Supplementary Information for Context-dependent sensitivity: Do biological interactions magnify salinity effects?

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CONTENTS

Abstract

We examined whether biological interactions mediate the effects of a toxicant in communities. Salinity effects were examined between communities made of sensitive only, and tolerant-sensitive organisms, using mesocosms. To examine the effects of sensitive-tolerant taxa interactions on salinity effects we fit a lognormal hurdle model to the abundance of sensitive taxa, with separate parameters for each taxa, in each community (senstive only and tolerant/senstive). A hurdle model assumes that zero and non-zero data come from separate data-generating processes, such that the positive relative abundances are conditional on a Bernoulli probability of being observed. For our purposes, we assume that each taxa has a different probability of being observed at the end of the experiment in either treatment. Estimated intercepts and slopes, for each taxa in each treatment, are then conditional on the probability of each taxa being observed. We tested whether the response of halosensitive species was mediated by tolerant taxa. Intercepts may differ between treatments through either or both of two processes: they were of initally higher density in the control community, or have been reduced due to competition with halotolerant taxa. However, because the estimated slopes are conditional on the probability of being observed and relative to the estimated intercept in either treatment, we can test for an interaction between sensitivity and competition with halotolerant taxa. If the effect of competition/biotic interaction

increases with salinity, taxa will have reduced slopes in the tolerant/senstitive mixed community, relative to the senstivie only community.

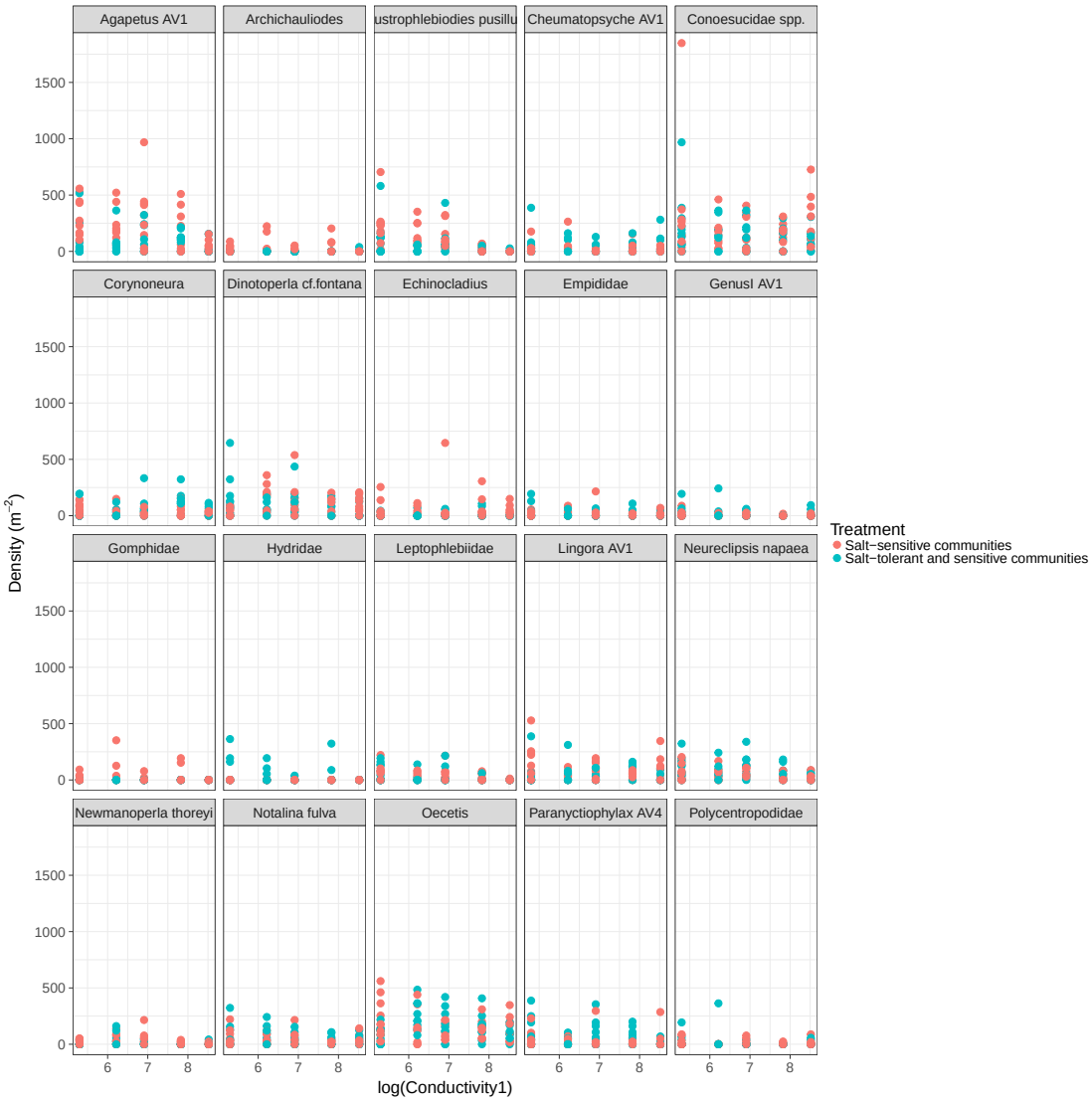
I. Raw data load and first exploration

```
# Load community dataset, convert to long format
communities <- read_csv("Cotter01RA_3.csv") %>%
  gather(sp, abun, -MesoRep)

# Get list of 20 most abundant species
common <- group_by(communities, sp) %>%
  tally(abun) %>%
  top_n(20)

# Filter full dataset for common species only
species <- filter(communities, sp %in% common$sp)

# Load covariates, scale conductivity
env_covariates <- read_csv("env5w18.csv") %>%
  dplyr::select(MesoRep, Mesocosm, Rep, Treatment, Conductivity1) %>%
  mutate(Treatment = ifelse(Treatment == "1Control",
                            "Salt-sensitive communities",
                            "Salt-tolerant and sensitive communities"),
         Conductivity = scale(Conductivity1))

# Join the covariates to the community data
dat <- left_join(species, env_covariates, by = "MesoRep")
```

A. Density for each species vs. conductivity

Simplest representation of the data.

```
dat %>%
  ggplot(aes(x = log(Conductivity1 ), y = abun, colour = Treatment)) +
  geom_point(size = 4) +
  facet_wrap(~sp) +
  ylab(expression(paste("Density (", m^{-2}, ")")))
```

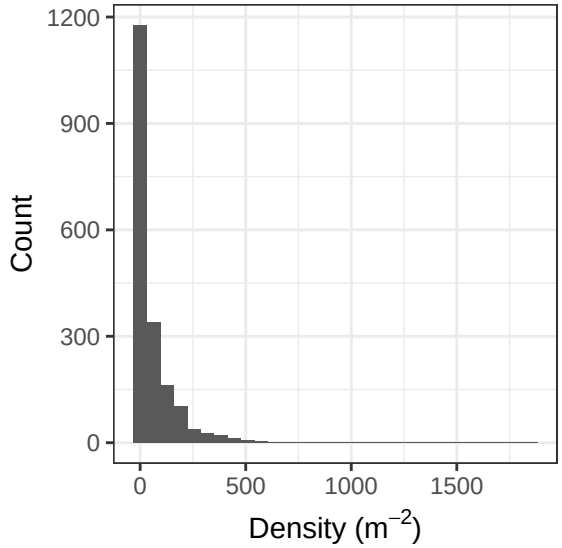


B. Distribution of the relative abundance

We look at the representation of the densities to understand what error model should be chosen. A large zero-inflated distribution appears:

```
dat %>%
  ggplot(aes(x = abun)) +
  geom_histogram() +
  theme_bw() +
  xlab(expression(paste("Density (", m^{-2}, ")"))) +
  ylab('Count')
```

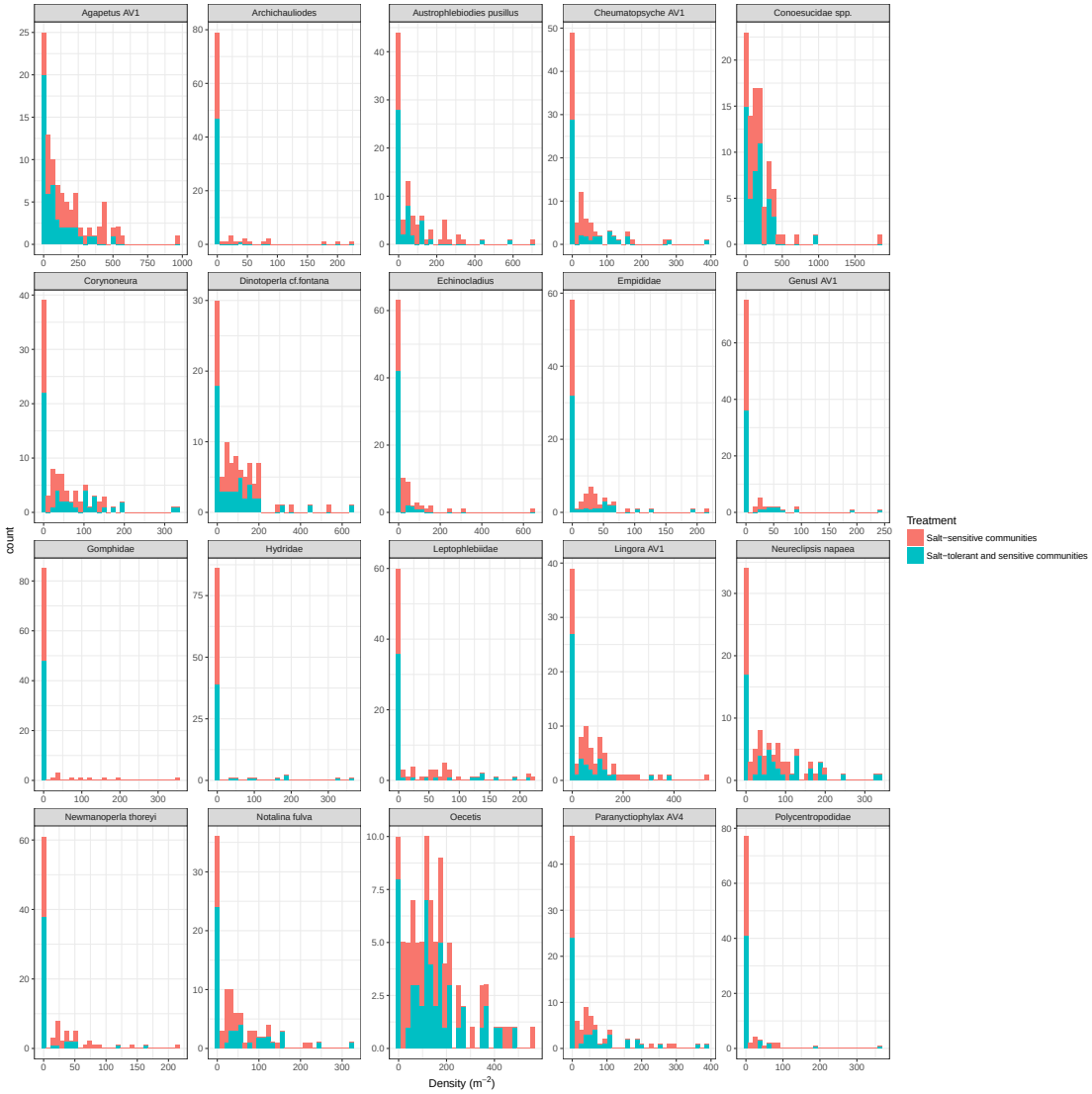
```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



The representation by species also exhibits this zero-inflated distribution.

```
dat %>%
  ggplot(aes(x = abun, fill = Treatment)) +
  geom_histogram() +
  facet_wrap(~sp, scales = 'free') +
  theme_bw() +
  xlab(expression(paste("Density (", m^{-2}, ")")))
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

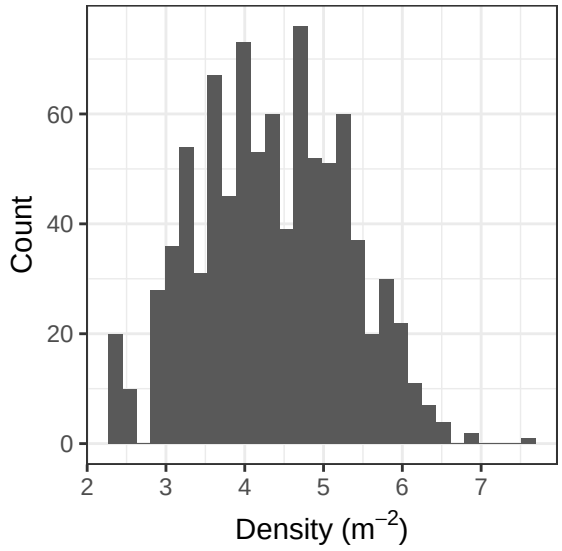


C. *Log-transformation of the data*

Ignoring the 0 of the distribution for the moment, how are the non-zero values distributed ? They look fairly logNormally distributed.

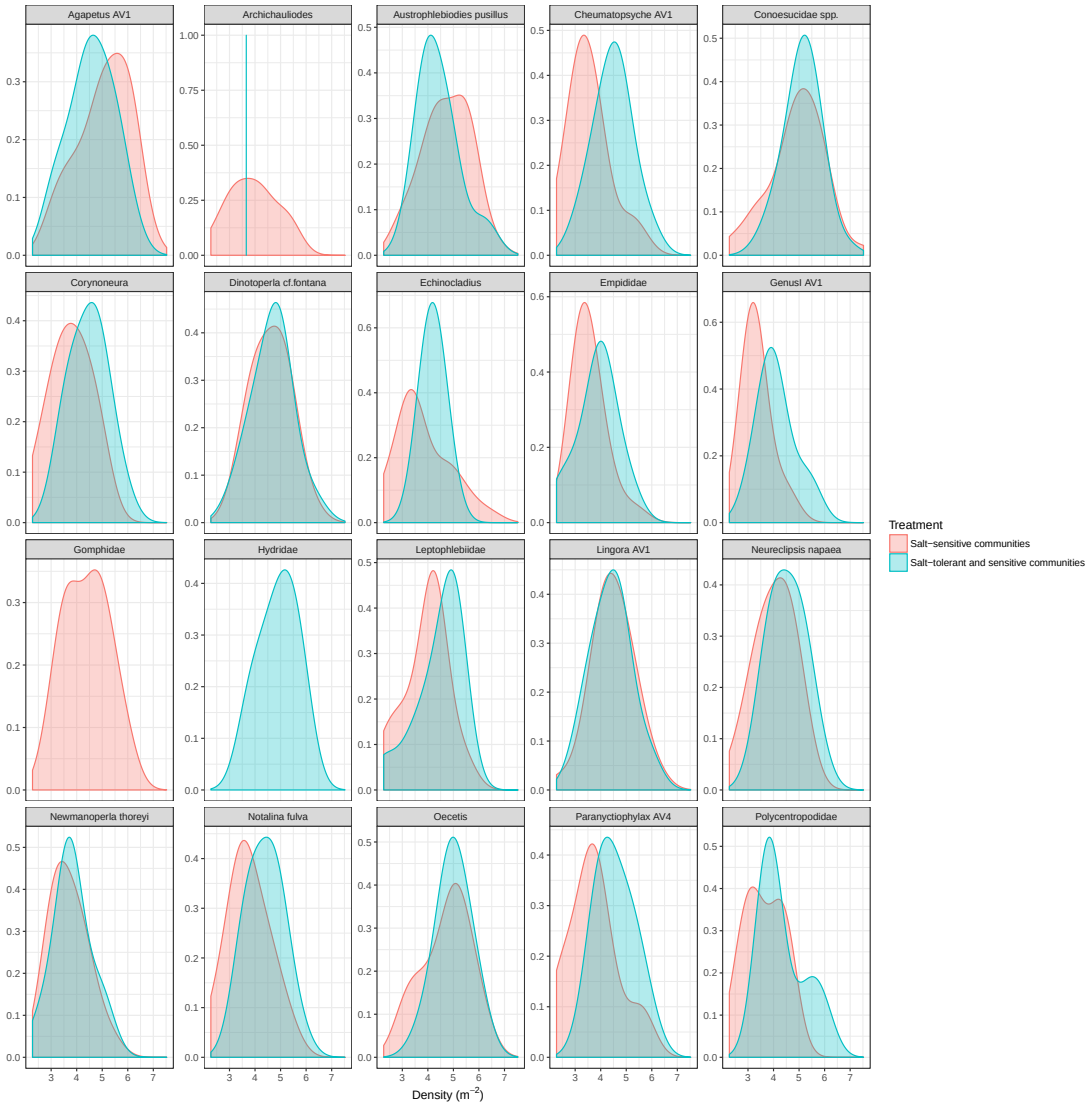
```
dat %>%
  filter(abun>0) %>%
  ggplot(aes(x = log(abun))) +
  geom_histogram() +
  theme_bw() +
  xlab(expression(paste("Density (", m^{-2}, ")"))) +
  ylab('Count')
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



The logNormal distribution also looks reasonable if you look at it by species. Some species are only present in one community.

```
dat %>%
  filter(abun>0) %>%
  ggplot(aes(x = log(abun), colour = Treatment, fill = Treatment)) +
  geom_density(bw = 0.5, alpha = 0.3) +
  facet_wrap(~sp, scales = 'free_y') +
  theme_bw() +
  xlab(expression(paste("Density (", m^{-2}, ")"))) +
  ylab('')
```



II. Modelling directly the abundances: a logNormal hurdle model

For the non-zero values, a logNormal model seem reasonable. To accomodate for the large number of 0 values, we consider a hurdle model, which mixes a point distribution at 0 and a distribution with support on the strictly positive values. w gives the probability of a species being absent $y = 0$, then positive values are conditional on $(1 - w)$:

$$f^h(y_i|w_i, \theta_i) = \begin{cases} w_i & \text{if } y_i = 0 \\ \frac{(1-w)f(y_i|\theta)}{1-F(0|\theta_i)} & \text{if } y_i > 0 \end{cases}$$

For a logNormal hurdle model, this amounts to:

$$\begin{aligned} f^h_{\text{lnNormal}}(y_i|w_i, \mu_i, \sigma) &= \begin{cases} w_i & \text{if } y_i = 0 \\ (1 - w_i)\mathcal{N}(\ln y_i|\mu_i, \sigma) & \text{if } y_i > 0 \end{cases} \\ \mu_i &= \alpha_{\text{species}_i,\text{Treatment}_i} + \beta_{\text{species}_i,\text{Treatment}_i}\text{Conductivity} \\ w_i &= w_{\text{species}_i,\text{Treatment}_i} \\ \sigma &\sim \pi_\sigma \\ \alpha_{\text{species}_i,\text{Treatment}_i} &\sim \pi_\alpha \\ \beta_{\text{species}_i,\text{Treatment}_i} &\sim \pi_\beta \\ w_{\text{species}_i,\text{Treatment}_i} &\sim \pi_w \end{aligned}$$

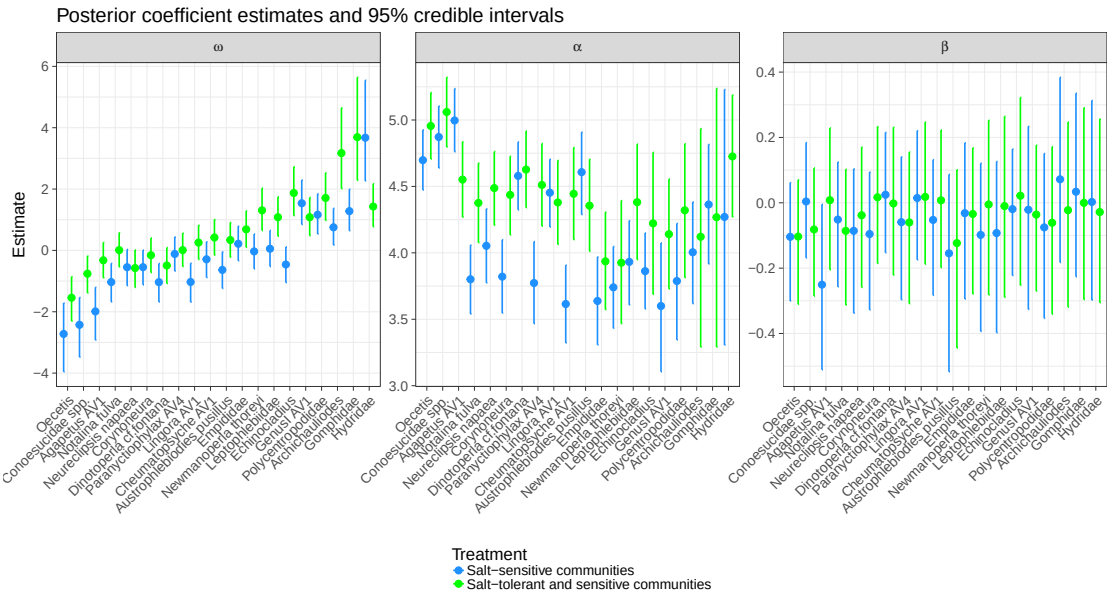
We used the 'brms' package with the default settings. 4000 posterior samples were drawn from each of four Markov chains, the first 2000 of which were discarded. α and β parameters were modelled using a log link function, while w hurdle parameters were modelled using a logit link. Weakly informative priors were used for all parameters and convergence was assessed using the Rubin-Gelman test statistic and the inspection of traceplots for adequate mixing. Sufficient sampling depth was confirmed by looking at the effective number of posterior samples obtained.

```
abundance_salinity_lognormal_hurdle_model = dat %>%
  brm(data = ., formula = bf(abun ~ Conductivity|sp:Treatment,
    hu ~ 1|sp:Treatment), family = hurdle_lognormal(), iter = 4000)
```

A. Posterior distribution for the parameters

The following figure plots the probability of observation, intercept and slope parameters for each species and treatment. Lower w mean species are less absent, higher intercepts mean greater average density across all salinity levels and higher slopes mean less sensitivity to salinity, conditional on a species being present at the end of the experiment. Some species are very similar between treatments, while others show larger differences.

```
posterior_coef <-
  coef(abundance_salinity_lognormal_hurdle_model) %>%
  as.data.frame() %>%
  rownames_to_column("sp_treatment") %>%
  gather(par, value, -sp_treatment) %>%
  mutate(quantile = str_extract(par, "Estimate|Q2.5|Q97.5"),
         parameter =
           str_extract(par, "Intercept|Conductivity|hu_Intercept") %>%
           factor(., labels = c("omega", "alpha", "beta"),
                  levels = c("hu_Intercept",
                             "Intercept",
                             "Conductivity"))) %>%
  separate(sp_treatment, c("Species", "Treatment"), sep = "_") %>%
  select(-par) %>%
  filter(!is.na(quantile)) %>%
  spread(quantile, value)

ggplot(posterior_coef, aes(x = reorder(Species, Estimate),
                           y = Estimate, color = Treatment)) +
  geom_point(position = position_dodge(width = 1), size = 4) +
  geom_errorbar(aes(ymin = Q2.5, ymax = Q97.5),
    position = position_dodge(width = 1), width = 0, size = 1) +
  scale_x_discrete(expand = c(0.01, 0.01)) +
  scale_color_manual(values = c("dodgerblue", "green")) +
  labs(x = "",
       title =
         "Posterior coefficient estimates and 95% credible intervals") +
  facet_wrap(~ parameter, scales = "free", labeller = label_parsed) +
  theme(axis.text.x = element_text(angle = 45, hjust = 1),
    aspect.ratio = 1, legend.position = "bottom",
    legend.direction = "vertical")
```



III. Difference between hurdles

Species are on average absent from the control community 41% of the time, and 57% of the time in the competition community.

```
# Hurdles use logit link
unlogit <- function(x) exp(x)/(1 + exp(x))

par_id <- select(dat, sp, Treatment) %>%
  distinct() %>%
  arrange(sp)

hurdles <- posterior_samples(abundance_salinity_lognormal_hurdle_model,
                             par = "r_sp:Treatment__hu") %>%
  t() %>%
  as.data.frame() %>%
  bind_cols(par_id) %>%
  gather(draw, value, -sp, -Treatment) %>%
  mutate(value = unlogit(value)) %>%
  group_by(Treatment) %>%
  summarise(mean = round(mean(value), 2),
```

```
            Q2.5 = round(quantile(value, 0.025), 2),
            Q97.5 = round(quantile(value, 0.975), 2))

hurdles
```

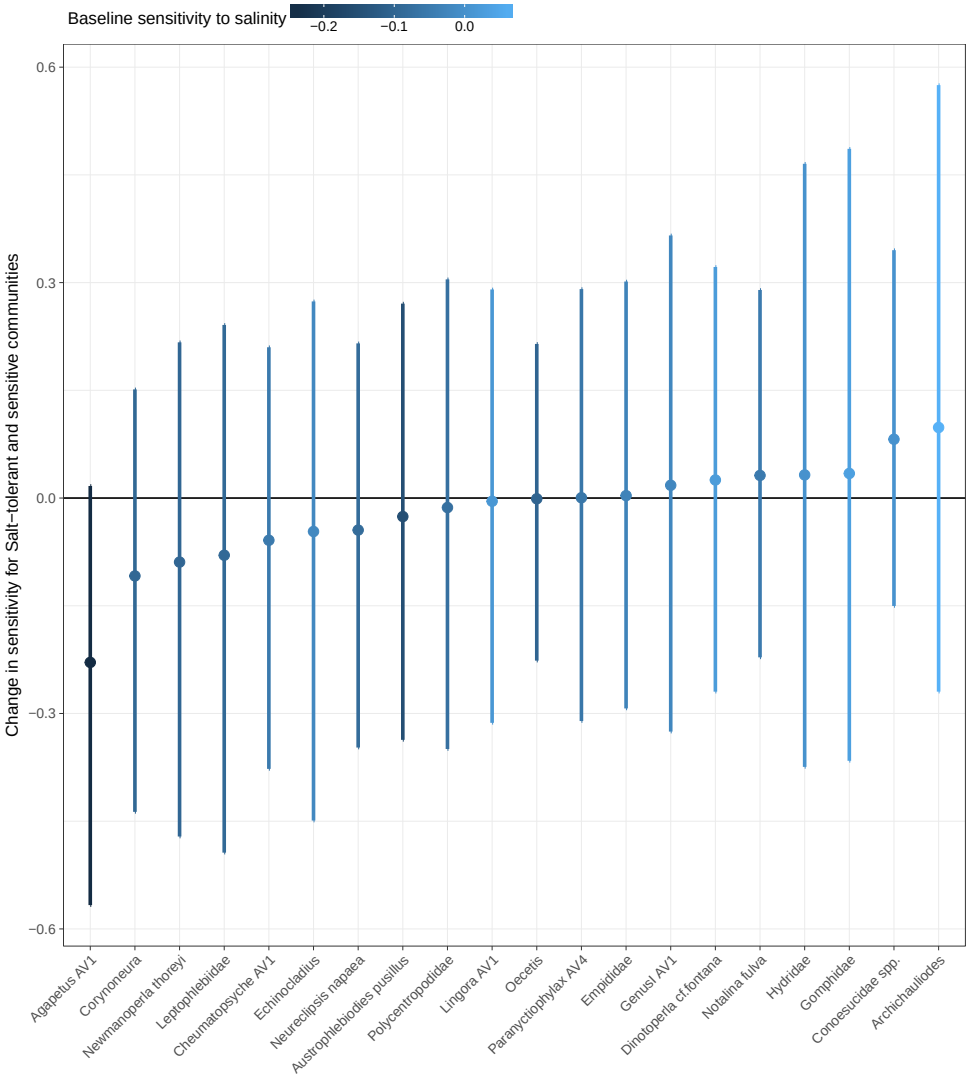
```
## # A tibble: 2 x 4
##   Treatment                                  mean  Q2.5 Q97.5
##   <chr>                                     <dbl> <dbl> <dbl>
## 1 Salt-sensitive communities                0.41   0.04  0.97
## 2 Salt-tolerant and sensitive communities 0.570   0.15  0.98
```

IV. Interaction between salinity and competition

Species that are least sensitive under control treatments show more similar responses to salinity in the competition treatment.

```
## Calculate difference between treatments
par_id <- select(dat, sp, Treatment) %>%
  distinct() %>%
  arrange(sp)

control_slopes <- coef(abundance_salinity_lognormal_hurdle_model) %>%
  as.data.frame() %>%
  rownames_to_column("par") %>%
  separate(par, c("sp", "Treatment"), sep = "_") %>%
  filter(grepl("Salt-sensitive", Treatment)) %>%
  select(sp, control_slope_mean = sp.Treatment.Estimate.Conductivity)

slope_diff <- posterior_samples(
                abundance_salinity_lognormal_hurdle_model,
                par = c("Conductivity")) %>%
  t() %>%
  as.data.frame() %>%
  rownames_to_column("par") %>%
  filter(grepl("^r_sp", par)) %>%
  select(-par) %>%
  bind_cols(par_id) %>%
  gather(draw, value, -sp, -Treatment) %>%
  mutate(value = exp(value)) %>%
  spread(Treatment, value) %>%
  mutate(diff = `Salt-sensitive communities` -
           `Salt-tolerant and sensitive communities`) %>%
  group_by(sp) %>%
  summarise(Difference = mean(diff),
            Q2.5 = quantile(diff, 0.025),
            Q97.5 = quantile(diff, 0.975)) %>%
  left_join(control_slopes)
```

```
pl = ggplot(slope_diff, aes(x = reorder(sp, Difference),
                            y = Difference,
                            colour = control_slope_mean)) +
  geom_hline(aes(yintercept = 0), size = 1) +
  geom_point(size = 6) +
  geom_errorbar(aes(ymin = Q2.5, ymax = Q97.5), width = 0, size = 2.2) +
  labs(x = "",
       y = "Change in sensitivity for Salt-tolerant and sensitive communities",
       colour = "Baseline sensitivity to salinity")+
  guides(colour = guide_colorbar(barwidth = 20)) +
  theme(axis.text.x = element_text(angle = 45, hjust = 1),
        aspect.ratio = 1, legend.position = "top",
        legend.justification = 'left')

ggsave(filename = 'Fig4B_difference_in_sensitivity.pdf', plot = pl,
       width = 12, height = 12)
plot(pl)
```

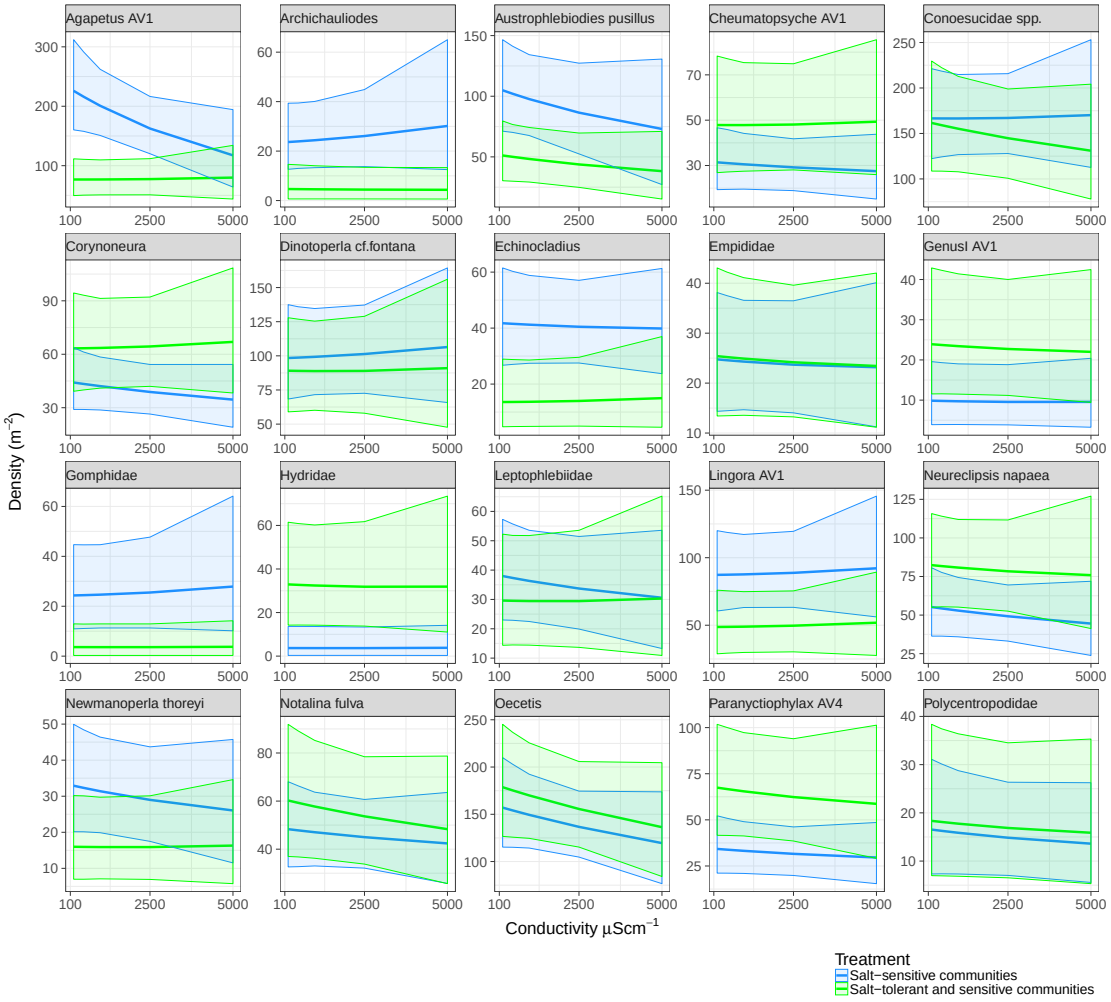


A. Scatter plot and fitted relative abundance

Scatter plots of the 20 most common taxa showing linear fits and 95% credible intervals for the expected density associated with conductivity and biological treatments. Even though we expect differences in density between treatments overall, we can still see differences in slopes for some species.

```
compute_expected_density = function(brms_fit){
  dat %>%
    select(Conductivity1, sp, Treatment, Conductivity) %>%
    unique() %>%
    rowid_to_column() %>%
    (function(ddf) fitted(brms_fit, newdata = ddf) %>%
       as_tibble() %>%
       rowid_to_column() %>%
```

```
       left_join(ddf) )
}

plot_expected_density = function(brms_fit){
  brms_fit %>%
    compute_expected_density %>%
      ggplot(aes(x = Conductivity1,
                 colour = Treatment,
                 fill = Treatment)) +
      #geom_point(data = dat, aes(y = abun), size = 2) +
      facet_wrap(~sp, scales = 'free') +
      scale_x_continuous(breaks = c(100, 2500, 5000)) +
      scale_colour_manual(values = c("dodgerblue", "green")) +
      scale_fill_manual(values = c("dodgerblue", "green")) +
      ylab(expression(paste("Density (", m^{-2}, ")"))) +
      xlab(expression(paste("Conductivity ", mu, S, cm^{-1}))) +
      geom_line(aes(y = Estimate), size = 1.5) +
      geom_ribbon(aes(ymin = Q2.5, ymax = Q97.5), alpha = 0.1) +
      #scale_x_log10() +
      theme(aspect.ratio = 1,
        legend.position = "bottom",
        legend.direction = "vertical",
        legend.justification = 'right') +
  theme(strip.text.x = element_text(angle = 0, hjust = 0))
}

pl = abundance_salinity_lognormal_hurdle_model %>%
  plot_expected_density

## Joining, by = "rowid"

ggsave(filename = 'Fig4a_predicted_densities.pdf', plot = pl)

## Saving 20 x 20 in image

plot(pl)
```



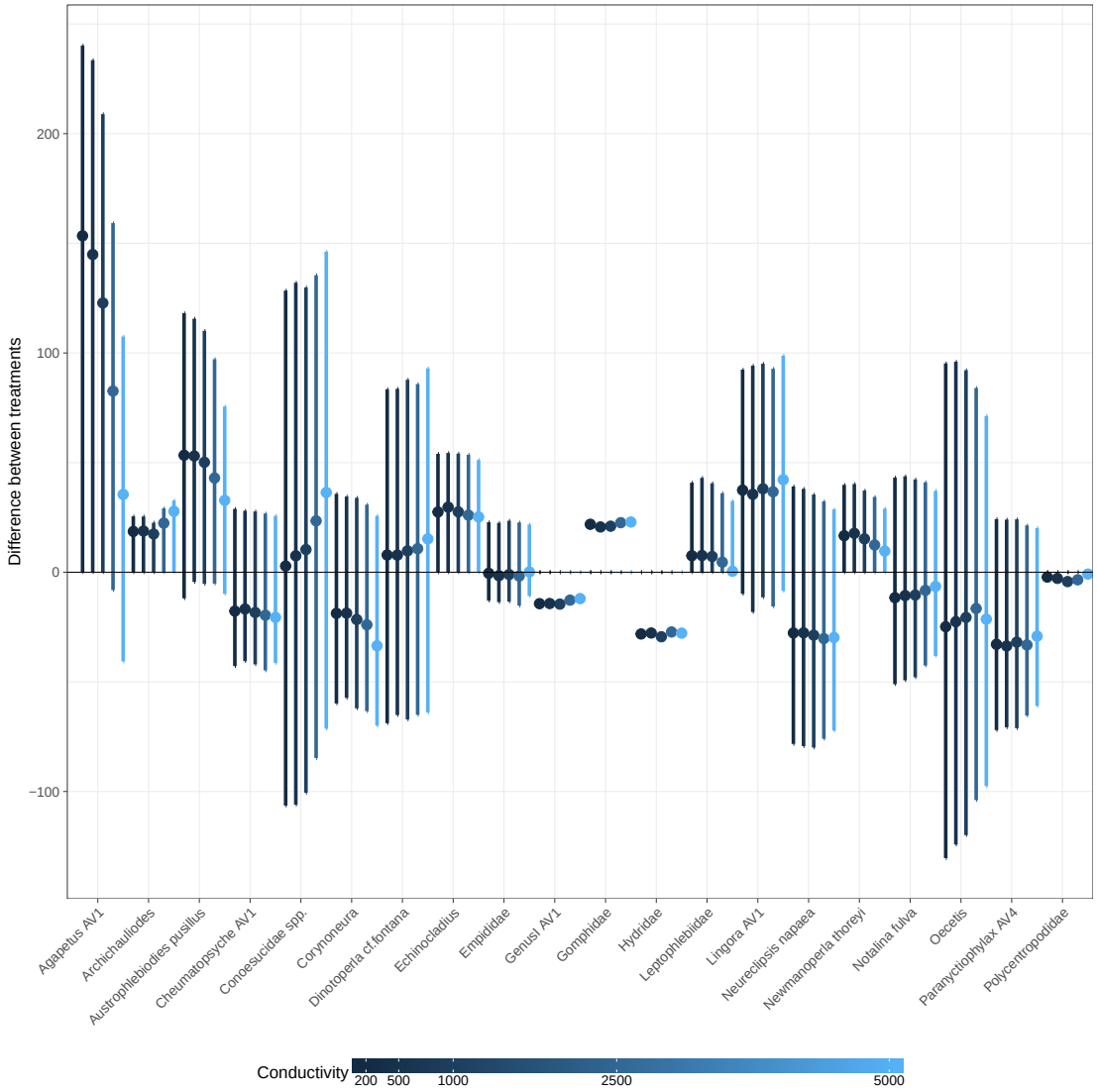
B. Differences in predicted densities

We can see if the difference in density between treatments changes between conductivity levels:

```
difference_between_treatments = function(abundance_model,
                                         species,
                                         Conductivity,
                                         Conductivity1){
  # Compute the difference for one species at one concentration.
  tibble(sp = species,
         Conductivity = Conductivity,
         Conductivity1 = Conductivity1,
         Treatment = c("Salt-sensitive communities", #Input covariates
                       "Salt-tolerant and sensitive communities")) %>%
```

```
    #Get a sample from the posterior
    posterior_predict(abundance_model,
                      newdata = .) %>%
    #Compute the difference between Low and Strong biotic interactions
    (function(x) x[,1] - x[,2]) %>%
    (function(vec){ # Compute summaries of the posteriors
      quantile(vec, probs = c(0.025,0.25,0.75,0.975)) %>%
        t %>%
        as_tibble() %>%
        setNames(c("inf95CI", "inf50CI", "sup50CI", "sup95CI")) %>%
        mutate(Estimate = mean(vec)) %>%
        return()
    }) %>%
    # Package results as a dataframe
    mutate(sp = species, Conductivity1 = Conductivity1)
}

cmp_difference_between_treatments = function(abundance_model){
  dat %>%
    select(sp, Conductivity, Conductivity1) %>%
    unique() %>%
    (function(df){
      parallel::mcmapply(FUN = function(species,
                                        Conductivity,
                                        Conductivity1)
        difference_between_treatments(abundance_model,
                                      species,
                                      Conductivity,
                                      Conductivity1),
        df$sp, df$Conductivity, df$Conductivity1, SIMPLIFY = F)
    }) %>%
    bind_rows()
}

plot_abundance_difference_between_treatments_and_concentration =
  function(posterior_differences_between_treatments){
    posterior_differences_between_treatments %>%
      mutate(offset = 0.2 * (as.numeric(as.factor(Conductivity1)) -
                               0.5*length(unique(Conductivity1)))) %>%
      mutate(x = sp %>% as.factor() %>% as.numeric() + offset) %>%
      ggplot(aes(x = sp, colour = Conductivity1)) +
      geom_point(aes(y = Estimate), alpha = 0) +
      geom_point(aes(x = x, y = Estimate), size = 6) +
      geom_errorbar(aes(x = x, ymin = inf50CI, ymax = sup50CI),
                    width = 0,
                    size = 2.2) +
      labs(x = "",
           y = "Difference between treatments",
```

```
           colour = "Conductivity") +
      scale_colour_continuous(
        breaks =
          unique(posterior_differences_between_treatments$Conductivity1)) +
      guides(colour = guide_colourbar(barwidth = 50)) +
      theme(axis.text.x = element_text(angle = 45, hjust = 1),
            legend.position = "bottom") +
      geom_hline(yintercept = 0)
  }

plot_abundance_difference_between_treatments_and_concentration_from_fit =
  function(abundance_model){
    abundance_model %>%
      cmp_difference_between_treatments %>%
      plot_abundance_difference_between_treatments_and_concentration
  }


abundance_salinity_lognormal_hurdle_model %>%
  plot_abundance_difference_between_treatments_and_concentration_from_fit
```



V. Order level differences

We repeat this analysis after aggregating taxa into fewer groups to examine the effects of large numbers of species absences on our analysis. We use the three most abundant orders, Ephemeroptera, Plecoptera and Trichoptera and the total densities of all oberved taxa. Aggregating into only a few groups means we only observe 41 absences across all mesocosms.

```
orders <- read_csv("order_key.csv")

## Parsed with column specification:
## cols(
##   order = col_character(),
##   sp = col_character()
## )
```

```
agg_dat <- left_join(communities, orders) %>%
  group_by(MesoRep, order) %>%
  summarise(order_abun = sum(abun)) %>%
  mutate(Total = sum(order_abun)) %>%
  ungroup() %>%
  spread(order, order_abun) %>%
  select(MesoRep, Ephemeroptera, Plecoptera, Trichoptera, Total) %>%
  gather(group, abun, -MesoRep) %>%
  left_join(env_covariates)
```

```
## Joining, by = "sp"
## Joining, by = "MesoRep"
```

```
sum(agg_dat$abun == 0)
```

```
## [1] 41
```

```
grouped_salinity_lognormal_hurdle_model = agg_dat %>%
  brm(data = ., formula = bf(abun ~ Conductivity|group:Treatment,
    hu ~ 1|group:Treatment),
    family = hurdle_lognormal(),
    iter = 4000,
    control = list(adapt_delta = 0.99, max_treedepth = 15))
```

```
## Compiling the C++ model
```

```
## In file included from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/BH/include
##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/BH/include
##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/StanHeader
##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/StanHeader
##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/StanHeader
##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/StanHeader
##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/StanHeader
##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/StanHeader
##                  from file60643afc5fb9.cpp:8:
## /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/BH/include/boost/smart_ptr/detai
##      explicit shared_count( std::auto_ptr<Y> & r ): pi_( new sp_counted_impl_p<Y>(
##                                     ^
## In file included from /usr/include/c++/5/bits/locale_conv.h:41:0,
##                  from /usr/include/c++/5/locale:43,
##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/BH/include
##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/BH/include
##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/BH/include
##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/BH/include
##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/BH/include
##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/BH/include
##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/StanHeader
##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/StanHeader
##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/StanHeader
##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/StanHeader
```

```
##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/StanHeader
##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/StanHeader
##                  from file60643afc5fb9.cpp:8:
## /usr/include/c++/5/bits/unique_ptr.h:49:28: note: declared here
##    template<typename> class auto_ptr;
##                            ^
## In file included from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/BH/include
##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/StanHeader
##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/StanHeader
##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/StanHeader
##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/StanHeader
##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/StanHeader
##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/StanHeader
##                  from file60643afc5fb9.cpp:8:
## /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/BH/include/boost/smart_ptr/share
##  template< class T, class R > struct sp_enable_if_auto_ptr< std::auto_ptr< T >, R
##                                                                ^
## In file included from /usr/include/c++/5/bits/locale_conv.h:41:0,
##                  from /usr/include/c++/5/locale:43,
##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/BH/include
##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/BH/include
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##                  from file60643afc5fb9.cpp:8:
## /usr/include/c++/5/bits/unique_ptr.h:49:28: note: declared here
##    template<typename> class auto_ptr;
##                            ^
## In file included from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/BH/include
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##                  from file60643afc5fb9.cpp:8:
## /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/BH/include/boost/smart_ptr/share
##      explicit shared_ptr( std::auto_ptr<Y> & r ): px(r.get()), pn()
##                               ^
## In file included from /usr/include/c++/5/bits/locale_conv.h:41:0,
##                  from /usr/include/c++/5/locale:43,
```

```
##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/BH/include
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##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/StanHeader
##                  from file60643afc5fb9.cpp:8:
## /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/BH/include/boost/smart_ptr/share
##      shared_ptr( std::auto_ptr<Y> && r ): px(r.get()), pn()
##                        ^
## In file included from /usr/include/c++/5/bits/locale_conv.h:41:0,
##                  from /usr/include/c++/5/locale:43,
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```

```
##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/StanHeader
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##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/StanHeader
##                  from file60643afc5fb9.cpp:8:
## /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/BH/include/boost/smart_ptr/share
##      shared_ptr & operator=( std::auto_ptr<Y> & r )
##                                   ^
## In file included from /usr/include/c++/5/bits/locale_conv.h:41:0,
##                  from /usr/include/c++/5/locale:43,
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## /usr/include/c++/5/bits/unique_ptr.h:49:28: note: declared here
##    template<typename> class auto_ptr;
##                             ^
## In file included from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/BH/include
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##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/StanHeader
##                  from file60643afc5fb9.cpp:8:
## /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/BH/include/boost/smart_ptr/share
##      shared_ptr & operator=( std::auto_ptr<Y> && r )
##                                   ^
## In file included from /usr/include/c++/5/bits/locale_conv.h:41:0,
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```

```
##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/StanHeader
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##    template<typename> class auto_ptr;
##                             ^
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##                  from file60643afc5fb9.cpp:8:
## /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/BH/include/boost/smart_ptr/share
## /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/BH/include/boost/smart_ptr/share
##          this_type( static_cast< std::auto_ptr<Y> && >( r ) ).swap( *this );
##                                            ^
## In file included from /usr/include/c++/5/bits/locale_conv.h:41:0,
##                  from /usr/include/c++/5/locale:43,
##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/BH/include
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##                             ^
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##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/BH/include
##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/StanHeader
##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/StanHeader
```

```
##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/StanHeader
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##                  from file60643afc5fb9.cpp:8:
## /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/BH/include/boost/get_pointer.hpp
## /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/BH/include/boost/get_pointer.hpp
##  template<class T> T * get_pointer(std::auto_ptr<T> const& p)
##                                                ^
## In file included from /usr/include/c++/5/bits/locale_conv.h:41:0,
##                  from /usr/include/c++/5/locale:43,
##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/BH/include
##                  from /home/guillaume/R/x86_64-pc-linux-gnu-library/3.4/BH/include
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##                  from file60643afc5fb9.cpp:8:
## /usr/include/c++/5/bits/unique_ptr.h:49:28: note: declared here
##    template<typename> class auto_ptr;
##                             ^
## Start sampling
```
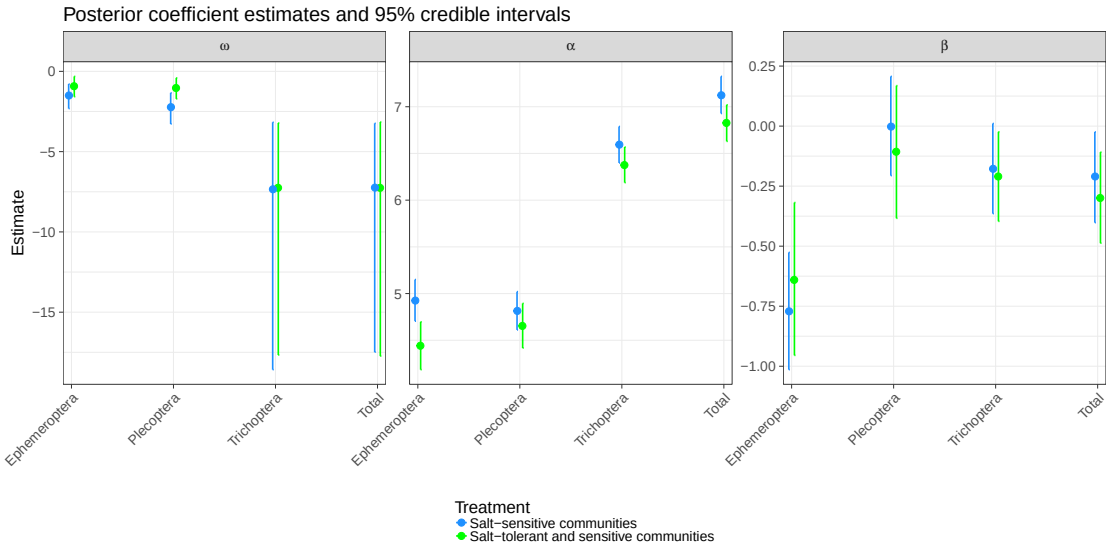

Trichoptera are present in all mesocosms. Ephemeroptera show the greatest sensitivty in the control community, but are less sensitive to salinity in the competition community. Plecoptera and all taxa, on average, show an increased sensitivty within Salt-tolerant and sensitive communities rather than Salt-sensitive only communities.

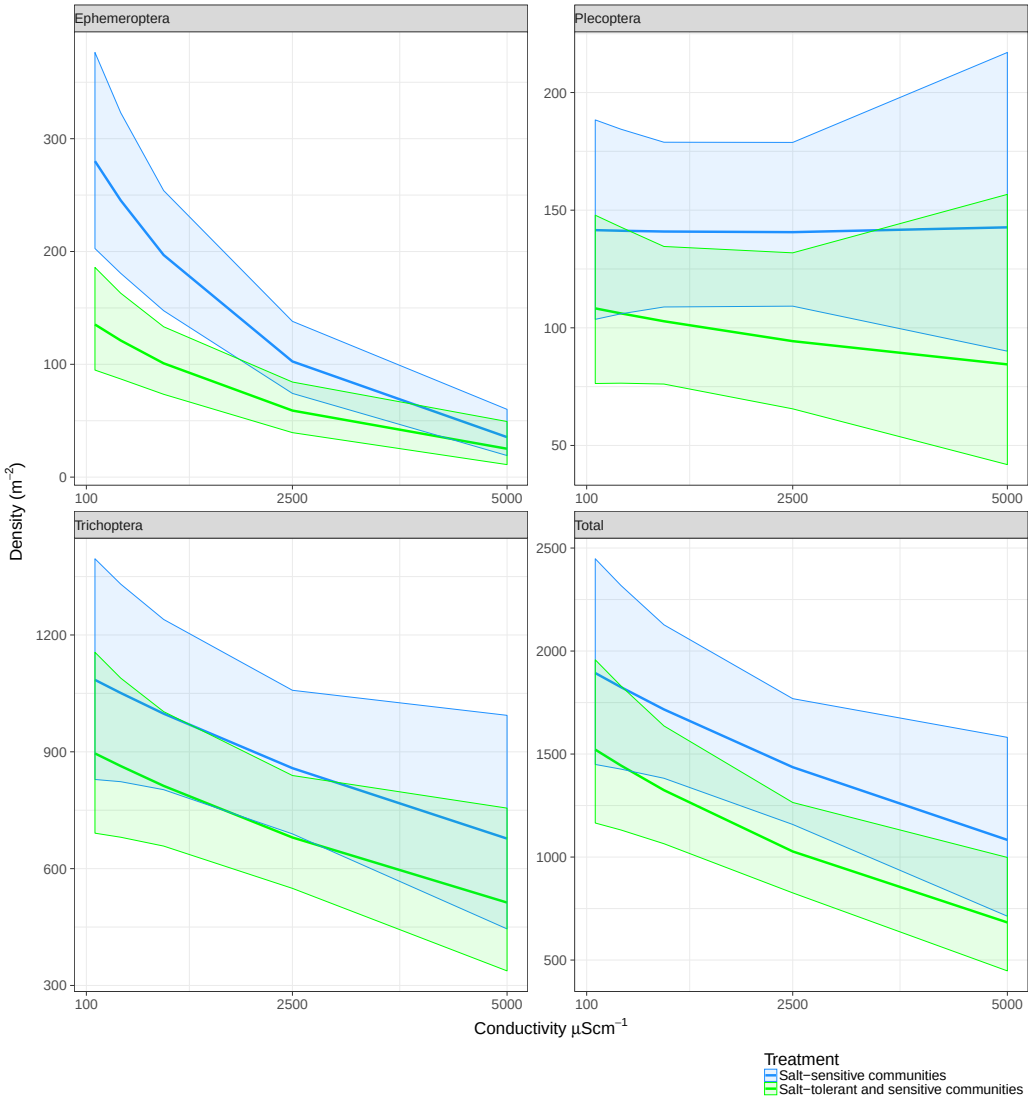
```
group_coef <-
  coef(grouped_salinity_lognormal_hurdle_model) %>%
  as.data.frame() %>%
  rownames_to_column("group_treatment") %>%
  gather(par, value, -group_treatment) %>%
  separate(group_treatment, c("Group", "Treatment"), sep = "_") %>%
  mutate(quantile = str_extract(par, "Estimate|Q2.5|Q97.5"),
         parameter = str_extract(par,
                                 "Intercept|Conductivity|hu_Intercept") %>%
                       factor(., labels = c("omega", "alpha", "beta"),
                         levels = c("hu_Intercept",
                                    "Intercept",
                                    "Conductivity")),
         Group = factor(Group, levels = c("Ephemeroptera",
```

```
                                                "Plecoptera",
                                                "Trichoptera",
                                                "Total"))) %>%
  select(-par) %>%
  filter(!is.na(quantile)) %>%
  spread(quantile, value)

ggplot(group_coef, aes(x = Group, y = Estimate, color = Treatment)) +
  geom_point(position = position_dodge(width = 0.1), size = 4) +
  geom_errorbar(aes(ymin = Q2.5, ymax = Q97.5),
    position = position_dodge(width = 0.11), width = 0, size = 1) +
  scale_x_discrete(expand = c(0.01, 0.01)) +
  scale_color_manual(values = c("dodgerblue", "green")) +
  labs(x = "",
       title = "Posterior coefficient estimates and 95% credible intervals")+
  facet_wrap(~ parameter, scales = "free", labeller = label_parsed) +
  theme(axis.text.x = element_text(angle = 45, hjust = 1),
    aspect.ratio = 1,
    legend.position = "bottom",
    legend.direction = "vertical")
```




```
pred_dat <- select(agg_dat,
                   group,
                   Treatment,
                   Conductivity,
                   Conductivity1) %>%
  distinct() %>%
```

```
  mutate(group = factor(group, levels = c("Ephemeroptera",
                                          "Plecoptera",
                                          "Trichoptera",
                                          "Total")))

pred_density <- fitted(grouped_salinity_lognormal_hurdle_model,
                       newdata = pred_dat) %>%
  as.data.frame() %>%
  bind_cols(pred_dat)

pl = ggplot(pred_density, aes(x = Conductivity1,
                              colour = Treatment,
                              fill = Treatment)) +
  facet_wrap(~ group, scales = 'free') +
  scale_x_continuous(breaks = c(100, 2500, 5000)) +
  scale_colour_manual(values = c("dodgerblue", "green")) +
  scale_fill_manual(values = c("dodgerblue", "green")) +
  ylab(expression(paste("Density (", m^{-2}, ")"))) +
  xlab(expression(paste("Conductivity ", mu, S, cm^{-1}))) +
  geom_line(aes(y = Estimate), size = 1.5) +
  geom_ribbon(aes(ymin = Q2.5, ymax = Q97.5), alpha = 0.1) +
  theme(aspect.ratio = 1,
        legend.position = "bottom",
        legend.direction = "vertical",
        legend.justification = 'right')  +
  theme(strip.text.x = element_text(angle = 0, hjust = 0))

ggsave(filename = 'Fig4c_predicted_order_densities.pdf',
       plot = pl,
       width = 12,
       height = 12)
plot(pl)
```



VI. Supplementary information 1

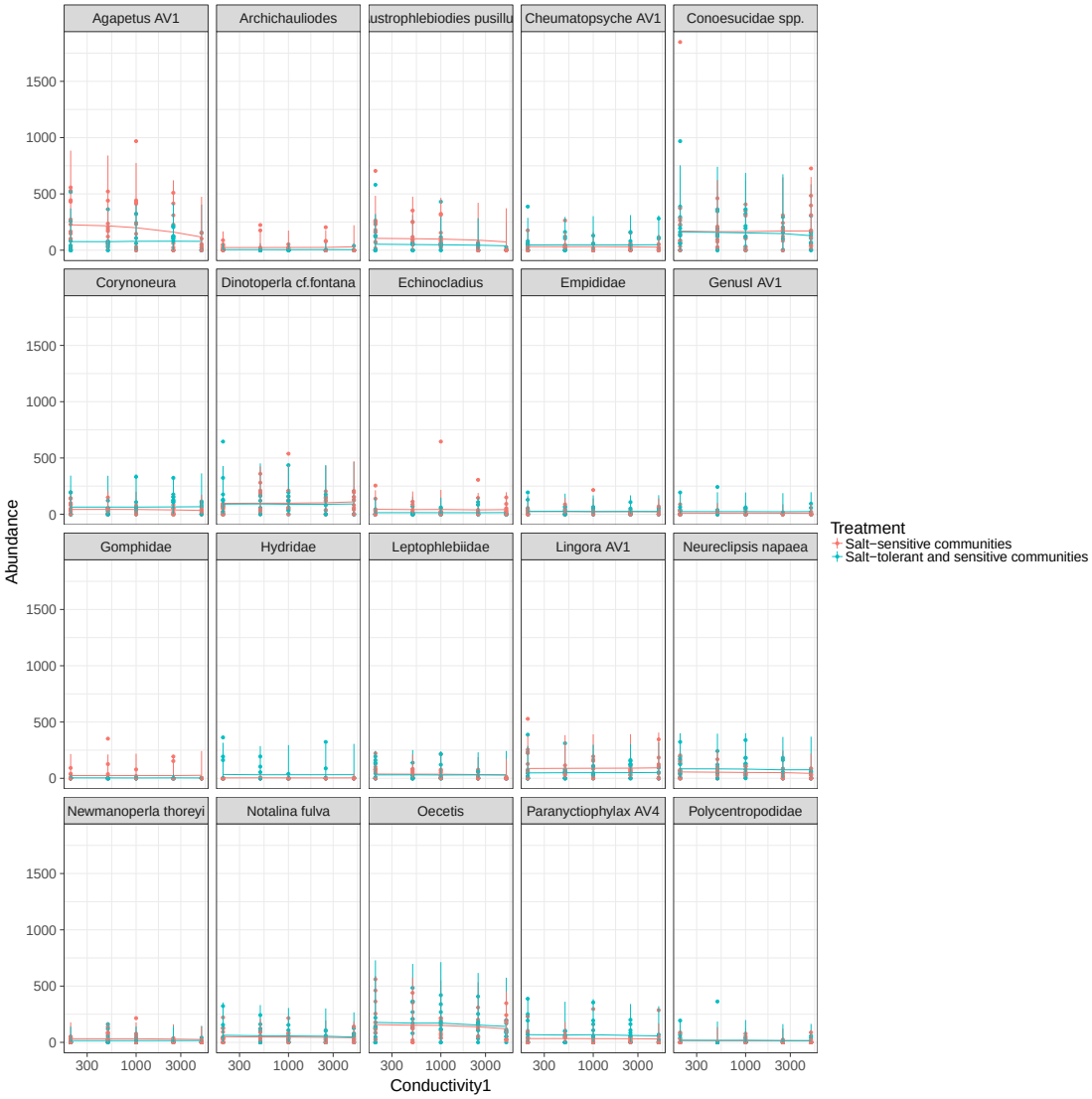
A. *Posterior predictive checks for the logNormal hurdle model*

1) *Coverage of the credible intervals:*

```
cmp_predicted_data = function(abundance_model){
  dat %>%
    dplyr::select(Conductivity1, sp, Treatment, Conductivity) %>%
    unique() %>%
    rowid_to_column() %>%
    (function(ddf) predict(abundance_model, newdata = ddf) %>%
       as_tibble() %>%
       rowid_to_column() %>%
```

```
        left_join(ddf) )
}

plot_coverage_credible_intervals = function(abundance_model){
  abundance_model %>%
    cmp_predicted_data %>%
    ggplot(aes(x = Conductivity1, colour = Treatment)) +
    geom_point(data = dat, aes(y = abun)) +
    facet_wrap(~sp) +
    ylab("Abundance") +
    geom_line(aes(y = Estimate)) +
    geom_linerange(aes(ymin = Q2.5, ymax = Q97.5)) +
    scale_x_log10()
}

plot_coverage_credible_intervals(abundance_salinity_lognormal_hurdle_model)
```

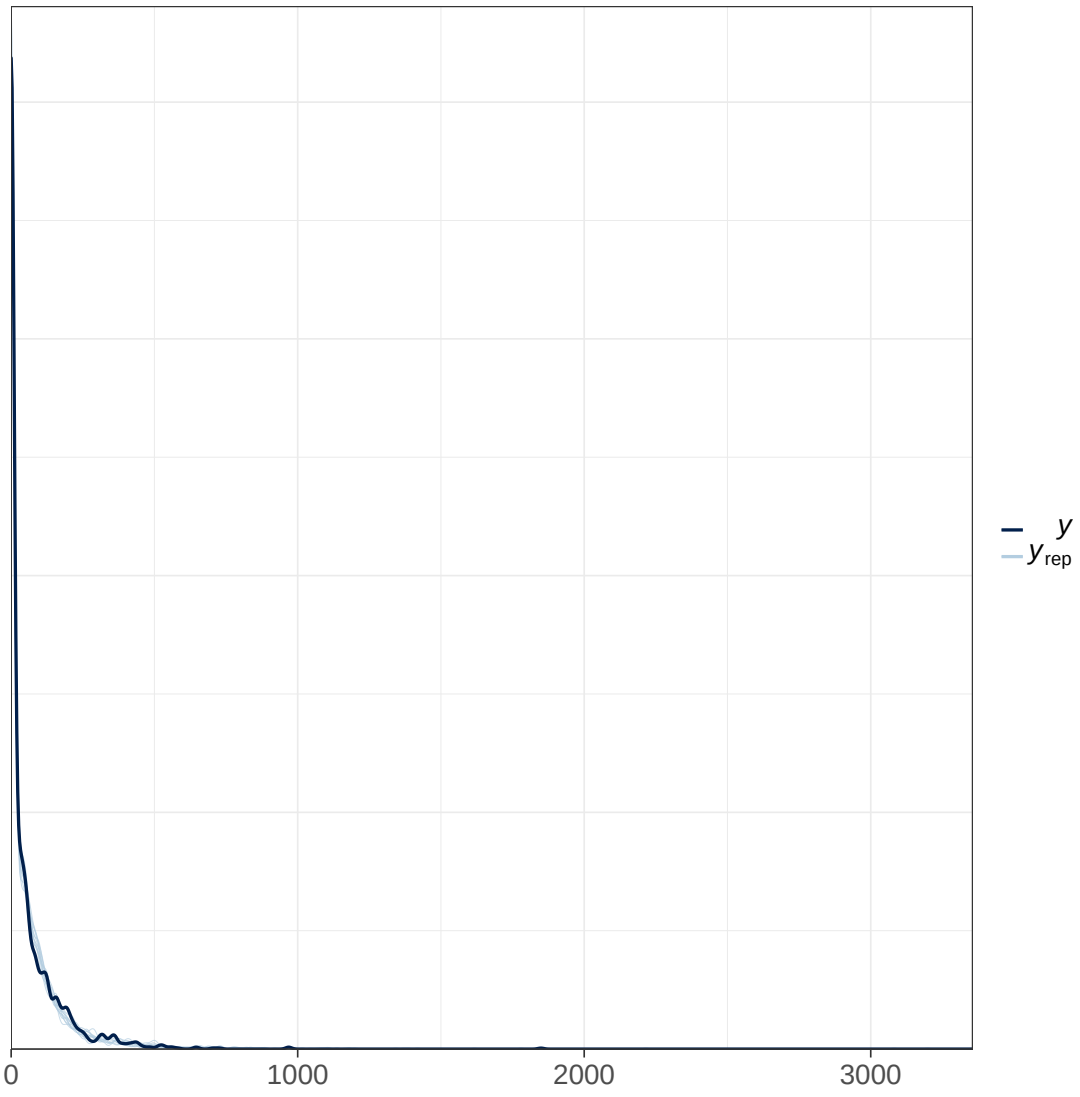
```
## Joining, by = "rowid"
```



2) Appropriateness of the distributional assumption (lognormal hurdle model):

```
pp_check(abundance_salinity_lognormal_hurdle_model)
```

```
## Using 10 posterior samples for ppc type 'dens_overlay' by default.
```



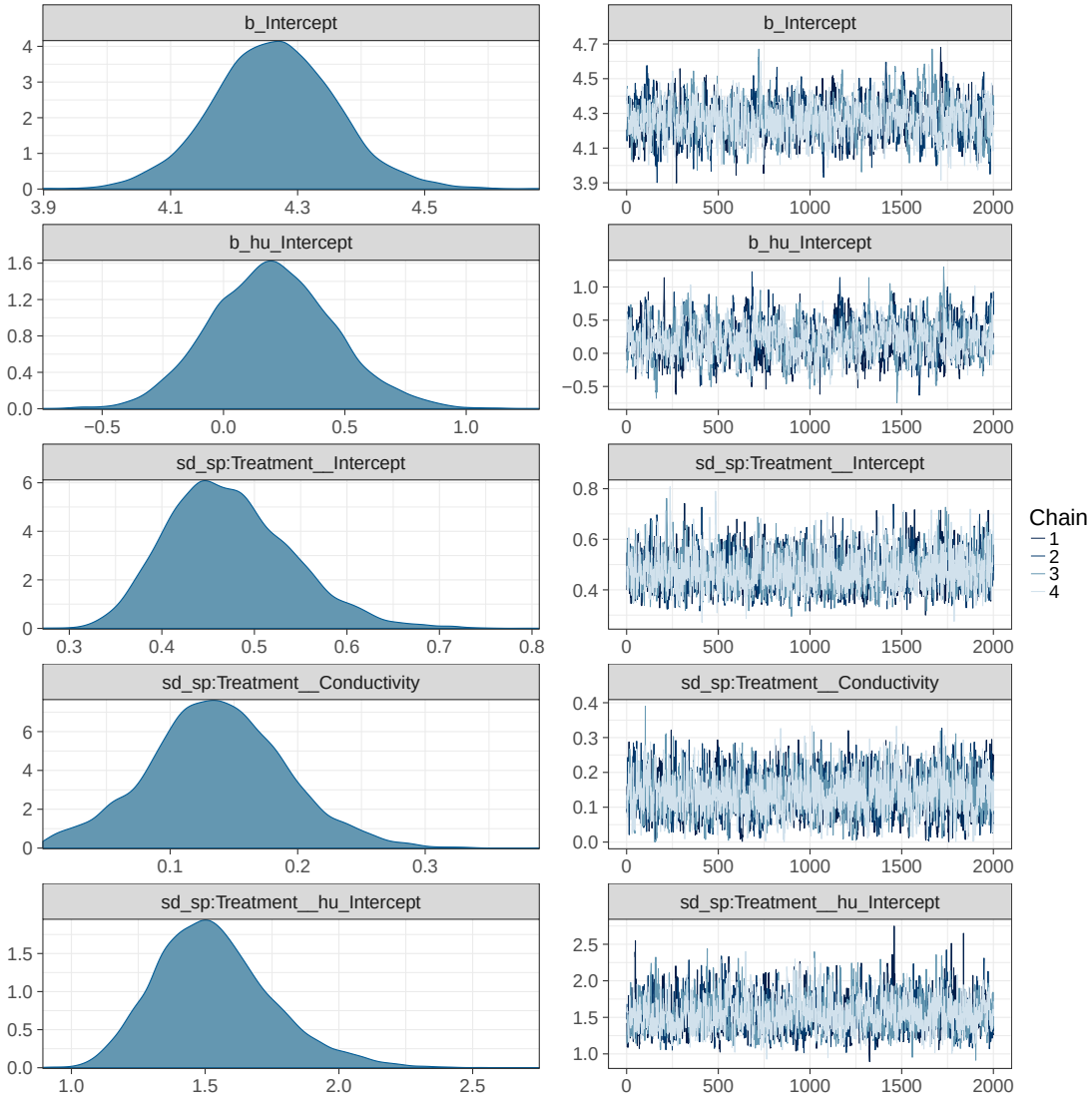
B. Convergence of the MCMC algorithm

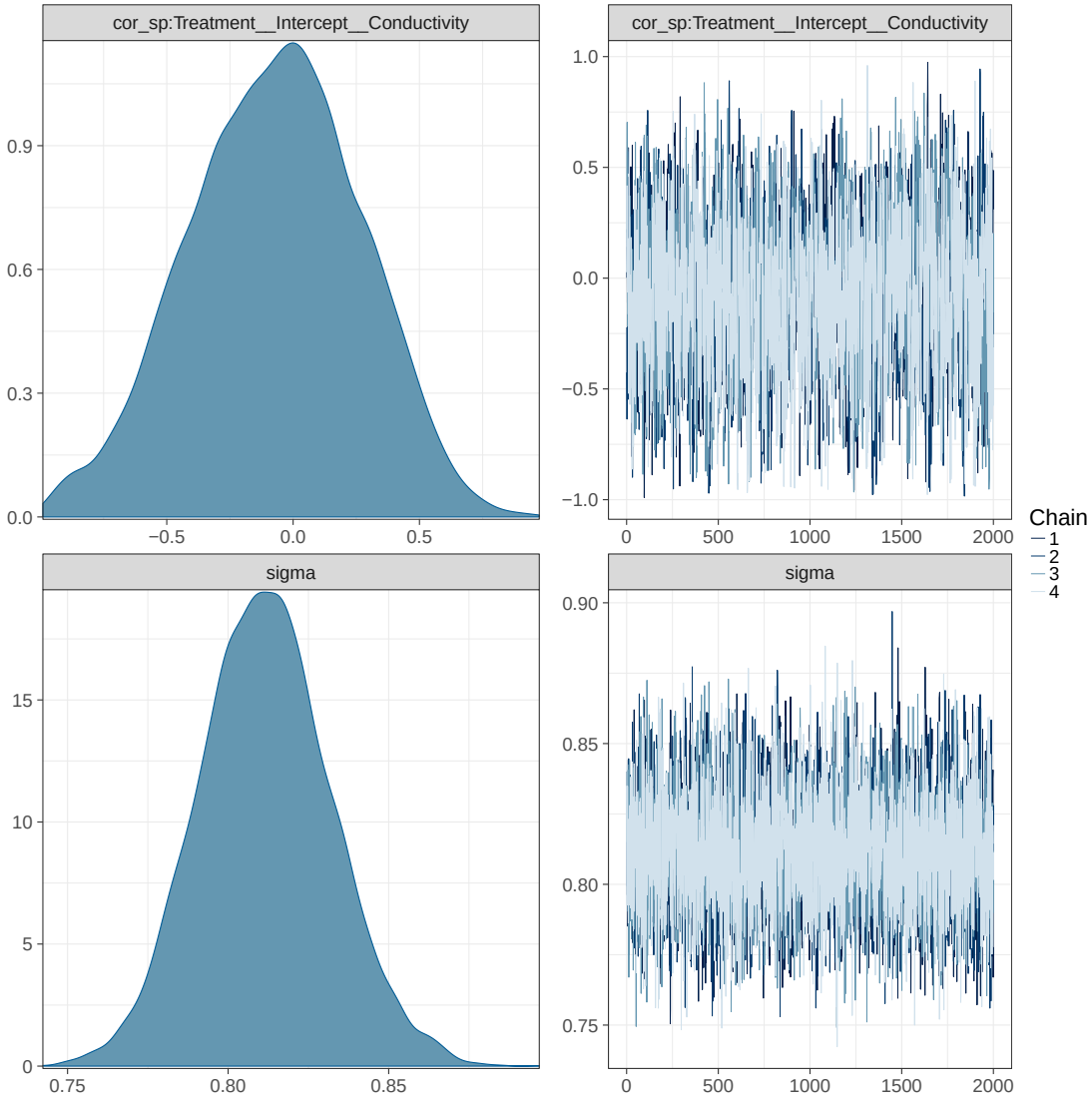
```
summary(abundance_salinity_lognormal_hurdle_model)
```

```
##  Family: hurdle_lognormal
##   Links: mu = identity; sigma = identity; hu = logit
## Formula: abun ~ Conductivity | sp:Treatment
##          hu ~ 1 | sp:Treatment
##    Data: . (Number of observations: 1900)
## Samples: 4 chains, each with iter = 4000; warmup = 2000; thin = 1;
##          total post-warmup samples = 8000
##
```

```
## Group-Level Effects:
## ~sp:Treatment (Number of levels: 40)
##                               Estimate Est.Error l-95% CI u-95% CI
## sd(Intercept)                     0.47      0.07     0.36     0.62
## sd(Conductivity)                  0.14      0.05     0.03     0.25
## sd(hu_Intercept)                  1.53      0.22     1.16     2.03
## cor(Intercept,Conductivity)      -0.07      0.34    -0.75     0.55
##                               Eff.Sample Rhat
## sd(Intercept)                       1895 1.00
## sd(Conductivity)                    1542 1.00
## sd(hu_Intercept)                    1137 1.00
## cor(Intercept,Conductivity)         1633 1.00
##
## Population-Level Effects:
##              Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat
## Intercept        4.26      0.10     4.07     4.46        835 1.00
## hu_Intercept     0.20      0.25    -0.27     0.72        621 1.01
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat
## sigma     0.81      0.02     0.77     0.85       8000 1.00
##
## Samples were drawn using sampling(NUTS). For each parameter, Eff.Sample
## is a crude measure of effective sample size, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

```
plot(abundance_salinity_lognormal_hurdle_model)
```


b_Intercept
b_Intercept
b_hu_Intercept
b_hu_Intercept
sd_sp:Treatment__Intercept
sd_sp:Treatment__Intercept
sd_sp:Treatment__Conductivity
sd_sp:Treatment__Conductivity
sd_sp:Treatment__hu_Intercept
sd_sp:Treatment__hu_Intercept
Chain
1
2
3
4


cor_sp:Treatment__Intercept__Conductivity
cor_sp:Treatment__Intercept__Conductivity
sigma
sigma
Chain
1
2
3
4