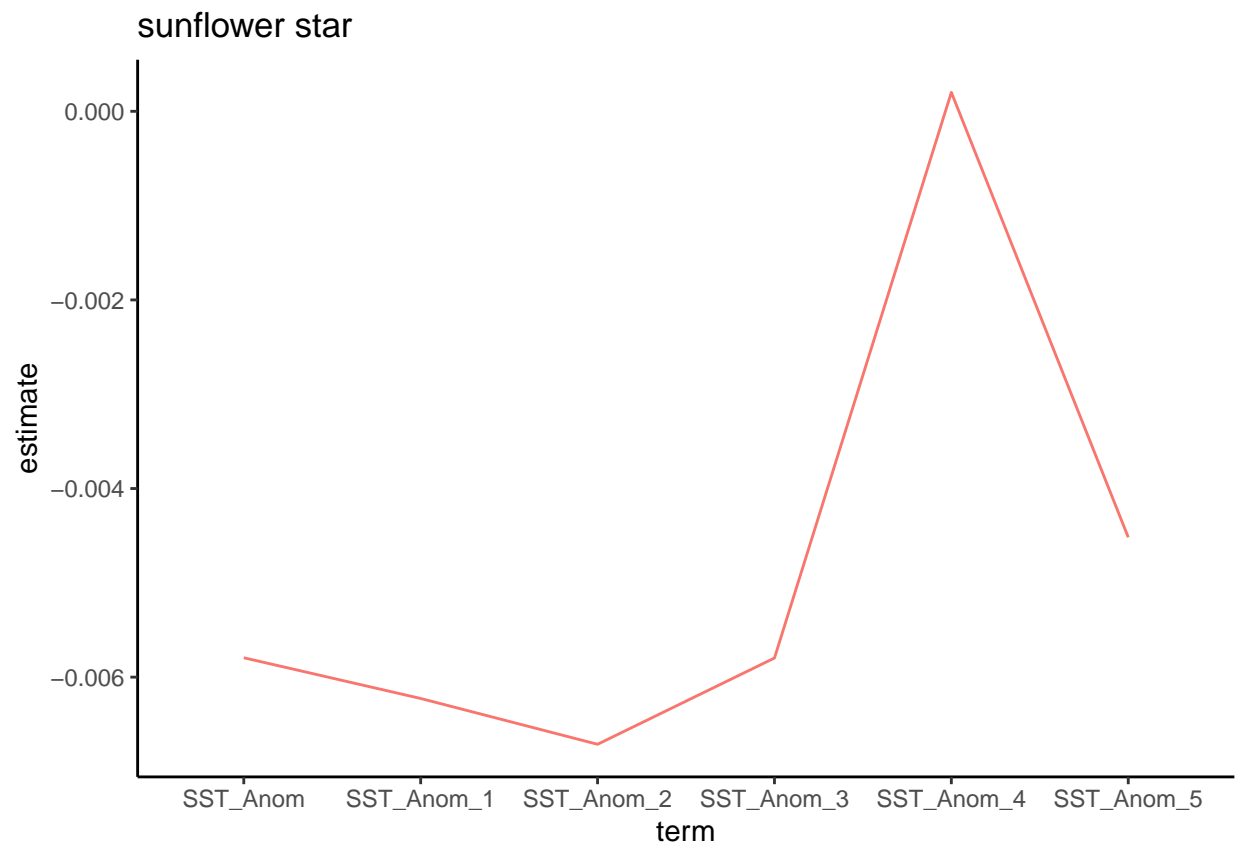


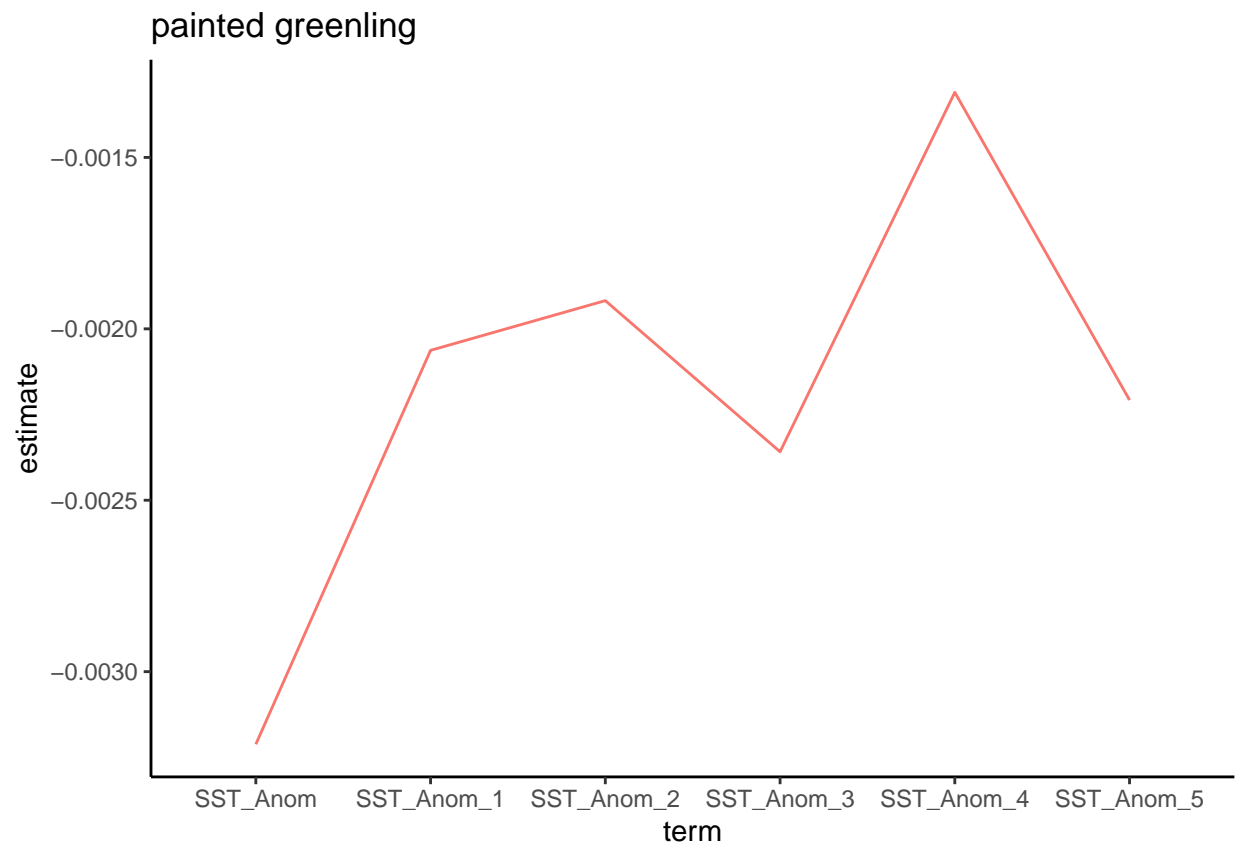


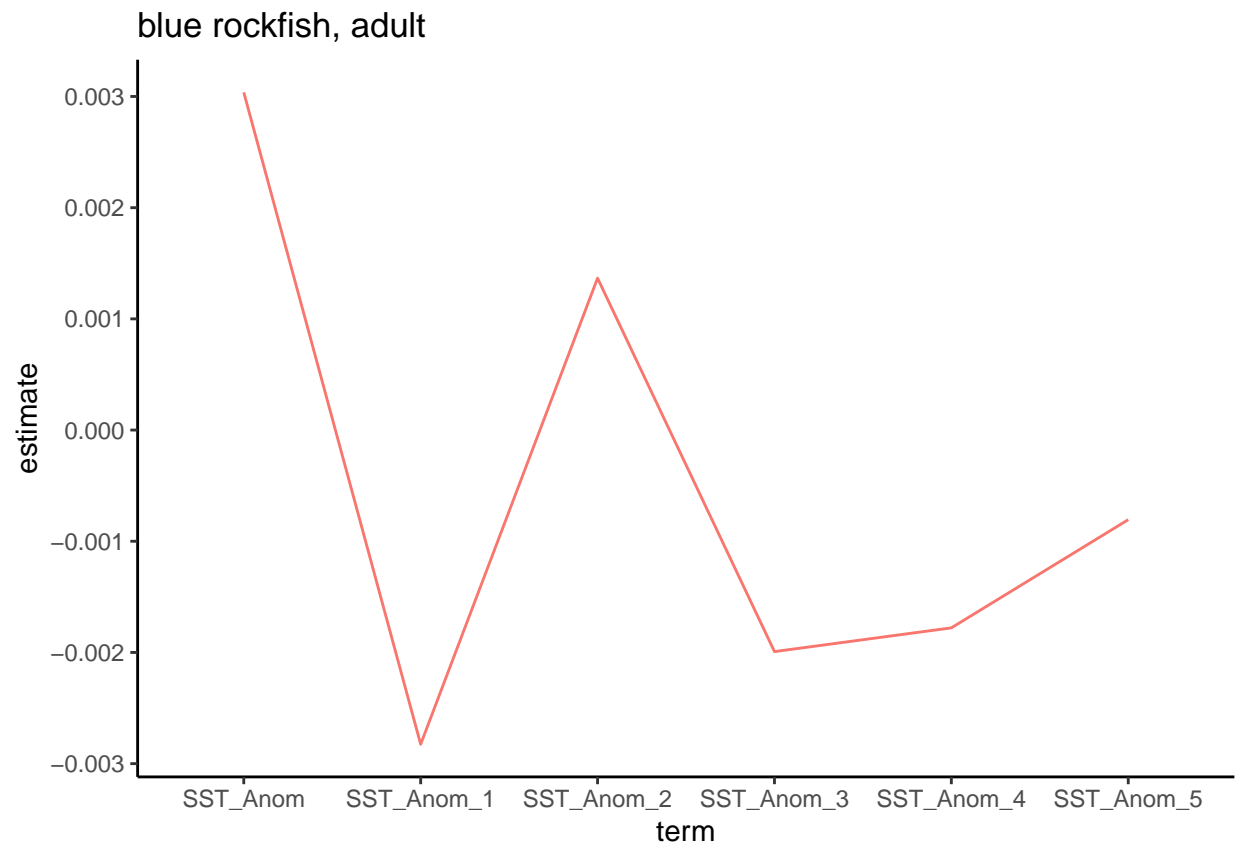




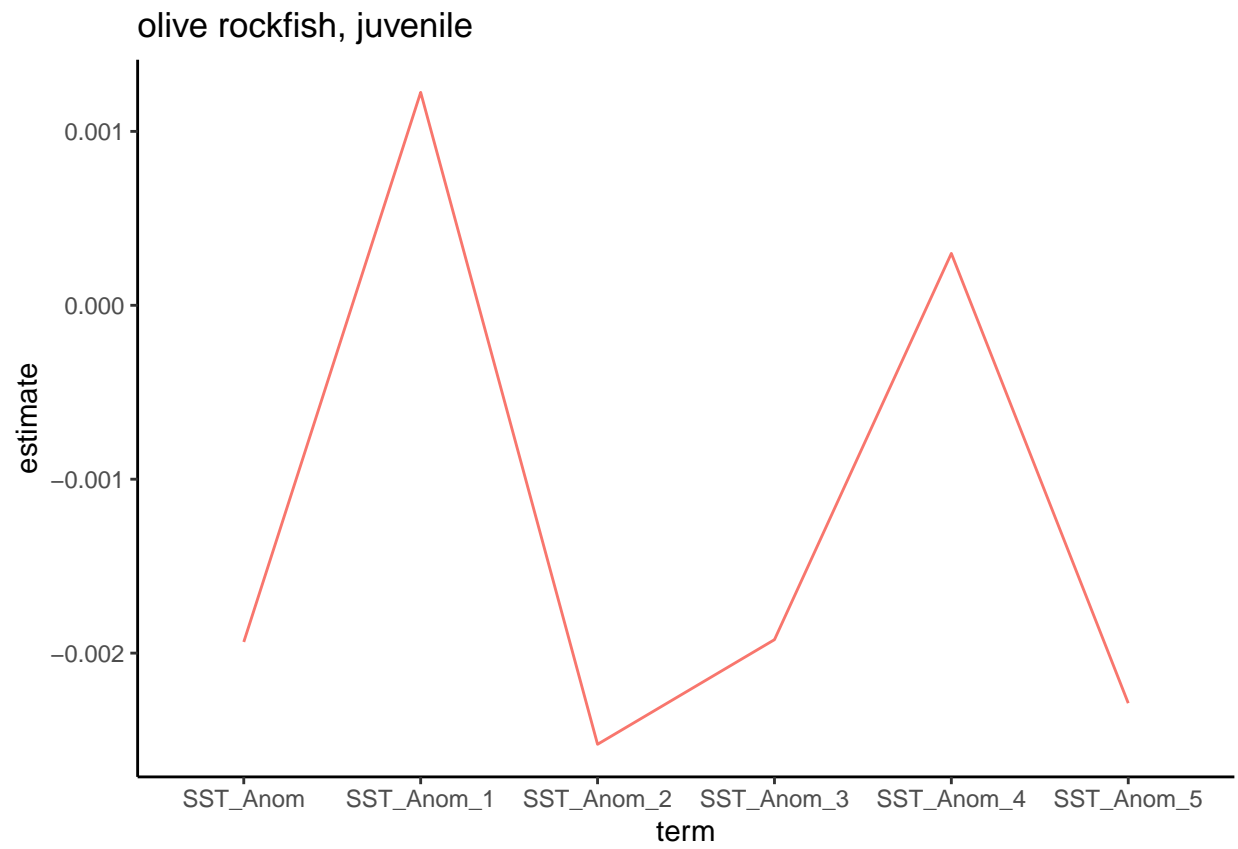


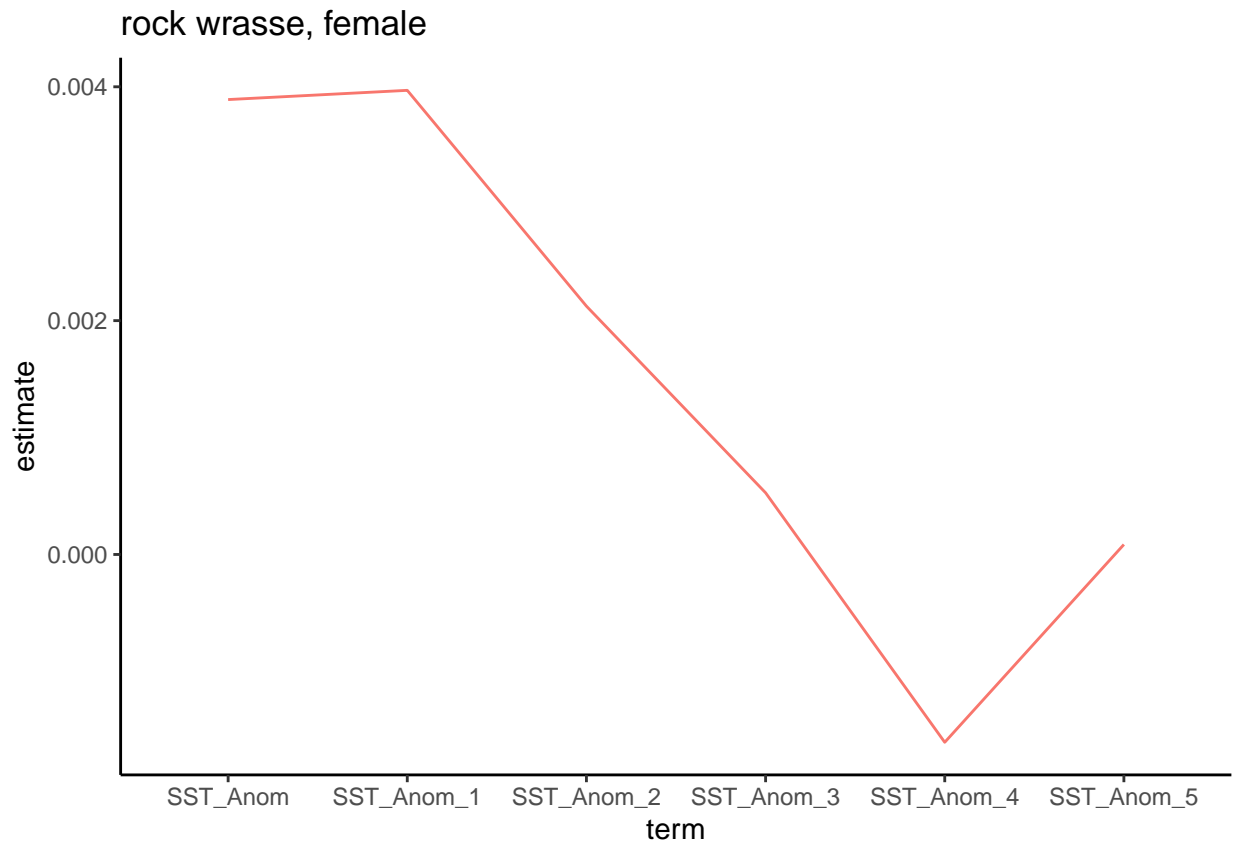


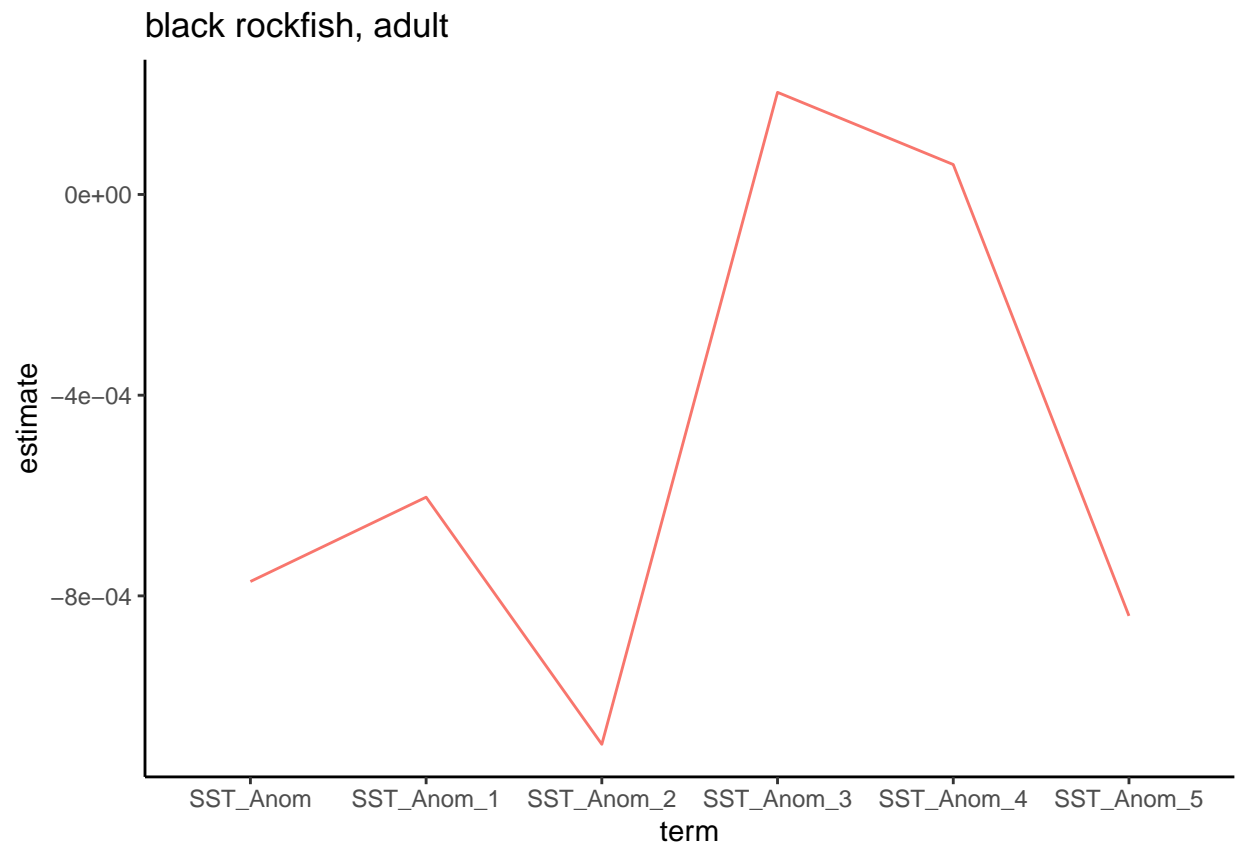


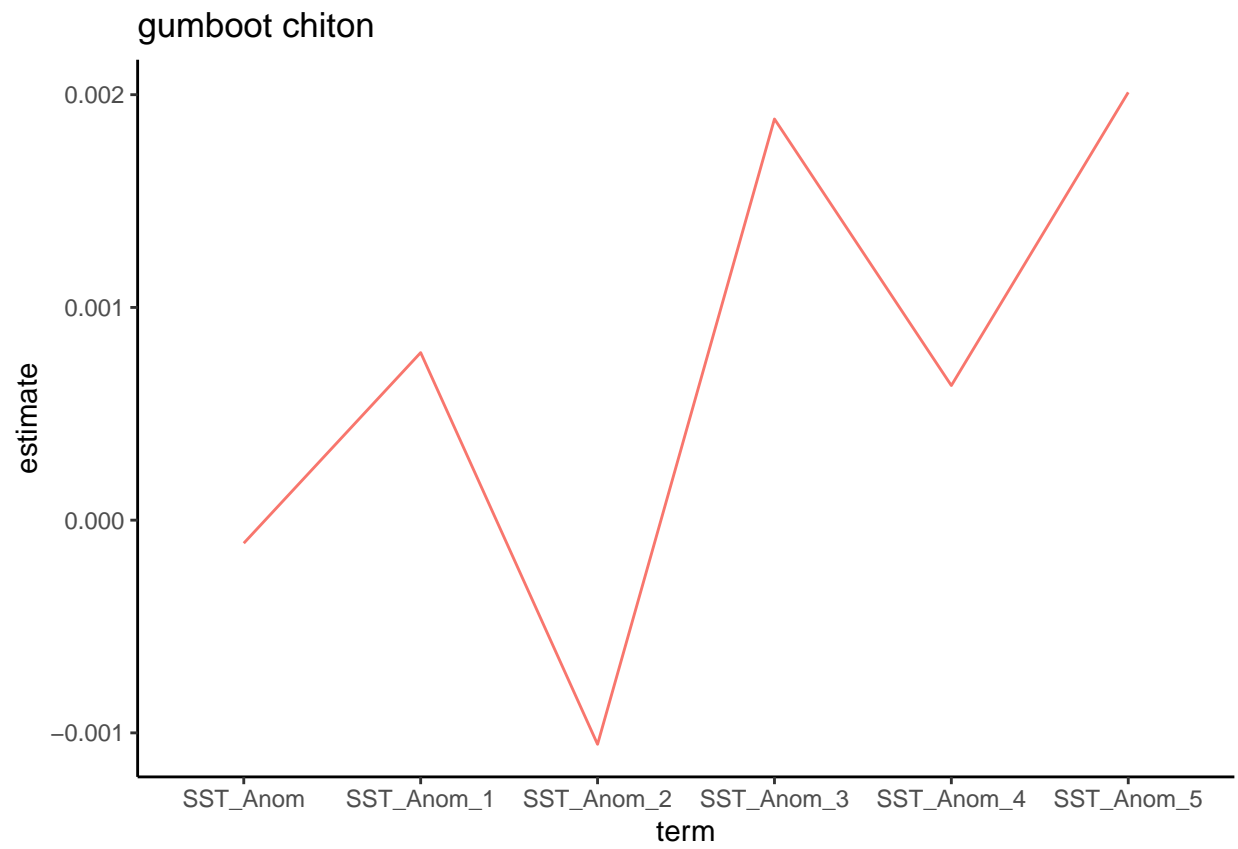


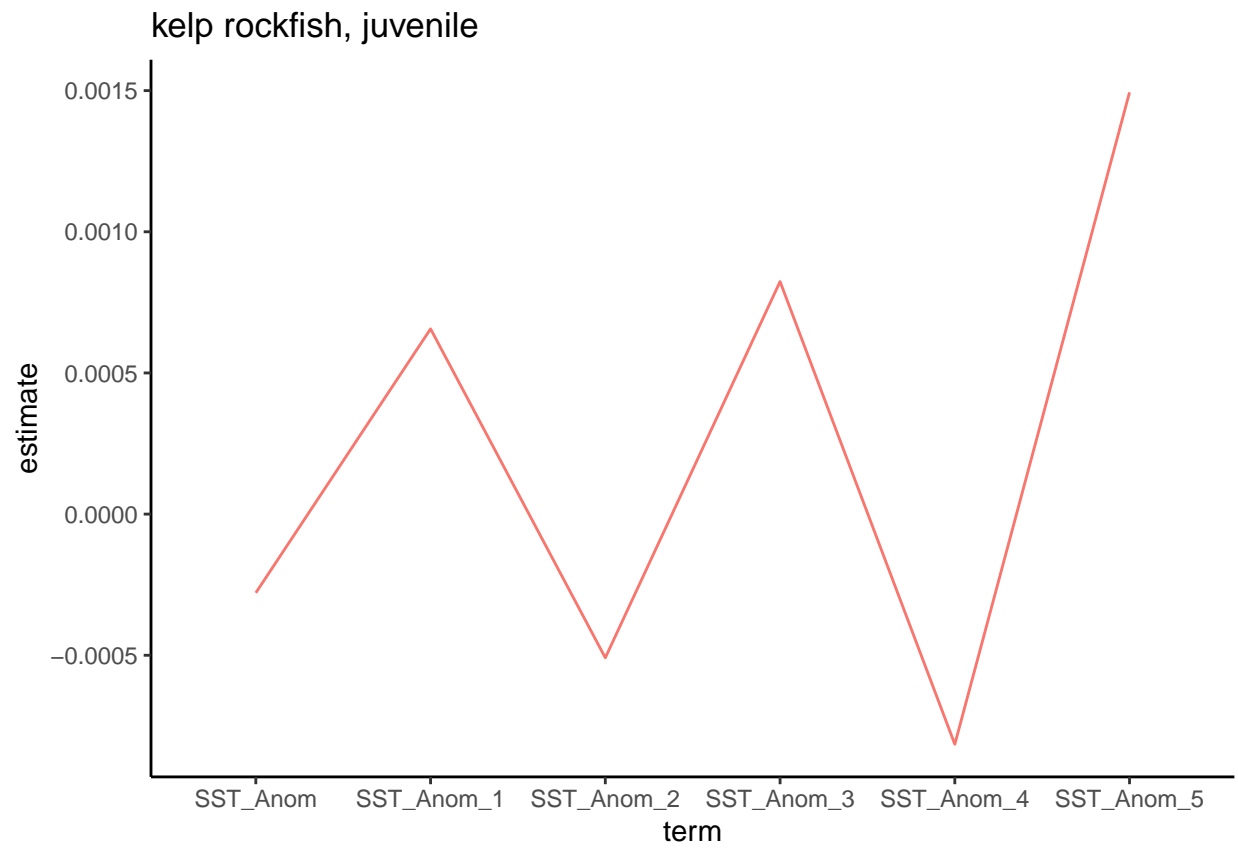


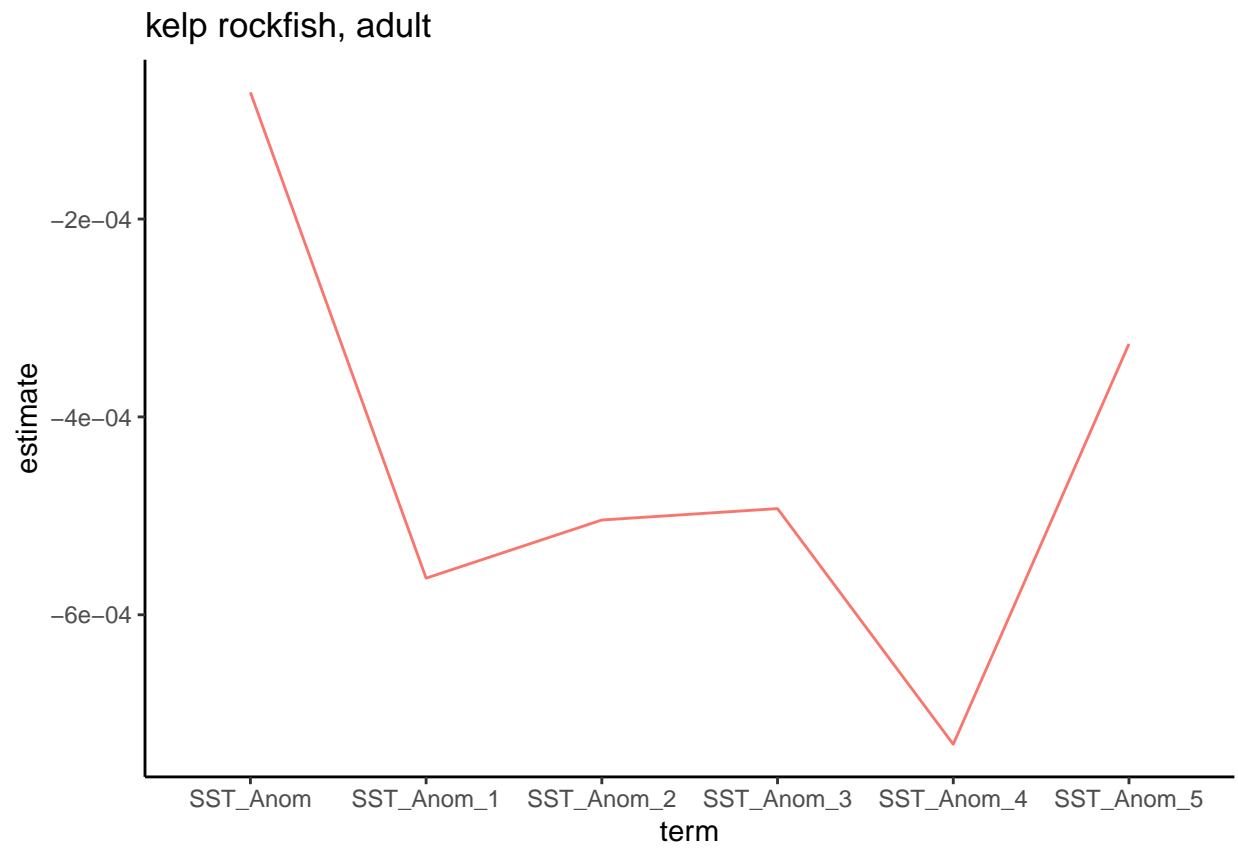


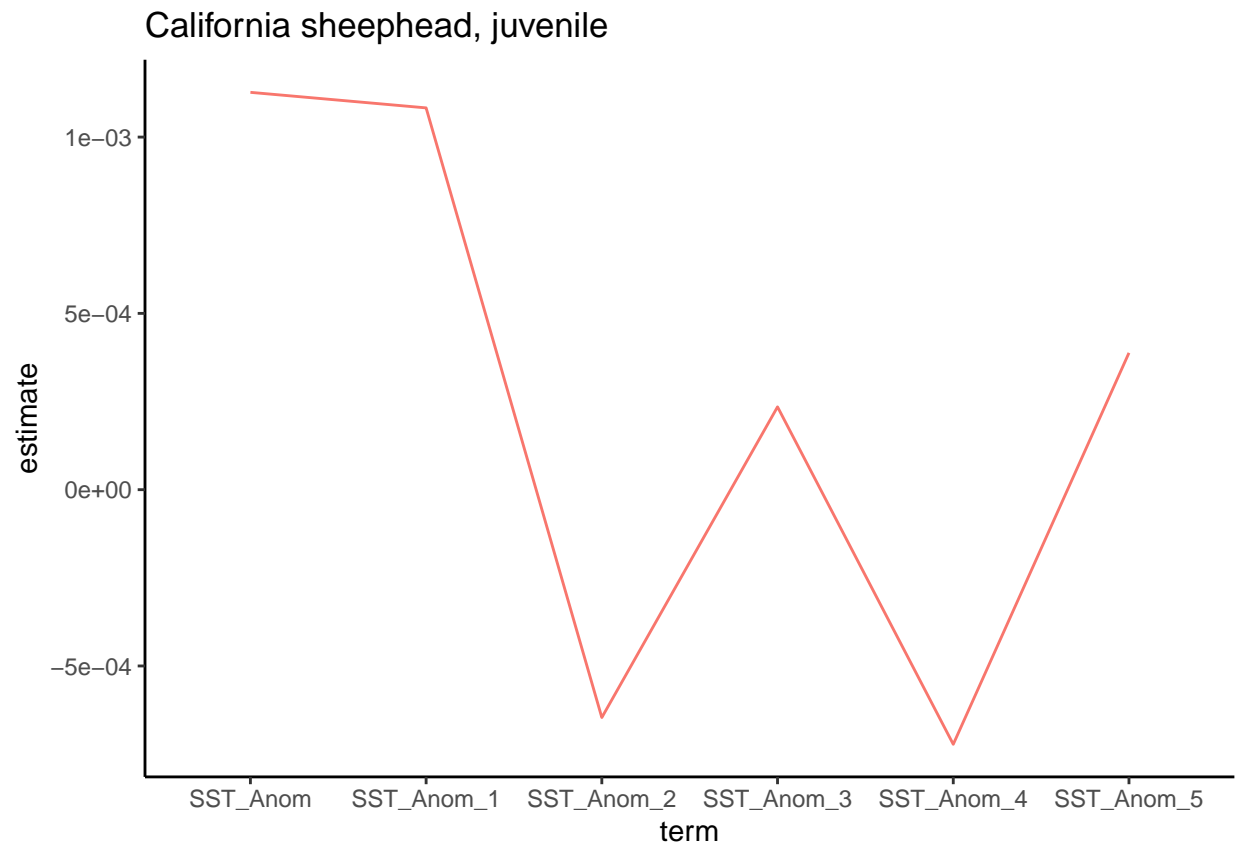


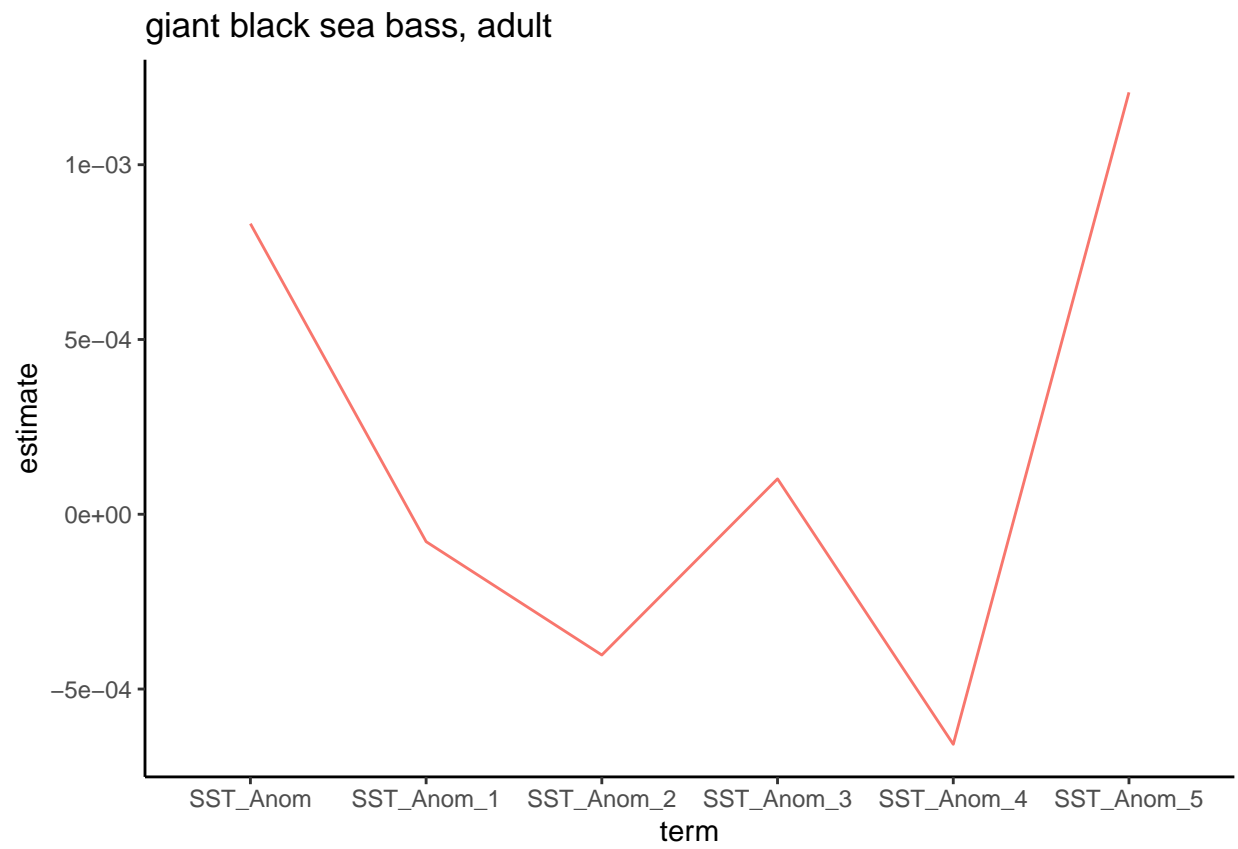




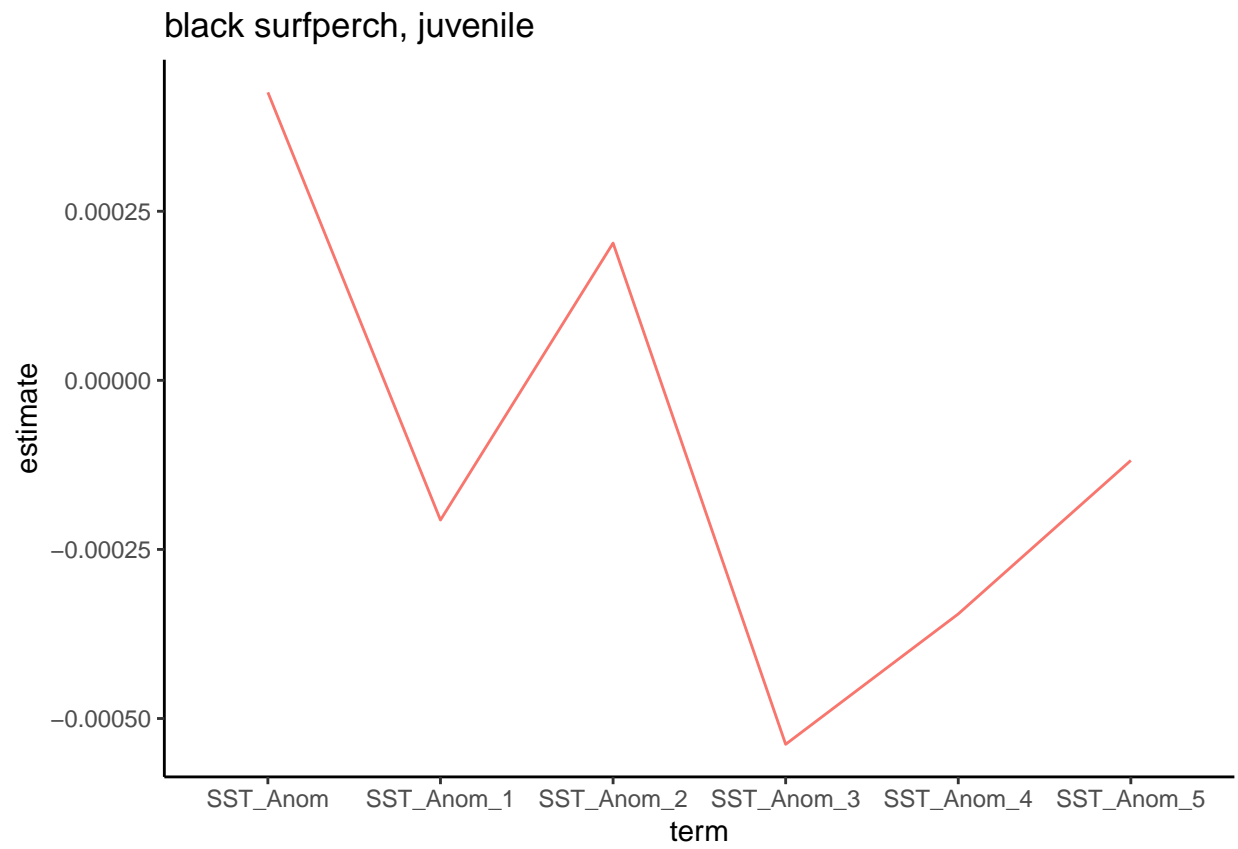


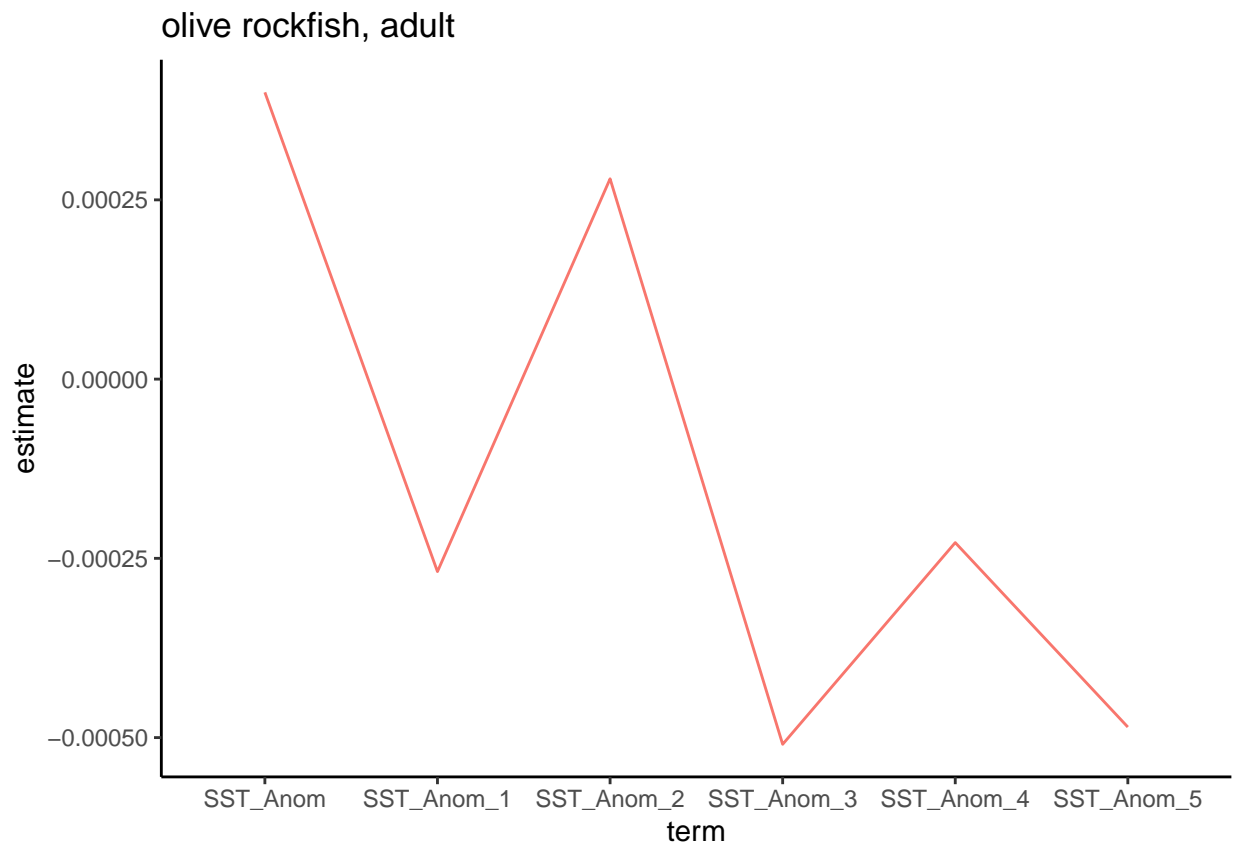


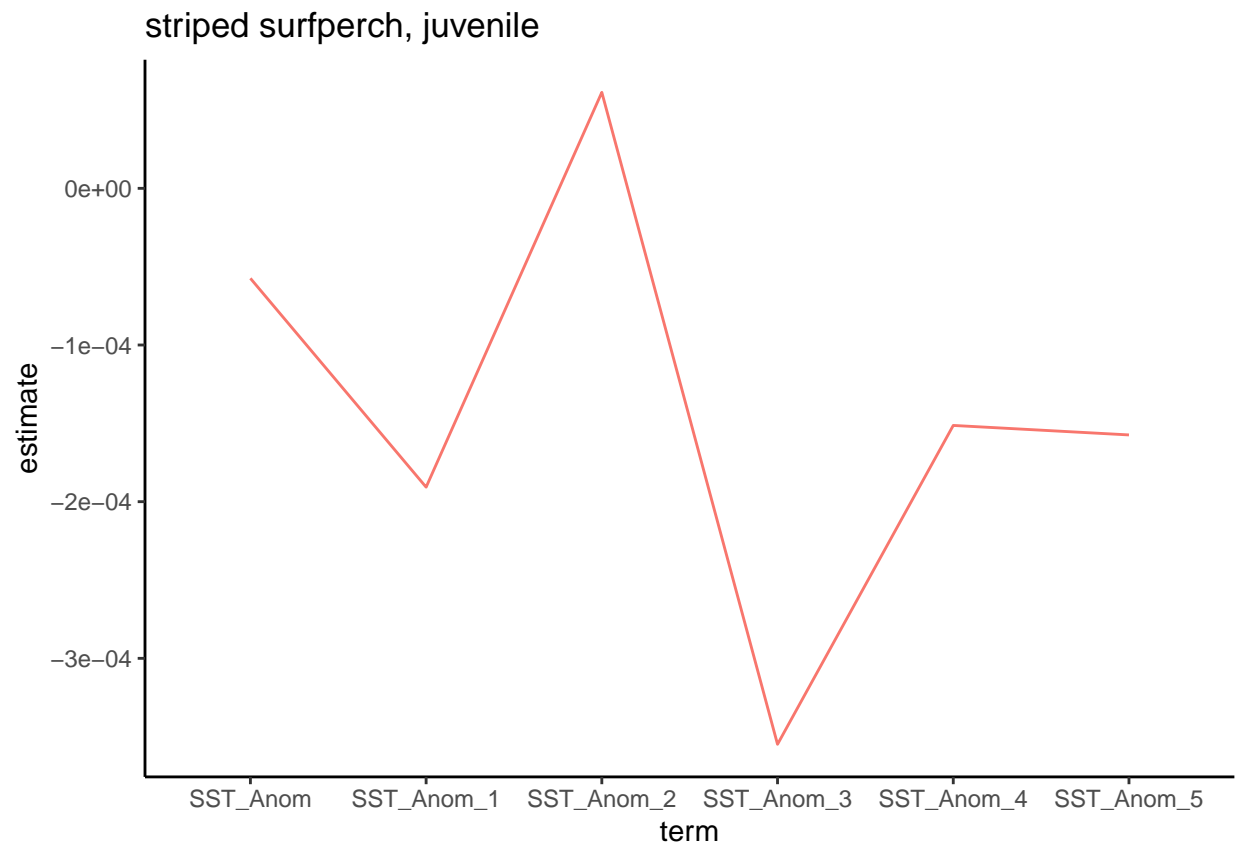


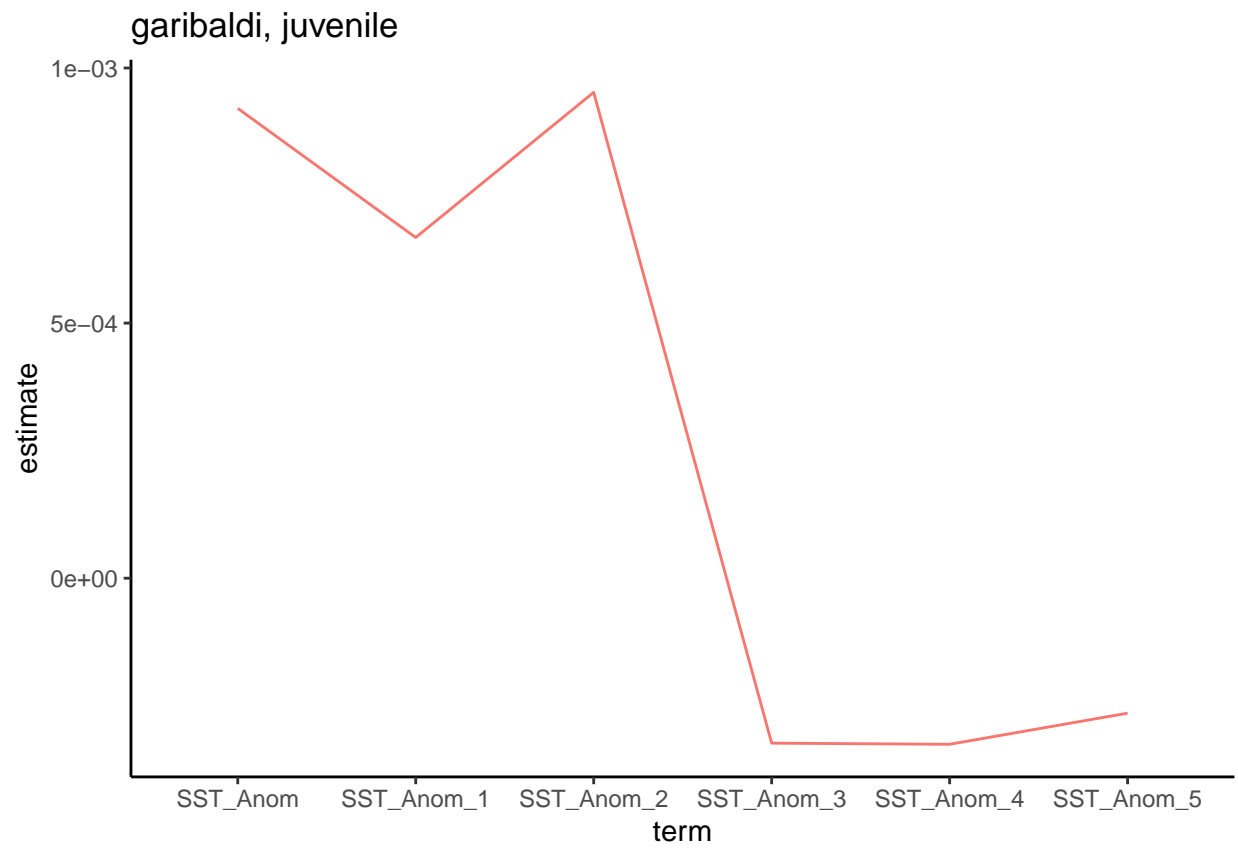


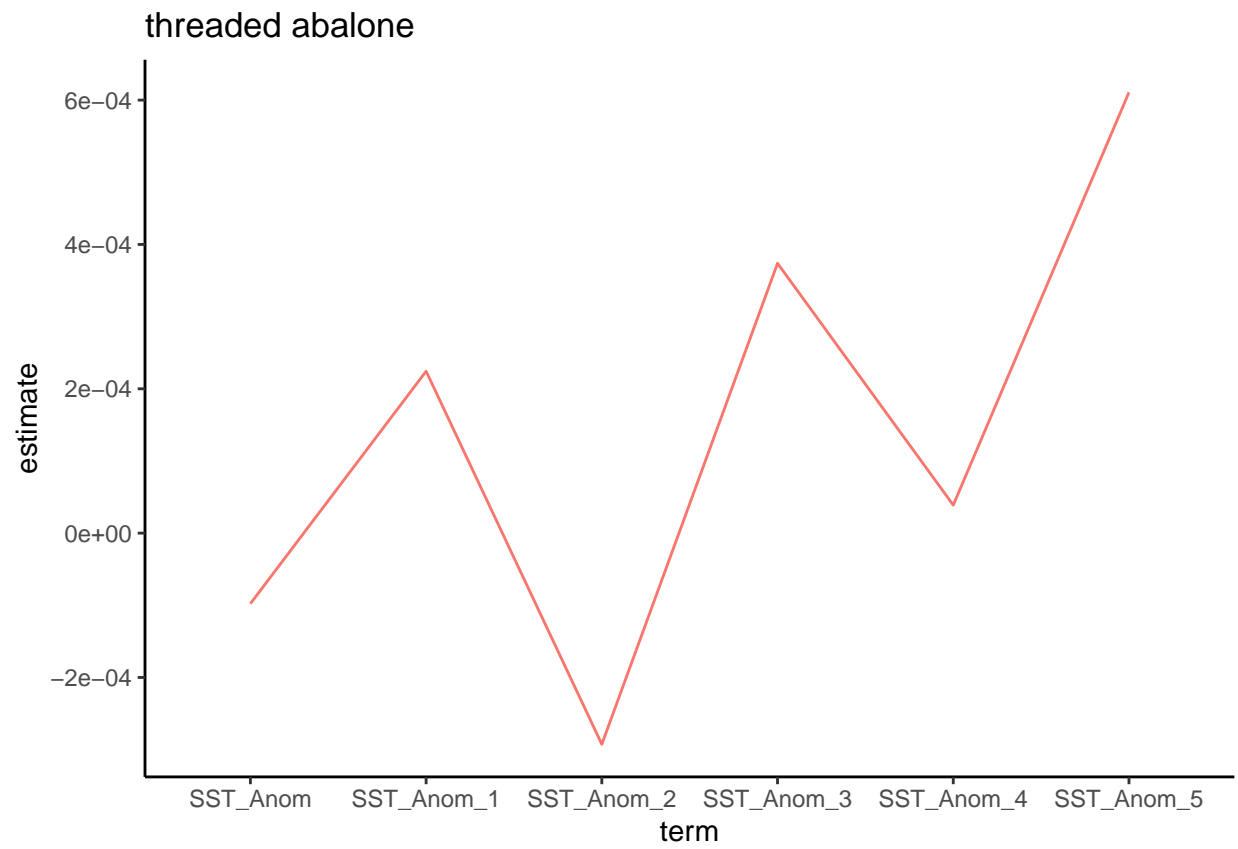


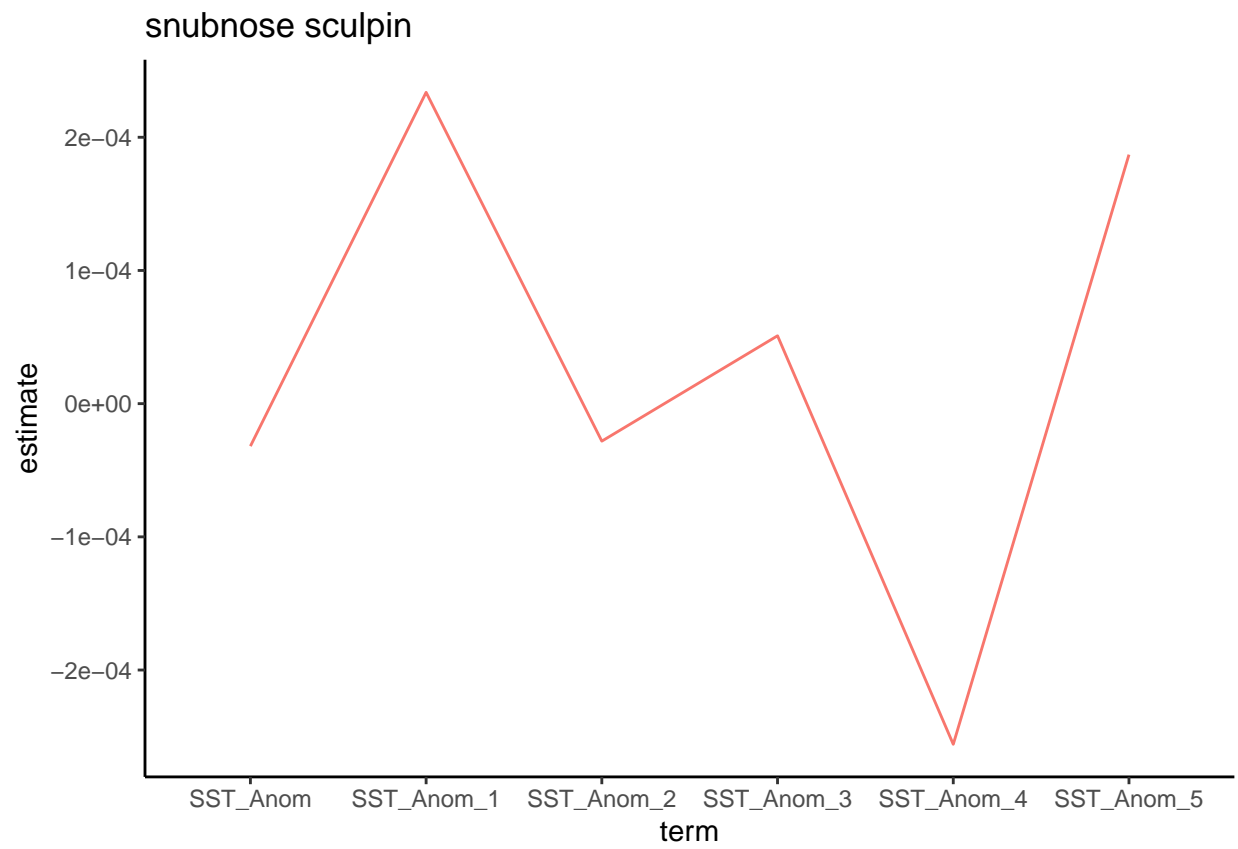


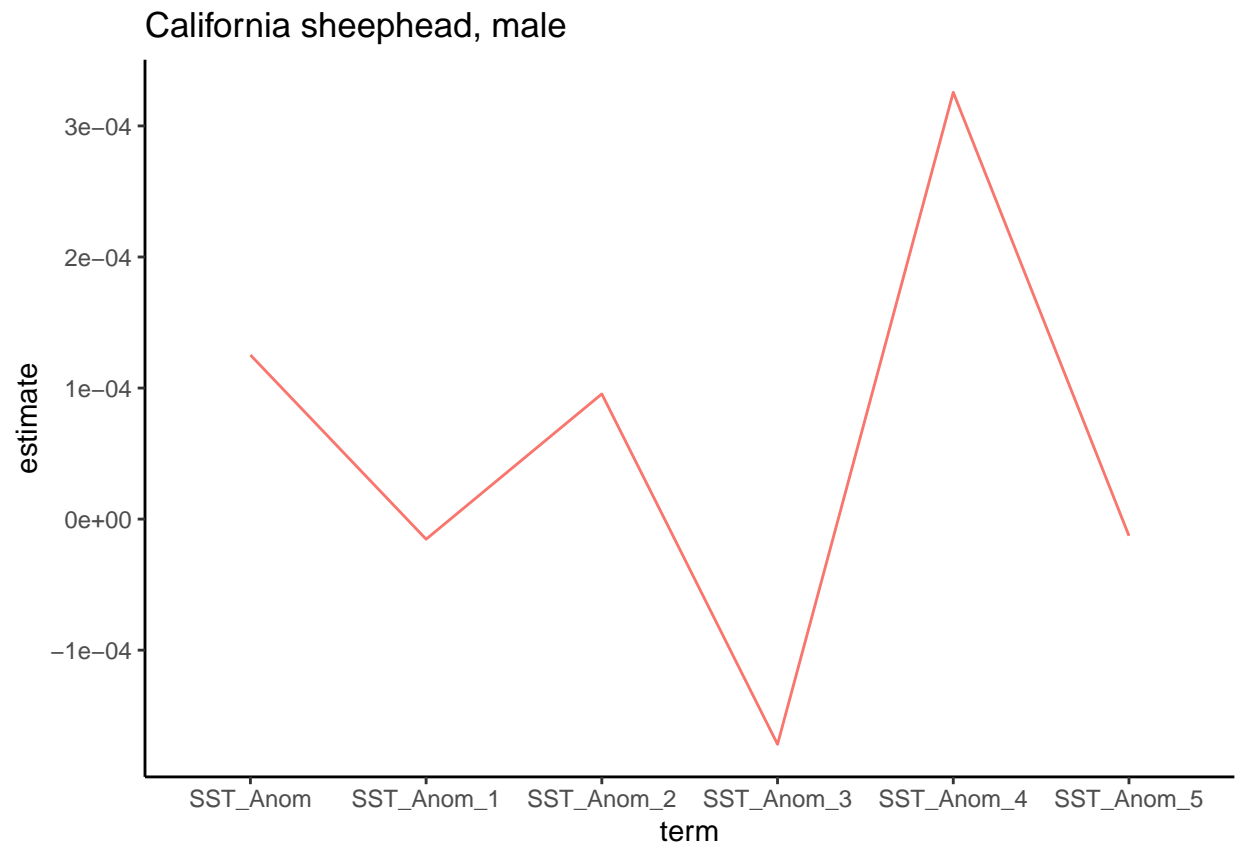


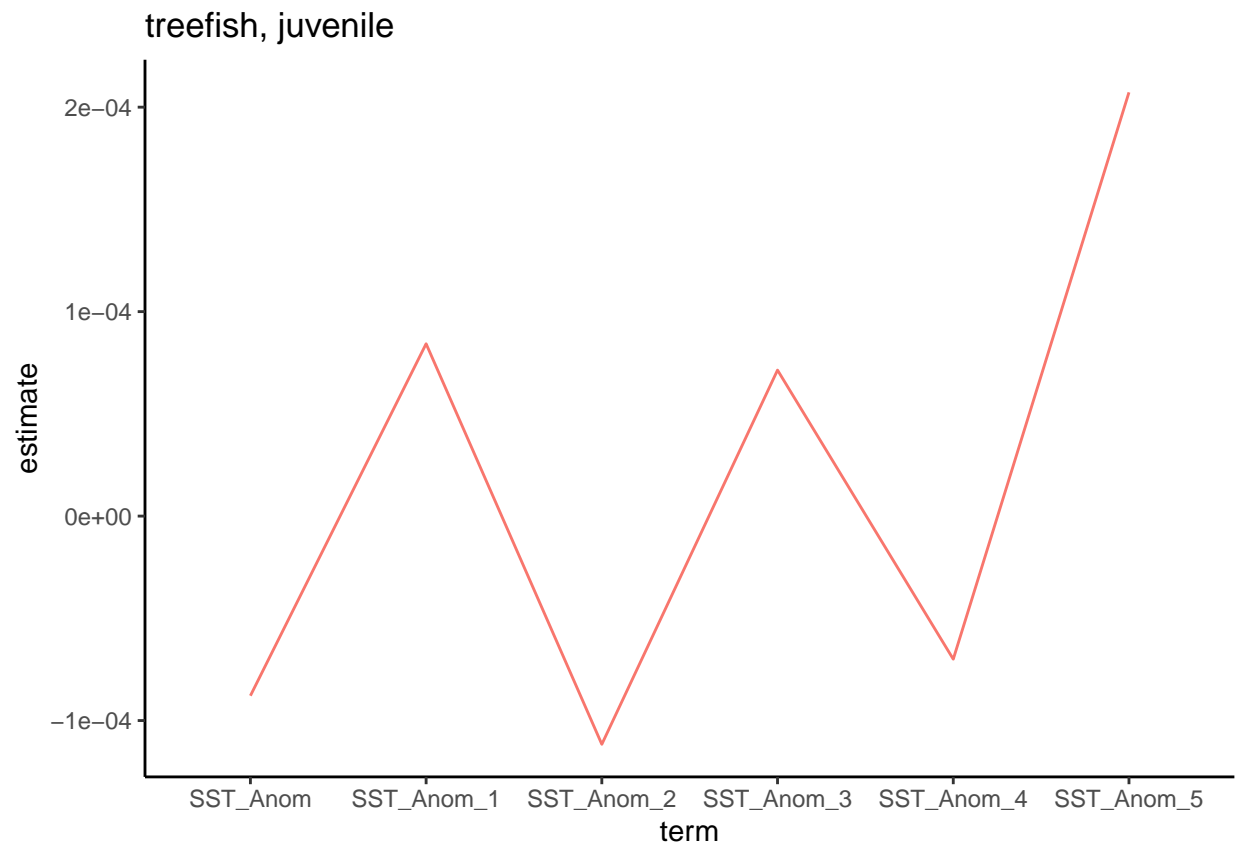






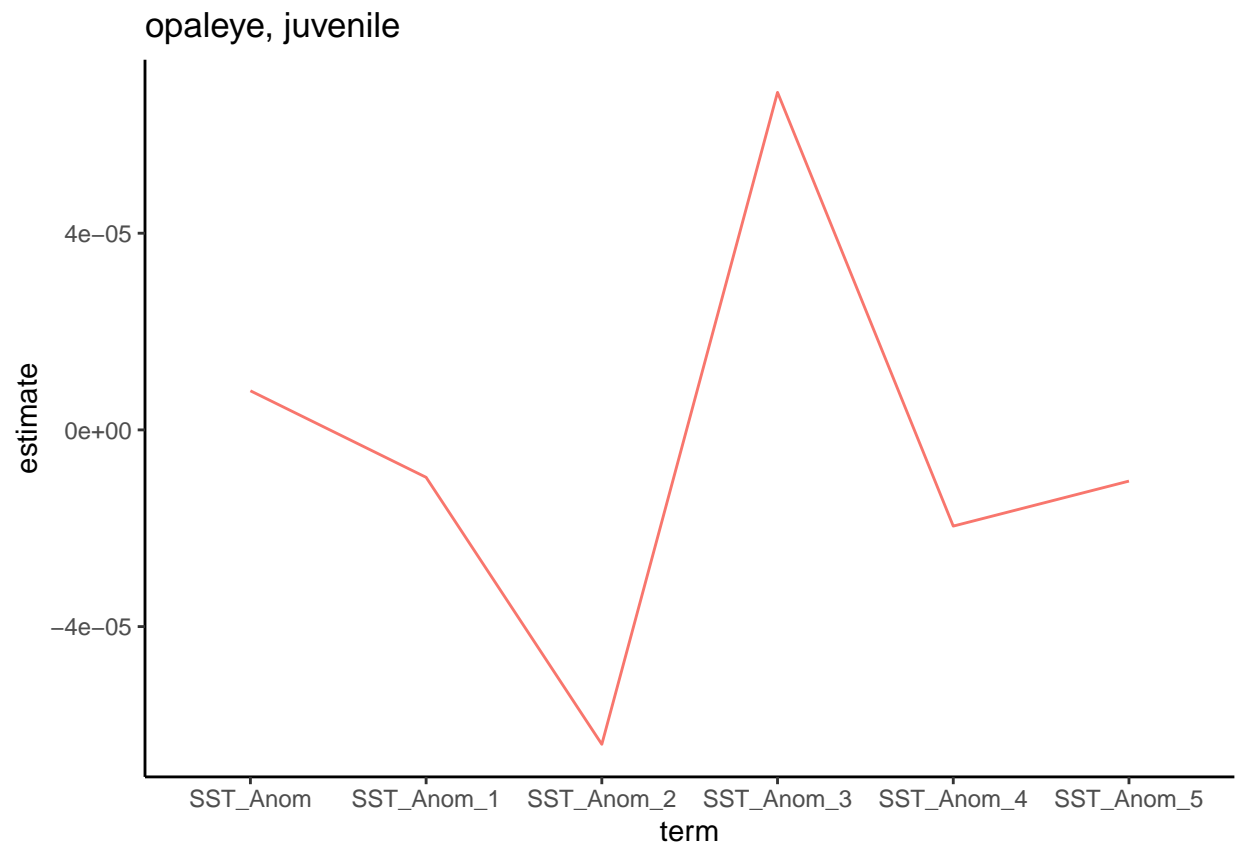


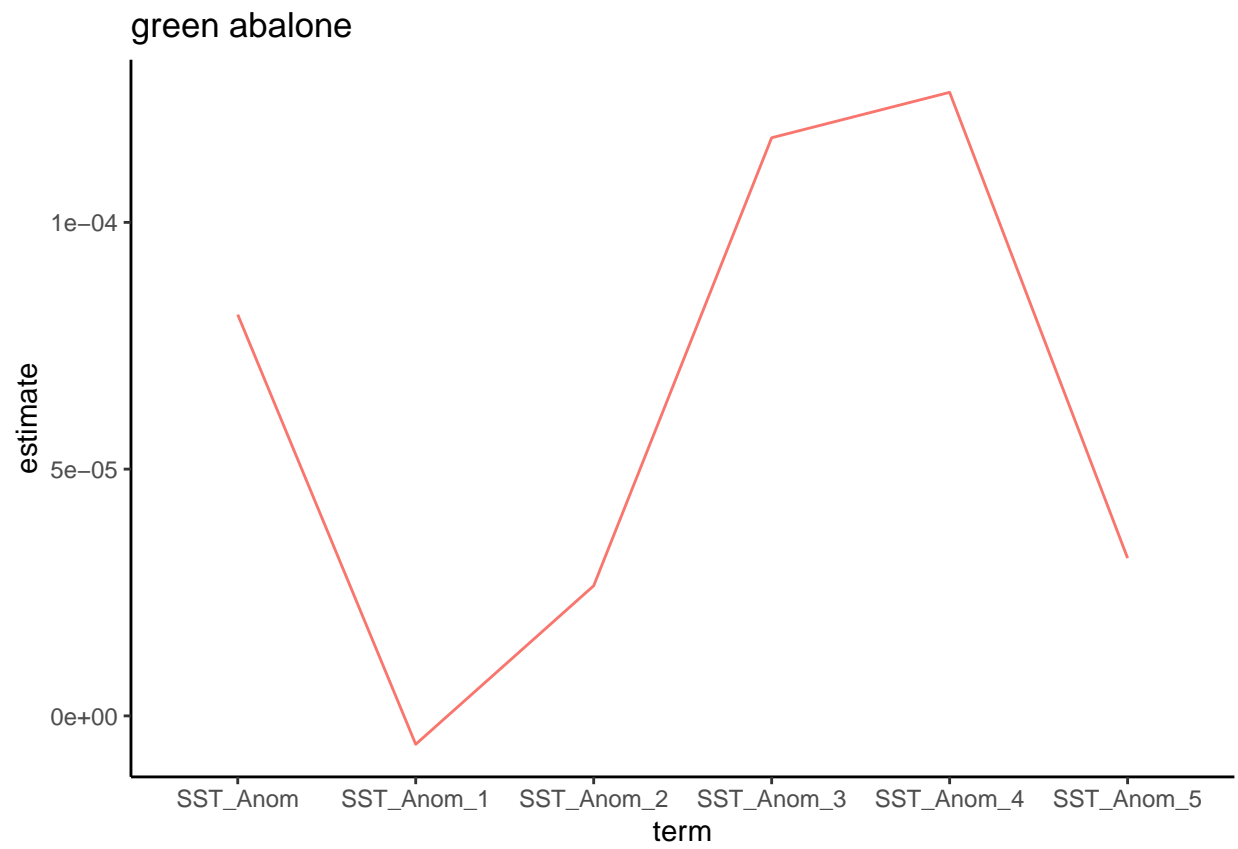


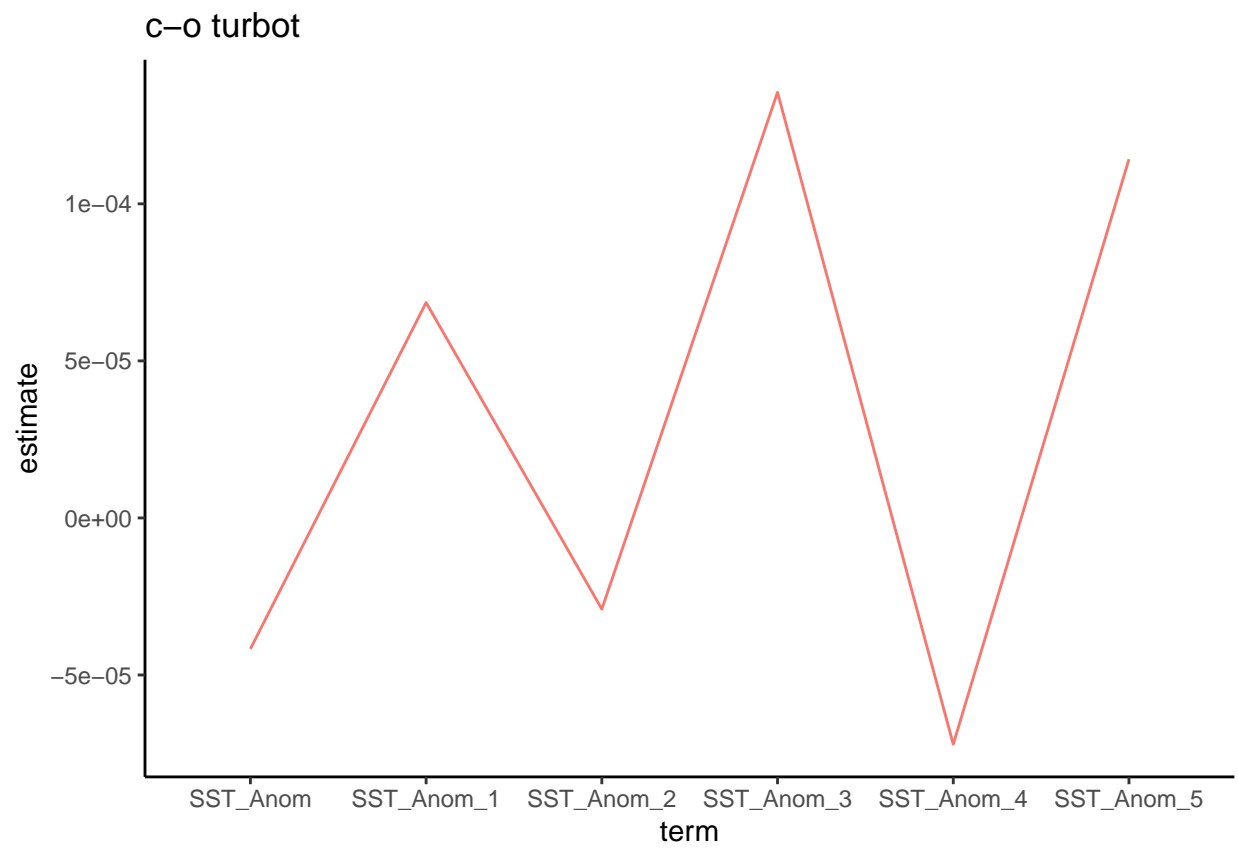


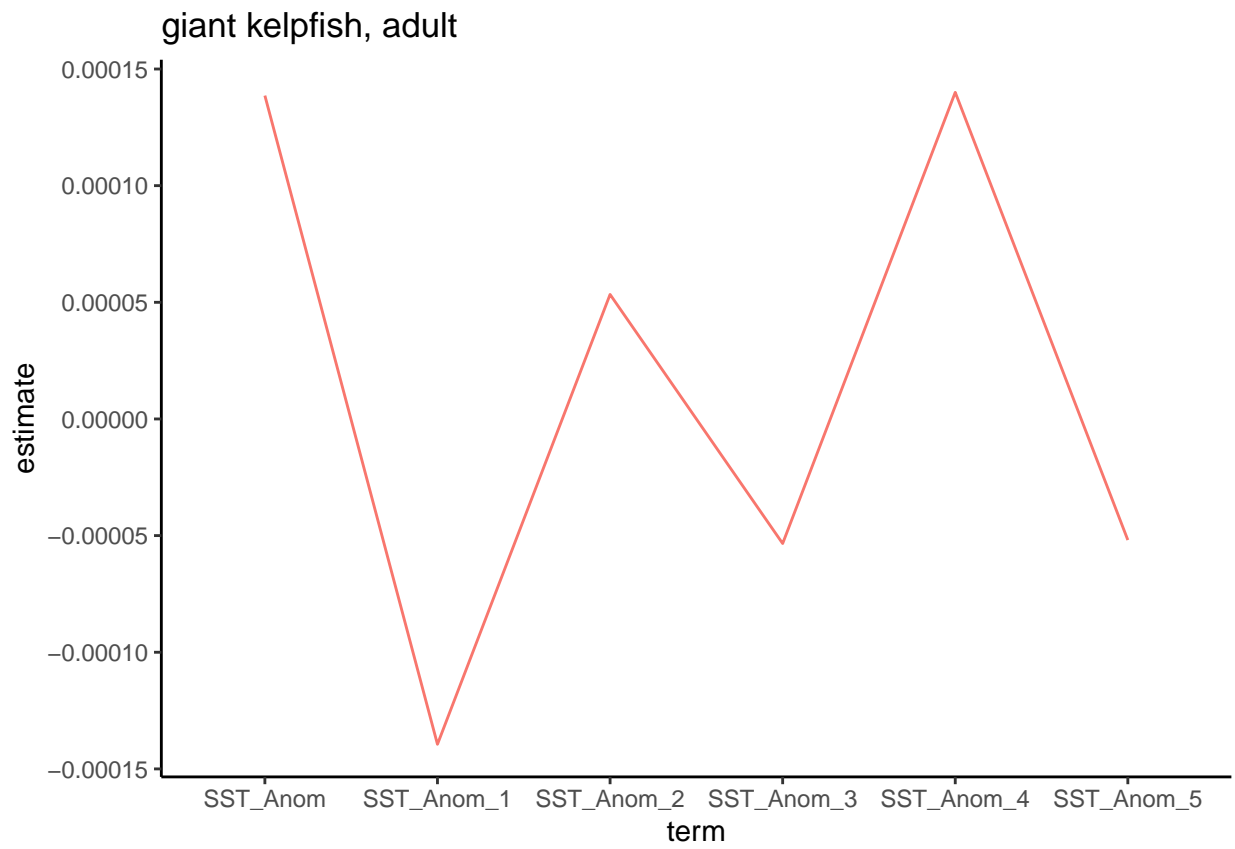


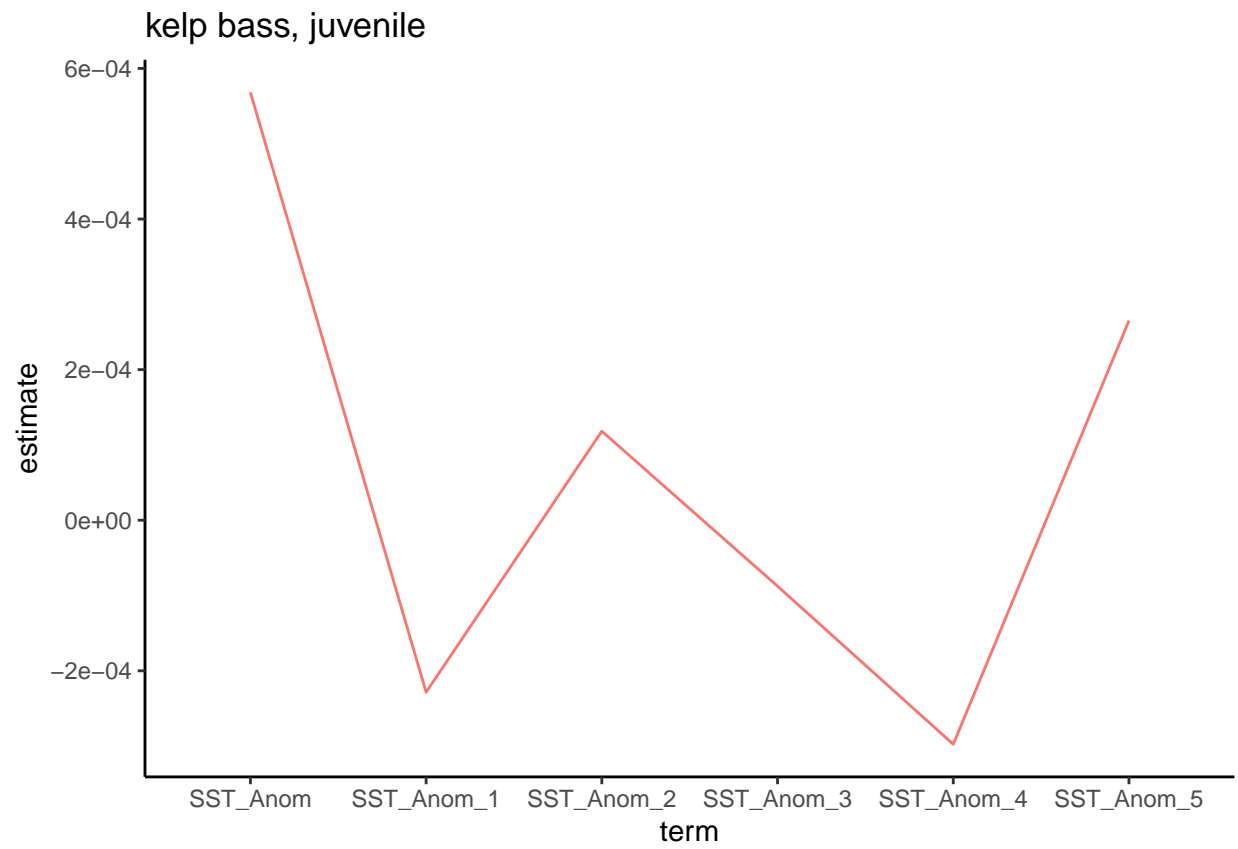


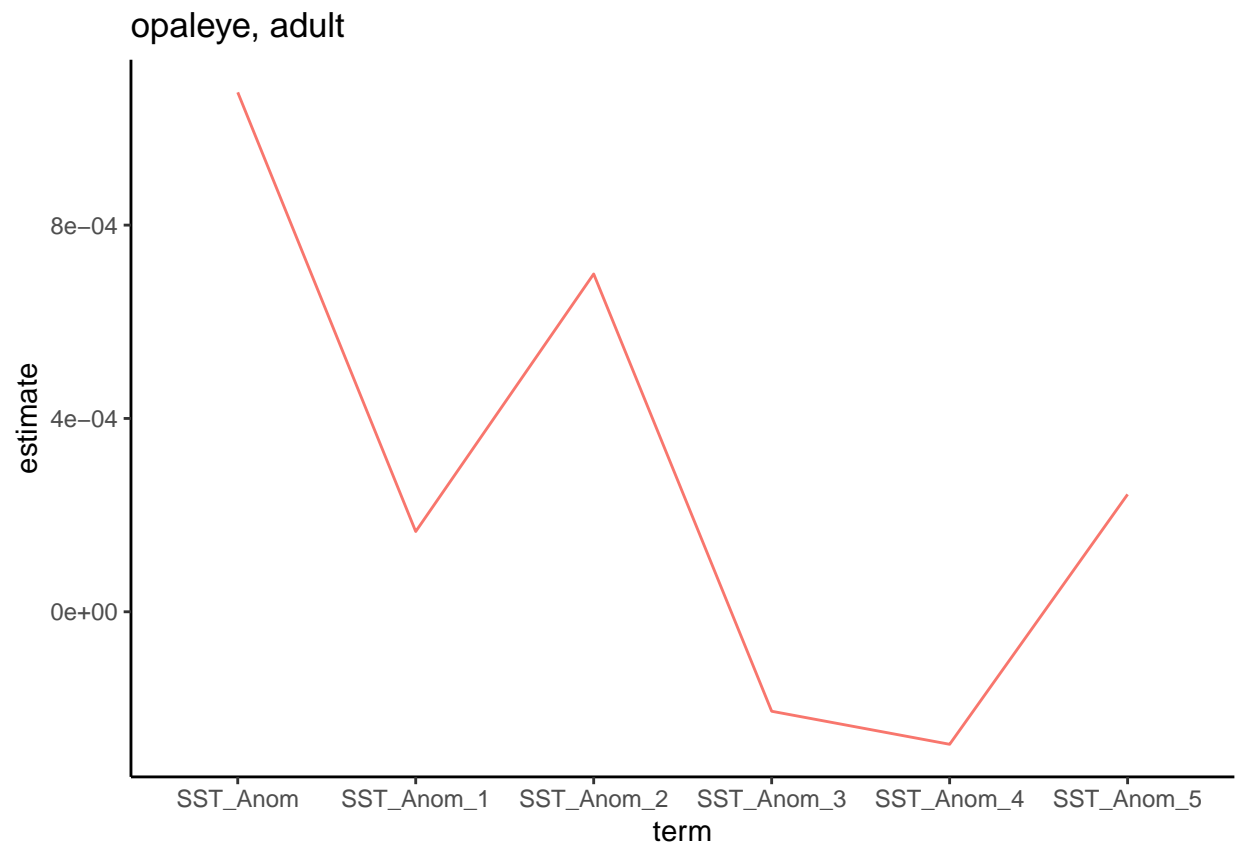


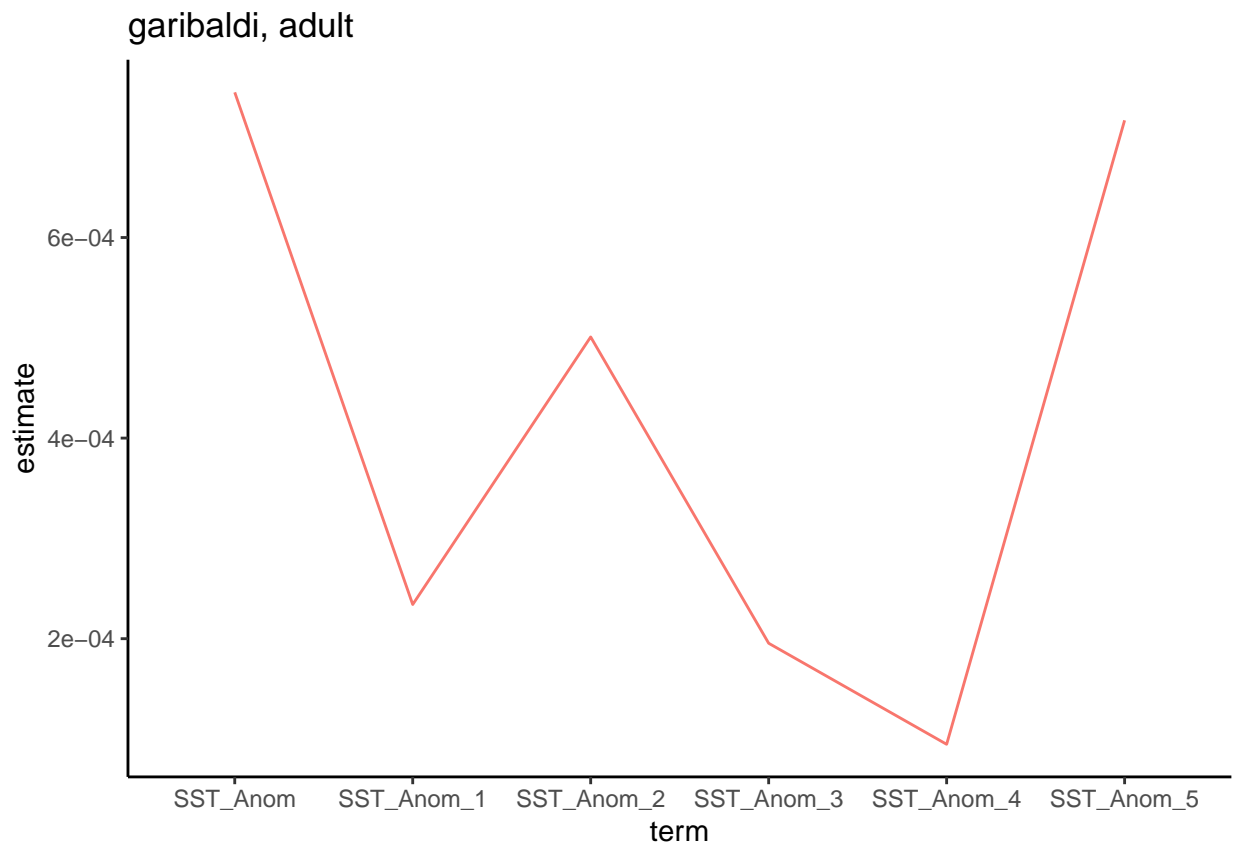






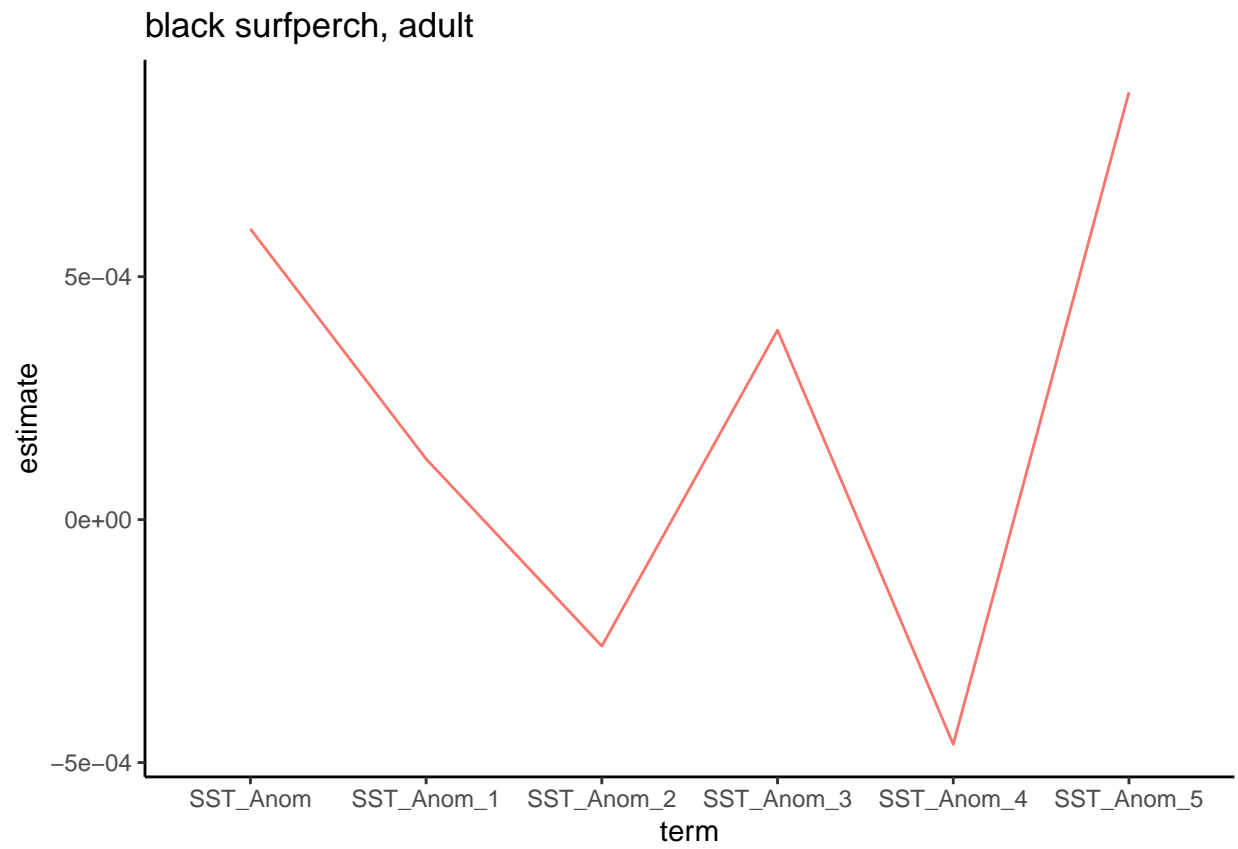




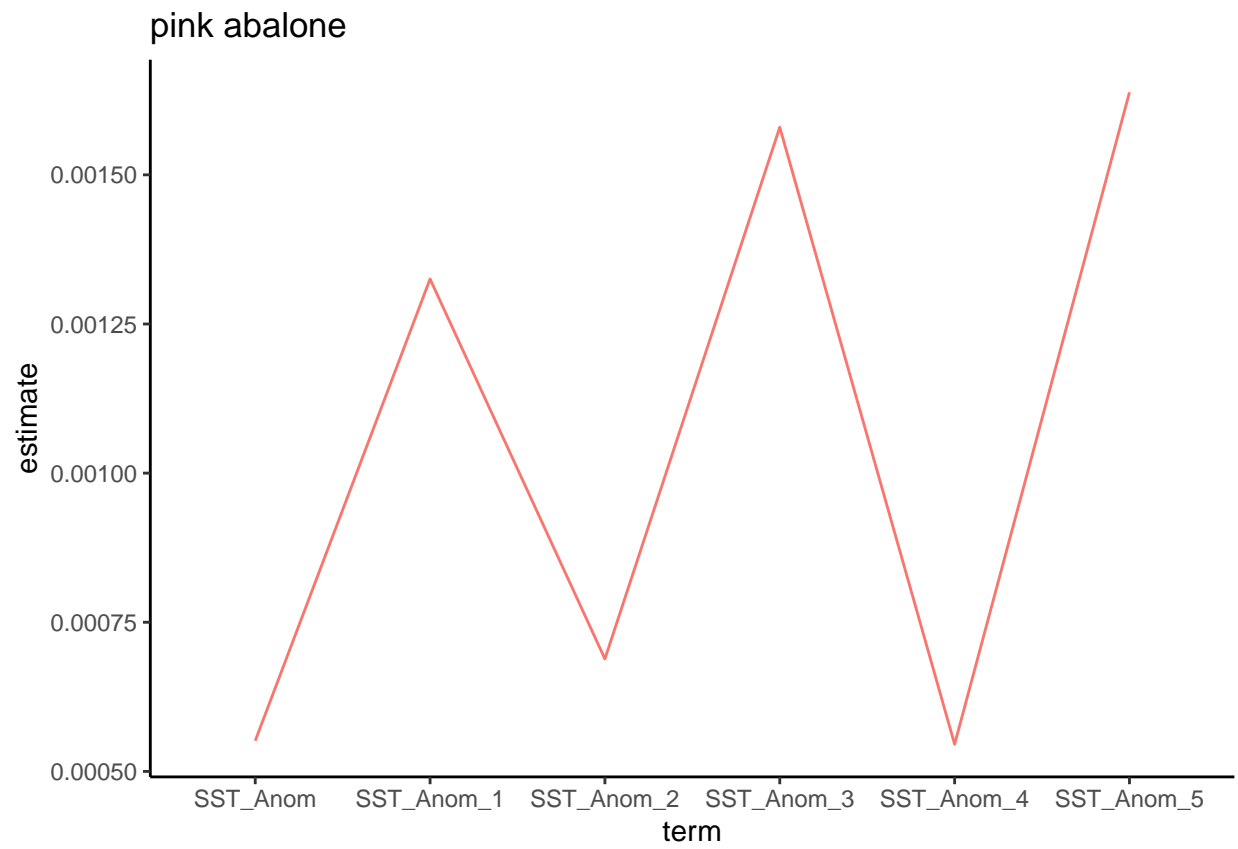


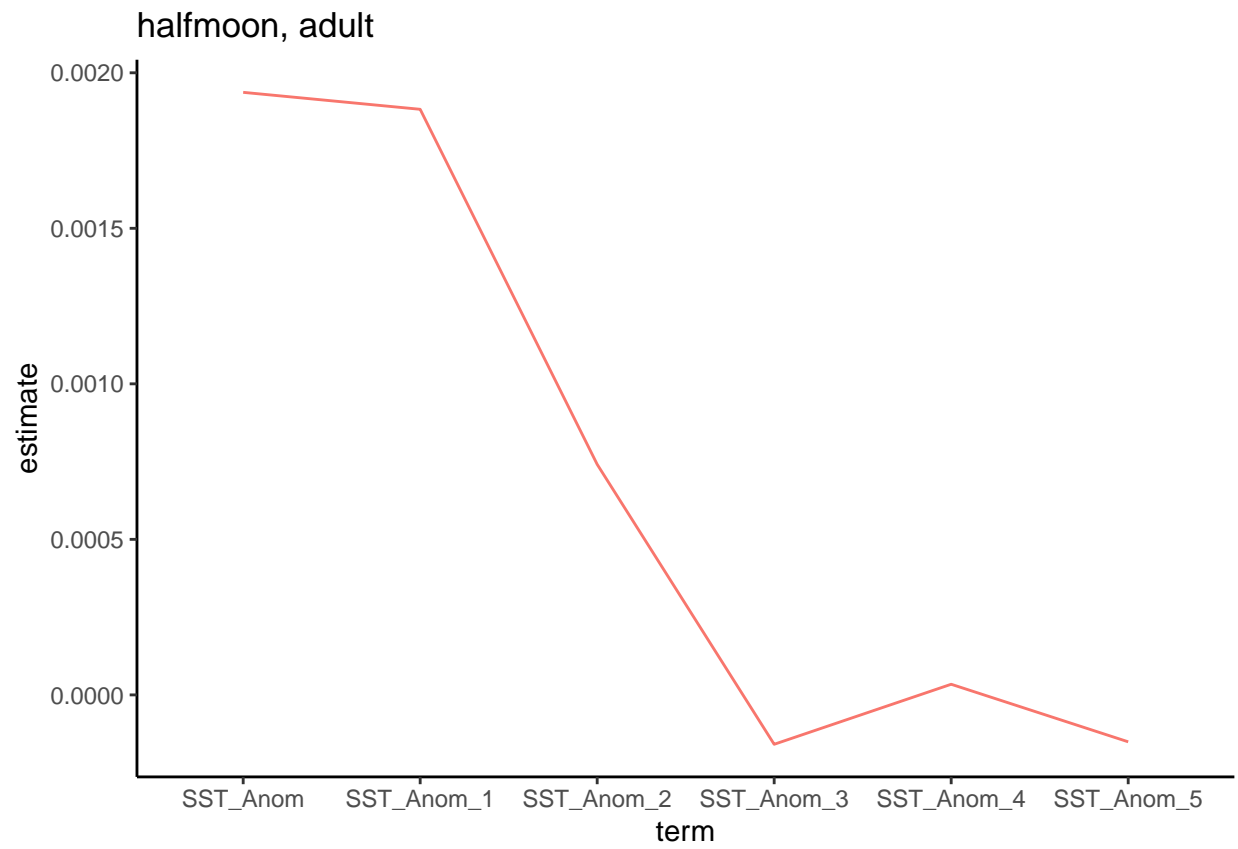


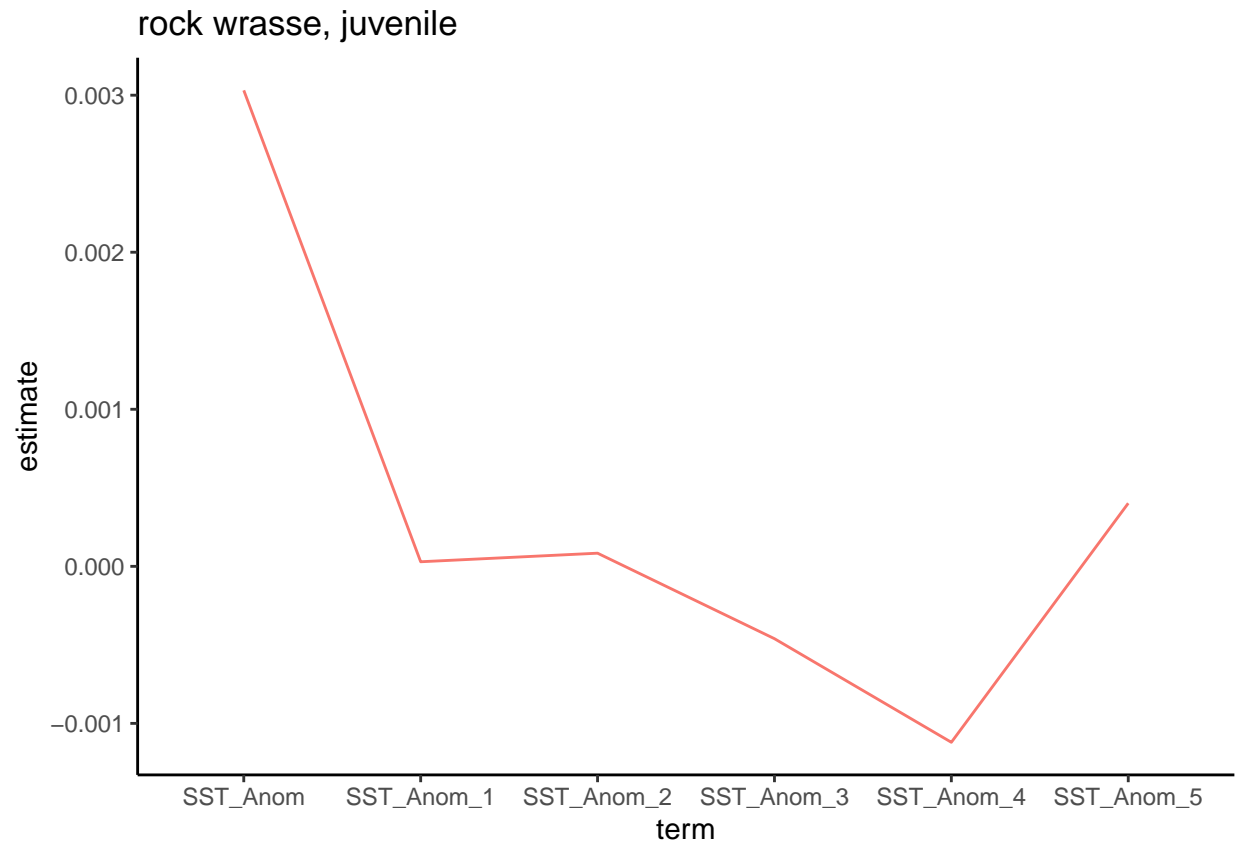


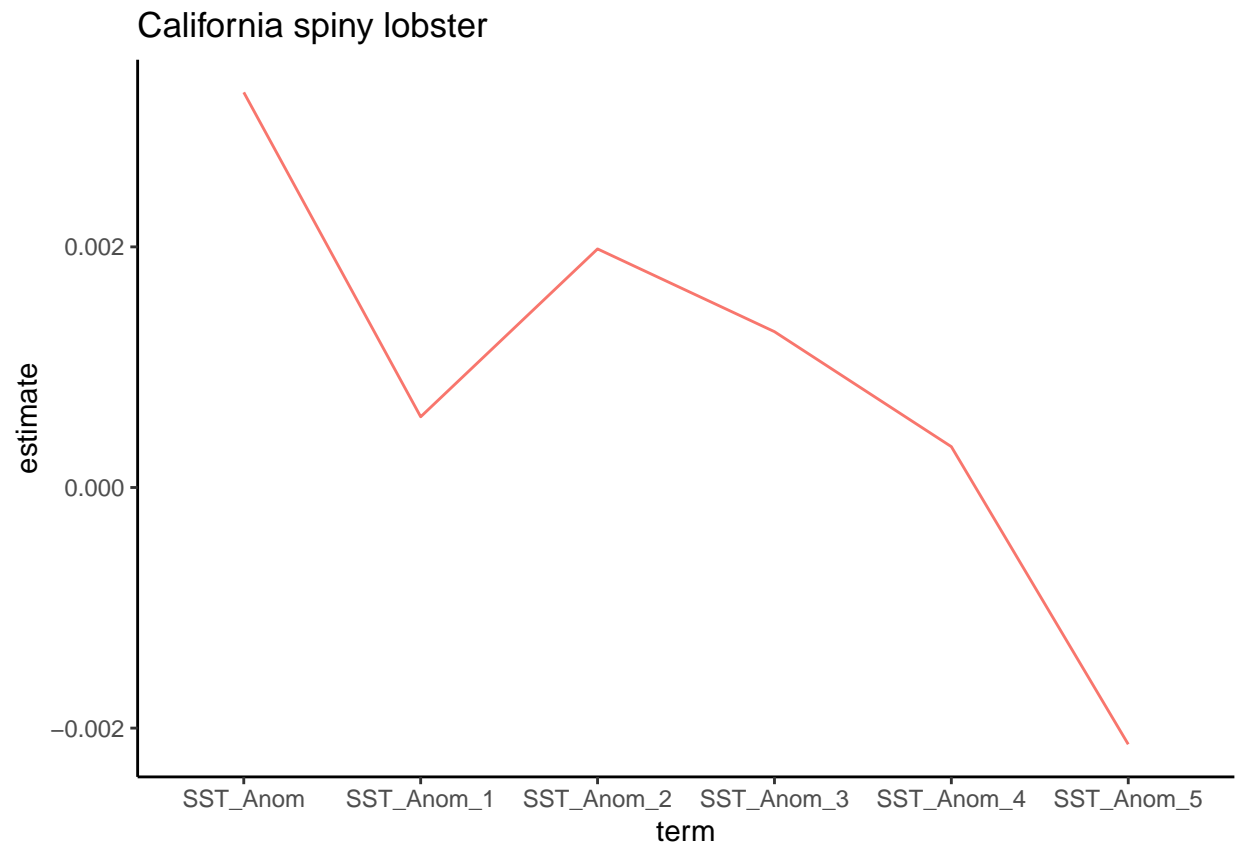


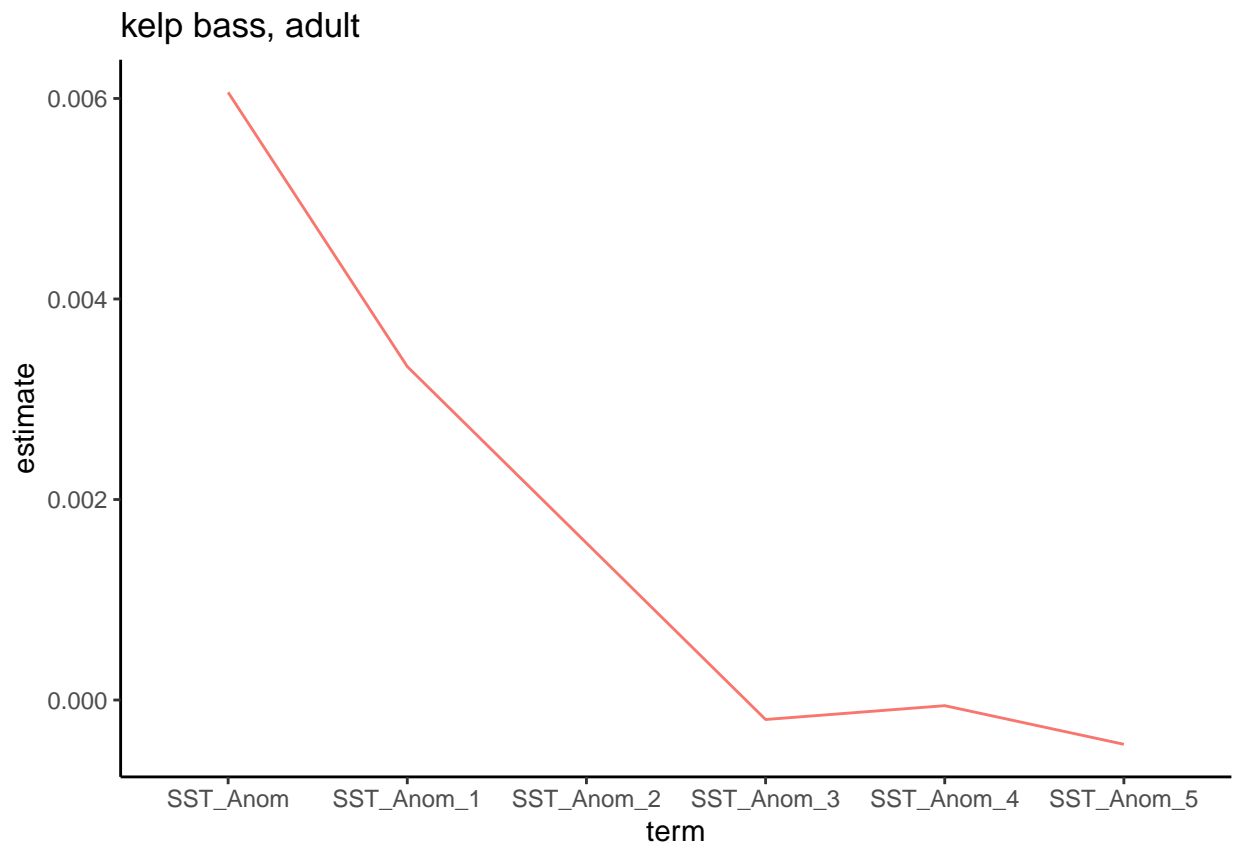




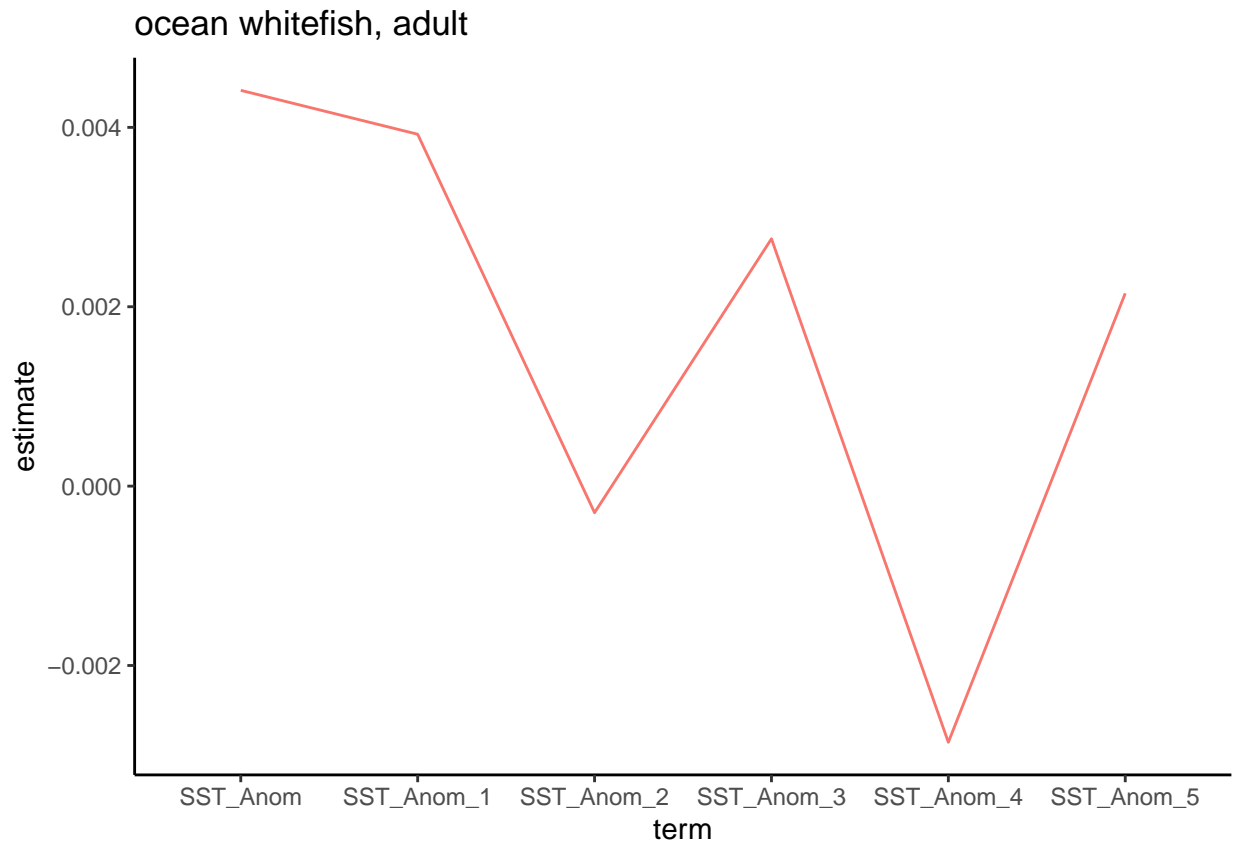


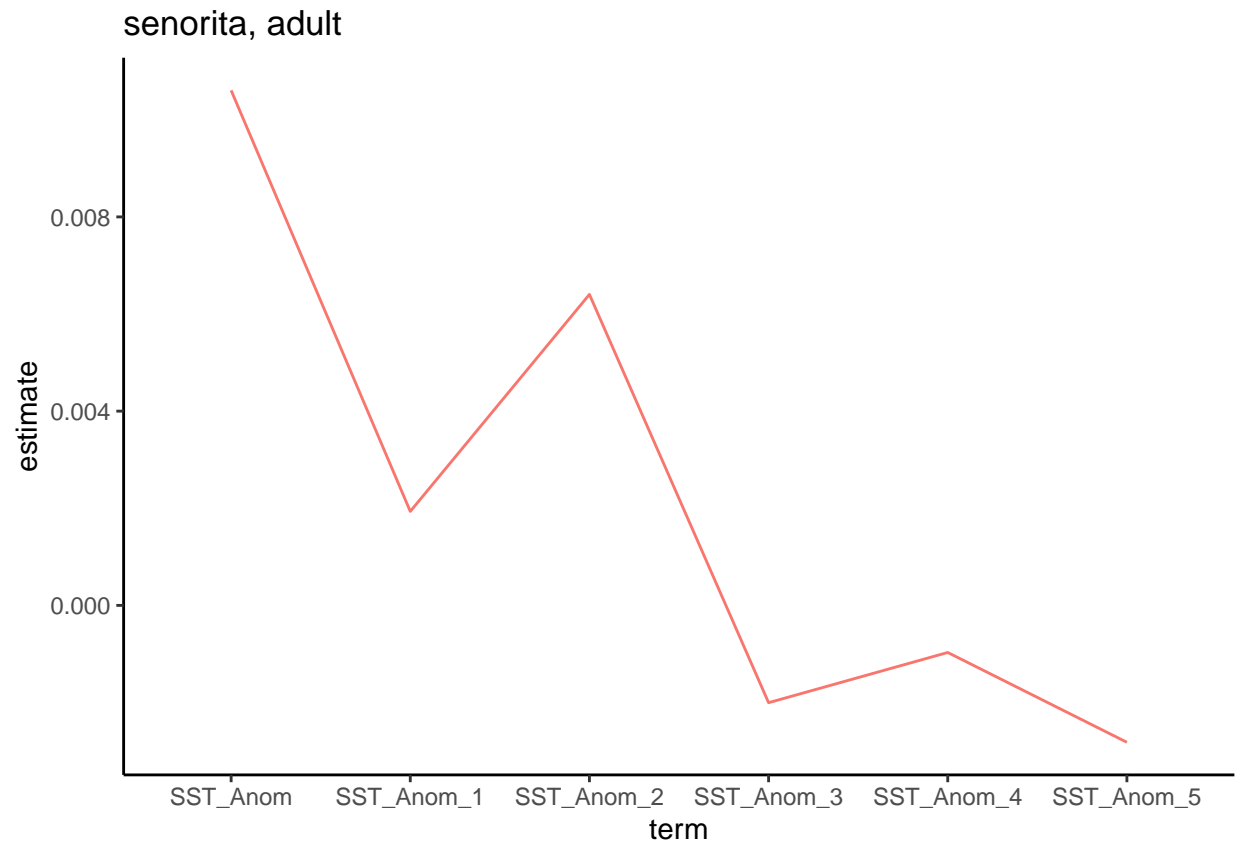


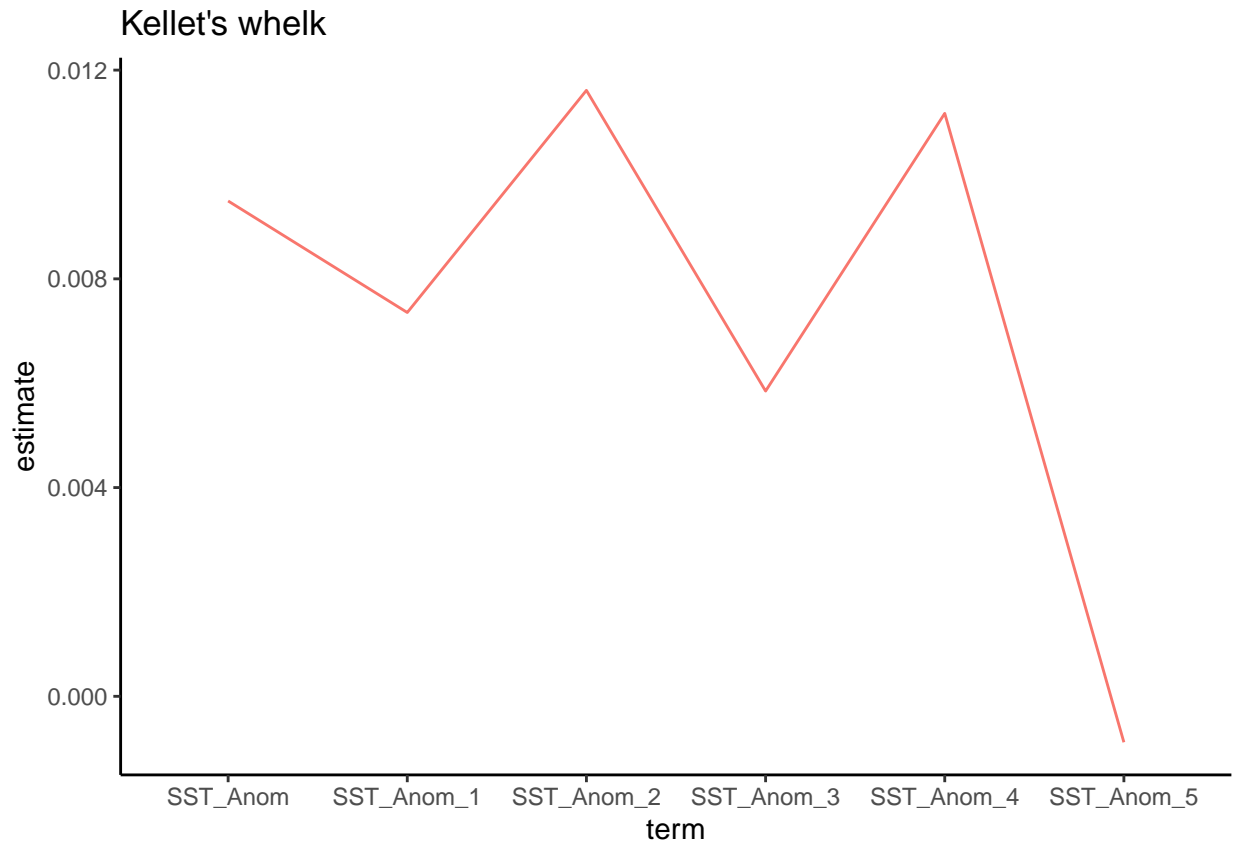


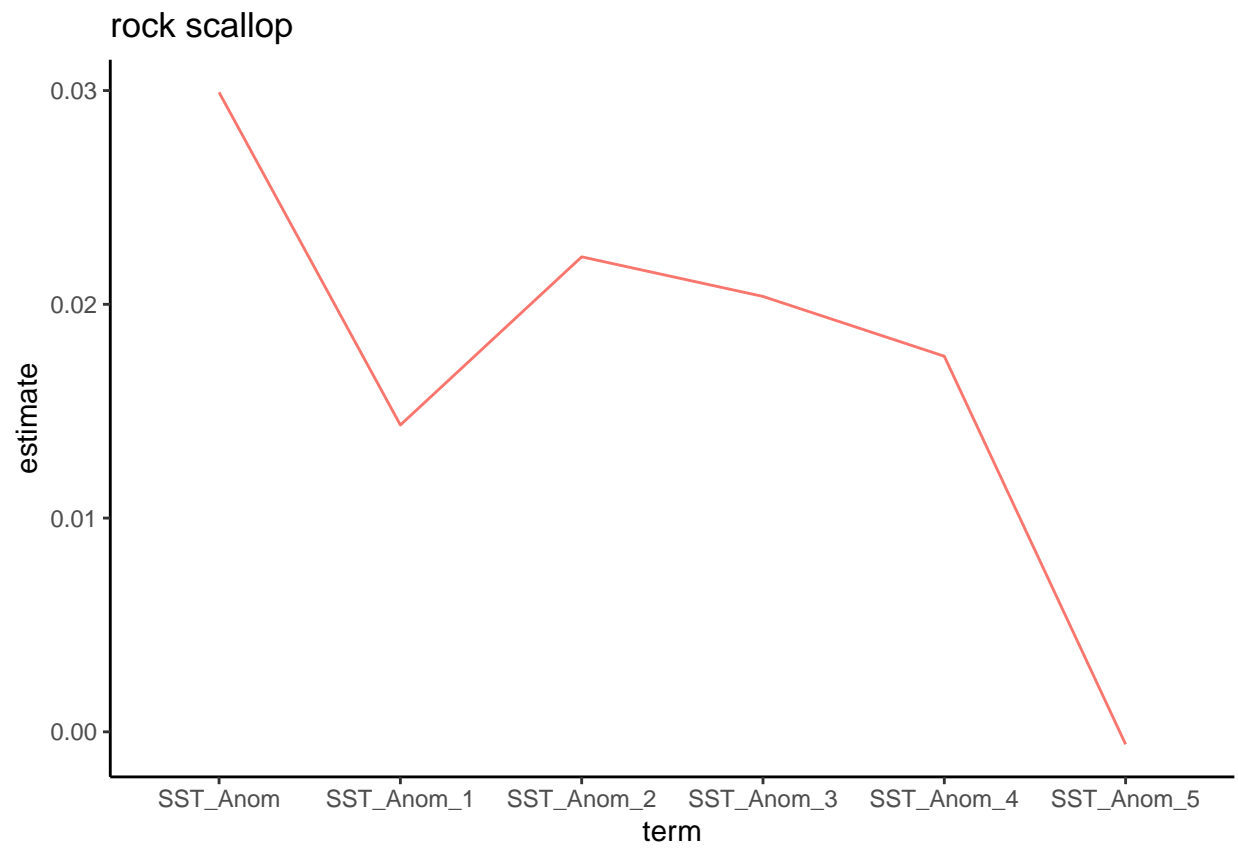


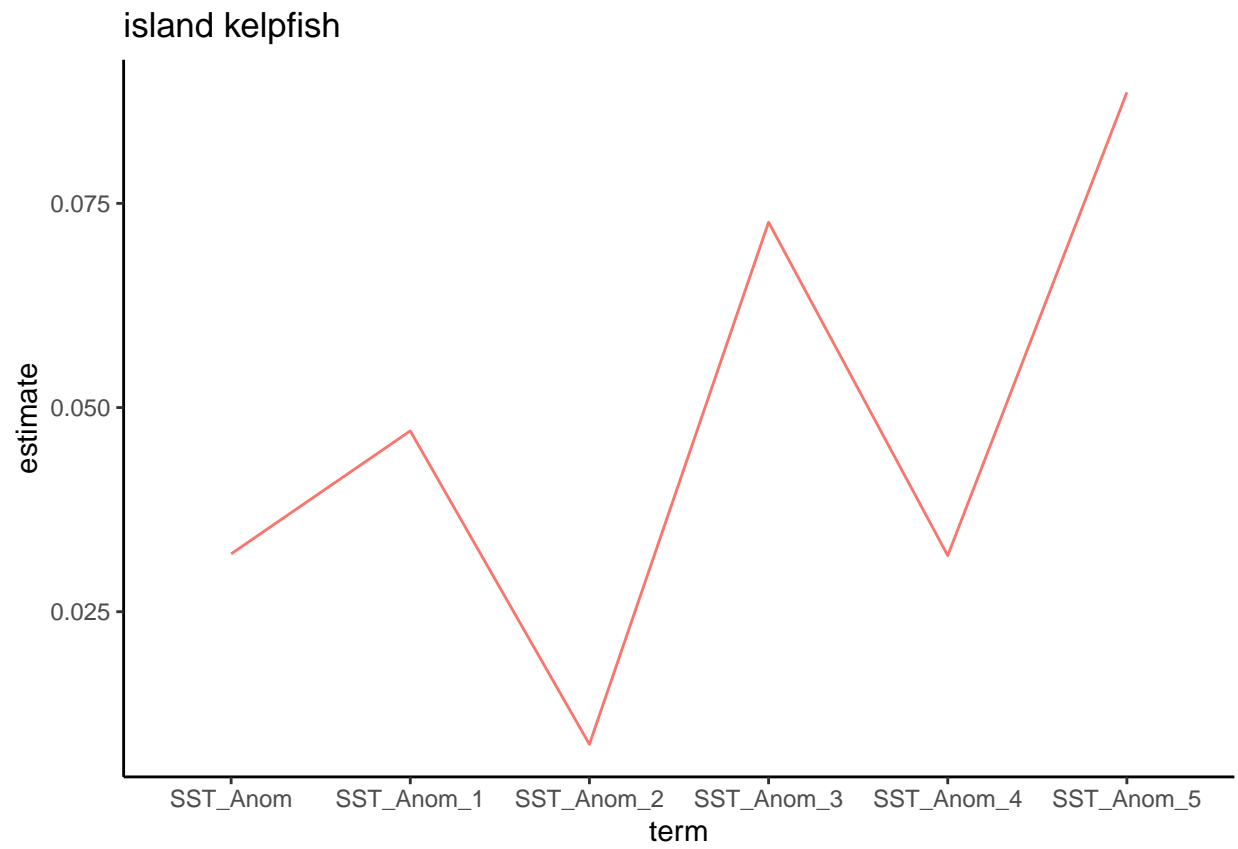


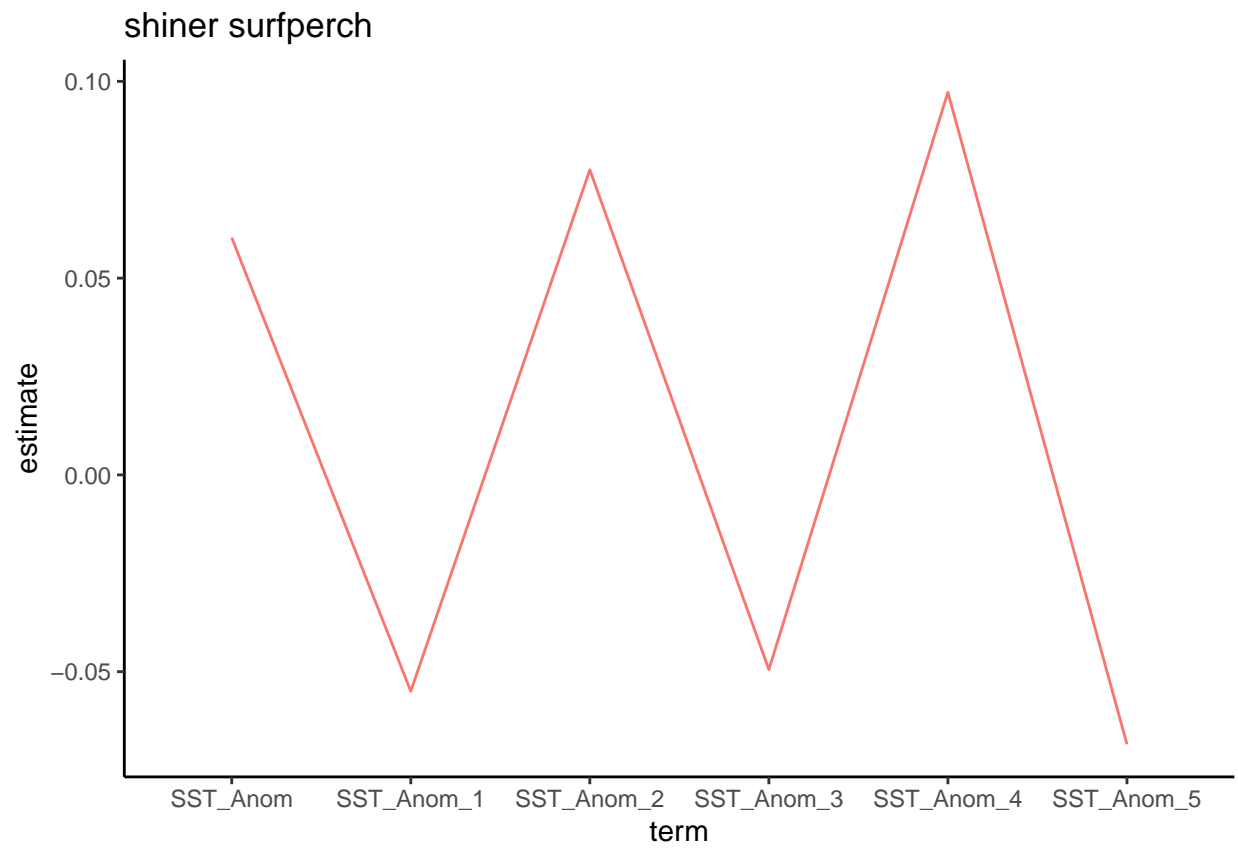






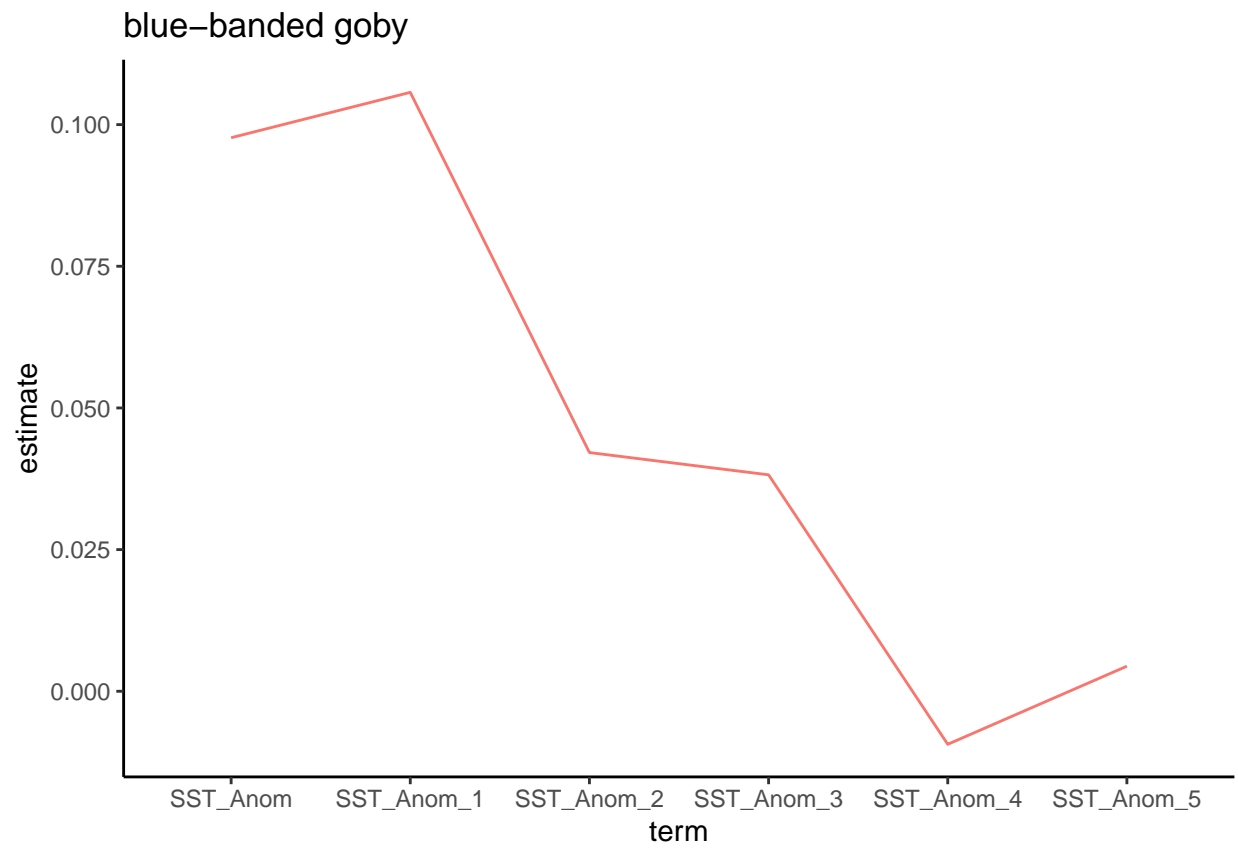




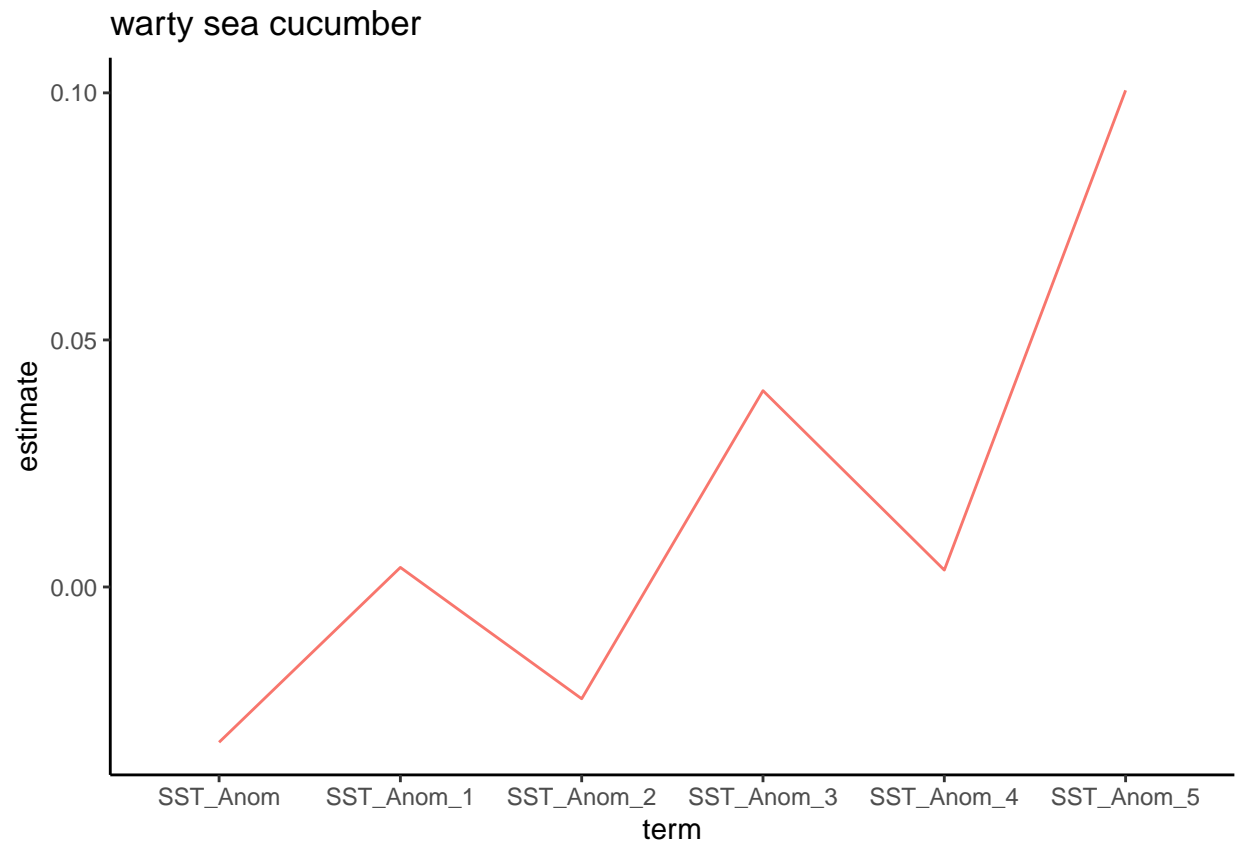


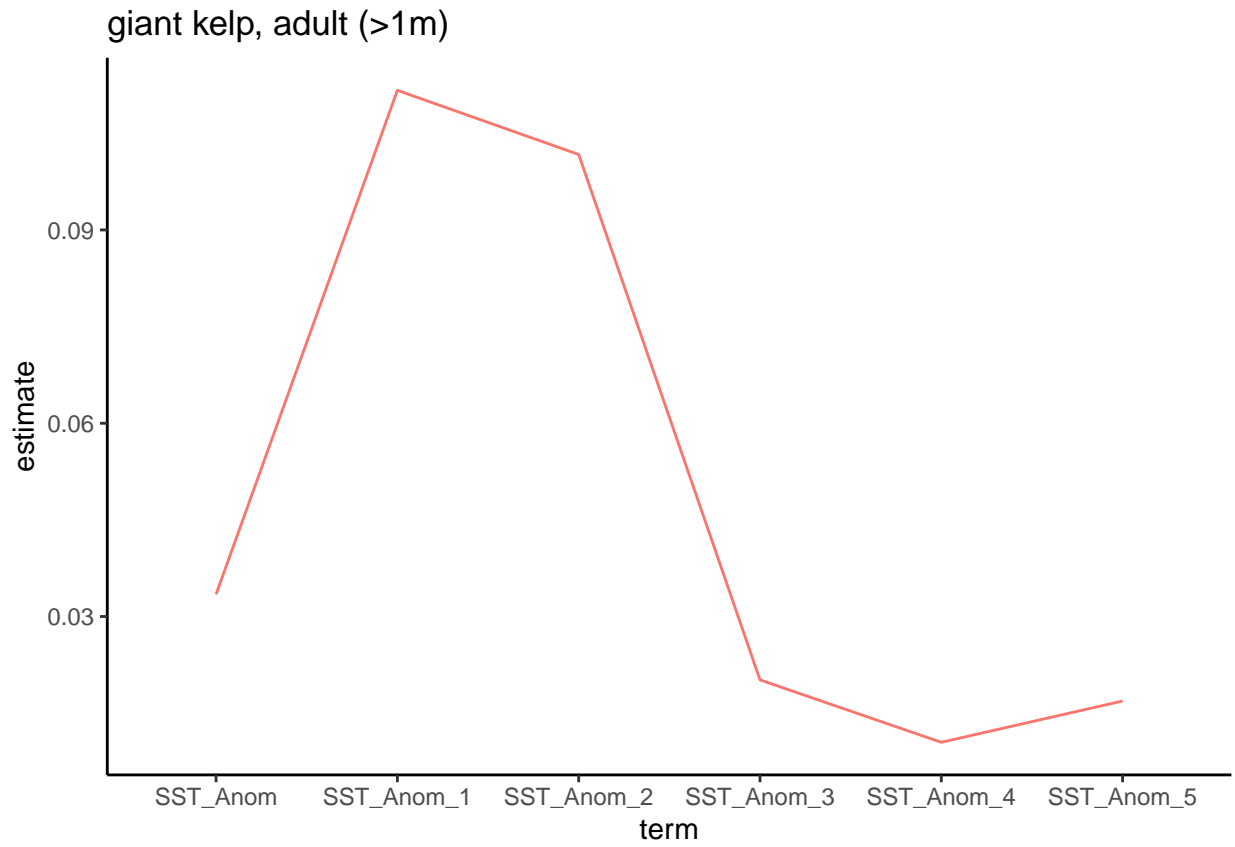
giant kelp, subadult (>1m and no haptera above the primary dichotomy)

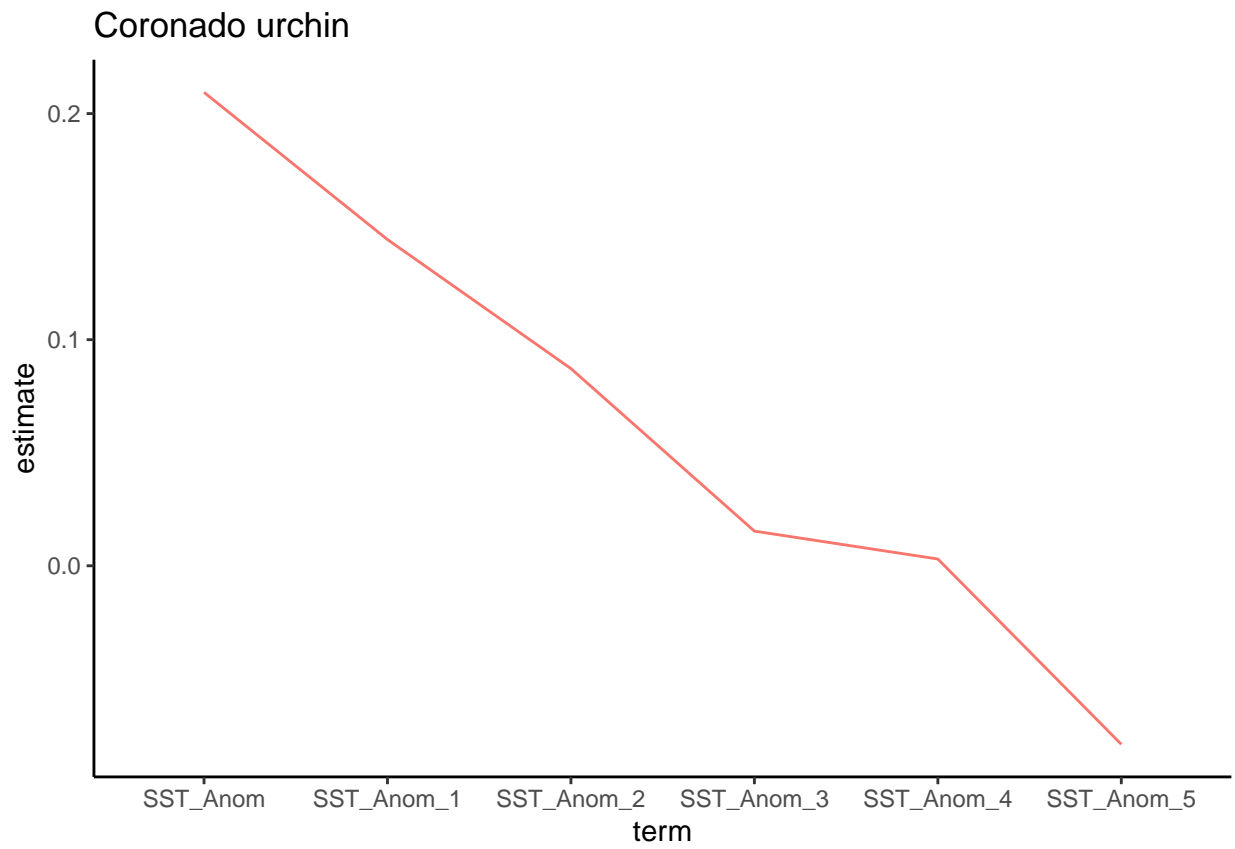


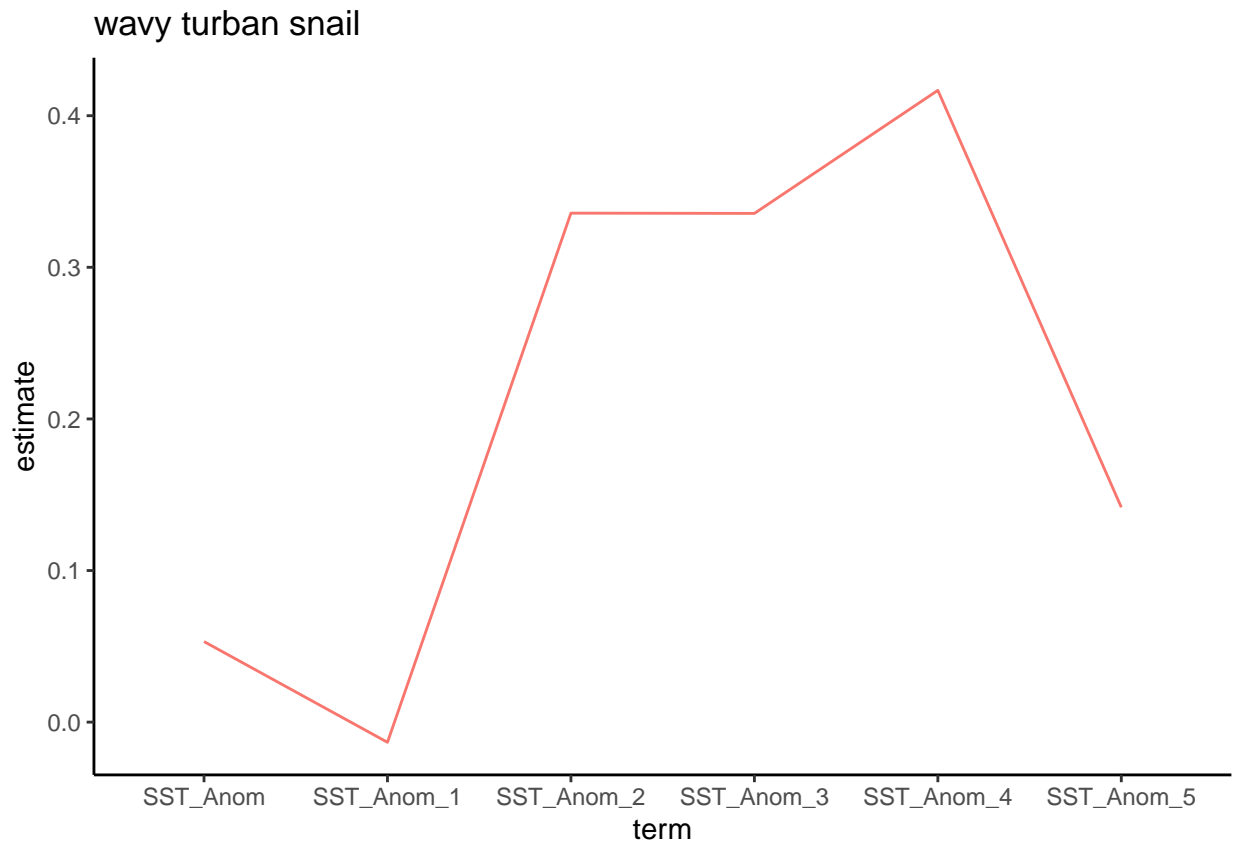


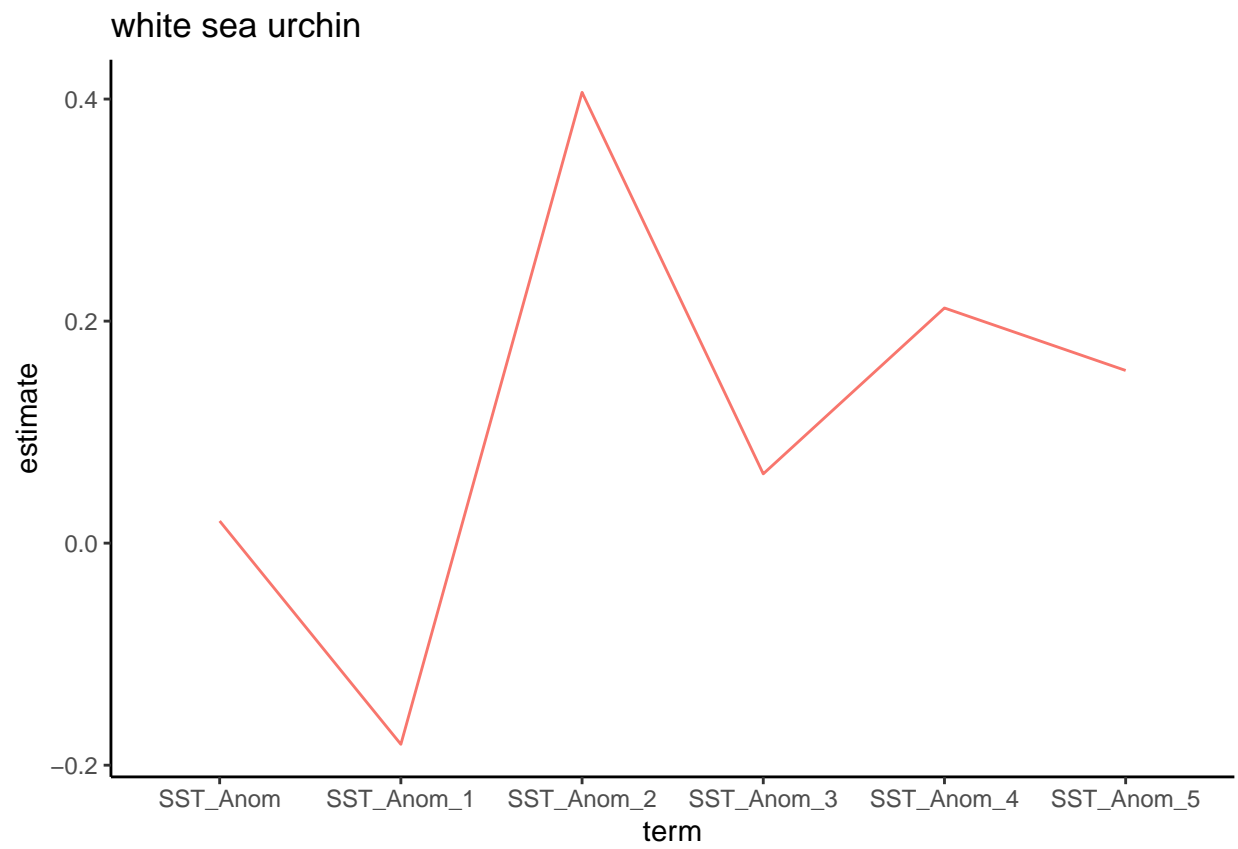


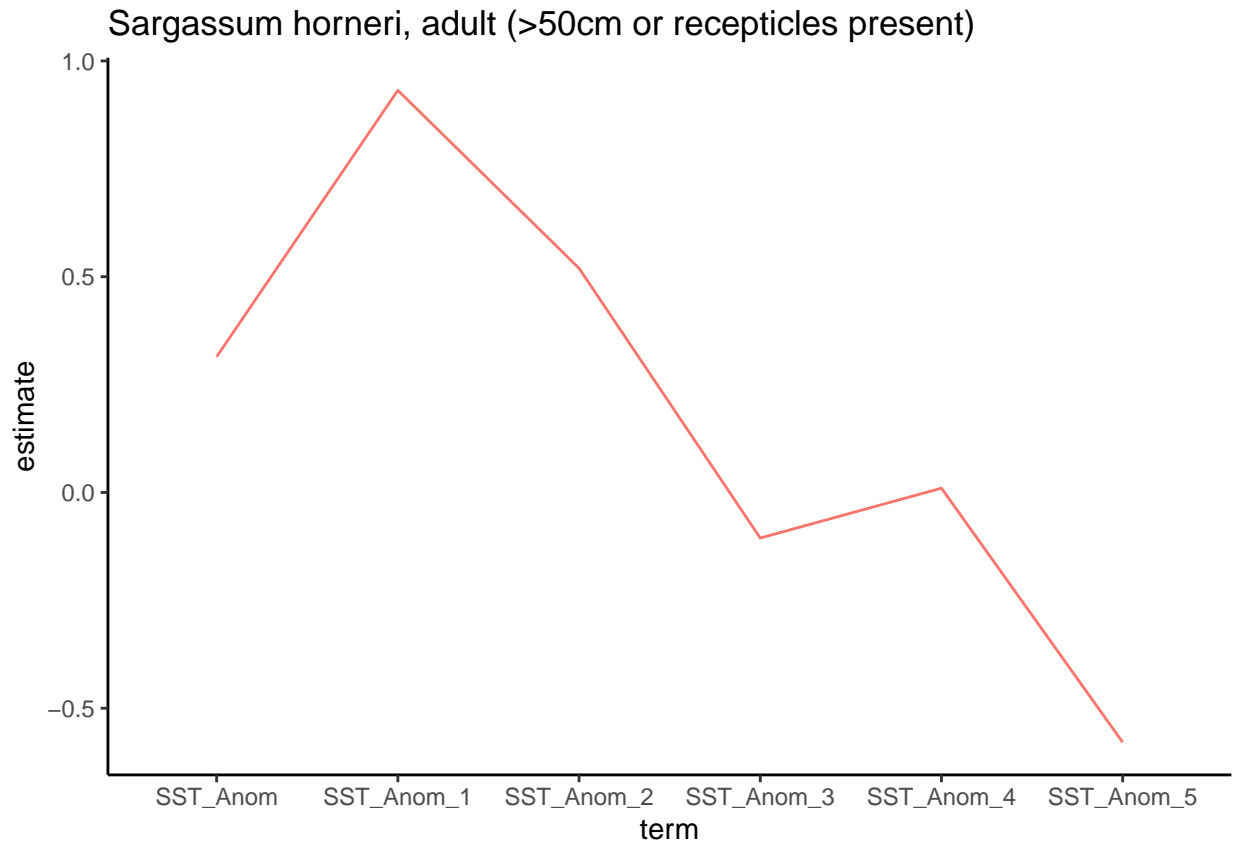


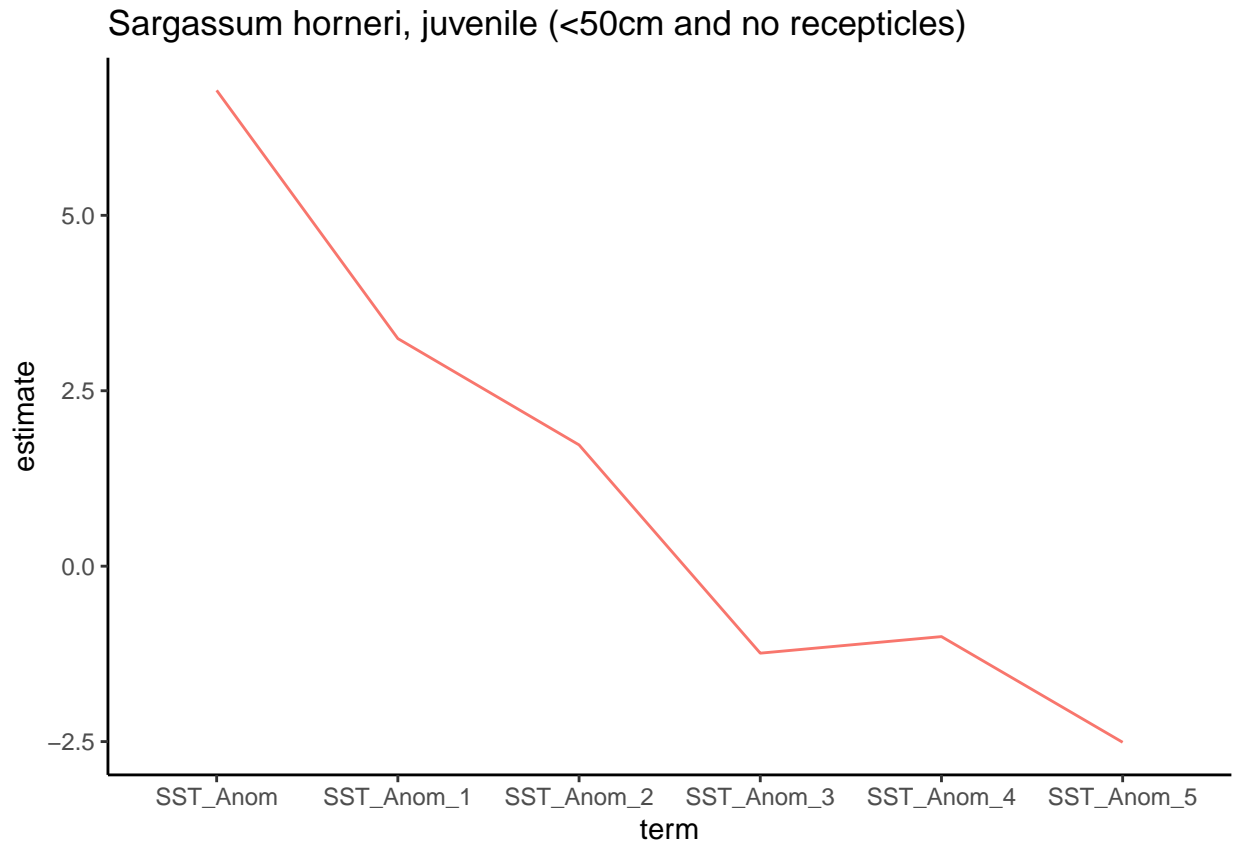


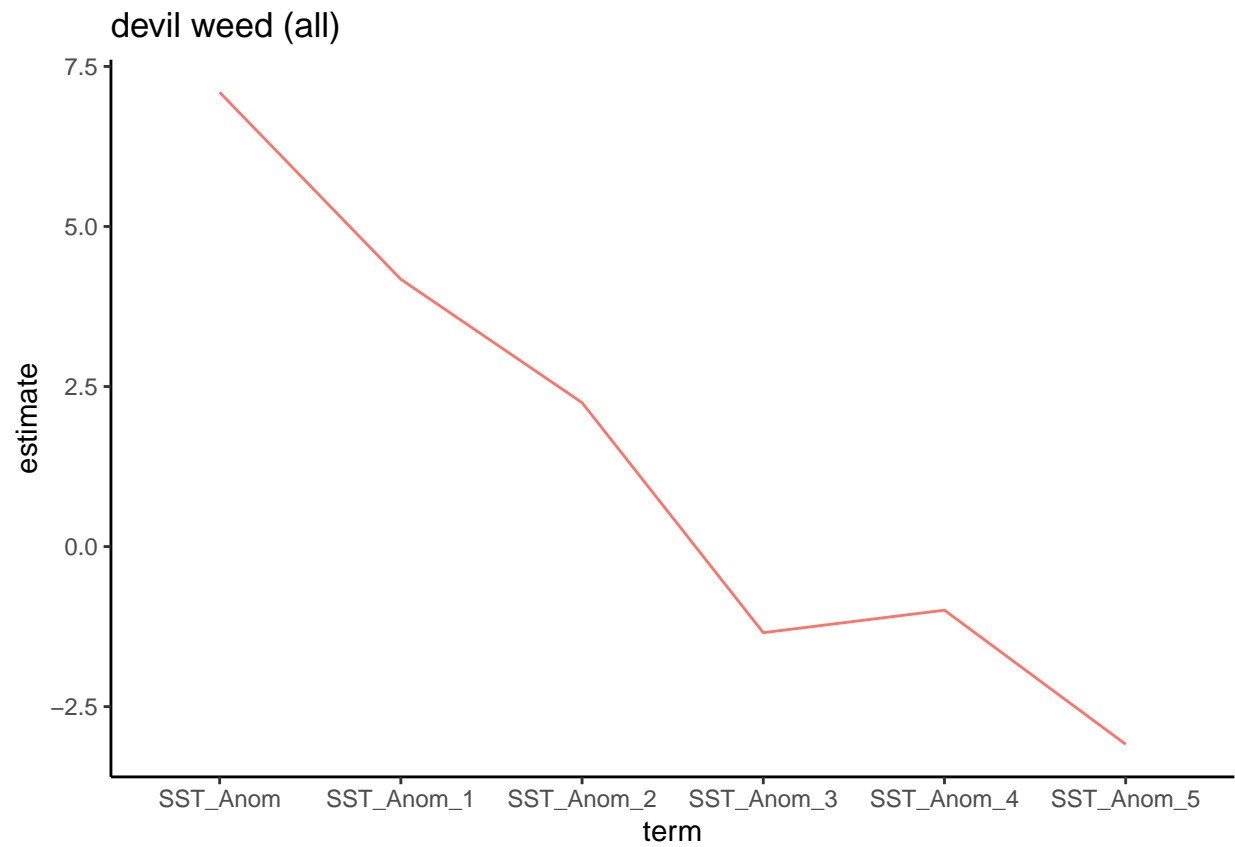






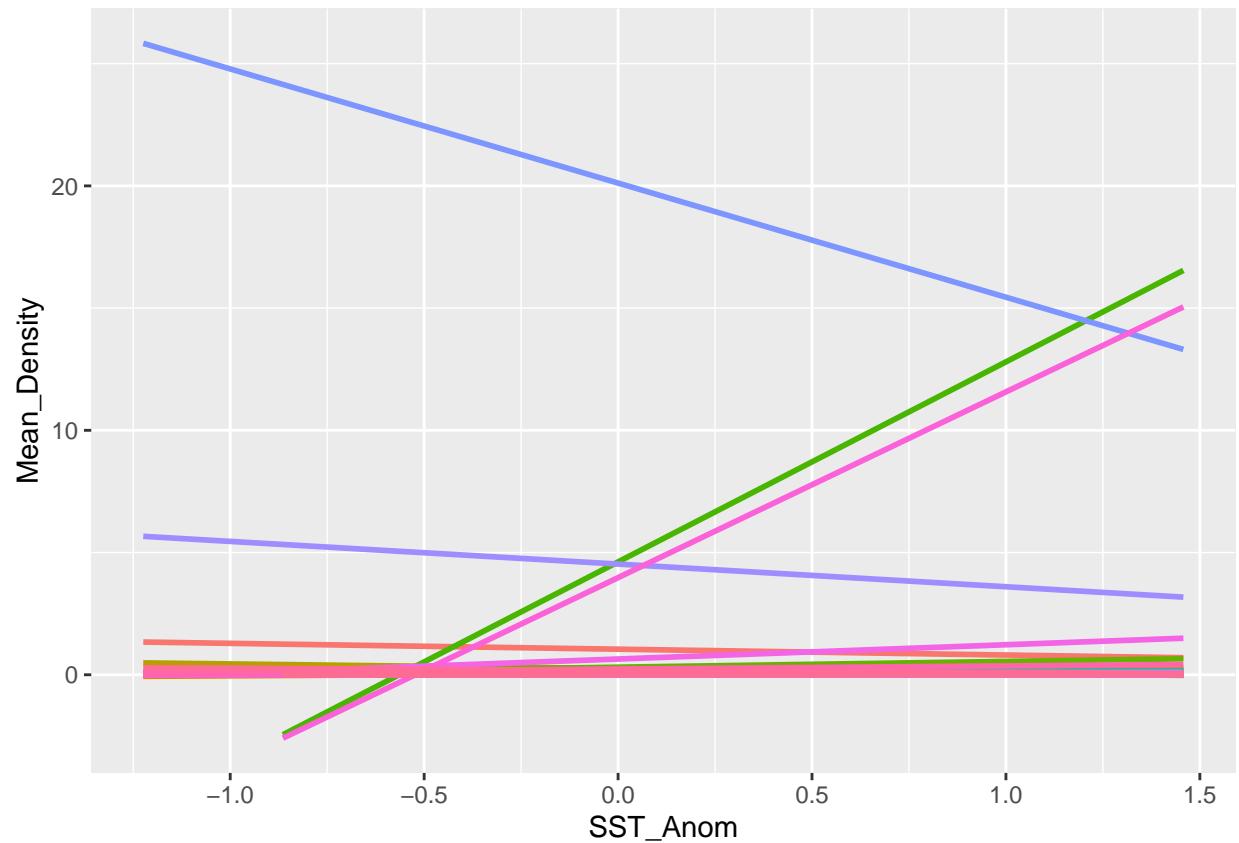






```
plt <- density %>%  
  filter(CommonName %in% unique(Results$`Response Variable`))  
  
ggplot(data = plt, aes(y = Mean_Density, x = SST_Anom, color = CommonName)) +  
  geom_smooth(method = lm, formula = "y~x", show.legend = F, se = FALSE)
```





```
for (sp in unique(Results_lag$`Response Variable`)) {
  p <- density %>%
    filter(CommonName == sp) %>%
    ggplot(aes(y = Mean_Density, x = SST_Anom)) +
    geom_point() +
    geom_smooth(method = lm, formula = "y~x") +
    labs(title = sp) +
    theme_classic()

  print(p)
}
```

```
## Warning: Unknown or uninitialised column: 'Response Variable'.
```