visualise

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This Rmarkdown contains all code necassary to re-produce plots and key statistics within the paper

Load packages

```
library(dplyr)
library(ggplot2)
library(ggpubr)
library(tidyr)
library(maptools)  ## For wrld_simpl
library(raster)
library(RColorBrewer)
library(ggtree)
library(ape)
library(phytools)
library(INLA)
library(brinla)
```

Descriptives

Overall summary, reporting on the number of populations, species and sites contained within the overall dataset

```
compiled_data = readRDS("../data/derived_data/compiled_data.rds")
length(unique(compiled_data$site_spec))
```

```
## [1] 30730
```

```r
length(unique(compiled_data$species))
```

```
## [1] 3141
```

```r
length(unique(compiled_data$site))
```

```
## [1] 5991
```

Summaries per dataset Here we report the spatial, taxonomic and temporal extent of each dataset. This information feeds directly into Table S1.

```r
analysis_list = readRDS("../data/derived_data/analysis_list.rds")
descriptives_df = NULL
for(a in names(analysis_list)){
  tmp_df = analysis_list[[a]][[1]]
  tmp_df = subset(tmp_df, !is.na(log_abundance))
  tmp_descriptives_df = data.frame(
    Dataset = a,
    Observations = nrow(tmp_df),
    Populations = length(unique(tmp_df$site_spec_code)),
    Species = length(unique(tmp_df$tips_code)),
    Sites = length(unique(tmp_df$site_code)),
    Timeframe = paste0(min(tmp_df$date), " - ", max(tmp_df$date)),
    Latitude = paste0(round(min(tmp_df$latitude),1), " - ", round(max(tmp_df$latitude),1)),
    Longitude = paste0(round(min(tmp_df$longitude),1), " - ", round(max(tmp_df$longitude),1))
  )
  descriptives_df = rbind(descriptives_df, tmp_descriptives_df)
}

print(descriptives_df)
```

```
##            Dataset Observations Populations Species Sites   Timeframe
## 1           BioTIME       243993       12065    1233   438 1933 - 2018
## 2         CaPTrends         2670         279      26   165 1880 - 2019
## 3           EA_NFPD         2999         359      16   179 1984 - 2019
## 4          FishGlob        67908        2286     152   229 1977 - 2020
## 5               LPI        77773        3613    1333  1244 1950 - 2020
```

```
## 6           NAm_BBS       164317        8718     361   584 1966 - 2019
## 7           Pilotto        11353         582     356    67 1974 - 2018
## 8  ReSurvey_Germany         4954         356      93     7 1966 - 2016
## 9           RivFish        40834        2386     191   197 1975 - 2019
## 10         TimeFISH          262          86      52    12 2008 - 2022
##         Latitude      Longitude
## 1   -77.6 - 68.6 -179.8 - 179.2
## 2     -40 - 71.6    -158 - 99.2
## 3    50.4 - 55.4     -3.9 - 0.5
## 4        26 - 62      -178 - 21
## 5   -77.8 - 78.9   -179.6 - 180
## 6     25.9 - 67 -165.3 - -55.4
## 7    40.1 - 67.8    -8.9 - 29.6
## 8    49.8 - 53.1     8.6 - 13.9
## 9   -28.3 - 67.9 -122.4 - 153.4
## 10 -27.7 - -27.1  -48.5 - -48.3
```

Model fit per dataset Here we explore variance partiioning within each model

```
model_sum = read.csv("../outputs/model_summary.csv")
model_compare_df = NULL
for(a in seq(1,30,3)){
  df_tmp = model_sum[c(a:(a+2)),]
  df_tmp2 = data.frame(
    code = df_tmp$code[1],
    phy_h = df_tmp$tip_h[3]/(df_tmp$tip[3] + df_tmp$tip_h[3] + df_tmp$gen[3]), #Contribution of phylogenetic covariance, relative to all t
    spa_h = df_tmp$sit_h[3]/(df_tmp$sit[3] + df_tmp$sit_h[3] + df_tmp$squ[3]), #Contribution of spatial covariance, relative to all spatia
    temp = df_tmp$obv_auto[3]/(df_tmp$obv[3] + df_tmp$obv_auto[3]),
    temp_phi = df_tmp$phi[3], #Rho correlation between abundances
    temp_v = sum(c(df_tmp$obv[3], df_tmp$obv_auto[3]),na.rm = T)/sum(c( #Proportion of variance captured by temporal model components
      df_tmp$fix[3],
      df_tmp$obv[3],
      df_tmp$obv_auto[3],
      df_tmp$tip[3],
      df_tmp$tip_h[3],
      df_tmp$gen[3],
      df_tmp$sit[3],
      df_tmp$sit_h[3],
      df_tmp$squ[3],
```

```
    df_tmp$sig[3]
  ),na.rm = T),
  sit_v = sum(c(df_tmp$sit[3],df_tmp$sit_h[3], df_tmp$squ[3]),na.rm = T)/sum(c( #Proportion of variance captured by spatial model compor
    df_tmp$fix[3],
    df_tmp$obv[3],
    df_tmp$obv_auto[3],
    df_tmp$tip[3],
    df_tmp$tip_h[3],
    df_tmp$gen[3],
    df_tmp$sit[3],
    df_tmp$sit_h[3],
    df_tmp$squ[3],
    df_tmp$sig[3]
  ),na.rm = T),
  phy_v = sum(c(df_tmp$tip[3],df_tmp$tip_h[3], df_tmp$gen[3]),na.rm = T)/sum(c( #Proportion of variance captured by phylogentic model co
    df_tmp$fix[3],
    df_tmp$obv[3],
    df_tmp$obv_auto[3],
    df_tmp$tip[3],
    df_tmp$tip_h[3],
    df_tmp$gen[3],
    df_tmp$sit[3],
    df_tmp$sit_h[3],
    df_tmp$squ[3],
    df_tmp$sig[3]
  ),na.rm = T),
  res_v = sum(c(df_tmp$sig[3]),na.rm = T)/sum(c( #Proportion of variance captured by residuals
    df_tmp$fix[3],
    df_tmp$obv[3],
    df_tmp$obv_auto[3],
    df_tmp$tip[3],
    df_tmp$tip_h[3],
    df_tmp$gen[3],
    df_tmp$sit[3],
    df_tmp$sit_h[3],
    df_tmp$squ[3],
    df_tmp$sig[3]
  ),na.rm = T),
```

```
    fix_v = sum(c(df_tmp$fix[3]),na.rm = T)/sum(c( #Proportion of variance captured by fixed effect
      df_tmp$fix[3],
      df_tmp$obv[3],
      df_tmp$obv_auto[3],
      df_tmp$tip[3],
      df_tmp$tip_h[3],
      df_tmp$gen[3],
      df_tmp$sit[3],
      df_tmp$sit_h[3],
      df_tmp$squ[3],
      df_tmp$sig[3]
    ),na.rm = T)

  )
  model_compare_df = rbind(model_compare_df, df_tmp2)

}
```

Proportion of variance captured by temporal componenents

```
round(mean(model_compare_df$temp_v),2)
```

```
## [1] 0.37
```

```
round(sd(model_compare_df$temp_v),2)
```

```
## [1] 0.13
```

Proportion of variance captured by spatial componenents

```
round(mean(model_compare_df$sit_v, na.rm = T),2)
```

```
## [1] 0.08
```

```r
round(sd(model_compare_df$sit_v, na.rm = T),2)
```

```
## [1] 0.05
```

Proportion of variance captured by phylogenetic componenents

```r
round(mean(model_compare_df$phy_v),2)
```

```
## [1] 0.05
```

```r
round(sd(model_compare_df$phy_v),2)
```

```
## [1] 0.06
```

Proportion of variance captured by residual componenents

```r
round(mean(model_compare_df$res_v),2)
```

```
## [1] 0.24
```

```r
round(sd(model_compare_df$res_v),2)
```

```
## [1] 0.24
```

Proportion of variance captured by fixed effect componenents

```r
round(mean(model_compare_df$fix_v),2)
```

```
## [1] 0.25
```

```r
round(sd(model_compare_df$fix_v),2)
```

```
## [1] 0.13
```

Correlation between sequential abundance values

```r
round(mean(model_compare_df$temp_phi),2)
```

```
## [1] 0.31
```

```r
round(sd(model_compare_df$temp_phi),2)
```

```
## [1] 0.42
```

H2 of phylo component i.e. the amount of variance captured by the phylogeny relative to the combined variance captured by the phylogeny and taxonomy

```r
round(mean(model_compare_df$phy_h),2)
```

```
## [1] 0.41
```

```r
round(sd(model_compare_df$phy_h),2)
```

```
## [1] 0.28
```

H2 of spatial componenents i.e. the amount of variance captured by space relative to the combined variance captured by the space and the hierarchical space nesting

```r
round(mean(model_compare_df$spa_h, na.rm = T),2)
```

```
## [1] 0.34
```

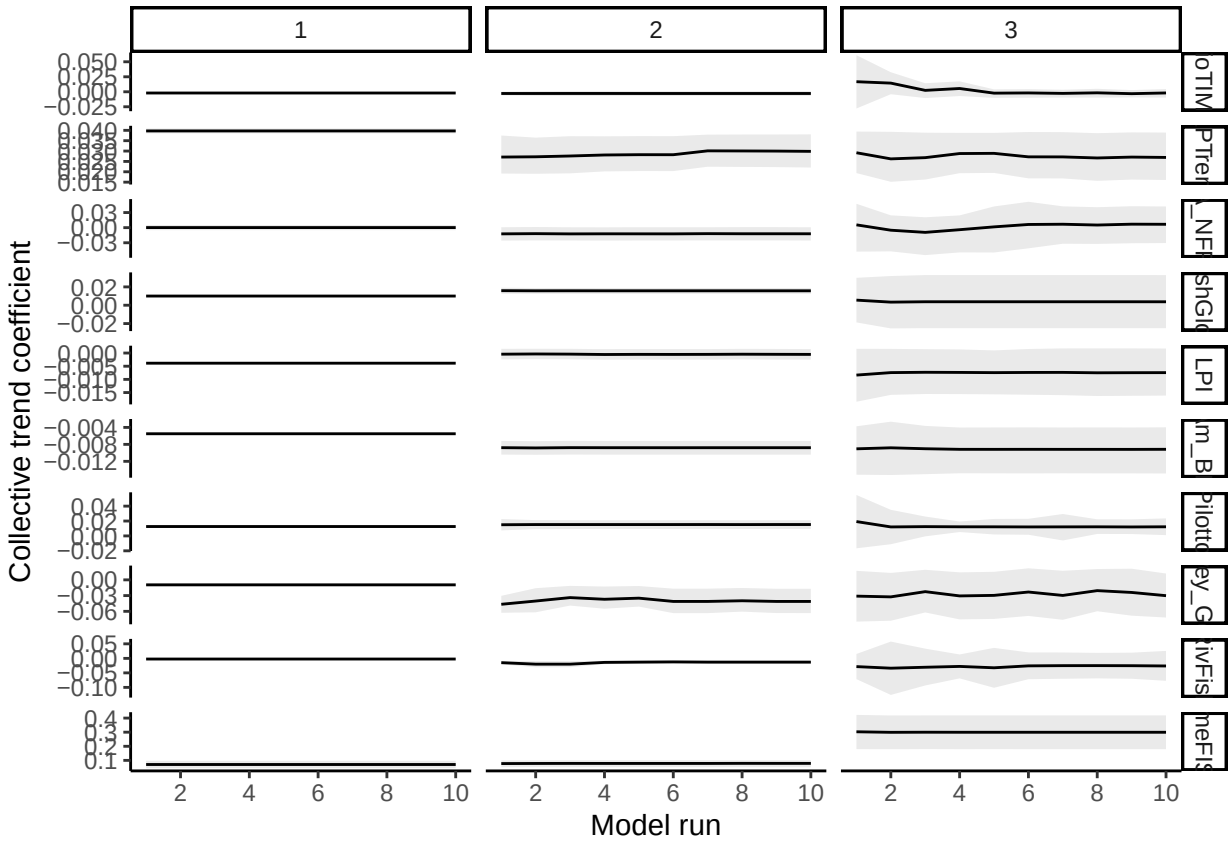
```r
round(sd(model_compare_df$spa_h, na.rm = T),2)
```

```
## [1] 0.3
```

Assumptions

We first check the models have converged. Under MCMC Bayesian approaches, convergence can be checked by ensuring independent chains arrive at similar parameter values. This is not possible in INLA where parameters are approximated, but the same princple applies i.e. if the model is re-run multiple times and arrives at similar parameter values, we can be somewhat confident the results are robust. With this in mind, we re-run each model 10 times, using the paramter mode values from the prior run as the intial values in the current run. In the first run, we used the randomly generated initial values. We assess convergence by looking at the main parameter of interest, the coefficient and credible intervals around the collective trend, and its apparent that after the first 5 runs, parameters begin to stabilise.

```
conv = read.csv("../outputs/model_summary_convergence.csv")
ggplot(conv) +
  geom_ribbon(aes(x = run, ymin = low, ymax = upp), alpha = 0.1) +
  geom_line(aes(x = run, y = coef)) +
  facet_grid(dataset~model, scales = "free") +
  scale_x_continuous(breaks = c(0,2,4,6,8,10)) +
  labs(x = "Model run", y = "Collective trend coefficient") +
  theme_classic()
```



We calculate residuals by subtracting the true abundance values by the median predicted values. We also identify populations with particulary extreme residual values +- 2 standard deviations from the mean residual in each population.

```
analysis_list = readRDS("../data/derived_data/analysis_list.rds")

assumptions_df = NULL
for(a in names(analysis_list)[c(1:10)]){
  tmp_model = readRDS(paste0("../outputs/model_output_convergence10_",a,".rds"))
  for(b in 1:3){
    if(b == 1){
      pred = tmp_model[[b]]$summary.fitted.values[,4]
```

```
      pred = head(pred,-100)
      true = analysis_list[[a]][[1]]$log_abundance
      true = head(true,-100)
      res = (true - pred)
    } else {
      pred = tmp_model[[b]]$summary.fitted.values[,4]
      pred = head(pred,-100)
      true = analysis_list[[a]][[1]]$cent_abundance
      true = head(true,-100)
      res = (true - pred)
    }
    tmp_assumptions_df = data.frame(
      dataset = a,
      model = b,
      site_spec = head(analysis_list[[a]][[1]]$site_spec,-100),
      pred = pred,
      true = true,
      res = res,
      year = head(analysis_list[[a]][[1]]$date,-100))
    res_sum = tmp_assumptions_df %>%
      group_by(site_spec) %>%
      summarise(mean_res = mean(abs(res)), low_cut = mean(res) - (sd(res)*2), high_cut = mean(res) + (sd(res)*2))
    cut = quantile(res_sum$mean_res, probs = 0.5)
    res_sum$hq = ifelse((res_sum$mean_res < cut & res_sum$mean_res > -cut), "Keep", "Remove")
    tmp_assumptions_df = left_join(tmp_assumptions_df, res_sum)
    assumptions_df = rbind(assumptions_df, tmp_assumptions_df)
  }
}

dataset_rename = data.frame(
  dataset = c("BioTIME", "CaPTrends", "EA_NFPD", "FishGlob", "LPI", "NAm_BBS", "Pilotto", "ReSurvey_Germany", "RivFish", "TimeFISH"),
  dataset_code = c("A) BioTIME", "J) Large carnivores", "F) UK riverine fishes", "D) FishGlob", "B) Living Planet", "C) NA Breeding Birds"
)
assumptions_df = left_join(assumptions_df, dataset_rename)
assumptions_df$model = as.character(assumptions_df$model)
assumptions_df$plot_code = paste0(assumptions_df$dataset_code, ": ", assumptions_df$model)
```

Plot median residuals and quantiles against year (the independent variable) to assess heteroscedasaticy

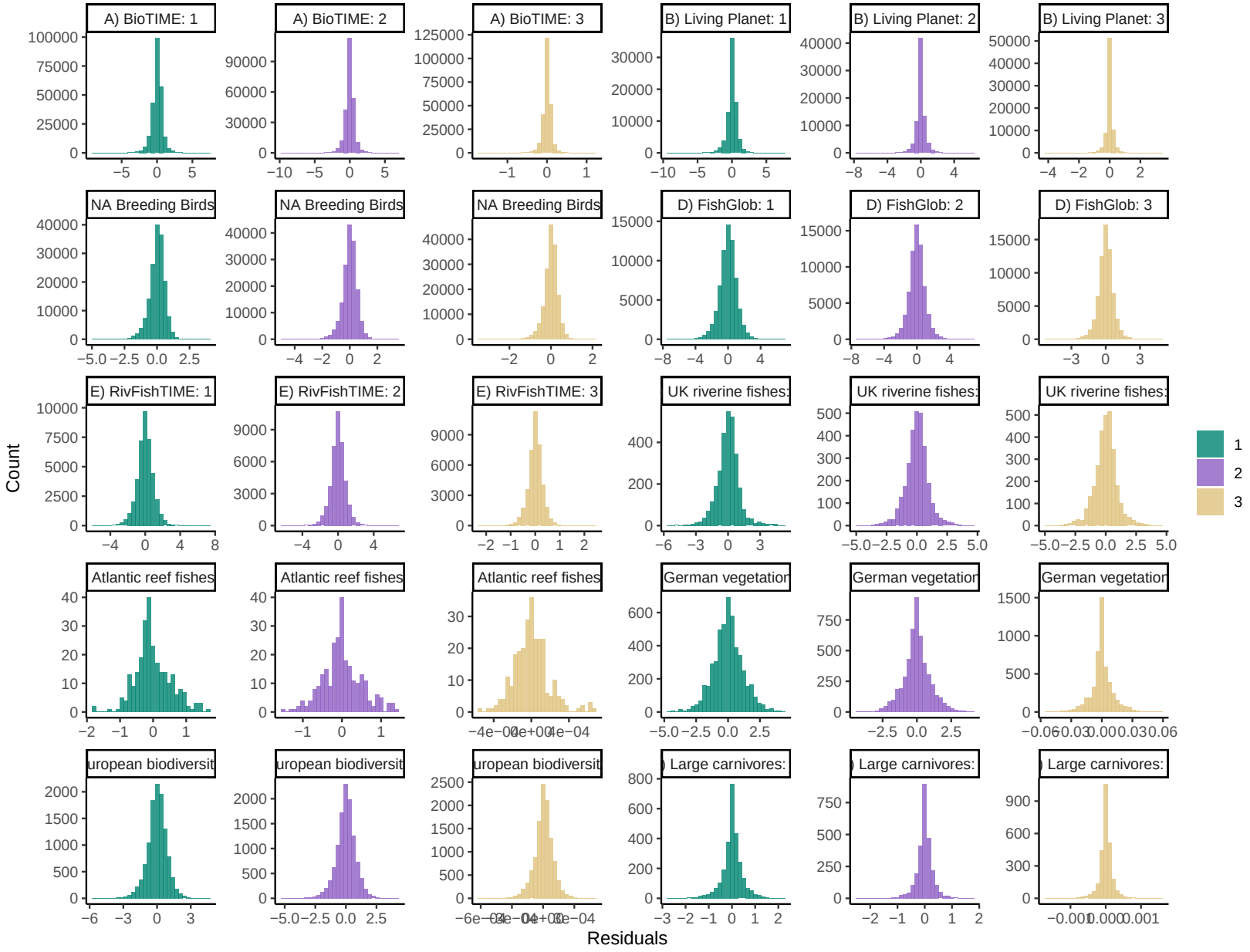
```r
ggplot(data = assumptions_df) +
  geom_boxplot(aes(x = year, y = res, fill = model, colour = model, group = year), alpha = 0.5, outlier.shape = NA) +
  scale_fill_manual(values = c("#018571", "#8f60c4", "#dfc27d"), name = NULL) +
  scale_colour_manual(values = c("#018571", "#8f60c4", "#dfc27d"), name = NULL) +
  facet_wrap(plot_code~., scales = "free") +
  labs(x = "Year", y = "Residuals") +
  theme_classic()
```


A) BioTIME: 1
A) BioTIME: 2
A) BioTIME: 3
B) Living Planet: 1
B) Living Planet: 2
B) Living Planet: 3
NA Breeding Birds:
NA Breeding Birds:
NA Breeding Birds:
D) FishGlob: 1
D) FishGlob: 2
D) FishGlob: 3
E) RivFishTIME: 1
E) RivFishTIME: 2
E) RivFishTIME: 3
UK riverine fishes:
UK riverine fishes:
UK riverine fishes:
Atlantic reef fishes:
Atlantic reef fishes:
Atlantic reef fishes:
German vegetation
German vegetation
German vegetation
European biodiversity
European biodiversity
European biodiversity
Large carnivores:
Large carnivores:
Large carnivores:
Residuals
Year
1
2
3

```r
ggsave("../outputs/figures/assumption_hetero.png",width = 13, height = 7, units = "in", device = "png")
```

Histogram of residuals for each dataset and model combinations to check for normality

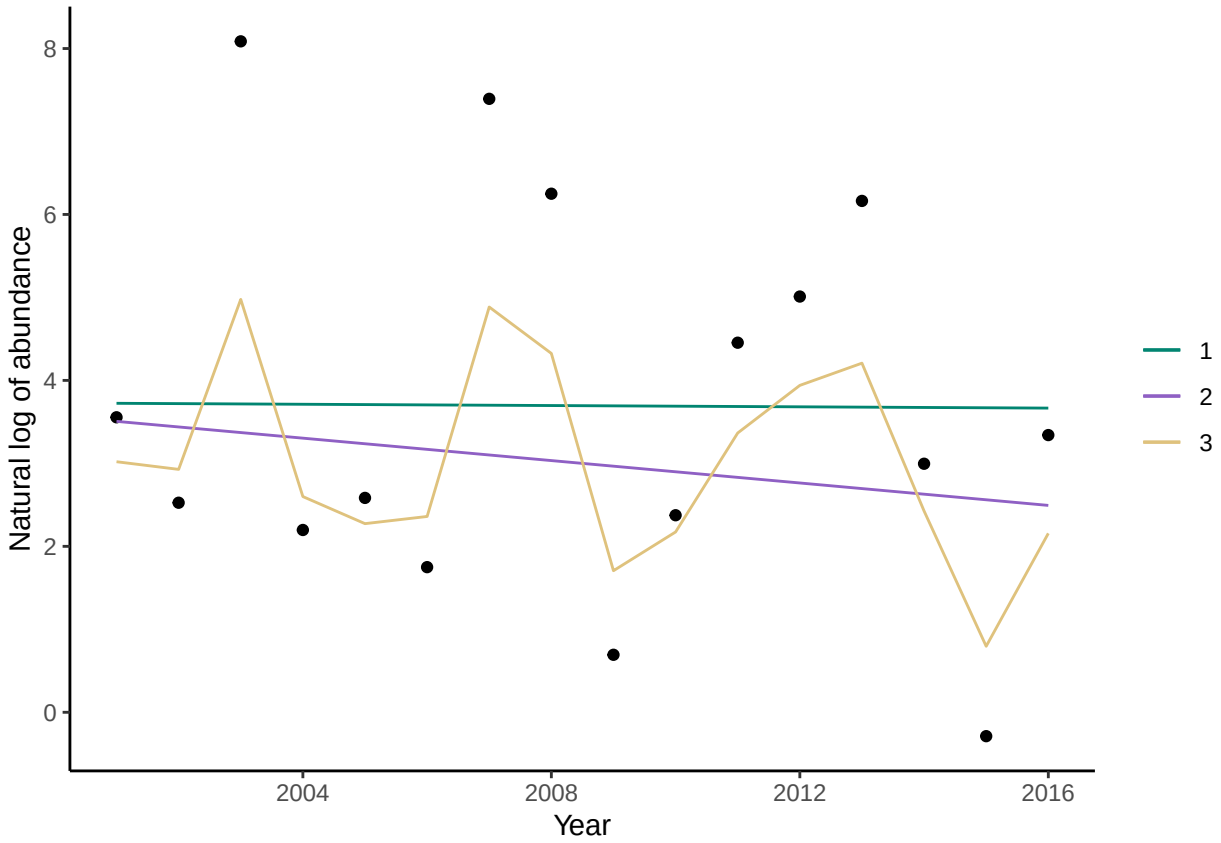
```r
ggplot(data = assumptions_df) +
  geom_histogram(aes(x = res, fill = model), alpha = 0.8, position = "identity") +
  scale_fill_manual(values = c("#018571", "#8f60c4", "#dfc27d"), name = NULL) +
  facet_wrap(plot_code~., scales = "free") +
  labs(x = "Residuals", y = "Count") +
  theme_classic()
```


A) BioTIME: 1
A) BioTIME: 2
A) BioTIME: 3
B) Living Planet: 1
B) Living Planet: 2
B) Living Planet: 3
NA Breeding Birds
NA Breeding Birds
NA Breeding Birds
D) FishGlob: 1
D) FishGlob: 2
D) FishGlob: 3
E) RivFishTIME: 1
E) RivFishTIME: 2
E) RivFishTIME: 3
UK riverine fishes:
UK riverine fishes:
UK riverine fishes:
Atlantic reef fishes
Atlantic reef fishes
Atlantic reef fishes
German vegetation
German vegetation
German vegetation
uropean biodiversit
uropean biodiversit
uropean biodiversit
) Large carnivores:
) Large carnivores:
) Large carnivores:
Count
Residuals
1
2
3

```
ggsave("../outputs/figures/assumption_normality1.png",width = 13, height = 7, units = "in", device = "png")
```

In some datasets, we see patterns of very heavy tails. These heavy tails tend to happen under two circumstances. 1) Example of population where the model poorly fits due to cyclical and highly variable abundance data

```
ggplot() +
  geom_point(data = assumptions_df[which(
    assumptions_df$site_spec == "Chen_2018_Yehliu power plant (site 2a)_25.209615_121.661948Siganus fuscescens_" & assumptions_df$model ==
  geom_line(data = assumptions_df[which(
    assumptions_df$site_spec == "Chen_2018_Yehliu power plant (site 2a)_25.209615_121.661948Siganus fuscescens_" & assumptions_df$model ==
  geom_line(data = assumptions_df[which(
    assumptions_df$site_spec == "Chen_2018_Yehliu power plant (site 2a)_25.209615_121.661948Siganus fuscescens_" & assumptions_df$model ==
  geom_line(data = assumptions_df[which(
    assumptions_df$site_spec == "Chen_2018_Yehliu power plant (site 2a)_25.209615_121.661948Siganus fuscescens_" & assumptions_df$model ==
  scale_colour_manual(values = c("#018571", "#8f60c4", "#dfc27d"), name = NULL) +
  labs(x = "Year", y = "Natural log of abundance") +
  theme_classic()
```

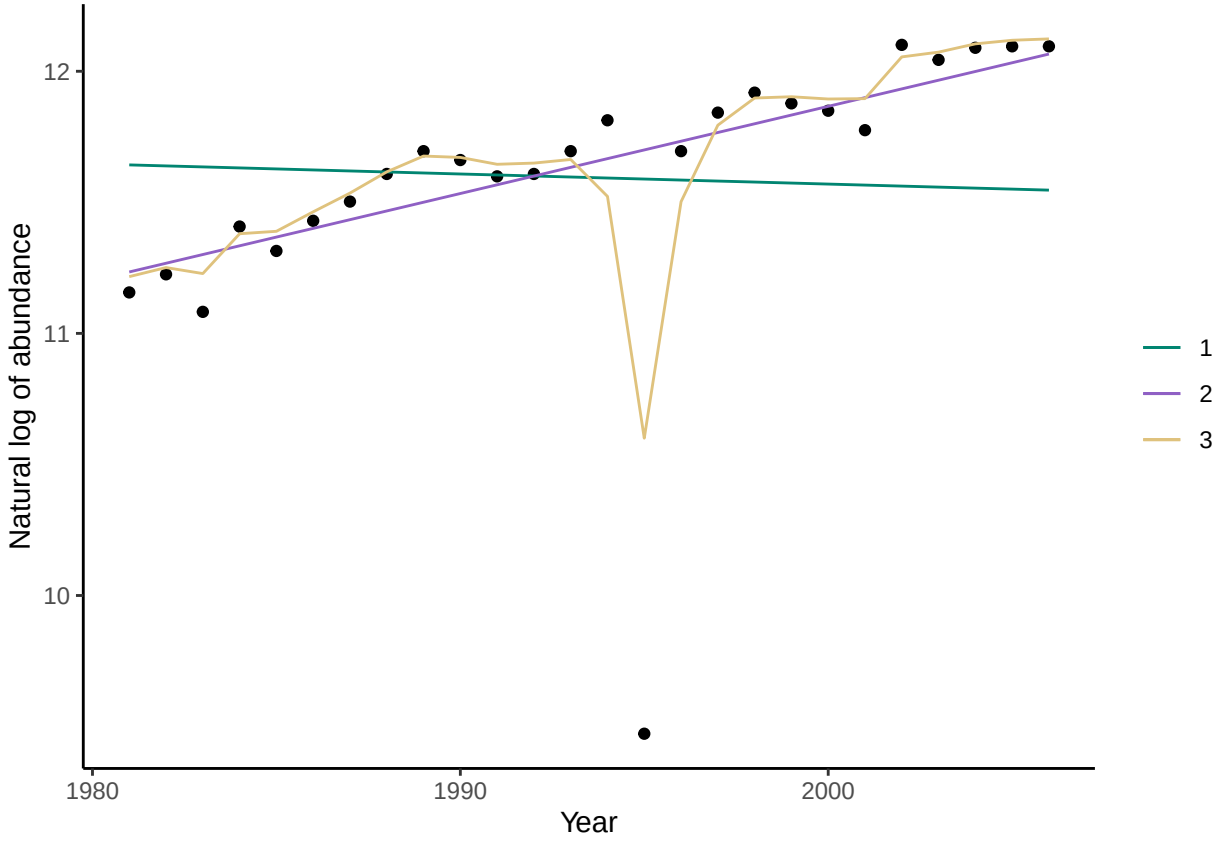



```
ggsave("../outputs/figures/assumption_poorfit1.png",width = 4, height = 4, units = "in", device = "png")
```

2) Example of population with generally well fitting data, but just one extreme abundance

```
ggplot() +
  geom_point(data = assumptions_df[which(
    assumptions_df$site_spec == "Rolley_2006_Western Forest, Wisconsin, USA_44.77778_-91.99472Odocoileus virginianus_" & assumptions_df$mo
  geom_line(data = assumptions_df[which(
    assumptions_df$site_spec == "Rolley_2006_Western Forest, Wisconsin, USA_44.77778_-91.99472Odocoileus virginianus_" & assumptions_df$mo
  geom_line(data = assumptions_df[which(
```

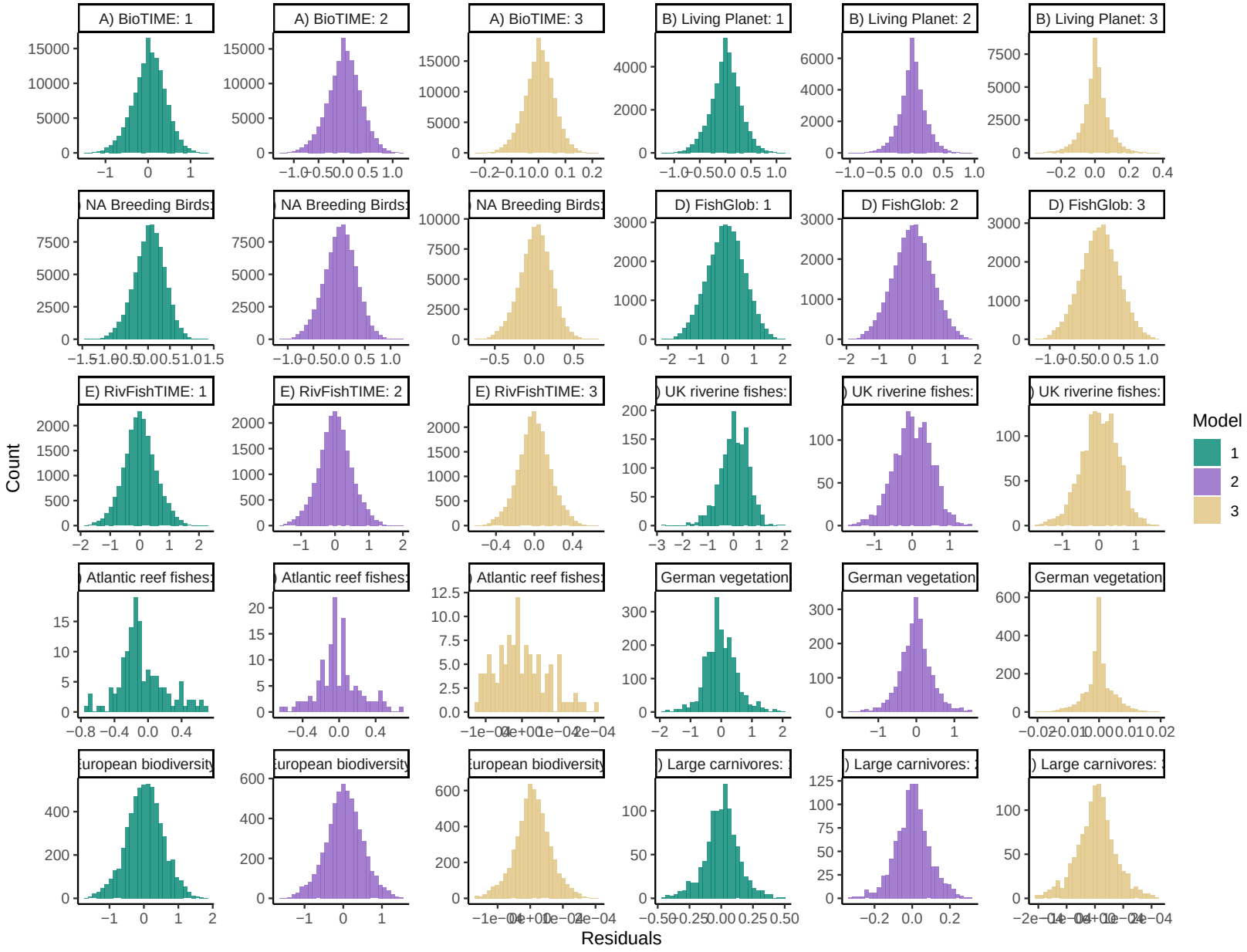
```
  assumptions_df$site_spec == "Rolley_2006_Western Forest, Wisconsin, USA_44.77778_-91.99472Odocoileus virginianus_" & assumptions_df$mo
geom_line(data = assumptions_df[which(
  assumptions_df$site_spec == "Rolley_2006_Western Forest, Wisconsin, USA_44.77778_-91.99472Odocoileus virginianus_" & assumptions_df$mo
scale_colour_manual(values = c("#018571", "#8f60c4", "#dfc27d"), name = NULL) +
labs(x = "Year", y = "Natural log of abundance") +
theme_classic()
```




```
ggsave("../outputs/figures/assumption_poorfit2.png",width = 4, height = 4, units = "in", device = "png")
```

When we check the residuals after removing poorly fitting populations and extreme values, the residuals are looking far more normal

```r
ggplot(data = assumptions_df[which(assumptions_df$hq == "Keep" & assumptions_df$res > assumptions_df$low_cut & assumptions_df$res < assump
  geom_histogram(aes(x = res, fill = model), alpha = 0.8, position = "identity") +
  scale_fill_manual(values = c("#018571", "#8f60c4", "#dfc27d"), name = "Model") +
  facet_wrap(plot_code~., scales = "free") +
  labs(x = "Residuals", y = "Count") +
  theme_classic()
```


A) BioTIME: 1
A) BioTIME: 2
A) BioTIME: 3
B) Living Planet: 1
B) Living Planet: 2
B) Living Planet: 3
NA Breeding Birds:
NA Breeding Birds:
NA Breeding Birds:
D) FishGlob: 1
D) FishGlob: 2
D) FishGlob: 3
E) RivFishTIME: 1
E) RivFishTIME: 2
E) RivFishTIME: 3
UK riverine fishes:
UK riverine fishes:
UK riverine fishes:
Atlantic reef fishes:
Atlantic reef fishes:
Atlantic reef fishes:
German vegetation
German vegetation
German vegetation
uropean biodiversity
uropean biodiversity
uropean biodiversity
Large carnivores:
Large carnivores:
Large carnivores:
Count
Residuals
Model
1
2
3

```
ggsave("../outputs/figures/assumption_normality2.png",width = 13, height = 7, units = "in", device = "png")
```

To ensure our inference is robust to heavy tails, we remove extrme values from the dataset with the heaviest tails (LPI) and re-model

```
lpi_trim = subset(assumptions_df, dataset == "LPI" & model == "3")
lpi_sub = head(analysis_list[["LPI"]][[1]],-100)
lpi_sub = cbind(lpi_sub, lpi_trim[,c(6,9,10,11)])
lpi_sub$log_abundance = ifelse(lpi_sub$res > lpi_sub$high_cut, NA, lpi_sub$log_abundance)
lpi_sub$log_abundance = ifelse(lpi_sub$res < lpi_sub$low_cut, NA, lpi_sub$log_abundance)
lpi_sub$log_abundance = ifelse(lpi_sub$hq == "Remove", NA, lpi_sub$log_abundance)
lpi_sub$cent_abundance = ifelse(lpi_sub$res > lpi_sub$high_cut, NA, lpi_sub$cent_abundance)
lpi_sub$cent_abundance = ifelse(lpi_sub$res < lpi_sub$low_cut, NA, lpi_sub$cent_abundance)
lpi_sub$cent_abundance = ifelse(lpi_sub$hq == "Remove", NA, lpi_sub$cent_abundance)

analysis_list_lpi = list(lpi_sub, analysis_list[["LPI"]][[2]], analysis_list[["LPI"]][[3]])
#source("modelling_lpi_assumption.R")
```

We detect the same pattern of an increasing standard deviation (from m1 to m2 to m3) around the collective trend. Inference appears robust

```
lpi_models = readRDS("../outputs/model_output_lpi_assumption.rds")
data.frame(
  model = c(1,2,3),
  uncertainty = c(
    lpi_models[[1]]$summary.fixed[2,2],
    lpi_models[[2]]$summary.fixed[2,2],
    lpi_models[[3]]$summary.fixed[2,2]))
```

```
##   model  uncertainty
## 1     1 0.0002001832
## 2     2 0.0047850804
## 3     3 0.0499042094
```

Figure 2

Load data from 'modelling core'

```r
model_summary_core = read.csv("../outputs/model_summary.csv")
```

Assess average change in uncertainty and coefficient as you progress through the models

```r
dataset_rename = data.frame(
  code = c("BioTIME", "CaPTrends", "EA_NFPD", "FishGlob", "LPI", "NAm_BBS", "Pilotto", "ReSurvey_Germany", "RivFish", "TimeFISH"),
  dataset_code = c("A) BioTIME", "J) Large carnivores", "F) UK riverine fishes", "D) FishGlob", "B) Living Planet", "C) NA Breeding Birds"
)
model_summary_core = left_join(model_summary_core, dataset_rename)



stre = data.frame(
  name = c(rep("2",10), rep("1",10)),
  diff_rate = c((model_summary_core[which(model_summary_core$model == 1),"coef"]) - (model_summary_core[which(model_summary_core$model ==
                (model_summary_core[which(model_summary_core$model == 2),"coef"]) - (model_summary_core[which(model_summary_core$model ==
  diff_sd = c((model_summary_core[which(model_summary_core$model == 3),"coef_sd"])/(model_summary_core[which(model_summary_core$model == 1
              (model_summary_core[which(model_summary_core$model == 3),"coef_sd"])/(model_summary_core[which(model_summary_core$model == 2
)

stre_sum = stre %>%
  dplyr::group_by(name) %>%
  summarise(mn1 = mean(abs(diff_rate)), sd1 = sd(abs(diff_rate)), mn2 = mean(log10(diff_sd)), sd2 = sd(log10(diff_sd)))

m1_col = "#018571"
m2_col = "#8f60c4"
m3_col = "#dfc27d"

tmp_mod = lm(log(diff_sd) ~ 0 + name, data = stre)
exp(coef(tmp_mod))
```

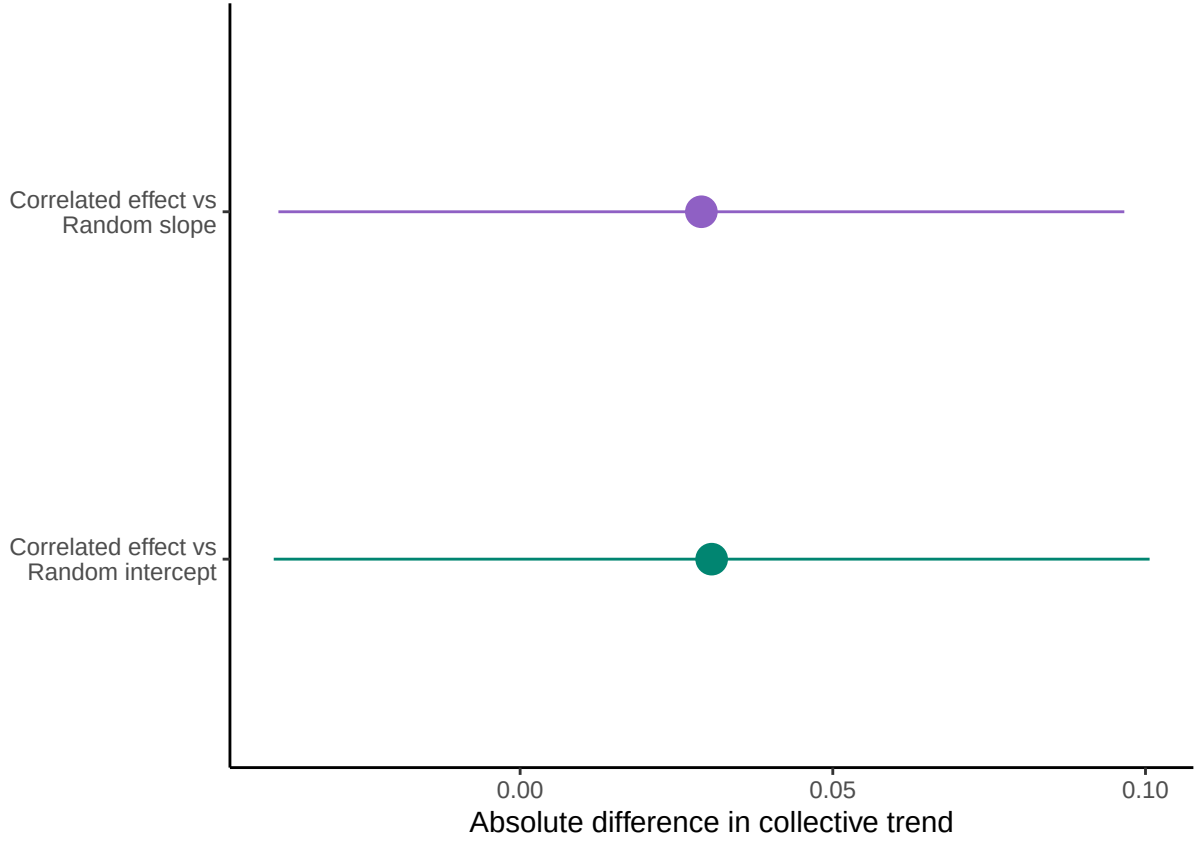
```
##    name1    name2
##  3.38590 25.71641
```

```r
exp(confint(tmp_mod))
```

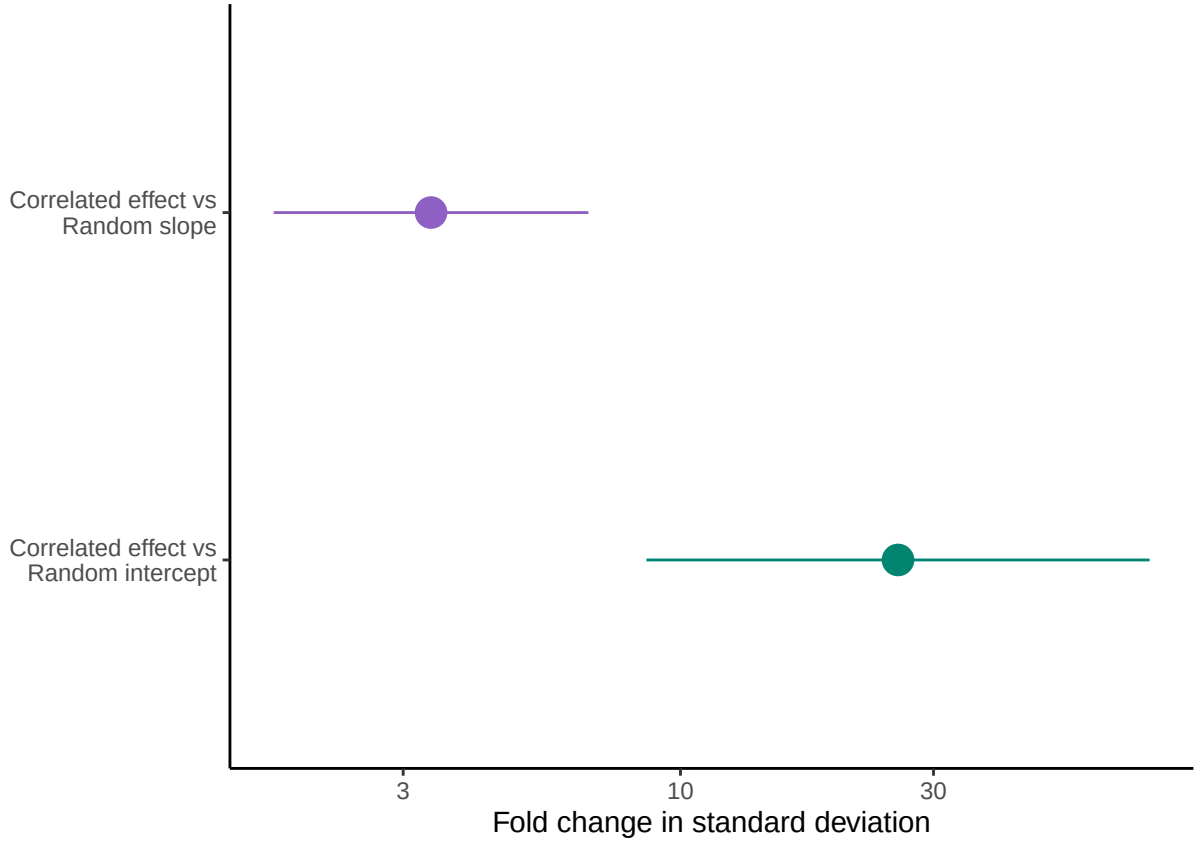
```
##           2.5 %    97.5 %
```

```
## name1  1.848509  6.201928
## name2 14.039699 47.104571
```

```
ggplot() +
  geom_pointrange(data = stre_sum, aes(y = rev(name), xmin = mn1 - sd1, x = mn1, xmax = mn1 + sd1, colour = name), size = 1.1) +
  scale_y_discrete(labels=c("1" = "Correlated effect vs\nRandom intercept",
                            "2" = "Correlated effect vs\nRandom slope")) +
  scale_colour_manual(values = c(m2_col, m1_col), guide = "none") +
  labs(x = "Absolute difference in collective trend", y = "") +
  theme_classic()
```



```
ggplot() +
  geom_pointrange(data = stre_sum, aes(y = rev(name), xmin = 10^(mn2 - sd2), x = 10^(mn2), xmax = 10^(mn2 + sd2), colour = name), size = 1
  scale_y_discrete(labels=c("1" = "Correlated effect vs\nRandom intercept",
                            "2" = "Correlated effect vs\nRandom slope")) +
  scale_x_log10() +
  #coord_cartesian(xlim = c(0, 0.025)) +
  scale_colour_manual(values = c(m2_col, m1_col), guide = "none") +
  labs(x = "Fold change in standard deviation", y = "") +
  theme_classic()
```



Next, we use the coefficients and 50% credible intervals from each model, against a baseline abundance of 100, and project abundance patterns for

each abundance datatset.

```
projections_cmb = NULL
for(a in c(1:10)){
  cde = unique(model_summary_core$code)[a]
  df_tmp = subset(model_summary_core, code == cde)
  df_tmp2 = analysis_list[[cde]][[1]]

  run = length(min(df_tmp2$date, na.rm = T):max(df_tmp2$date, na.rm = T))-1
  y1 = c(100)
  y2 = c(100)
  y3 = c(100)
  for(tim in 1:(run)){
    y1 = c(y1,y1[tim]*(1 + df_tmp$coef[1]))
    y2 = c(y2,y2[tim]*(1 + df_tmp$coef[2]))
    y3 = c(y3,y3[tim]*(1 + df_tmp$coef[3]))
  }


  lc1 = c(100)
  lc2 = c(100)
  lc3 = c(100)
  for(tim in 1:(run)){
    lc1 = c(lc1,lc1[tim]*(1 + df_tmp$coef_lc5[1]))
    lc2 = c(lc2,lc2[tim]*(1 + df_tmp$coef_lc5[2]))
    lc3 = c(lc3,lc3[tim]*(1 + df_tmp$coef_lc5[3]))
  }


  uc1 = c(100)
  uc2 = c(100)
  uc3 = c(100)
  for(tim in 1:(run)){
    uc1 = c(uc1,uc1[tim]*(1 + df_tmp$coef_uc5[1]))
    uc2 = c(uc2,uc2[tim]*(1 + df_tmp$coef_uc5[2]))
    uc3 = c(uc3,uc3[tim]*(1 + df_tmp$coef_uc5[3]))
  }

  projections_tmp = data.frame(
```

```
    code = df_tmp$dataset_code[1],
    year = c(min(df_tmp2$date, na.rm = T):max(df_tmp2$date, na.rm = T)),
    y1 = y1, y2 = y2, y3 = y3,
    lc1 = lc1, lc2 = lc2, lc3 = lc3,
    uc1 = uc1, uc2 = uc2, uc3 = uc3)
  projections_cmb = rbind(projections_cmb, projections_tmp)
}



plt1 = ggplot(data = projections_cmb[projections_cmb$code  %in% unique(projections_cmb$code)[1],]) +
  geom_line(aes(x = year, y1), colour = m1_col) +
  geom_ribbon(aes(x = year, ymin = lc1, ymax = uc1), alpha = 0.1, fill = m1_col) +
  geom_line(aes(x = year, y2), colour = m2_col) +
  geom_ribbon(aes(x = year, ymin = lc2, ymax = uc2), alpha = 0.1, fill = m2_col) +
  geom_line(aes(x = year, y3), colour = m3_col) +
  geom_ribbon(aes(x = year, ymin = lc3, ymax = uc3), alpha = 0.1, fill = m3_col) +
  geom_hline(aes(yintercept = 100), colour= "grey", linetype = "dotted") +
  scale_x_continuous(expand = c(0,0), breaks = c(1950,1980,2010)) +
  scale_y_log10(expand = c(0,0), breaks = c(50,75,100,125)) +
  coord_cartesian(xlim = c(1948,2016), ylim = c(45,130)) +
  labs(x = " ", y = "Abundance") +
  theme_classic() +
  theme(axis.text = element_text(size=12))


plt2 = ggplot(data = projections_cmb[projections_cmb$code  %in% unique(projections_cmb$code)[5],]) +
  geom_line(aes(x = year, y1), colour = m1_col) +
  geom_ribbon(aes(x = year, ymin = lc1, ymax = uc1), alpha = 0.1, fill = m1_col) +
  geom_line(aes(x = year, y2), colour = m2_col) +
  geom_ribbon(aes(x = year, ymin = lc2, ymax = uc2), alpha = 0.1, fill = m2_col) +
  geom_line(aes(x = year, y3), colour = m3_col) +
  geom_ribbon(aes(x = year, ymin = lc3, ymax = uc3), alpha = 0.1, fill = m3_col) +
  geom_hline(aes(yintercept = 100), colour= "grey", linetype = "dotted") +
  scale_x_continuous(expand = c(0,0), breaks = c(1960,1985,2010)) +
  scale_y_log10(expand = c(0,0), breaks =  c(50,75,100,125)) +
  coord_cartesian(ylim = c(45,130)) +
  labs(x = " ", y = "") +
```

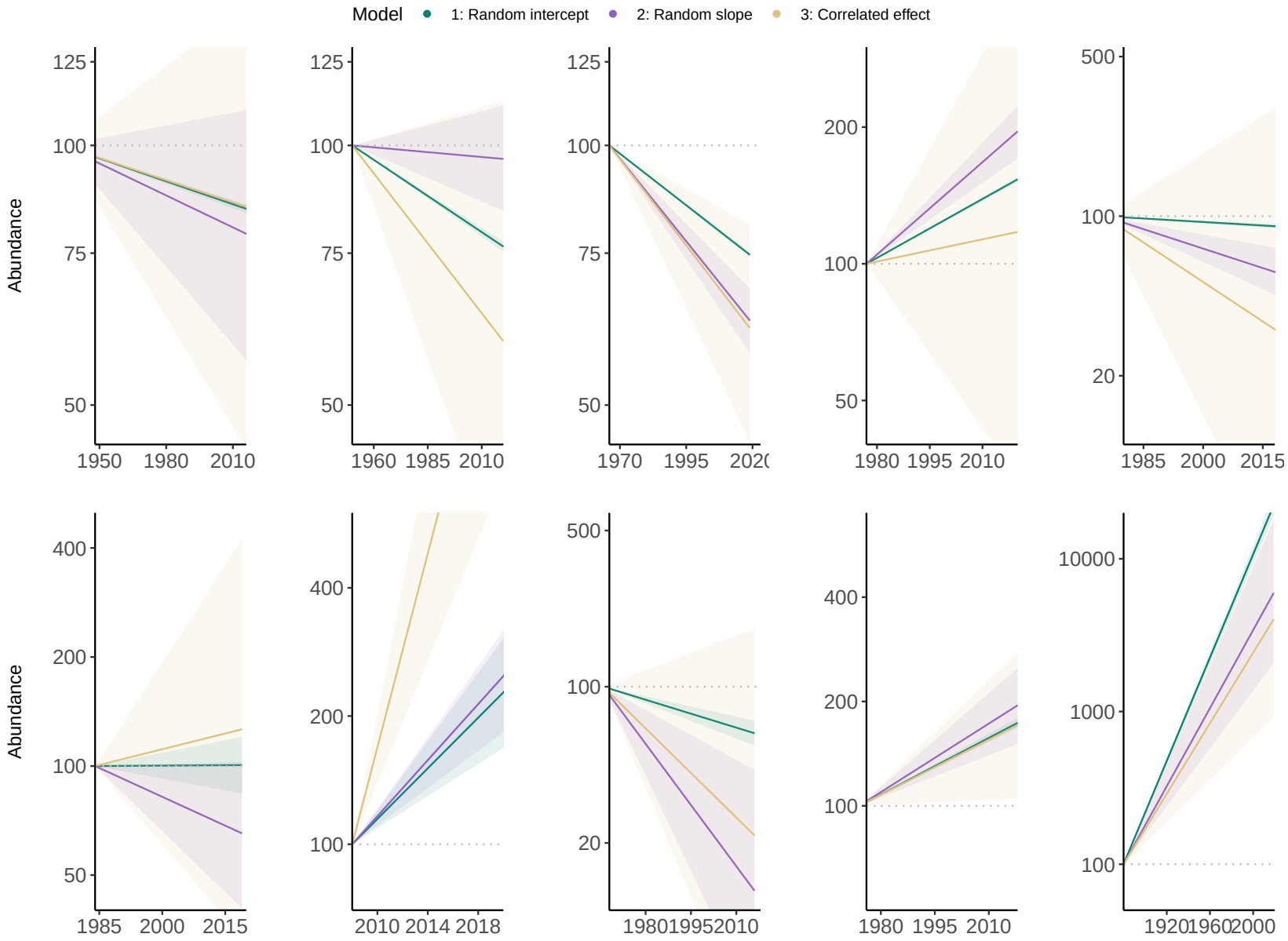
```
  theme_classic() +
  theme(axis.title.y=element_blank(),
        axis.text = element_text(size=12))


plt3 =   ggplot(data = projections_cmb[projections_cmb$code  %in% unique(projections_cmb$code)[6],]) +
  geom_line(aes(x = year, y1), colour = m1_col) +
  geom_ribbon(aes(x = year, ymin = lc1, ymax = uc1), alpha = 0.1, fill = m1_col) +
  geom_line(aes(x = year, y2), colour = m2_col) +
  geom_ribbon(aes(x = year, ymin = lc2, ymax = uc2), alpha = 0.1, fill = m2_col) +
  geom_line(aes(x = year, y3), colour = m3_col) +
  geom_ribbon(aes(x = year, ymin = lc3, ymax = uc3), alpha = 0.1, fill = m3_col) +
  geom_hline(aes(yintercept = 100), colour= "grey", linetype = "dotted") +
  scale_x_continuous(expand = c(0,0), breaks = c(1970,1995,2020), limits = c(1966, 2023)) +
  scale_y_log10(expand = c(0,0), breaks =  c(50,75,100,125)) +
  coord_cartesian(ylim = c(45,130)) +
  labs(x = " ", y = "") +
  theme_classic() +
  theme(axis.title.y=element_blank(),
        axis.text = element_text(size=12))


plt4 = ggplot(data = projections_cmb[projections_cmb$code  %in% unique(projections_cmb$code)[4],]) +
  geom_line(aes(x = year, y1), colour = m1_col) +
  geom_ribbon(aes(x = year, ymin = lc1, ymax = uc1), alpha = 0.1, fill = m1_col) +
  geom_line(aes(x = year, y2), colour = m2_col) +
  geom_ribbon(aes(x = year, ymin = lc2, ymax = uc2), alpha = 0.1, fill = m2_col) +
  geom_line(aes(x = year, y3), colour = m3_col) +
  geom_ribbon(aes(x = year, ymin = lc3, ymax = uc3), alpha = 0.1, fill = m3_col) +
  geom_hline(aes(yintercept = 100), colour= "grey", linetype = "dotted") +
  scale_x_continuous(expand = c(0,0), breaks = c(1980,1995,2010)) +
  scale_y_log10(expand = c(0,0), breaks = c(50,100,200)) +
  coord_cartesian(ylim = c(40,300)) +
  labs(x = " ", y = "") +
  theme_classic() +
  theme(axis.title.y=element_blank(),
        axis.text = element_text(size=12))
```

```r
plt5 = ggplot(data = projections_cmb[projections_cmb$code  %in% unique(projections_cmb$code)[9],]) +
  geom_line(aes(x = year, y1), colour = m1_col) +
  geom_ribbon(aes(x = year, ymin = lc1, ymax = uc1), alpha = 0.1, fill = m1_col) +
  geom_line(aes(x = year, y2), colour = m2_col) +
  geom_ribbon(aes(x = year, ymin = lc2, ymax = uc2), alpha = 0.1, fill = m2_col) +
  geom_line(aes(x = year, y3), colour = m3_col) +
  geom_ribbon(aes(x = year, ymin = lc3, ymax = uc3), alpha = 0.1, fill = m3_col) +
  geom_hline(aes(yintercept = 100), colour= "grey", linetype = "dotted") +
  scale_x_continuous(expand = c(0,0), breaks = c(1985,2000,2015)) +
  scale_y_log10(expand = c(0,0), breaks = c(20,100,500)) +
  coord_cartesian(xlim = c(1980,2018), ylim = c(10,550)) +
  labs(x = " ", y = "") +
  theme_classic() +
  theme(axis.title.y=element_blank(),
        axis.text = element_text(size=12))


plt6 = ggplot(data = projections_cmb[projections_cmb$code  %in% unique(projections_cmb$code)[3],]) +
  geom_line(aes(x = year, y1), colour = m1_col) +
  geom_ribbon(aes(x = year, ymin = lc1, ymax = uc1), alpha = 0.1, fill = m1_col) +
  geom_line(aes(x = year, y2), colour = m2_col) +
  geom_ribbon(aes(x = year, ymin = lc2, ymax = uc2), alpha = 0.1, fill = m2_col) +
  geom_line(aes(x = year, y3), colour = m3_col) +
  geom_ribbon(aes(x = year, ymin = lc3, ymax = uc3), alpha = 0.1, fill = m3_col) +
  geom_hline(aes(yintercept = 100), colour= "grey", linetype = "dotted") +
  scale_x_continuous(expand = c(0,0), breaks = c(1985,2000,2015)) +
  scale_y_log10(expand = c(0,0), breaks = c(50,100,200,400)) +
  coord_cartesian(xlim = c(1984,2020), ylim = c(40,500)) +
  labs(x = " ", y = "Abundance") +
  theme_classic() +
  theme(axis.text = element_text(size=12))



plt7 = ggplot(data = projections_cmb[projections_cmb$code  %in% unique(projections_cmb$code)[10],]) +
  geom_line(aes(x = year, y1), colour = m1_col) +
  geom_ribbon(aes(x = year, ymin = lc1, ymax = uc1), alpha = 0.1, fill = m1_col) +
```

```
  geom_line(aes(x = year, y2), colour = m2_col) +
  geom_ribbon(aes(x = year, ymin = lc2, ymax = uc2), alpha = 0.1, fill = m2_col) +
  geom_line(aes(x = year, y3), colour = m3_col) +
  geom_ribbon(aes(x = year, ymin = lc3, ymax = uc3), alpha = 0.1, fill = m3_col) +
  geom_hline(aes(yintercept = 100), colour= "grey", linetype = "dotted") +
  scale_x_continuous(expand = c(0,0), breaks = c(2010,2014,2018)) +
  scale_y_log10(expand = c(0,0), breaks = c(100,200,400)) +
  coord_cartesian(xlim = c(2008,2020), ylim = c(70,600)) +
  labs(x = " ", y = "") +
  theme_classic() +
  theme(axis.title.y=element_blank(),
        axis.text = element_text(size=12))


plt8 = ggplot(data = projections_cmb[projections_cmb$code  %in% unique(projections_cmb$code)[8],]) +
  geom_line(aes(x = year, y1), colour = m1_col) +
  geom_ribbon(aes(x = year, ymin = lc1, ymax = uc1), alpha = 0.1, fill = m1_col) +
  geom_line(aes(x = year, y2), colour = m2_col) +
  geom_ribbon(aes(x = year, ymin = lc2, ymax = uc2), alpha = 0.1, fill = m2_col) +
  geom_line(aes(x = year, y3), colour = m3_col) +
  geom_ribbon(aes(x = year, ymin = lc3, ymax = uc3), alpha = 0.1, fill = m3_col) +
  geom_hline(aes(yintercept = 100), colour= "grey", linetype = "dotted") +
  scale_x_continuous(expand = c(0,0), breaks = c(1980,1995,2010), limits = c(1968, 2018)) +
  scale_y_log10(expand = c(0,0), breaks = c(20,100,500)) +
  coord_cartesian(ylim = c(10,600)) +
  labs(x = " ", y = "") +
  theme_classic() +
  theme(axis.title.y=element_blank(),
        axis.text = element_text(size=12))


plt9 = ggplot(data = projections_cmb[projections_cmb$code  %in% unique(projections_cmb$code)[7],]) +
  geom_line(aes(x = year, y1), colour = m1_col) +
  geom_ribbon(aes(x = year, ymin = lc1, ymax = uc1), alpha = 0.1, fill = m1_col) +
  geom_line(aes(x = year, y2), colour = m2_col) +
  geom_ribbon(aes(x = year, ymin = lc2, ymax = uc2), alpha = 0.1, fill = m2_col) +
  geom_line(aes(x = year, y3), colour = m3_col) +
  geom_ribbon(aes(x = year, ymin = lc3, ymax = uc3), alpha = 0.1, fill = m3_col) +
```

```
  geom_hline(aes(yintercept = 100), colour= "grey", linetype = "dotted") +
  scale_x_continuous(expand = c(0,0), breaks = c(1980,1995,2010), limits = c(1976, 2018)) +
  scale_y_log10(expand = c(0,0), breaks = c(100,200,400)) +
  coord_cartesian(ylim = c(50,700)) +
  labs(x = " ", y = "") +
  theme_classic() +
  theme(axis.title.y=element_blank(),
        axis.text = element_text(size=12))

legend_creator = data.frame(
  id = c("1","2","3"),
  x = 1000,
  y = 100
)

plt10 = ggplot(data = projections_cmb[projections_cmb$code  %in% unique(projections_cmb$code)[2],]) +
  geom_line(aes(x = year, y1), colour = m1_col) +
  geom_ribbon(aes(x = year, ymin = lc1, ymax = uc1), alpha = 0.1, fill = m1_col) +
  geom_line(aes(x = year, y2), colour = m2_col) +
  geom_ribbon(aes(x = year, ymin = lc2, ymax = uc2), alpha = 0.1, fill = m2_col) +
  geom_line(aes(x = year, y3), colour = m3_col) +
  geom_ribbon(aes(x = year, ymin = lc3, ymax = uc3), alpha = 0.1, fill = m3_col) +
  geom_hline(aes(yintercept = 100), colour= "grey", linetype = "dotted") +
  geom_point(data = legend_creator, aes(x = x, y = y, colour = id)) +
  scale_x_continuous(expand = c(0,0), breaks = c(1920,1960,2000), limits = c(1880,2020)) +
  scale_y_log10(expand = c(0,0), breaks = c(100,1000,10000)) +
  coord_cartesian(ylim = c(50,20000)) +
  labs(x = " ", y = "") +
  theme_classic() +
  scale_colour_manual(name = "Model", labels = c(
    "1: Random intercept",
    "2: Random slope",
    "3: Correlated effect"
  ), values = c(
    m1_col,
    m2_col,
    m3_col
  )) +
```

```
  theme_classic() +
  theme(axis.title.y=element_blank(),
        axis.text = element_text(size=12),
        legend.position = "bottom")


ggarrange(plt1, plt2, plt3, plt4, plt5, plt6, plt7, plt8, plt9, plt10, ncol = 5, nrow = 2, common.legend = T, legend = "top", align = "hv"
```


Model
1: Random intercept
2: Random slope
3: Correlated effect
Abundance
Abundance

```
write.csv(projections_cmb, "../data/derived_data/fig2.csv")
```

#Figure 3

Here we plot the abundance observations and assoicated predictions for a series of species in a specific site. We plot this data under each model to show how each model fits to the data

```
example_dat = readRDS("../outputs/model_output_convergence10_LPI.rds")
df = readRDS("../data/derived_data/analysis_list.rds")[[5]][[1]]

pop_level = data.frame(id = rownames(example_dat[[1]]$summary.fitted.values))
pop_level$m1_pred = example_dat[[1]]$summary.fitted.values$`0.5quant`
pop_level$m1_pred_lc = example_dat[[1]]$summary.fitted.values$`0.025quant`
pop_level$m1_pred_uc = example_dat[[1]]$summary.fitted.values$`0.975quant`
pop_level$m2_pred = example_dat[[2]]$summary.fitted.values$`0.5quant`
pop_level$m2_pred_lc = example_dat[[2]]$summary.fitted.values$`0.025quant`
pop_level$m2_pred_uc = example_dat[[2]]$summary.fitted.values$`0.975quant`
pop_level$m3_pred = example_dat[[3]]$summary.fitted.values$`0.5quant`
pop_level$m3_pred_lc = example_dat[[3]]$summary.fitted.values$`0.025quant`
pop_level$m3_pred_uc = example_dat[[3]]$summary.fitted.values$`0.975quant`
pop_level = cbind(df, pop_level)

obs_by_site_species = pop_level %>%
  group_by(site_code, species) %>%
  summarise(N = n())

trends_by_site = pop_level %>%
  group_by(site_code, latitude, longitude, species) %>%
  summarise(N = n())

site_freq = as.data.frame(table(unique(pop_level[,c("site_code","latitude", "longitude", "species")])$site_code))
site_freq = subset(site_freq, Freq == 3)

#Select site 566 as a good example
trends_by_site = trends_by_site[trends_by_site$site_code %in% site_freq$Var1, ]

plt_m1_a = ggplot(data = pop_level[which(pop_level$site_code == 566),]) +
  geom_line(aes(x = date, y = (exp(m1_pred)), colour = species)) +
  geom_ribbon(aes(x = date, ymin =  (exp(m1_pred_lc)), ymax = (exp(m1_pred_uc)), fill = species), alpha = 0.1) +
```

```
  geom_point(aes(x = date, y = exp(log_abundance), colour = species)) +
  scale_x_continuous(expand = c(0,0), breaks = c(1990, 2000, 2010), limits = c(1987, 2015)) +
  scale_y_continuous(expand = c(0,0)) +
  coord_cartesian(ylim = c(1,600), xlim = c(1987, 2015)) +
  scale_colour_manual(
    name = "",
    labels = c("M. daubentoni", "M. emarginatus", "M. nattereri"),
    values = c("#9fbdbf", "#1885d9", "#1c50d4")) +
  scale_fill_manual(
    name = "",
    labels = c("M. daubentoni", "M. emarginatus", "M. nattereri"),
    values = c("#9fbdbf", "#1885d9", "#1c50d4")) +
  labs(x = "", y = "Abundance", title = "Random intercept") +
  theme_classic() +
  theme(plot.title = element_text(size=10, face="italic"))

plt_m2_a = ggplot(data = pop_level[which(pop_level$site_code == 566),]) +
  geom_line(aes(x = date, y = (exp(m2_pred + mean_log)), colour = species)) +
  geom_ribbon(aes(x = date, ymin =  (exp(m2_pred_lc + mean_log)), ymax = (exp(m2_pred_uc + mean_log)), fill = species), alpha = 0.1) +
  geom_point(aes(x = date, y = exp(cent_abundance + mean_log), colour = species)) +
  scale_x_continuous(expand = c(0,0), breaks = c(1990, 2000, 2010), limits = c(1987, 2015)) +
  scale_y_continuous(expand = c(0,0)) +
  coord_cartesian(ylim = c(1,600), xlim = c(1987, 2015)) +
  scale_colour_manual(
    name = "",
    labels = c("M. daubentoni", "M. emarginatus", "M. nattereri"),
    values = c("#9fbdbf", "#1885d9", "#1c50d4")) +
  scale_fill_manual(
    name = "",
    labels = c("M. daubentoni", "M. emarginatus", "M. nattereri"),
    values = c("#9fbdbf", "#1885d9", "#1c50d4")) +
  labs(x = "", y = "Abundance", title = "Random slope") +
  theme_classic() +
  theme(plot.title = element_text(size=10, face="italic"))


plt_m3_a = ggplot(data = pop_level[which(pop_level$site_code == 566),]) +
  geom_line(aes(x = date, y = (exp(m3_pred + mean_log)), colour = species)) +
```

```
  geom_ribbon(aes(x = date, ymin =  (exp(m3_pred_lc + mean_log)), ymax = (exp(m3_pred_uc + mean_log)), fill = species), alpha = 0.1) +
  geom_point(aes(x = date, y = exp(cent_abundance + mean_log), colour = species)) +
  scale_x_continuous(expand = c(0,0), breaks = c(1990, 2000, 2010), limits = c(1987, 2015)) +
  scale_y_continuous(expand = c(0,0)) +
  coord_cartesian(ylim = c(1,600), xlim = c(1987, 2015)) +
  scale_colour_manual(
    name = "",
    labels = c("M. daubentoni", "M. emarginatus", "M. nattereri"),
    values = c("#9fbdbf", "#1885d9", "#1c50d4")) +
  scale_fill_manual(
    name = "",
    labels = c("M. daubentoni", "M. emarginatus", "M. nattereri"),
    values = c("#9fbdbf", "#1885d9", "#1c50d4")) +
  labs(x = "", y = "Abundance", title = "Correlated effect") +
  theme_classic() +
  theme(plot.title = element_text(size=10, face="italic"))

write.csv(pop_level[which(pop_level$site_code == 566),], "../data/derived_data/fig3a.csv")
```

Under the same site described above, we plot the predicted site level trend. In this trend we only show uncertainty in the rate of change, the primary paramter of interest, not the intercept. This allows direct comparisons in uncertainty between the model types

```
site_level = example_dat[[1]]$summary.random$site_code[,c(1,4,5,6)]
site_level = cbind(site_level, example_dat[[2]]$summary.random$site_code[,c(4,5,6)])
site_level = cbind(site_level, example_dat[[3]]$summary.random$site_code2[,c(4,5,6)] + example_dat[[3]]$summary.random$site_code2[,c(4,5,6
colnames(site_level) = c("site_code", "m1_lc_a", "m1_med_a", "m1_uc_a", "m2_lc_a", "m2_med_a", "m2_uc_a", "m3_lc_a", "m3_med_a", "m3_uc_a"

region_level = example_dat[[1]]$summary.random$region_code[,c(1,5)]
region_level = cbind(region_level, example_dat[[2]]$summary.random$region_code[,c(5)])
region_level = cbind(region_level, example_dat[[3]]$summary.random$region_code[,c(5)])
colnames(region_level) = c("region_code","m1_med_b","m2_med_b","m3_med_b")

region_site_link = unique(df[,c("region_code", "site_code")])
region_site_link = left_join(region_site_link, site_level)
region_site_link = left_join(region_site_link, region_level, by = "region_code")

region_site_link$m1_lc = region_site_link$m1_lc_a + region_site_link$m1_med_b
region_site_link$m1_med = region_site_link$m1_med_a + region_site_link$m1_med_b
```

```
region_site_link$m1_uc = region_site_link$m1_uc_a + region_site_link$m1_med_b
region_site_link$m2_lc = region_site_link$m2_lc_a + region_site_link$m2_med_b
region_site_link$m2_med = region_site_link$m2_med_a + region_site_link$m2_med_b
region_site_link$m2_uc = region_site_link$m2_uc_a + region_site_link$m2_med_b
region_site_link$m3_lc = region_site_link$m3_lc_a + region_site_link$m3_med_b
region_site_link$m3_med = region_site_link$m3_med_a + region_site_link$m3_med_b
region_site_link$m3_uc = region_site_link$m3_uc_a + region_site_link$m3_med_b

region_site_link_trim = subset(region_site_link, region_site_link$site_code == 566)


sit_level = data.frame(
  year = df$year_centre[c((nrow(example_dat[[1]]$summary.fitted.values)-99):nrow(example_dat[[1]]$summary.fitted.values))],
  mn1 = 4.72 + region_site_link_trim$m1_med + example_dat[[1]]$summary.fixed[2,4]*df$year_centre[c((nrow(example_dat[[1]]$summary.fitted.v
  lc1 = 4.72 + region_site_link_trim$m1_med + example_dat[[1]]$summary.fixed[2,3]*df$year_centre[c((nrow(example_dat[[1]]$summary.fitted.v
  uc1 = 4.72 + region_site_link_trim$m1_med + example_dat[[1]]$summary.fixed[2,5]*df$year_centre[c((nrow(example_dat[[1]]$summary.fitted.v
  mn2 = 4.72 + (region_site_link_trim$m2_med + example_dat[[2]]$summary.fixed[2,4])*df$year_centre[c((nrow(example_dat[[2]]$summary.fitted
  lc2 = 4.72 + (region_site_link_trim$m2_lc + example_dat[[2]]$summary.fixed[2,3])*df$year_centre[c((nrow(example_dat[[2]]$summary.fitted.
  uc2 = 4.72 + (region_site_link_trim$m2_uc + example_dat[[2]]$summary.fixed[2,5])*df$year_centre[c((nrow(example_dat[[2]]$summary.fitted.
  mn3 = 4.72 + (region_site_link_trim$m3_med + example_dat[[3]]$summary.fixed[2,4])*df$year_centre[c((nrow(example_dat[[3]]$summary.fitted
  lc3 = 4.72 + (region_site_link_trim$m3_lc + example_dat[[3]]$summary.fixed[2,3])*df$year_centre[c((nrow(example_dat[[3]]$summary.fitted.
  uc3 = 4.72 + (region_site_link_trim$m3_uc + example_dat[[3]]$summary.fixed[2,5])*df$year_centre[c((nrow(example_dat[[3]]$summary.fitted.
)

plt_m1_b = ggplot() +
  geom_line(data = pop_level[which(pop_level$site_code == 566),], aes(x = date, y = (exp(m1_pred)), colour = species), alpha = 0.5) +
  geom_line(data = sit_level, aes(x = year+2001, y = exp(mn1)), colour = "black") +
  geom_ribbon(data = sit_level, aes(x = year+2001, ymin =  exp(lc1), ymax = exp(uc1)), alpha = 0.2, fill = "black") +
  scale_x_continuous(expand = c(0,0), breaks = c(1990, 2000, 2010)) +
  scale_y_continuous(expand = c(0,0)) +
  coord_cartesian(ylim = c(1,600), xlim = c(1987, 2015)) +
  scale_colour_manual(
    name = "",
    labels = c("M. daubentoni", "M. emarginatus", "M. nattereri"),
    values = c("#9fbdbf", "#1885d9", "#1c50d4")) +
  scale_fill_manual(
    name = "",
    labels = c("M. daubentoni", "M. emarginatus", "M. nattereri"),
```

```
    values = c("#9fbdbf", "#1885d9", "#1c50d4")) +
  labs(x = "", y = "", title = "") +
  theme_classic() +
  theme(plot.title = element_text(size=10, face="italic"))


plt_m2_b = ggplot(data = pop_level[which(pop_level$site_code == 566),]) +
  geom_line(aes(x = date, y = (exp(m2_pred + mean_log)), colour = species), alpha = 0.5) +
  geom_line(data = sit_level, aes(x = year+2001, y = exp(mn2)), colour = "black") +
  geom_ribbon(data = sit_level, aes(x = year+2001, ymin =  exp(lc2), ymax = exp(uc2)), alpha = 0.2, fill = "black") +
  scale_x_continuous(expand = c(0,0), breaks = c(1990, 2000, 2010)) +
  scale_y_continuous(expand = c(0,0)) +
  coord_cartesian(ylim = c(1,600), xlim = c(1987, 2015)) +
  scale_colour_manual(
    name = "",
    labels = c("M. daubentoni", "M. emarginatus", "M. nattereri"),
    values = c("#9fbdbf", "#1885d9", "#1c50d4")) +
  scale_fill_manual(
    name = "",
    labels = c("M. daubentoni", "M. emarginatus", "M. nattereri"),
    values = c("#9fbdbf", "#1885d9", "#1c50d4")) +
  labs(x = "", y = "", title = "") +
  theme_classic() +
  theme(plot.title = element_text(size=10, face="italic"))


plt_m3_b = ggplot() +
  geom_line(data = pop_level[which(pop_level$site_code == 566),],aes(x = date, y = (exp(m3_pred + mean_log)), colour = species), alpha = 0
  geom_line(data = sit_level, aes(x = year+2001, y = exp(mn3)), colour = "black") +
  geom_ribbon(data = sit_level, aes(x = year+2001, ymin =  exp(lc3), ymax = exp(uc3)), alpha = 0.2, fill = "black") +
  scale_x_continuous(expand = c(0,0), breaks = c(1990, 2000, 2010)) +
  scale_y_continuous(expand = c(0,0)) +
  coord_cartesian(ylim = c(1,600), xlim = c(1987, 2015)) +
  scale_colour_manual(
    name = "",
    labels = c("M. daubentoni", "M. emarginatus", "M. nattereri"),
    values = c("#9fbdbf", "#1885d9", "#1c50d4")) +
  scale_fill_manual(
```

```
    name = "",
    labels = c("M. daubentoni", "M. emarginatus", "M. nattereri"),
    values = c("#9fbdbf", "#1885d9", "#1c50d4")) +
  labs(x = "", y = "", title = "") +
  labs(x = "", y = "", title = "") +
  theme_classic() +
  theme(plot.title = element_text(size=10, face="italic"))

write.csv(sit_level, "../data/derived_data/fig3b.csv")
```

Next we plot all site level trends to depict heterogeniety in spatial trend variation, and then display the global trend over this site level variability, indicating that random intercept and random slope models are a poor representation of this heterogeniety. In this trend we only show uncertainty in the rate of change, the primary paramter of interest, not the intercept. This allows direct comparisons in uncertainty between the model types.

```
expand_reg_sit_link = unique(df[,c("site_code", "mean_log", "mean_year")])
cmb_df = NULL
for(a in 1:nrow(region_site_link)){
  mn_lg = mean(subset(expand_reg_sit_link, site_code == region_site_link$site_code[a])$mean_log)[1]
  tmp_df = data.frame(
    site_code = subset(expand_reg_sit_link, site_code == region_site_link$site_code[a])$site_code[1],
    year_centre = seq(-20,20,length.out = 30),
    year_adj = seq(-20,20,length.out = 30) + subset(expand_reg_sit_link, site_code == region_site_link$site_code[a])$mean_year[1],
    mn_lg = mn_lg,
    y1 = 4.72 + -0.004*c(seq(-20,20,length.out = 30)) + region_site_link$m1_med[a], #2.801 -0.002
    y2 = 4.72 + (-0.001 + region_site_link$m2_med[a])*c(seq(-20,20,length.out = 30)), #-0.002
    y3 = 4.72 + (-0.008 + region_site_link$m3_med[a])*c(seq(-20,20,length.out = 30))) #-0.002
  cmb_df = rbind(cmb_df, tmp_df)
}



glob_level = data.frame(
  year = df$year_centre[c((nrow(example_dat[[1]]$summary.fitted.values)-99):nrow(example_dat[[1]]$summary.fitted.values))],
  mn1 = example_dat[[1]]$summary.fixed[2,4]*df$year_centre[c((nrow(example_dat[[1]]$summary.fitted.values)-99):nrow(example_dat[[1]]$summa
  lc1 = example_dat[[1]]$summary.fixed[2,3]*df$year_centre[c((nrow(example_dat[[1]]$summary.fitted.values)-99):nrow(example_dat[[1]]$summa
  uc1 = example_dat[[1]]$summary.fixed[2,5]*df$year_centre[c((nrow(example_dat[[1]]$summary.fitted.values)-99):nrow(example_dat[[1]]$summa
  mn2 = example_dat[[2]]$summary.fitted.values[c((nrow(example_dat[[1]]$summary.fitted.values)-99):nrow(example_dat[[1]]$summary.fitted.va
  lc2 = example_dat[[2]]$summary.fitted.values[c((nrow(example_dat[[1]]$summary.fitted.values)-99):nrow(example_dat[[1]]$summary.fitted.va
```

```
  uc2 = example_dat[[2]]$summary.fitted.values[c((nrow(example_dat[[1]]$summary.fitted.values)-99):nrow(example_dat[[1]]$summary.fitted.va
  mn3 = example_dat[[3]]$summary.fitted.values[c((nrow(example_dat[[1]]$summary.fitted.values)-99):nrow(example_dat[[1]]$summary.fitted.va
  lc3 = example_dat[[3]]$summary.fitted.values[c((nrow(example_dat[[1]]$summary.fitted.values)-99):nrow(example_dat[[1]]$summary.fitted.va
  uc3 = example_dat[[3]]$summary.fitted.values[c((nrow(example_dat[[1]]$summary.fitted.values)-99):nrow(example_dat[[1]]$summary.fitted.va
)

m1_col = "#018571"
m2_col = "#8f60c4"
m3_col = "#dfc27d"



plt_m1_c = ggplot() +
  geom_line(data = cmb_df,
            aes(x = year_centre+2001, y = exp(y1), group = site_code), alpha = 0.02, colour = "grey") +
  geom_line(data = glob_level, aes(x = year+2001, y = exp(mn1+4.72)), colour = "#018571", size = 1.5) +
  geom_ribbon(data = glob_level, aes(x = year+2001, ymin =  exp(lc1+4.72), ymax = exp(uc1+4.72)), alpha = 0.4, fill = "#018571") +
  scale_x_continuous(expand = c(0,0), breaks = c(1990, 2000, 2010)) +
  scale_y_continuous(expand = c(0,0)) +
  coord_cartesian(ylim = c(0,200), xlim = c(1987, 2015)) +
  labs(x = "", y = "", title = "") +
  theme_classic()


plt_m2_c = ggplot() +
  geom_line(data = cmb_df,
          aes(x = year_centre+2001, y = exp(y3), group = site_code), alpha = 0.02, colour = "grey") +
  geom_line(data = glob_level, aes(x = year+2001, y = exp(mn2+4.72)), colour = "#8f60c4", size = 1.5) +
  geom_ribbon(data = glob_level, aes(x = year+2001, ymin =  exp(lc2+4.72), ymax = exp(uc2+4.72)), alpha = 0.4, fill = "#8f60c4") +
  scale_x_continuous(expand = c(0,0), breaks = c(1990, 2000, 2010)) +
  scale_y_continuous(expand = c(0,0)) +
  coord_cartesian(ylim = c(50,200), xlim = c(1987, 2015)) +
  labs(x = "", y = "", title = "") +
  theme_classic()


plt_m3_c = ggplot() +
  geom_line(data = cmb_df,
```

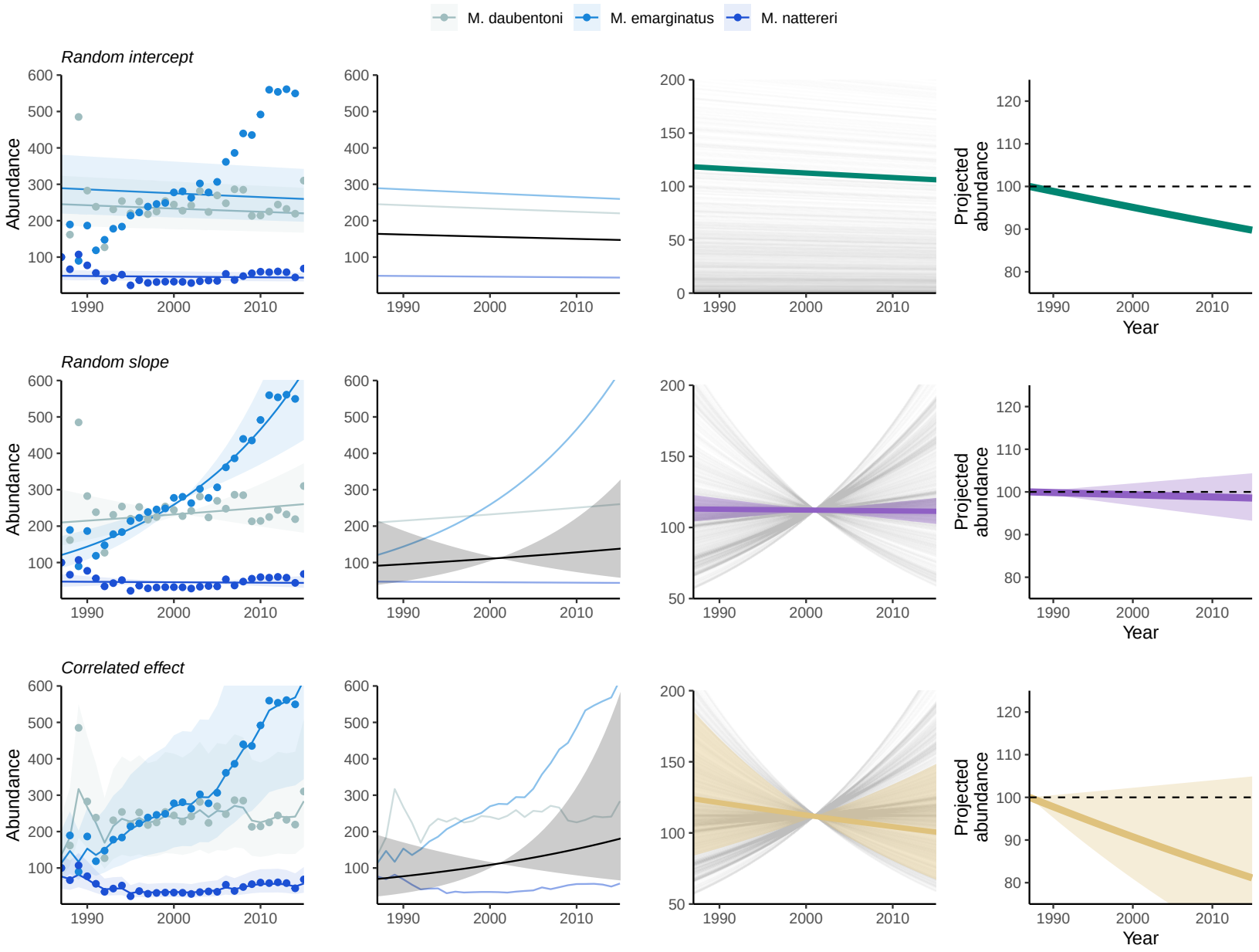
```
            aes(x = year_centre+2001, y = exp(y3), group = site_code), alpha = 0.02, colour = "grey") +
  geom_line(data = glob_level, aes(x = year+2001, y = exp(mn3+4.72)), colour = "#dfc27d", size = 1.5) +
  geom_ribbon(data = glob_level, aes(x = year+2001, ymin =  exp(lc3+4.72), ymax = exp(uc3+4.72)), alpha = 0.4, fill = "#dfc27d") +
  scale_x_continuous(expand = c(0,0), breaks = c(1990, 2000, 2010)) +
  scale_y_continuous(expand = c(0,0)) +
  coord_cartesian(ylim = c(50,200), xlim = c(1987, 2015)) +
  labs(x = "", y = "", title = "") +
  theme_classic()


write.csv(glob_level, "../data/derived_data/fig3c.csv")
```

We then take global level trend coefficients and 50% credible intervals to project abundance trends over time

```
ab_lc = c(100)
ab_mn = c(100)
ab_uc = c(100)
for(a in c(1:28)){
  ab_lc = c(ab_lc,ab_lc[a]*(1 + inla.hpdmarginal(0.5, example_dat[[1]]$marginals.fixed[[2]])[1]))
  ab_mn = c(ab_mn,ab_mn[a]*(1 + example_dat[[1]]$summary.fixed$`0.5quant`[2]))
  ab_uc = c(ab_uc,ab_uc[a]*(1 + inla.hpdmarginal(0.5, example_dat[[1]]$marginals.fixed[[2]])[2]))
}
example_dat_proj_m1 = data.frame(
  year = c(1987:2015),
  ab_lc = ab_lc,
  ab_mn = ab_mn,
  ab_uc = ab_uc
)


plt_m1_d = ggplot(example_dat_proj_m1) +
  geom_line(aes(x = year, y = ab_mn), colour = "#018571", size = 2) +
  geom_ribbon(aes(x = year, ymin = ab_lc, ymax = ab_uc), alpha = 0.3, fill = "#018571") +
  geom_hline(aes(yintercept = 100), linetype = "dashed") +
  scale_y_continuous(expand = c(0,0)) +
  scale_x_continuous(expand = c(0,0), breaks = c(1990, 2000, 2010)) +
  coord_cartesian(ylim  = c(75,125)) +
  theme_classic() +
```

```
  labs(x = "Year", y = "Projected\nabundance", title = "")



ab_lc = c(100)
ab_mn = c(100)
ab_uc = c(100)
for(a in c(1:28)){
  ab_lc = c(ab_lc,ab_lc[a]*(1 + inla.hpdmarginal(0.5, example_dat[[2]]$marginals.fixed[[2]])[1]))
  ab_mn = c(ab_mn,ab_mn[a]*(1 + example_dat[[2]]$summary.fixed$`0.5quant`[2]))
  ab_uc = c(ab_uc,ab_uc[a]*(1 + inla.hpdmarginal(0.5, example_dat[[2]]$marginals.fixed[[2]])[2]))
}
example_dat_proj_m2 = data.frame(
  year = c(1987:2015),
  ab_lc = ab_lc,
  ab_mn = ab_mn,
  ab_uc = ab_uc
)

plt_m2_d = ggplot(example_dat_proj_m2) +
  geom_line(aes(x = year, y = ab_mn), colour = "#8f60c4", size = 2) +
  geom_ribbon(aes(x = year, ymin = ab_lc, ymax = ab_uc), alpha = 0.3, fill = "#8f60c4") +
  geom_hline(aes(yintercept = 100), linetype = "dashed") +
  scale_y_continuous(expand = c(0,0)) +
  scale_x_continuous(expand = c(0,0), breaks = c(1990, 2000, 2010)) +
  coord_cartesian(ylim  = c(75,125)) +
  theme_classic() +
  labs(x = "Year", y = "Projected\nabundance", title = "")



ab_lc = c(100)
ab_mn = c(100)
ab_uc = c(100)
for(a in c(1:28)){
  ab_lc = c(ab_lc,ab_lc[a]*(1 + inla.hpdmarginal(0.5, example_dat[[3]]$marginals.fixed[[2]])[1]))
  ab_mn = c(ab_mn,ab_mn[a]*(1 + example_dat[[3]]$summary.fixed$`0.5quant`[2]))
  ab_uc = c(ab_uc,ab_uc[a]*(1 + inla.hpdmarginal(0.5, example_dat[[3]]$marginals.fixed[[2]])[2]))
```

```
}
example_dat_proj_m3 = data.frame(
  year = c(1987:2015),
  ab_lc = ab_lc,
  ab_mn = ab_mn,
  ab_uc = ab_uc
)

plt_m3_d = ggplot(example_dat_proj_m3) +
  geom_line(aes(x = year, y = ab_mn), colour = "#dfc27d", size = 2) +
  geom_ribbon(aes(x = year, ymin = ab_lc, ymax = ab_uc), alpha = 0.3, fill = "#dfc27d") +
  geom_hline(aes(yintercept = 100), linetype = "dashed") +
  scale_y_continuous(expand = c(0,0)) +
  scale_x_continuous(expand = c(0,0), breaks = c(1990, 2000, 2010)) +
  coord_cartesian(ylim  = c(75,125)) +
  theme_classic() +
  labs(x = "Year", y = "Projected\nabundance", title = "")


ggarrange(
  plt_m1_a,
  plt_m1_b,
  plt_m1_c,
  plt_m1_d,
  plt_m2_a,
  plt_m2_b,
  plt_m2_c,
  plt_m2_d,
  plt_m3_a,
  plt_m3_b,
  plt_m3_c,
  plt_m3_d,
  ncol =4, nrow = 3, common.legend = T)
```


M. daubentoni
M. emarginatus
M. nattereri
Random intercept
Random slope
Correlated effect
Abundance
Projected abundance
Year
1990
2000
2010

```
write.csv(rbind(example_dat_proj_m1, example_dat_proj_m2, example_dat_proj_m3), "../data/derived_data/fig3d.csv")
```

Figure 4

Here we plot estimates of abundance change over space for one high profile species - American Robin. To calculate this abundance change in a given location, we sum: population trend + species trend + genus trend + phylogeny trend + site trend + region trend + spatial trend + overall trend. We then take uncertainty around spatial trends to estimate whether a trend would be significant at a selection of thresholds. This model is based on BioTIME data.

```
m3 = readRDS("../outputs/model_output_predict2_BioTIME.rds")
m3 = m3[[3]]
tmp_df = readRDS("../data/derived_data/analysis_list_predict2.rds")
tmp_df = tmp_df[[1]][[1]]
link_df = unique(tmp_df[,c("site_spec","site_spec_code","site_code","region_code","tips_code","genus_code", "lat_round", "lon_round", "spe
link_df = link_df[c(12066:14976),]


tips_code_med = m3$summary.random$tips_code[,c(1,2)]
colnames(tips_code_med) = c("ID","val_tips_code_mn")
link_df = left_join(link_df, tips_code_med, by = c("tips_code" = "ID"))

tips_code2_med = m3$summary.random$tips_code2[,c(1,2)]
colnames(tips_code2_med) = c("ID","val_tips_code2_mn")
link_df = left_join(link_df, tips_code2_med, by = c("tips_code" = "ID"))

genus_code_med = m3$summary.random$genus_code[,c(1,2)]
colnames(genus_code_med) = c("ID","val_genus_code_mn")
link_df = left_join(link_df, genus_code_med, by = c("genus_code" = "ID"))

site_code_med = m3$summary.random$site_code[,c(1,2)]
colnames(site_code_med) = c("ID","val_site_code_mn")
link_df = left_join(link_df, site_code_med, by = c("site_code" = "ID"))

site_code2_med = m3$summary.random$site_code2[,c(1,2)]
colnames(site_code2_med) = c("ID","val_site_code2_mn")
link_df = left_join(link_df, site_code2_med, by = c("site_code" = "ID"))
```

```r
site_spec_code_med = m3$summary.random$site_spec_code[,c(1,2,3)]
colnames(site_spec_code_med) = c("ID","val_site_spec_code_mn", "val_site_spec_code_sd")
site_spec_code_med$site_spec_qt400 = site_spec_code_med$val_site_spec_code_mn - (0.25*site_spec_code_med$val_site_spec_code_sd) #20% 0.25
site_spec_code_med$site_spec_qt600 = site_spec_code_med$val_site_spec_code_mn + (0.25*site_spec_code_med$val_site_spec_code_sd)
site_spec_code_med$site_spec_qt300 = site_spec_code_med$val_site_spec_code_mn - (0.52*site_spec_code_med$val_site_spec_code_sd) #40%
site_spec_code_med$site_spec_qt700 = site_spec_code_med$val_site_spec_code_mn + (0.52*site_spec_code_med$val_site_spec_code_sd)
site_spec_code_med$site_spec_qt200 = site_spec_code_med$val_site_spec_code_mn - (0.84*site_spec_code_med$val_site_spec_code_sd) #60%
site_spec_code_med$site_spec_qt800 = site_spec_code_med$val_site_spec_code_mn + (0.84*site_spec_code_med$val_site_spec_code_sd)
site_spec_code_med$site_spec_qt100 = site_spec_code_med$val_site_spec_code_mn - (1.28*site_spec_code_med$val_site_spec_code_sd) #80%
site_spec_code_med$site_spec_qt900 = site_spec_code_med$val_site_spec_code_mn + (1.28*site_spec_code_med$val_site_spec_code_sd)
link_df = left_join(link_df, site_spec_code_med, by = c("site_spec_code" = "ID"))

region_code_med = m3$summary.random$region_code[,c(1,2)]
colnames(region_code_med) = c("ID", "val_region_code_mn")
link_df = left_join(link_df, region_code_med, by = c("region_code" = "ID"))

link_df$pop_trend_sit_mn =
  link_df$val_tips_code_mn +
  link_df$val_tips_code2_mn +
  link_df$val_genus_code_mn +
  link_df$val_site_code_mn +
  link_df$val_site_code2_mn +
  link_df$val_region_code_mn +
  m3$summary.fixed$mean[2]

link_df$pop_trend_sit_100 =
  link_df$val_tips_code_mn +
  link_df$val_tips_code2_mn +
  link_df$val_genus_code_mn +
  link_df$val_site_code_mn +
  link_df$val_site_code2_mn +
  link_df$site_spec_qt100 +
  link_df$val_region_code_mn +
  m3$summary.fixed$mean[2]

link_df$pop_trend_sit_200 =
  link_df$val_tips_code_mn +
  link_df$val_tips_code2_mn +
```

```
  link_df$val_genus_code_mn +
  link_df$val_site_code_mn +
  link_df$val_site_code2_mn +
  link_df$site_spec_qt200 +
  link_df$val_region_code_mn +
  m3$summary.fixed$mean[2]

link_df$pop_trend_sit_300 =
  link_df$val_tips_code_mn +
  link_df$val_tips_code2_mn +
  link_df$val_genus_code_mn +
  link_df$val_site_code_mn +
  link_df$val_site_code2_mn +
  link_df$site_spec_qt300 +
  link_df$val_region_code_mn +
  m3$summary.fixed$mean[2]

link_df$pop_trend_sit_400 =
  link_df$val_tips_code_mn +
  link_df$val_tips_code2_mn +
  link_df$val_genus_code_mn +
  link_df$val_site_code_mn +
  link_df$val_site_code2_mn +
  link_df$site_spec_qt400 +
  link_df$val_region_code_mn +
  m3$summary.fixed$mean[2]

link_df$pop_trend_sit_600 =
  link_df$val_tips_code_mn +
  link_df$val_tips_code2_mn +
  link_df$val_genus_code_mn +
  link_df$val_site_code_mn +
  link_df$val_site_code2_mn +
  link_df$site_spec_qt600 +
  link_df$val_region_code_mn +
  m3$summary.fixed$mean[2]

link_df$pop_trend_sit_700 =
```

```
  link_df$val_tips_code_mn +
  link_df$val_tips_code2_mn +
  link_df$val_genus_code_mn +
  link_df$val_site_code_mn +
  link_df$val_site_code2_mn +
  link_df$site_spec_qt700 +
  link_df$val_region_code_mn +
  m3$summary.fixed$mean[2]

link_df$pop_trend_sit_800 =
  link_df$val_tips_code_mn +
  link_df$val_tips_code2_mn +
  link_df$val_genus_code_mn +
  link_df$val_site_code_mn +
  link_df$val_site_code2_mn +
  link_df$site_spec_qt800 +
  link_df$val_region_code_mn +
  m3$summary.fixed$mean[2]

link_df$pop_trend_sit_900 =
  link_df$val_tips_code_mn +
  link_df$val_tips_code2_mn +
  link_df$val_genus_code_mn +
  link_df$val_site_code_mn +
  link_df$val_site_code2_mn +
  link_df$site_spec_qt900 +
  link_df$val_region_code_mn +
  m3$summary.fixed$mean[2]




link_df_sum = link_df
link_df_sum$cat = NA
link_df_sum$cat = ifelse(link_df_sum$pop_trend_sit_400 > 0, "+20%", link_df_sum$cat)
link_df_sum$cat = ifelse(link_df_sum$pop_trend_sit_300 > 0, "+40%", link_df_sum$cat)
link_df_sum$cat = ifelse(link_df_sum$pop_trend_sit_200 > 0, "+60%", link_df_sum$cat)
link_df_sum$cat = ifelse(link_df_sum$pop_trend_sit_100 > 0, "+80%", link_df_sum$cat)
```

```r
link_df_sum$cat = ifelse(link_df_sum$pop_trend_sit_600 < 0, "-20%", link_df_sum$cat)
link_df_sum$cat = ifelse(link_df_sum$pop_trend_sit_700 < 0, "-40%", link_df_sum$cat)
link_df_sum$cat = ifelse(link_df_sum$pop_trend_sit_800 < 0, "-60%", link_df_sum$cat)
link_df_sum$cat = ifelse(link_df_sum$pop_trend_sit_900 < 0, "-80%", link_df_sum$cat)
link_df_sum$cat = ifelse(is.na(link_df_sum$cat), "0%", link_df_sum$cat)
link_df_sum$cat = factor(link_df_sum$cat, levels = c("-80%", "-60%", "-40%", "-20%", "0%", "+20%", "+40%", "+60%", "+80%"))
link_df_sum$cat_num = as.numeric(link_df_sum$cat)

## Example SpatialPolygonsDataFrame
data(wrld_simpl)
SPDF <- subset(wrld_simpl, ISO3=="USA" | ISO3=="CAN" | ISO3=="MEX" )

## Example RasterLayer
rst <- rasterFromXYZ(link_df_sum[,c("lon_round", "lat_round", "cat_num")], crs=proj4string(SPDF))
## crop and mask
rst <- crop(rst, extent(SPDF))
rst <- mask(rst, SPDF)

rst_df <- as(rst, "SpatialPixelsDataFrame")
rst_df <- as.data.frame(rst_df)
colnames(rst_df) <- c("value", "x", "y")


world <- map_data("world")

plt_map = ggplot() +
  geom_tile(data=rst_df, aes(x=x, y=y, fill=as.factor(value)), alpha=0.8) +
  geom_map(data = world, map = world, aes(long, lat, map_id = region), fill = NA, colour = "black", alpha = 0.4)  +
  #geom_polygon(data=SPDF, aes(x=long, y=lat, group=group),
  #             fill=NA, color="black", size=1) +
  coord_sf(xlim = c(-130,-60), ylim = c(20,60)) +
  scale_x_continuous(expand = c(0,0)) +
  scale_y_continuous(expand = c(0,0)) +
  scale_fill_brewer(palette = "RdBu", labels = c("-80", "-60", "-40", "-20", "0", "+20", "+40", "+60", "+80"), name = "Confidence interval
  labs (x = "Longitude", y = "Latitude") +
  theme_classic()
```

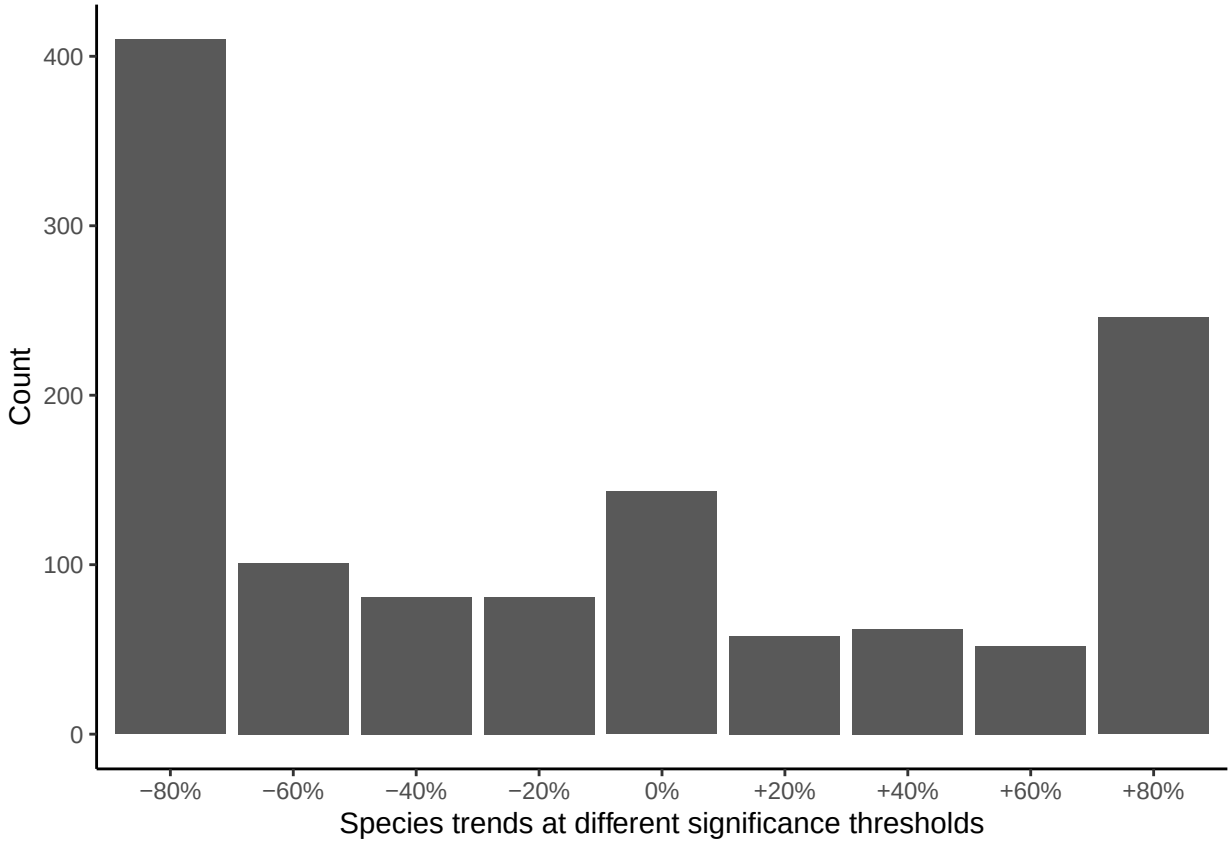
```
write.csv(rst_df, "../data/derived_data/fig4a.csv")
```

Here we plot estimates of abundance change over a phylogeny by taking the sum of: species trend + genus trend + phylogeny trend + overall trend. We then take uncertainty around phylogeny trends to estimate whether a trend would be significant at a selection of thresholds. This model is based on BioTIME data

```
m3 = readRDS("../outputs/model_output_convergence10_BioTIME.rds")
m3 = m3[[3]]
tmp_df = readRDS("../data/derived_data/analysis_list.rds")
tmp_df = tmp_df[[1]][[1]]
link_df = unique(tmp_df[,c("tips_code","genus_code","species")])


tips_code_med = m3$summary.random$tips_code[,c(1,2)]
colnames(tips_code_med) = c("ID","val_tips_code_mn")
link_df = left_join(link_df, tips_code_med, by = c("tips_code" = "ID"))

tips_code2_med = m3$summary.random$tips_code2[,c(1,2,3,4,6)]
colnames(tips_code2_med) = c("ID","val_tips_code2_mn", "val_tips_code2_sd","lc","uc")
tips_code2_med$tip_qt400 = tips_code2_med$val_tips_code2_mn - (0.25*tips_code2_med$val_tips_code2_sd) #20%
tips_code2_med$tip_qt600 = tips_code2_med$val_tips_code2_mn + (0.25*tips_code2_med$val_tips_code2_sd)
tips_code2_med$tip_qt300 = tips_code2_med$val_tips_code2_mn - (0.52*tips_code2_med$val_tips_code2_sd) #40%
tips_code2_med$tip_qt700 = tips_code2_med$val_tips_code2_mn + (0.52*tips_code2_med$val_tips_code2_sd)
tips_code2_med$tip_qt200 = tips_code2_med$val_tips_code2_mn - (0.84*tips_code2_med$val_tips_code2_sd) #60%
tips_code2_med$tip_qt800 = tips_code2_med$val_tips_code2_mn + (0.84*tips_code2_med$val_tips_code2_sd)
tips_code2_med$tip_qt100 = tips_code2_med$val_tips_code2_mn - (1.28*tips_code2_med$val_tips_code2_sd) #80%
tips_code2_med$tip_qt900 = tips_code2_med$val_tips_code2_mn + (1.28*tips_code2_med$val_tips_code2_sd)
link_df = left_join(link_df, tips_code2_med, by = c("tips_code" = "ID"))

genus_code_med = m3$summary.random$genus_code[,c(1,2)]
colnames(genus_code_med) = c("ID","val_genus_code_mn")
link_df = left_join(link_df, genus_code_med, by = c("genus_code" = "ID"))

link_df$pop_trend_tip_mn =
  link_df$val_tips_code_mn +
  link_df$val_tips_code2_mn +
  link_df$val_genus_code_mn +
  m3$summary.fixed$mean[2]
```

```
link_df$pop_trend_tip_100 =
  link_df$val_tips_code_mn +
  link_df$tip_qt100 +
  link_df$val_genus_code_mn +
  m3$summary.fixed$mean[2]

link_df$pop_trend_tip_200 =
  link_df$val_tips_code_mn +
  link_df$tip_qt200 +
  link_df$val_genus_code_mn +
  m3$summary.fixed$mean[2]

link_df$pop_trend_tip_300 =
  link_df$val_tips_code_mn +
  link_df$tip_qt300 +
  link_df$val_genus_code_mn +
  m3$summary.fixed$mean[2]

link_df$pop_trend_tip_400 =
  link_df$val_tips_code_mn +
  link_df$tip_qt400 +
  link_df$val_genus_code_mn +
  m3$summary.fixed$mean[2]

link_df$pop_trend_tip_600 =
  link_df$val_tips_code_mn +
  link_df$tip_qt600 +
  link_df$val_genus_code_mn +
  m3$summary.fixed$mean[2]

link_df$pop_trend_tip_700 =
  link_df$val_tips_code_mn +
  link_df$tip_qt700 +
  link_df$val_genus_code_mn +
  m3$summary.fixed$mean[2]

link_df$pop_trend_tip_800 =
  link_df$val_tips_code_mn +
```

```
  link_df$tip_qt800 +
  link_df$val_genus_code_mn +
  m3$summary.fixed$mean[2]

link_df$pop_trend_tip_900 =
  link_df$val_tips_code_mn +
  link_df$tip_qt900 +
  link_df$val_genus_code_mn +
  m3$summary.fixed$mean[2]

link_df_sum = link_df
link_df_sum$cat = NA
link_df_sum$cat = ifelse(link_df_sum$pop_trend_tip_400 > 0, "+20%", link_df_sum$cat)
link_df_sum$cat = ifelse(link_df_sum$pop_trend_tip_300 > 0, "+40%", link_df_sum$cat)
link_df_sum$cat = ifelse(link_df_sum$pop_trend_tip_200 > 0, "+60%", link_df_sum$cat)
link_df_sum$cat = ifelse(link_df_sum$pop_trend_tip_100 > 0, "+80%", link_df_sum$cat)
link_df_sum$cat = ifelse(link_df_sum$pop_trend_tip_600 < 0, "-20%", link_df_sum$cat)
link_df_sum$cat = ifelse(link_df_sum$pop_trend_tip_700 < 0, "-40%", link_df_sum$cat)
link_df_sum$cat = ifelse(link_df_sum$pop_trend_tip_800 < 0, "-60%", link_df_sum$cat)
link_df_sum$cat = ifelse(link_df_sum$pop_trend_tip_900 < 0, "-80%", link_df_sum$cat)
link_df_sum$cat = ifelse(is.na(link_df_sum$cat), "0%", link_df_sum$cat)
link_df_sum$cat = factor(link_df_sum$cat, levels = c("-80%", "-60%", "-40%", "-20%", "0%", "+20%", "+40%", "+60%", "+80%"))

ggplot(link_df_sum) +
  geom_bar(aes(cat)) +
  labs(x = "Species trends at different significance thresholds", y = "Count") +
  theme_classic()
```

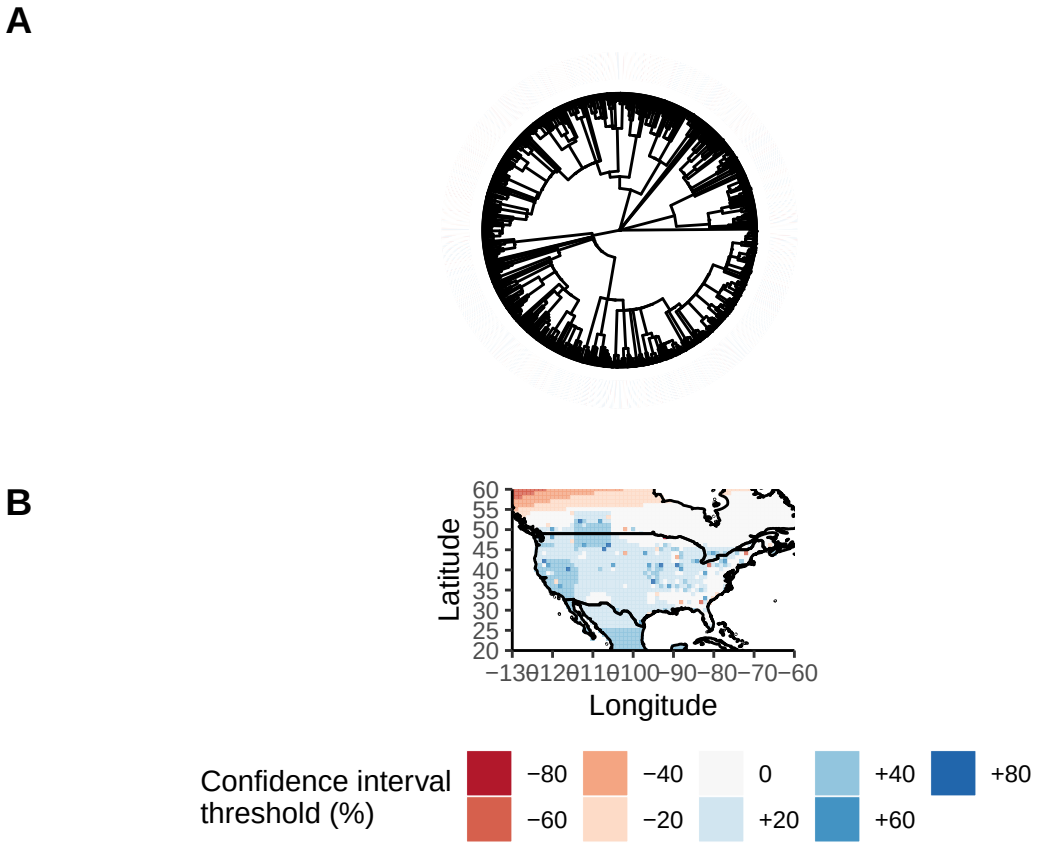



```
spec_link = unique(tmp_df[,c("tips_code", "tips_chr")])
spec_link = subset(spec_link, !is.na(tips_chr))
link_df_sum2 = left_join(link_df_sum[,c("tips_code", "cat")], spec_link, by = "tips_code")
link_df_sum2 = subset(link_df_sum2, !is.na(link_df_sum2$tips_chr))
keep = unique(link_df_sum2$tips_chr)



tr = readRDS("../data/derived_data/trees.rds")[[1]][[3]]
tr2 = keep.tip(tr, keep)
```

```r
tr2$edge.length = log(tr2$edge.length) - min(log(tr2$edge.length)) + 0.01
tr2 = force.ultrametric(tr2)
```

```
## ************************************************************
## *                         Note:                            *
## *    force.ultrametric does not include a formal method to    *
## *    ultrametricize a tree & should only be used to coerce    *
## *   a phylogeny that fails is.ultramtric due to rounding --   *
## *    not as a substitute for formal rate-smoothing methods.   *
## ************************************************************
```

```r
p = ggtree(tr2, layout = "circular")

plt_trends = data.frame(
  cat = link_df_sum2$cat
)
plt_trends$cat = as.factor(plt_trends$cat)
rownames(plt_trends) = link_df_sum2$tips_chr
plt_clad = gheatmap(p, plt_trends, width = 0.2, colnames = F) +
    scale_fill_brewer(palette = "RdBu", labels = c("-80", "-60", "-40", "-20", "0", "+20", "+40", "+60", "+80"), name = "Confidence interv


ggarrange(plt_clad, plt_map, ncol = 1, labels = c("A", "B"), common.legend = T, heights = c(1.2,0.65), legend = "bottom")
```




```
write.csv(plt_trends, "../data/derived_data/fig4b.csv")
```

Phylogeny - sensitivity analysis

Load data and develop a dataset summarising the three phylogeny models (A: Full - OTL, B: Restricted - OTL, C: Restricted - TimeTree). The OTL models use a phylogeny lacking branch lengths from the Open Tree of Life. The TimeTree phylogeny contains branch lengths, but has a 'restricted' taxonomic extent. In this restricted dataset, we only kept species occuring in both the Open Tree of Life and TimeTree.

```
model_summary_core = read.csv("../outputs/model_summary.csv")
model_summary_phylo = read.csv("../outputs/model_summary_phylo.csv")

model_summary_core = subset(model_summary_core, model == 3)
df_tmp = rbind(model_summary_core, model_summary_phylo)


df_tmp$phy_h = df_tmp$tip_h/(df_tmp$tip + df_tmp$tip_h + df_tmp$gen)
df_tmp$spa_h = df_tmp$sit_h/(df_tmp$sit + df_tmp$sit_h + df_tmp$squ)
df_tmp$temp = df_tmp$obv_auto/(df_tmp$obv + df_tmp$obv_auto)
df_tmp$temp_v = (df_tmp$obv + df_tmp$obv_auto)/(
  df_tmp$fix +
  df_tmp$obv +
  df_tmp$obv_auto +
  df_tmp$gen +
  df_tmp$sit +
  df_tmp$sit_h +
  df_tmp$squ +
  df_tmp$sig)
df_tmp$sit_v = (df_tmp$sit + df_tmp$sit_h + df_tmp$squ)/(
  df_tmp$fix +
  df_tmp$obv +
  df_tmp$obv_auto +
  df_tmp$gen +
  df_tmp$sit +
  df_tmp$sit_h +
  df_tmp$squ +
  df_tmp$sig)
df_tmp$phy_v = (df_tmp$tip + df_tmp$tip_h + df_tmp$gen)/(
  df_tmp$fix +
  df_tmp$obv +
  df_tmp$obv_auto +
  df_tmp$gen +
  df_tmp$sit +
  df_tmp$sit_h +
  df_tmp$squ +
  df_tmp$sig)
df_tmp$res_v = (df_tmp$sig)/(
```

```
  df_tmp$fix +
  df_tmp$obv +
  df_tmp$obv_auto +
  df_tmp$tip +
  df_tmp$tip_h +
  df_tmp$gen +
  df_tmp$sit +
  df_tmp$sit_h +
  df_tmp$squ +
  df_tmp$sig)
df_tmp$fix_v = (df_tmp$fix)/(
  df_tmp$fix +
  df_tmp$obv +
  df_tmp$obv_auto +
  df_tmp$gen +
  df_tmp$sit +
  df_tmp$sit_h +
  df_tmp$squ +
  df_tmp$sig)



dataset_rename = data.frame(
  code = c("BioTIME", "CaPTrends", "EA_NFPD", "FishGlob", "LPI", "NAm_BBS", "Pilotto", "ReSurvey_Germany", "RivFish", "TimeFISH"),
  dataset_code = c("A) BioTIME", "J) Large carnivores", "F) UK riverine fishes", "D) FishGlob", "B) Living Planet", "C) NA Breeding Birds"
)
df_tmp = left_join(df_tmp, dataset_rename)
```

Collective trends and estimates of unceertainty for each of the model and dataset combinations

```
ggplot(data = df_tmp) +
  geom_pointrange(aes(x = model, ymin = coef_lc, y = coef, ymax = coef_uc, colour = model)) +
  scale_colour_manual(values = c("grey10", "grey50","grey80"),labels = c("Full: OTL", "Restricted: OTL", "Restriced: TimeTree"), name = NU
  scale_x_discrete(labels = c("A", "B", "C")) +
  labs(x = "", y = expression(beta)) +
  #coord_flip() +
  facet_wrap(dataset_code~., scales = "free") +
  theme_classic() +
```

```
  theme(legend.position = "bottom")
```

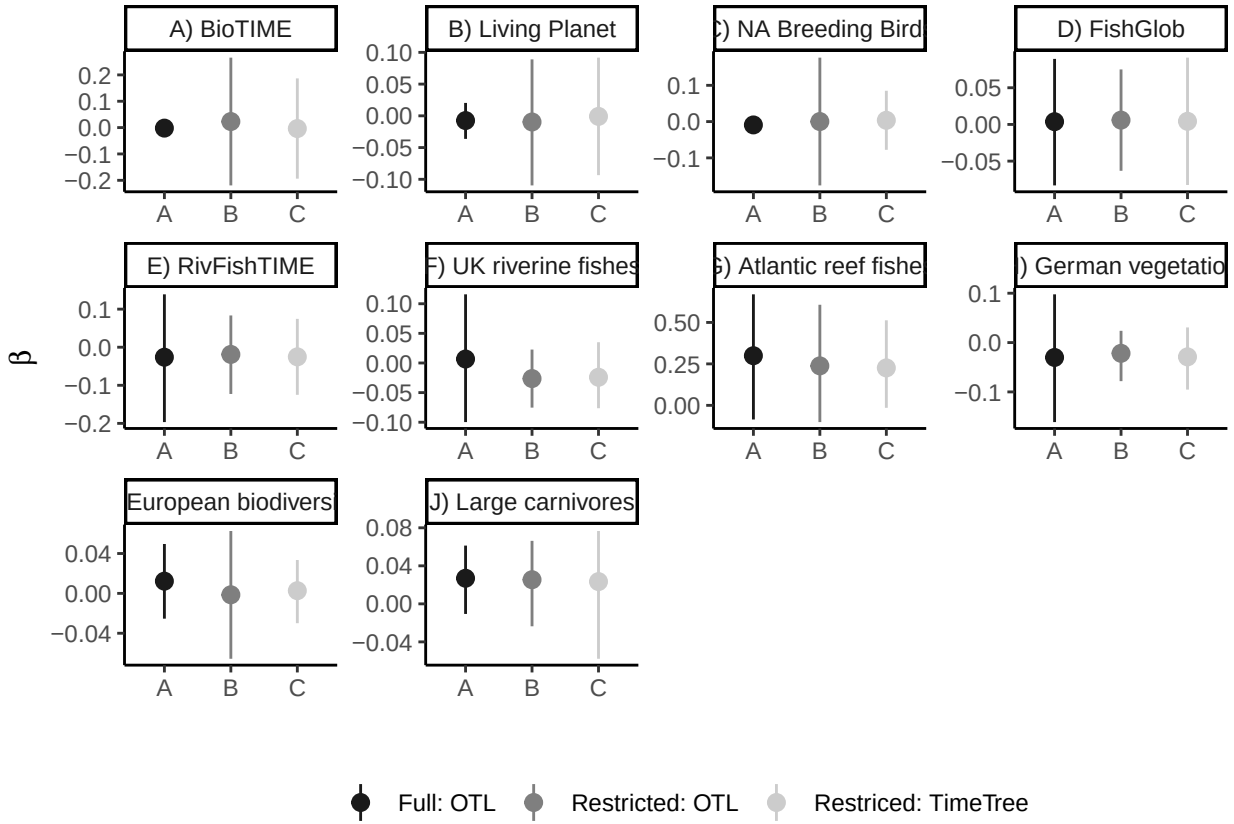
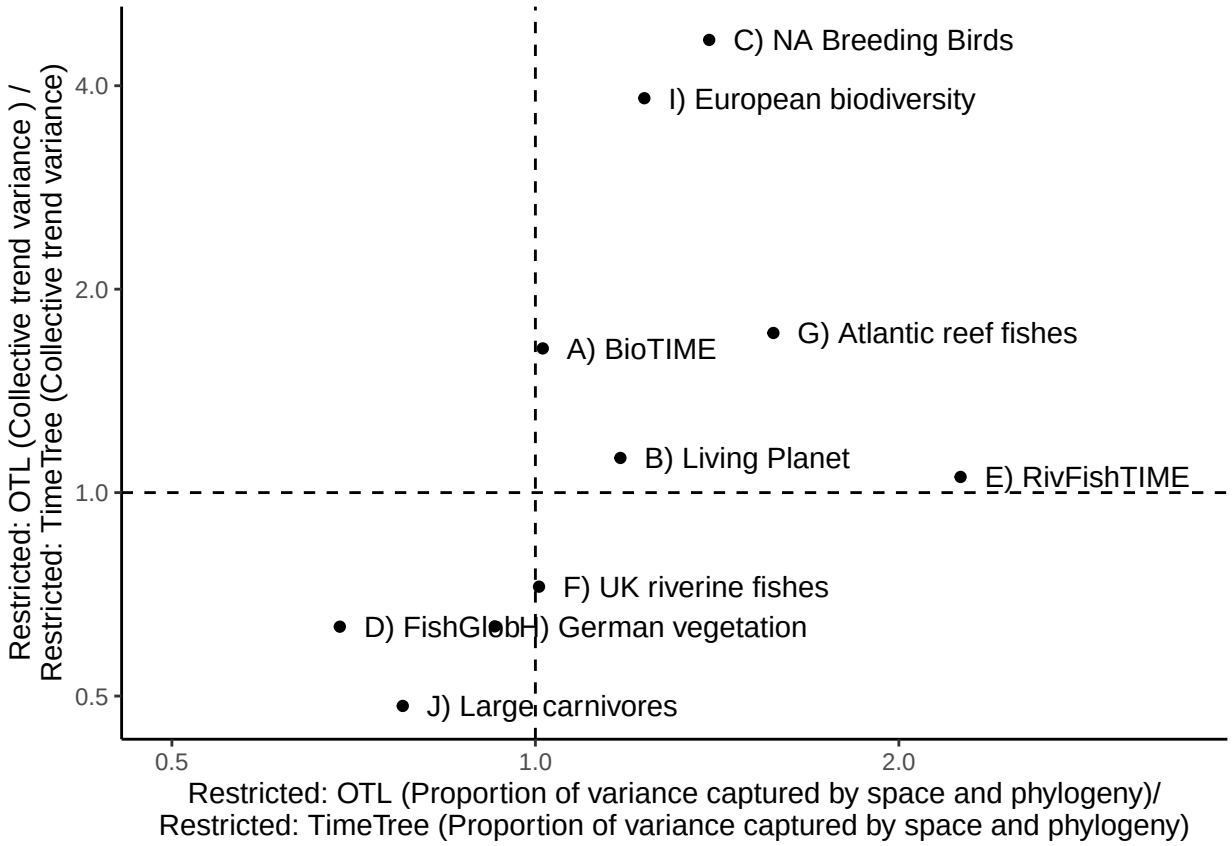


Figure describing how the porportion of variance captures by space and time are the driving forces behind the degree of uncertainty in the collective trend.

```
df_rotl_trim = subset(df_tmp,
                      model == "3_rotl_trim"
                  )
df_timetree_trim = subset(df_tmp,
                      model == "3_timetree"
```

```
)
df_compare = data.frame(
  name = df_rotl_trim$dataset_code,
  sd_div = df_rotl_trim$coef_sd^2/df_timetree_trim$coef_sd^2,
  var = (df_rotl_trim$sit_v + df_rotl_trim$phy_v)/
    (df_timetree_trim$sit_v + df_timetree_trim$phy_v))

ggplot(data = df_compare) +
  geom_point(aes(x = var, y = sd_div)) +
  geom_text(aes(x = var, y = sd_div, label = name), hjust = 0, nudge_x = 0.02) +
  scale_y_log10(breaks = c(0.5,1,2,4,8)) +
  scale_x_log10(breaks = c(0.5,1,2,4,8), limits = c(0.5,3.4)) +
  geom_hline(aes(yintercept = 1), linetype = "dashed") +
  geom_vline(aes(xintercept = 1), linetype = "dashed") +
  labs(x = "Restricted: OTL (Proportion of variance captured by space and phylogeny)/\nRestricted: TimeTree (Proportion of variance captur
  theme_classic()
```



Structure - sensitivity analysis

Load data

```
model_summary_core = read.csv("../outputs/model_summary.csv")
model_summary_struc = read.csv("../outputs/model_summary_structure.csv")
```

Manipulate data. Renaming columns. Calculating the collective trend variance difference between the random slope model and all other models

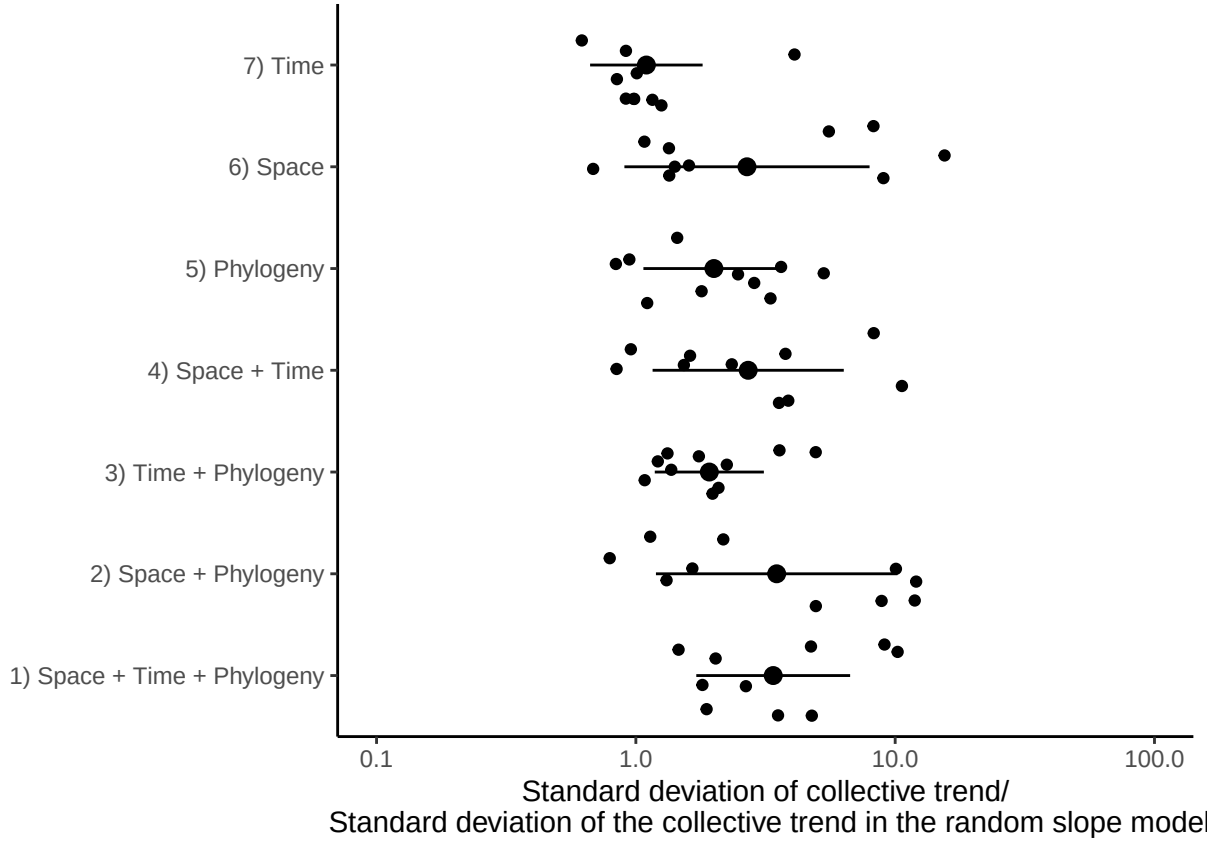
```
model_summary_core = subset(model_summary_core, model != 1, select = c(
  "X", "code", "model", "coef", "coef_sd", "coef_lc", "coef_uc"
))
colnames(model_summary_core)[3] = "model_type"

df_tmp = rbind(model_summary_core, model_summary_struc)

df_tmp = df_tmp %>% mutate(model_type=recode(model_type,
                                    '3'='1) Space + Time + Phylogeny',
                                    'Time absent'='2) Space + Phylogeny',
                                    'Space absent'='3) Time + Phylogeny',
                                    'Phylogeny absent'='4) Space + Time',
                                    'Time and space absent'='5) Phylogeny',
                                    'Time and phylogeny absent'='6) Space',
                                    'Space and phylogeny absent'='7) Time',
                                    '2'='8) Random slope model'
                                    ))

df_tmp2 = spread(df_tmp[,c(2,3,5)], model_type, coef_sd)
df_tmp2$`1) Space + Time + Phylogeny` = df_tmp2$`1) Space + Time + Phylogeny`/ df_tmp2$`8) Random slope model`
df_tmp2$`2) Space + Phylogeny` = df_tmp2$`2) Space + Phylogeny`/ df_tmp2$`8) Random slope model`
df_tmp2$`3) Time + Phylogeny` = df_tmp2$`3) Time + Phylogeny`/ df_tmp2$`8) Random slope model`
df_tmp2$`4) Space + Time` = df_tmp2$`4) Space + Time`/ df_tmp2$`8) Random slope model`
df_tmp2$`5) Phylogeny` = df_tmp2$`5) Phylogeny`/ df_tmp2$`8) Random slope model`
df_tmp2$`6) Space` = df_tmp2$`6) Space`/ df_tmp2$`8) Random slope model`
df_tmp2$`7) Time` = df_tmp2$`7) Time`/ df_tmp2$`8) Random slope model`

df_tmp3 = gather(df_tmp2, model, sd_div, `1) Space + Time + Phylogeny`:`7) Time`, factor_key=TRUE)
```

Calucalte average variance difference and standard deviation

```
df_tmp4 = df_tmp3 %>%
  group_by(model) %>%
  summarise(mn = mean(log(sd_div)), sd = sd(log(sd_div)))
```

Plot variance differences

```
ggplot() +
  geom_jitter(data = df_tmp3, aes(y = model, x = sd_div)) +
  geom_pointrange(data = df_tmp4, aes(y = model, x = exp(mn), xmin = exp(mn-sd), xmax = exp(mn+sd))) +
  coord_cartesian(xlim = c(0.1,100)) +
  labs(x = "Standard deviation of collective trend/\n Standard deviation of the collective trend in the random slope model", y = "") +
  scale_x_log10() +
  theme_classic()
```




```
ggsave("../outputs/figures/extended_data_fig2.tiff",width = 9, height = 7, device='tiff', dpi=300)
```

Prediction - trends

Here we take the predictions of missing trends in each dataaset and estimate the median absolute error in preciction. This predcitive error is then summarised across datasets, and then compared across models

```
miss_t = read.csv("../outputs/model_summary_miss_trends.csv")
mae_full = NULL
for(a in names(analysis_list)[c(1:10)]){
  tmp_df = subset(miss_t, code == a)
  tmp_mae_full = data.frame(
    code = a,
    mae2 = median(abs(abs(tmp_df$tr - tmp_df$m2)/tmp_df$tr)*100),
    mae3 = median(abs(abs(tmp_df$tr - tmp_df$m3)/tmp_df$tr)*100)
  )
  mae_full = rbind(mae_full, tmp_mae_full)
}

mean(mae_full$mae2)
```

```
## [1] 28.87288
```

```
sd(mae_full$mae2)
```

```
## [1] 25.50235
```

```
median(mae_full$mae2)
```

```
## [1] 15.92591
```

```
mean(mae_full$mae3)
```

```
## [1] 21.40227
```

```
sd(mae_full$mae3)
```

```
## [1] 15.63896
```

```r
median(mae_full$mae3)
```

```
## [1] 14.38674
```

```r
mean(mae_full$mae2)/mean(mae_full$mae3)
```

```
## [1] 1.349057
```

```r
median(mae_full$mae2)/median(mae_full$mae3)
```

```
## [1] 1.106985
```

Prediction - abundances

Here we take the predictions of missing abundance in each dataaset and estimate the median absolute error in preciction. This predcitive error is then summarised across datasets, and then compared across models

```r
cmb_preds = NULL
for(a in names(analysis_list)[c(1:10)]){
  print(a)
  tmp_df_predict = readRDS(paste0("../outputs/model_output_miss_abundance_", a,".rds"))

  tmp_preds = data.frame(
    code = a,
    log_abundance = tmp_df_predict[[4]]$log_abundance,
    mean_log = tmp_df_predict[[4]]$mean_log,
    miss = ifelse(is.na(tmp_df_predict[[4]]$log_abundance_trim),"Missing", "Complete"),
    pred1 = tmp_df_predict[[1]]$summary.fitted.values$mean,
    pred2 = tmp_df_predict[[2]]$summary.fitted.values$mean,
    pred3 = tmp_df_predict[[3]]$summary.fitted.values$mean
  )
  cmb_preds = rbind(cmb_preds, tmp_preds)
}
```

```
## [1] "BioTIME"
## [1] "CaPTrends"
## [1] "EA_NFPD"
## [1] "FishGlob"
## [1] "LPI"
## [1] "NAm_BBS"
## [1] "Pilotto"
## [1] "ReSurvey_Germany"
## [1] "RivFish"
## [1] "TimeFISH"
```

```
cmb_preds = subset(cmb_preds, miss == "Missing")
cmb_preds$pred2 = cmb_preds$pred2 + cmb_preds$mean_log
cmb_preds$pred3 = cmb_preds$pred3 + cmb_preds$mean_log
cmb_preds$diff1 = abs(abs(cmb_preds$log_abundance - cmb_preds$pred1)/cmb_preds$log_abundance)*100
cmb_preds$diff2 = abs(abs(cmb_preds$log_abundance - cmb_preds$pred2)/cmb_preds$log_abundance)*100
cmb_preds$diff3 = abs(abs(cmb_preds$log_abundance - cmb_preds$pred3)/cmb_preds$log_abundance)*100


sum_preds = cmb_preds %>%
  group_by(code) %>%
  summarise(mn1 = median(diff1), mn2 = median(diff2), mn3 = median(diff3))
#sum_preds$mn1 = signif(sum_preds$mn1, 3)
#sum_preds$mn2 = signif(sum_preds$mn2, 3)
#sum_preds$mn3 = signif(sum_preds$mn3, 3)
mean(sum_preds$mn1)
```

```
## [1] 24.44367
```

```
sd(sum_preds$mn1)
```

```
## [1] 16.17349
```

```
median(sum_preds$mn1)
```

```
## [1] 19.59994
```

```r
mean(sum_preds$mn2)
```

```
## [1] 18.293
```

```r
sd(sum_preds$mn2)
```

```
## [1] 10.53608
```

```r
median(sum_preds$mn2)
```

```
## [1] 16.93631
```

```r
mean(sum_preds$mn3)
```

```
## [1] 16.14866
```

```r
sd(sum_preds$mn3)
```

```
## [1] 7.501114
```

```r
median(sum_preds$mn3)
```

```
## [1] 17.18781
```

```r
mean(sum_preds$mn1)/mean(sum_preds$mn3)
```

```
## [1] 1.513665
```

```r
mean(sum_preds$mn2)/mean(sum_preds$mn3)
```

```
## [1] 1.132787
```

Driver of uncertainty

We now explore how the variance captured by spatial and phylogentic covariaince terms (relative to combined variance of covariance + hierarchical terms) impacts our inference

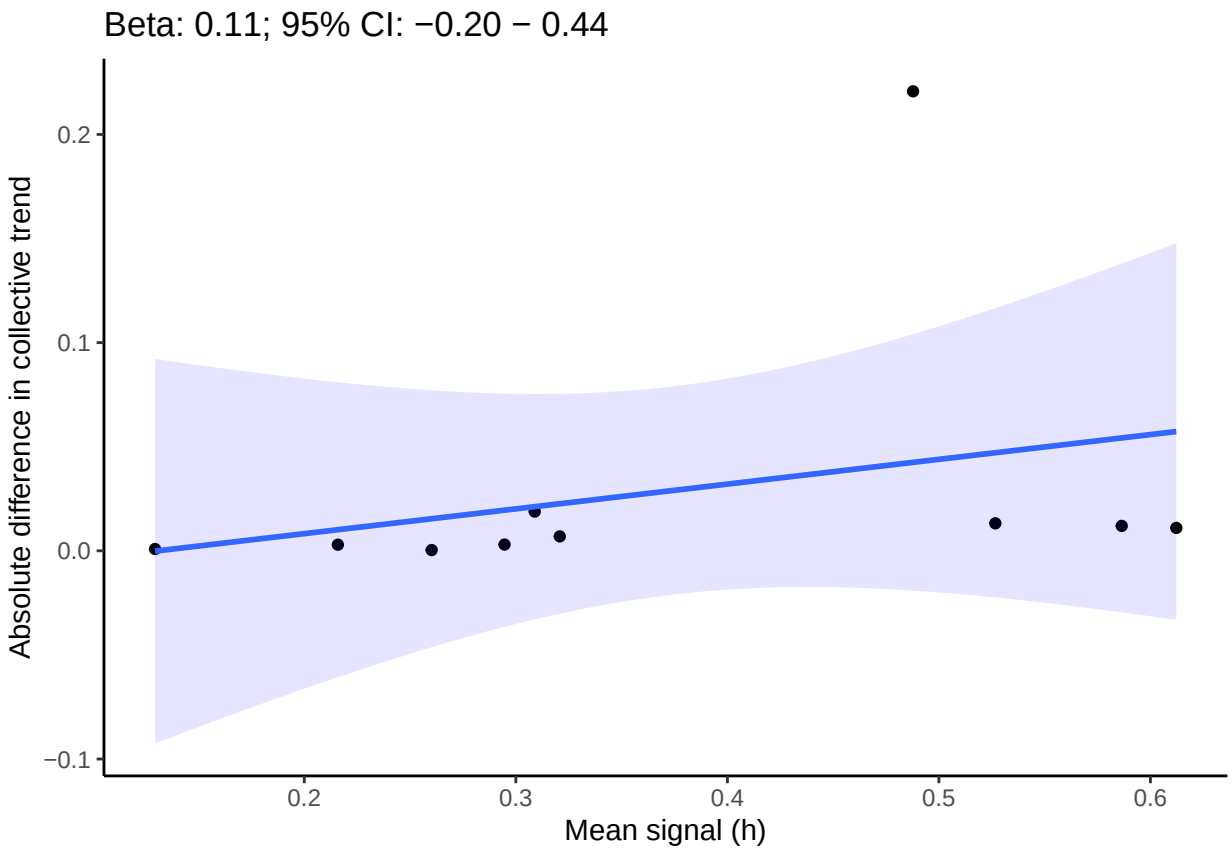
```
model_summary_core = read.csv("../outputs/model_summary.csv")

stre2 = data.frame(
  diff_rate = c((model_summary_core[which(model_summary_core$model == 2),"coef"]) - (model_summary_core[which(model_summary_core$model ==
  diff_sd = c((model_summary_core[which(model_summary_core$model == 3),"coef_sd"])/(model_summary_core[which(model_summary_core$model == 2
  var_tip = rowSums((model_summary_core[which(model_summary_core$model == 3),c("tip","gen","tip_h")])),
  var_phy = (model_summary_core[which(model_summary_core$model == 3),c("tip_h")]),
  var_loc = rowSums((model_summary_core[which(model_summary_core$model == 3),c("sit","squ","sit_h")])),
  var_spa = (model_summary_core[which(model_summary_core$model == 3),c("sit_h")])
)
stre2$phy_h = stre2$var_phy/stre2$var_tip
stre2$spa_h = stre2$var_spa/stre2$var_loc
stre2$mean_h = rowMeans(stre2[,c("phy_h", "spa_h")])

summary(lm(abs(diff_rate) ~ mean_h, data = stre2))
```

```
##
## Call:
## lm(formula = abs(diff_rate) ~ mean_h, data = stre2)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.046289 -0.029550 -0.015364 -0.003568  0.178205
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.01554    0.05581  -0.278    0.788
## mean_h       0.11895    0.13738   0.866    0.412
##
## Residual standard error: 0.06859 on 8 degrees of freedom
## Multiple R-squared:  0.08569,    Adjusted R-squared:  -0.0286
## F-statistic: 0.7498 on 1 and 8 DF,  p-value: 0.4118
```

```r
confint(lm(abs(diff_rate) ~ mean_h, data = stre2))
```

```
##                  2.5 %    97.5 %
## (Intercept) -0.1442316 0.1131511
## mean_h      -0.1978410 0.4357477
```

```r
ggplot(stre2) +
  geom_point(aes(x = mean_h, y = abs(diff_rate))) +
  geom_smooth(aes(x = mean_h, y = abs(diff_rate)), method = "lm", fill = "blue", alpha = 0.1) +
  labs(x = "Mean signal (h)", y = "Absolute difference in collective trend", title = "Beta: 0.11; 95% CI: -0.20 - 0.44") +
  theme_classic()
```




```
summary(lm(log10(diff_sd) ~ mean_h, data = stre2))
```

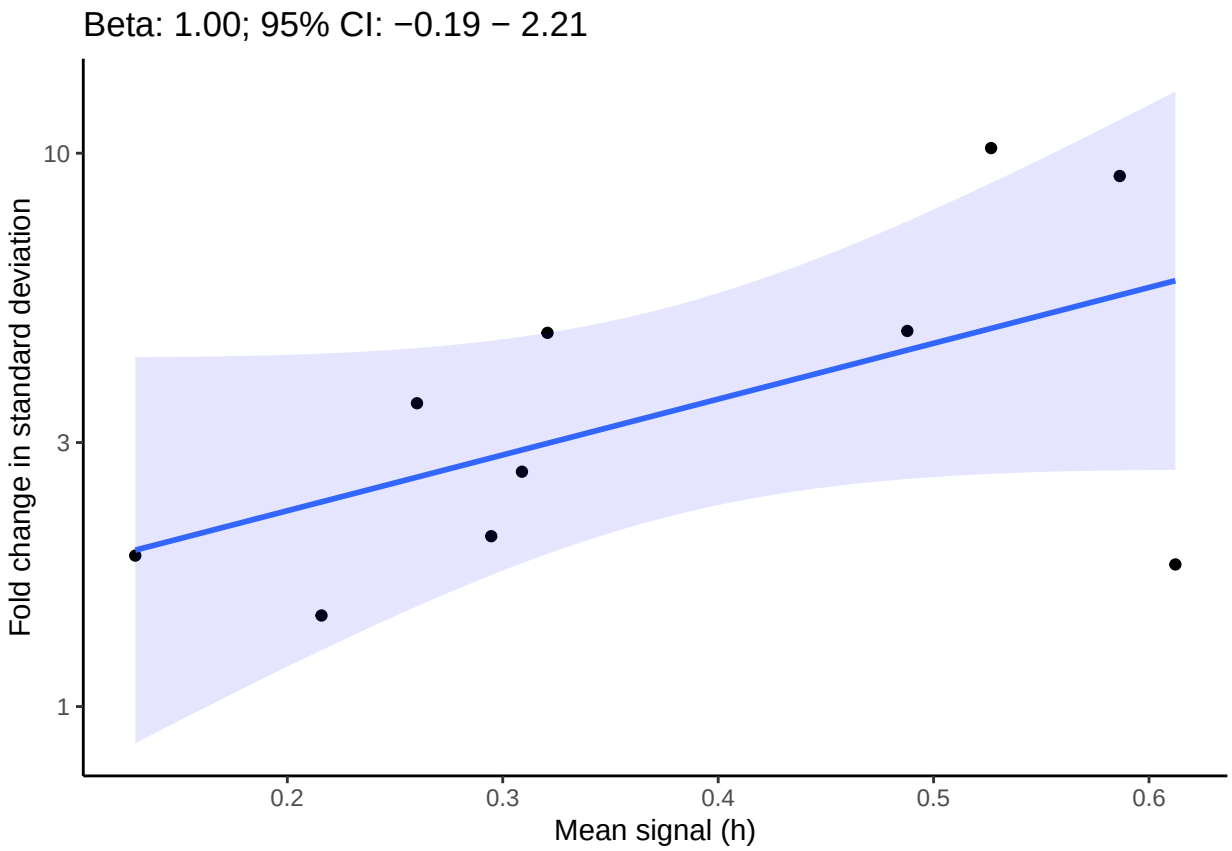
```
##
## Call:
## lm(formula = log10(diff_sd) ~ mean_h, data = stre2)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.51293 -0.11592  0.01238  0.18315  0.32588
##
```

```
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.1521     0.2110   0.721   0.4917
## mean_h        1.0088     0.5195   1.942   0.0881 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2594 on 8 degrees of freedom
## Multiple R-squared:  0.3203, Adjusted R-squared:  0.2354
## F-statistic: 3.771 on 1 and 8 DF,  p-value: 0.0881
```

```
confint(lm(log10(diff_sd) ~ mean_h, data = stre2))
```

```
##                  2.5 %    97.5 %
## (Intercept) -0.3345974 0.6387605
## mean_h      -0.1892213 2.2068549
```

```
ggplot(stre2) +
  geom_point(aes(x = mean_h, y = (diff_sd))) +
  geom_smooth(aes(x = mean_h, y = (diff_sd)), method = "lm", fill = "blue", alpha = 0.1) +
  scale_y_log10() +
  labs(x = "Mean signal (h)", y = "Fold change in standard deviation", title = "Beta: 1.00; 95% CI: -0.19 - 2.21") +
  theme_classic()
```




```
ggsave("../outputs/figures/extended_data_fig1.tiff",width = 4, height = 4, device='tiff', dpi=300)
```

Reproducibility

Date rendered

```
## [1] "2024-02-08 14:14:09 GMT"
```

Session info

```
## R version 4.2.3 (2023-03-15)
## Platform: aarch64-apple-darwin20 (64-bit)
## Running under: macOS Monterey 12.1
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/4.2-arm64/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.2-arm64/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] parallel  stats     graphics  grDevices utils     datasets  methods
## [8] base
##
## other attached packages:
##  [1] brinla_0.1.0       INLA_23.04.24      foreach_1.5.2      Matrix_1.5-3
##  [5] phytools_1.5-1     maps_3.4.1         ape_5.7-1          ggtree_3.6.2
##  [9] RColorBrewer_1.1-3 raster_3.6-23      maptools_1.1-8     sp_2.1-1
## [13] tidyr_1.3.0        ggpubr_0.6.0       ggplot2_3.4.4      dplyr_1.1.2
##
## loaded via a namespace (and not attached):
##  [1] nlme_3.1-162            sf_1.0-13               lubridate_1.9.2
##  [4] doParallel_1.0.17       numDeriv_2016.8-1.1     tools_4.2.3
##  [7] backports_1.4.1         utf8_1.2.4              R6_2.5.1
## [10] KernSmooth_2.23-20      mgcv_1.8-42             DBI_1.1.3
## [13] lazyeval_0.2.2          colorspace_2.1-0        withr_2.5.2
## [16] gridExtra_2.3           tidyselect_1.2.0        mnormt_2.1.1
## [19] phangorn_2.11.1         compiler_4.2.3          textshaping_0.3.6
## [22] cli_3.6.1               expm_0.999-7            labeling_0.4.3
## [25] scales_1.2.1            classInt_0.4-9          quadprog_1.5-8
## [28] proxy_0.4-27            systemfonts_1.0.4       digest_0.6.33
## [31] yulab.utils_0.0.9       foreign_0.8-84          rmarkdown_2.23
## [34] pkgconfig_2.0.3         htmltools_0.5.5         plotrix_3.8-2
## [37] fastmap_1.1.1           highr_0.10              rlang_1.1.2
## [40] rstudioapi_0.15.0       optimParallel_1.0-2     gridGraphics_0.5-1
## [43] generics_0.1.3          farver_2.1.1            combinat_0.0-8
## [46] jsonlite_1.8.7          car_3.1-2               magrittr_2.0.3
## [49] ggplotify_0.1.2         patchwork_1.1.3         Rcpp_1.0.11
```

```
## [52] munsell_0.5.0          fansi_1.0.5            abind_1.4-5
## [55] lifecycle_1.0.4        terra_1.7-39           scatterplot3d_0.3-44
## [58] yaml_2.3.7             carData_3.0-5          clusterGeneration_1.3.7
## [61] MASS_7.3-58.2          grid_4.2.3             lattice_0.20-45
## [64] cowplot_1.1.1          splines_4.2.3          knitr_1.43
## [67] pillar_1.9.0           igraph_1.5.0           ggsignif_0.6.4
## [70] codetools_0.2-19       fastmatch_1.1-3        glue_1.6.2
## [73] evaluate_0.21          ggfun_0.1.2            vctrs_0.6.4
## [76] treeio_1.22.0          gtable_0.3.4           purrr_1.0.1
## [79] cachem_1.0.8           xfun_0.39              broom_1.0.5
## [82] e1071_1.7-13           tidytree_0.4.5         coda_0.19-4
## [85] rstatix_0.7.2          class_7.3-21           ragg_1.2.5
## [88] tibble_3.2.1           iterators_1.0.14       aplot_0.2.0
## [91] memoise_2.0.1          units_0.8-2            timechange_0.2.0
```