How fractal is the data?

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Table of contents

0.1 Libraries

```r
rm(list=ls())

library(dplyr)
library(sf)
library(tidyr)
library(ggplot2)
library(viridis)
library(AICcmodavg)
```

```r
# folder path to atlas data
source_path <- "c:/Users/wolke/OneDrive - CZU v Praze/Datasets/Processed/Atlases/Replicate

# folder path to output folder
out_path <- "c:/Users/wolke/OneDrive - CZU v Praze/Dokumenty/GitHub/BEAST_General_Procedur
```

```r
# create path to read in data and grids from variables
data_path <- paste0(source_path,"Birds_Atlas_Czechia_beast_data.rds")
grid_path <-  paste0(source_path,"Birds_Atlas_Czechia_grid.gpkg")

# save names of layers from file (needed to read them in):
layers <- st_layers(grid_path)$name

# Define the desired order of factor levels
desired_levels <- factor(layers,
                        ordered = T,
                        levels = c("cell1grid", "cell2grid",
                                   "cell4grid", "cell8grid",
                                   "cell16grid", "cellfullgrid"))
```

0.2 Data

```r
# Species data
presence_data <- readRDS(data_path)

## sort the cell groupings ascending
presence_data <- presence_data %>%
  mutate(cell_grouping = factor(cell_grouping,
                                levels = desired_levels))

## add column for time period (tp)
start_times <- sort(unique(presence_data$start_year))
end_times <- sort(unique(presence_data$end_year))

time_periods <- data.frame(start_year = start_times,
                           end_year = end_times,
                           tp = seq_along(end_times))

presence_data <- merge(presence_data, time_periods,
                       by=c("start_year", "end_year"),
                       all.x=T)

# grid data
grid_list <- sapply(layers, function(i) {
  st_read(grid_path, paste(i), quiet = TRUE)
}, simplify = FALSE)
```

0.3 Occupancy calculation

- There are several ways we could calculate the occupancy.

  1. counting the number of occupied cells and calculating the proportion of all cells that were sampled
  2. Summing the areas of all occupied cells and calculating the proportion from the whole sampled area
  3. AOO based on IUCN standards: $AOO = Nr.ofoccupiedcells * areaofsingleacell$
  4. Modeling occupancy using occupancy-detection models

- Question: Do all of these yield the same measure for fractal dimension?

Anyway, here we calculate both (1), (2) and (3). (4) Will be done at a later stage of my PhD

```
occ_data_list <- list()

# We run the loop for each spatial grain (N = 8)
for (i in seq_along(grid_list)){

  # subset the grid_list and work on a single spatial grain:
  map_atlas <- grid_list[[i]]

  # Calculate total sampled area per time period:
  map_atlas <- map_atlas %>% mutate(
    Total_area1 = sum(map_atlas$area1s),
    Total_area2 = sum(map_atlas$area2s),
    Total_area3 = sum(map_atlas$area3s)
  )

  # Calculate total number of sampled cells per time period:
Total_Ncells1 <- map_atlas %>%
  filter(area1s > 0) %>%
  mutate(Total_Ncells1 = length(unique(cell_label))) %>%
  pull(Total_Ncells1) %>%
  unique()
Total_Ncells2 <- map_atlas %>%
  filter(area2s > 0) %>%
  mutate(Total_Ncells2 = length(unique(cell_label))) %>%
  pull(Total_Ncells2) %>%
  unique()
```

```
Total_Ncells3 <- map_atlas %>%
  filter(area3s > 0) %>%
  mutate(Total_Ncells3 = length(unique(cell_label))) %>%
  pull(Total_Ncells3) %>%
  unique()

  Total_Ncells <- data.frame(
    cell_grouping = unique(map_atlas$cell_grouping),
    Total_Ncells1, Total_Ncells2, Total_Ncells3)

  map_atlas <- merge(map_atlas, Total_Ncells)

  # map_atlas %>%
  #   pivot_longer(cols=c('Total_Ncells1', 'Total_Ncells2', 'Total_Ncells3'),
  #                names_to='year',
  #                values_to='Total_N_cells')

  # subset the presence/absence data to the current spatial grain:
  pres_data <- presence_data %>%
    filter(cell_grouping == unique(map_atlas$cell_grouping))

  # Merge sampled and unsampled cells for calculations:
  pres_data_full <- merge(pres_data, map_atlas,
                          by = intersect(names(pres_data), names(map_atlas)),
                          all = T)
  pres_data_full <- unique(pres_data_full)

  # Reduce columns needed for analysis:
  pres_data_full_reduced <- pres_data_full %>%
  ungroup() %>%
    mutate(
      area_sampled = case_when(
        tp == 1 ~ area1s,
        tp == 2 ~ area2s,
        tp == 3 ~ area3s),
      area_c = case_when(
        tp == 1 ~ area_cropped,
        tp == 2 ~ area_cropped,
        tp == 3 ~ area_cropped),
      Total_area =case_when(
        tp == 1 ~ Total_area1,
```

```r
        tp == 2 ~ Total_area2,
        tp == 3 ~ Total_area3),
      Total_Ncells = case_when(
        tp == 1 ~ Total_Ncells1,
        tp == 2 ~ Total_Ncells2,
        tp == 3 ~ Total_Ncells3)) %>%
    select(verbatim_name, tp, cell_grouping, cell_label,
           area_sampled, area_c, Total_area, Total_Ncells) %>%
    filter_all(any_vars(!is.na(.)))

## ========================================================================= ##
##  ========================== Calculate Occupancy ========================== ##
## ========================================================================= ##

occ_data <- pres_data_full_reduced %>%
  ungroup() %>%

# Remove unsampled cells:
  filter(!is.na(verbatim_name)) %>%

# Necessary grouping to calculate occupancy:
  group_by(verbatim_name, tp, cell_grouping) %>% unique() %>%

# Calculate Occupancy:
  # mutate(occupancy_area = sum(area_sampled)) %>%
  mutate(occupancy_Ncells = n_distinct(cell_label)) %>%

# Calculate AOO:
  mutate(AOO = occupancy_Ncells * mean(area_sampled)) %>%

# Calculate relative Occupancy:
  # mutate(relative_occupancy_area = occupancy_area/Total_area) %>%
  mutate(relative_occupancy_Ncells = occupancy_Ncells/Total_Ncells) %>%

# Round values to 2 digits after the comma:
  # mutate(relative_occupancy_area = round(relative_occupancy_area, 3)) %>%
  mutate(relative_occupancy_Ncells = round(relative_occupancy_Ncells, 2)) %>%

# Remove duplicated rows:
  distinct()

# save to list:
```

```
occ_data_list[[i]] <- occ_data

}

# Bind to one dataframe:
occ_data_full_df <- plyr::rbind.fill(occ_data_list, fill=T)
#occ_data_full_df %>%  filter_all(any_vars(is.na(.)))

# create scale column as a fraction of the full country:
occ_data_full_df <- occ_data_full_df %>% mutate(
      scale = case_when(
        cell_grouping == "cell1grid" ~ 1/32,
        cell_grouping == "cell2grid" ~ 1/16,
        cell_grouping == "cell4grid" ~ 1/8,
        cell_grouping == "cell8grid" ~ 1/4,
        cell_grouping == "cell16grid" ~ 1/2 ,
        cell_grouping == "cellfullgrid" ~ 1)) %>% unique()

# save reduced version of this to file:

species_data <- occ_data_full_df %>% select(-c(cell_label, area_sampled, area_c)) %>% dist
# species_data %>% write.csv(paste0(out_path, "Occupancy_table.csv"))
```

0.4 How fractal is the data?

(Work in progress, 18.12.2023)

0.4.1 1. at which scale do species saturate?

- a bit less than 50% of species saturate at cell8grid
- What does it mean if species saturate at which scales? (some Brainstorming…)
  - at cell1grid: saturation indicates a very cosmopolitan species that occurs in every grid cell at the sampling resolution
  - at cell2grid: saturation indicates a cosmopolitan species that occurs in every second grid cell at the sampling resolution
  - at cell4grid: wide spread but a bit fragmented
  - at cell8grid: a bit more fragmented but still wide spread
  - at cell16grid: country is divided into 6 squares: species only now covers all 6 squares, species distribution is wide spread but very fragmented. It still occurs in all directions of a country. (North/East/South/West)

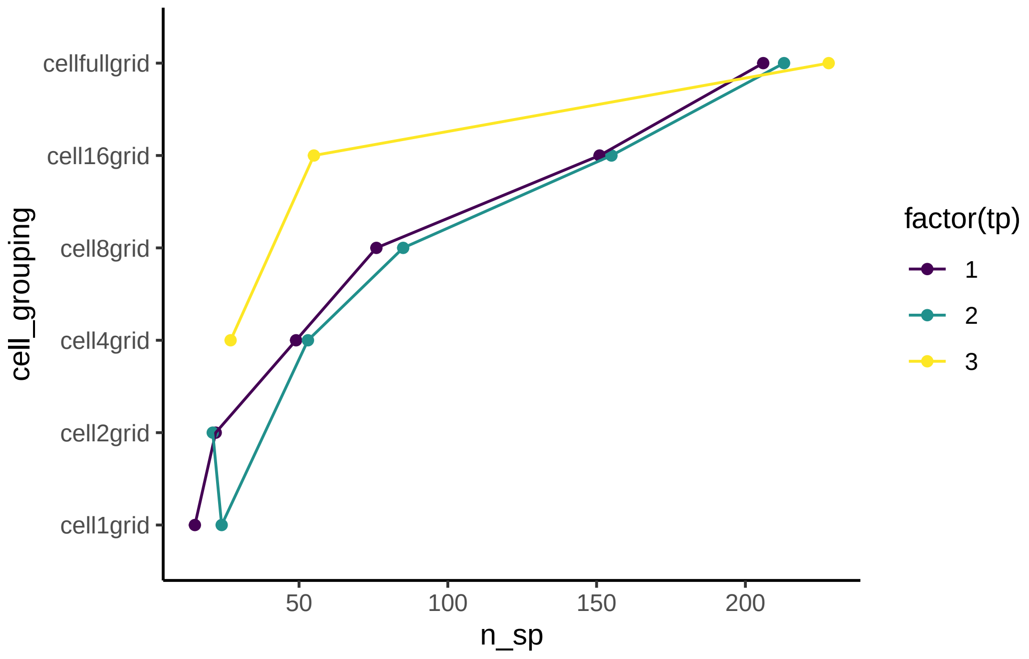
    - at cellfullgrid: species distribution is limited to certain area of the country

- in time period 3, much less species saturate at other scales than the full country grid. What's going on here?
- At cell2grid, less species saturate compared to time period 1. All other spatial grains suggest temporal increases (i.e., more species saturating at a given scale in tp2 compared to tp1)

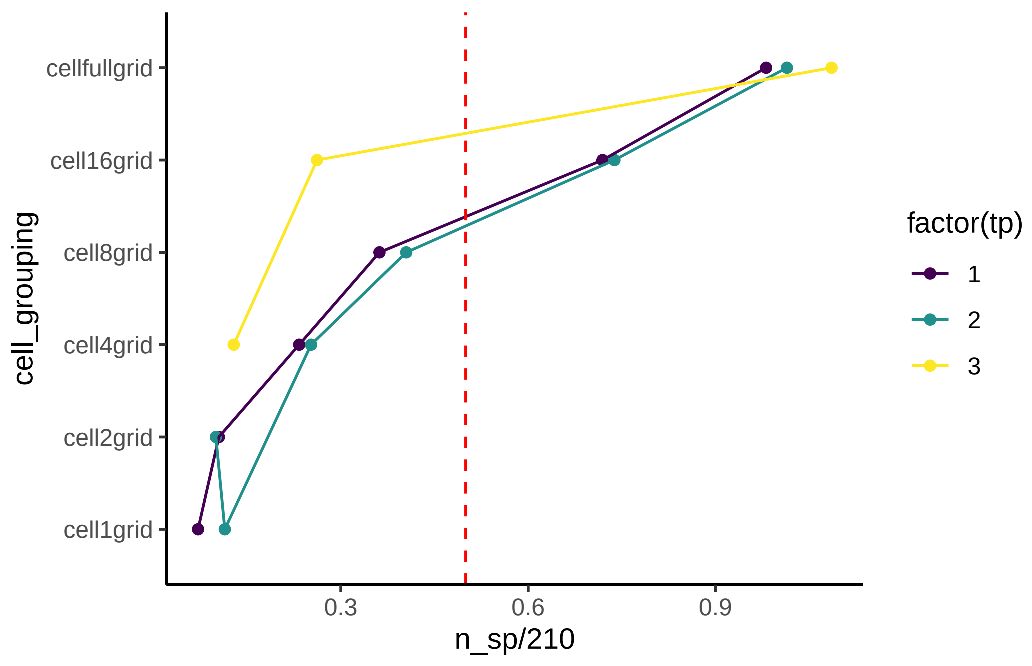
cell_grouping	*tp*	*n_sp*	*Comment*
cell1grid	1	4	
cell1grid	2	5	indicates population growth over time
cell2grid	1	22	
cell2grid	2	21	does not indicate growth anymore !
cell4grid	1	49	
cell4grid	2	53	Again indicated growth !
cell4grid	3	27	
cell8grid	1	76	0.37% of all species saturated
cell8grid	2	85	0.40% of all species saturated // Growth
cell16grid	1	151	0.73% of all species saturated
cell16grid	2	155	0.73 % of all species saturated // Growth
cell16grid	3	55	0.24% of all species saturated // what's going on here?
cellfullgrid	1	206	period 1 has the smallest overall SR
cellfullgrid	2	213	period 2 has an intermediate overall SR
cellfullgrid	3	228	period 3 has the highest overall SR

```
# species_data %>%
#   filter(relative_occupancy_Ncells == 1) %>%
#   group_by(cell_grouping, tp) %>%
#   summarize(n_sp = n_distinct(verbatim_name))

species_data %>%
  filter(relative_occupancy_Ncells == 1) %>%
  group_by(cell_grouping, tp) %>%
  summarize(n_sp = n_distinct(verbatim_name)) %>%
  ggplot(aes(y = cell_grouping, x = n_sp, col = factor(tp)))+
  geom_point()+
  geom_line(aes(group = tp))+
  scale_color_viridis(discrete = T)+
  theme_classic()
```



```
species_data %>%
  filter(relative_occupancy_Ncells == 1) %>%
  group_by(cell_grouping, tp) %>%
  summarize(n_sp = n_distinct(verbatim_name)) %>%
  ggplot(aes(y = cell_grouping, x = n_sp/210, col = factor(tp)))+
  geom_point()+
  geom_line(aes(group = tp))+
  geom_vline(xintercept = 0.5, color = "red", linetype = "dashed") +  # Adding a vertical
  scale_color_viridis(discrete = TRUE) +
  theme_classic()
```



0.4.2 2. Data sub-setting

What are important influences to consider how the scale-area curve looks?

- saturation –> exclude scales at which a species saturates for the calculation (i.e., relative occupancy = 1)
  - early saturation can lead to the exclusion of too many scales for the calculation –> could be worth sub-setting the data to all species that do not saturate within a range of scales (e.g., spatial grain 1-4 yields still > 50% species NOT saturated)
- temporal replication
  - ? exclude species for which we do not temporally replicated data for comparative reasons with whatever temporal change variable I want to assess –> not necessary when assessing how fractal the data is (!)
- sampling effort
- not all cells of the same grain have the same area
  - –> distribution of these across the country could be important: smaller cells will have less area, therefore less species will be present in such a cell. However, saturation of a species depends on a species occupying all cells. Here this affects all species the same way (as saturation is always = 1) and may thus be ignored (?)

```r
# exclude saturated species for all calculations
dd <- species_data %>%
  filter(relative_occupancy_Ncells < 1) %>% # exclude saturated scales
  unique() %>%
  filter_at(
    vars(c(
      cell_grouping, scale,
      AOO, occupancy_Ncells,
      relative_occupancy_Ncells
    )),
    any_vars(!is.na(.))
  )

#### Subset the data by at last 3 scales
#(minimum n needed to calculate 2nd degree poly relationship)
sp_3scales <- dd %>%
  select(verbatim_name, tp, cell_grouping) %>%
  distinct() %>%
  group_by(verbatim_name, tp) %>%
  summarize(n = n_distinct(cell_grouping)) %>%
  filter(n >= 3)

sp_3scales_tp1 <- sp_3scales %>% filter(tp == 1) %>% pull(verbatim_name)
sp_3scales_tp2 <- sp_3scales %>% filter(tp == 2) %>% pull(verbatim_name)
sp_3scales_tp3 <- sp_3scales %>% filter(tp == 3) %>% pull(verbatim_name)

length(unique(sp_3scales_tp1)) # 158 species
```

```
[1] 157
```

```r
length(unique(sp_3scales_tp2)) # 160 species
```

```
[1] 160
```

```r
length(unique(sp_3scales_tp3)) # 228 species
```

```
[1] 228
```

```r
length(unique(dd$verbatim_name)) # 237 species
```

```
[1] 237
```

0.4.3 3. Is the scale-area relationship linear or non-linear?

- this analysis requires species to not-saturate over 3 scales (as calculating 2nd degree polynomials requires at least 3 data points)
  –> therefore I exclude species that saturate at the third grain

```r
sumtab <- read.csv(paste0(out_path, "Linear_Poly_AICc_Summary.csv"))
sumtab
```

```
    X Modnames        model   n mean_cumWT Delta_AICc
1   1   linear          AOO 690      0.943      0.006
2   2   linear      occArea 690      0.943      0.006
3   3   linear    occNcells 627      0.946      0.001
4   4   linear   occRelArea 690      0.938      0.004
5   5   linear occRelNcells 651      0.912      0.034
6   6     poly          AOO  45      0.970      0.530
7   7     poly      occArea  45      0.970      0.530
8   8     poly    occNcells  84      0.964      0.388
9   9     poly   occRelArea  48      0.877      0.431
10 10     poly occRelNcells 132      0.919      0.457
```

```r
##

tp1_dd <- dd %>% filter(tp == 1 & verbatim_name %in% sp_3scales_tp1)
tp2_dd <- dd %>% filter(tp == 2 & verbatim_name %in% sp_3scales_tp2)
tp3_dd <- dd %>% filter(tp == 3 & verbatim_name %in% sp_3scales_tp3)
tp_dd_list <- list(tp1_dd, tp2_dd, tp3_dd)

# loop along tp_dd list, then along species

models_est_list <- list()
models_est_df_list <- list()
all_AIC_tabs <- list()
all_AIC_tabs_all <- list()
```

```r
for (y in seq_along(tp_dd_list)){

  temp_df <- tp_dd_list[[y]]

  for (i in seq_along(unique(temp_df$verbatim_name))){

    sp <- unique(temp_df$verbatim_name)[i]
    model_df <- temp_df %>% filter(verbatim_name == sp)

     m_lin <- lm(log(AOO) ~ log(scale), data = model_df)
     m_poly <- lm(log(AOO) ~ poly(scale, 2), data = model_df)



     aic.discrete <- setNames(c(AIC(m_lin), AIC(m_poly)), c("linear", "poly"))
     weights <- geiger::aicw(aic.discrete)

      AIC_tab <- data.frame(verbatim_name = sp,
                            tp = y,
                            aictab(list(m_lin, m_poly), modnames = c("linear", "poly")),
                            AIC = sapply(list(m_lin, m_poly), AIC),
                            weights)


      m_df1 <- data.frame(
      # row.names = c("linear"),
      verbatim_name = sp,
      tp = y,
      m_AOO = m_lin$coefficients[2],
      b_AOO = m_lin$coefficients[1],
      r2_AOO = summary(m_lin)$r.squared)


      all_AIC_tabs[[i]] <- AIC_tab
      models_est_list[[i]] <- m_df1

  }

    models_est_df <- plyr::rbind.fill(models_est_list, fill = T)
    models_est_df_list[[y]] <- models_est_df
    all_AIC_tabs_df <- plyr::rbind.fill(all_AIC_tabs, fill = T)
    all_AIC_tabs_all[[y]] <- all_AIC_tabs_df

}

all_AIC_tabs_df_all <- plyr::rbind.fill(all_AIC_tabs_all, fill = T)
models_est_df_all <- plyr::rbind.fill(models_est_df_list, fill = T)
rownames(models_est_df_all) <- NULL
models_est_df_all <- models_est_df_all[order(models_est_df_all$verbatim_name), ] # sort by
```

0.5 Big table

```
species_data_new <- merge(species_data,
                          models_est_df_all,
                          by=c(intersect(names(species_data), names(models_est_df_all))))

# Telfer:

telfer_results <- sparta::telfer(taxa = presence_data$verbatim_name,
                                site = presence_data$cell_label,
                                time_period = presence_data$tp,
                                minSite = 2)

telfer_results2 <- telfer_results %>%
  select(taxa, Telfer_1_2, Telfer_2_3, Telfer_1_3) %>%
  rename(verbatim_name = taxa)


species_data_new2 <- merge(species_data_new, telfer_results2, by="verbatim_name")
#%>% write.csv(file=paste0(out_path, "Big_table.csv"))
```

0.5.0.1 D ~ Telfer Plot

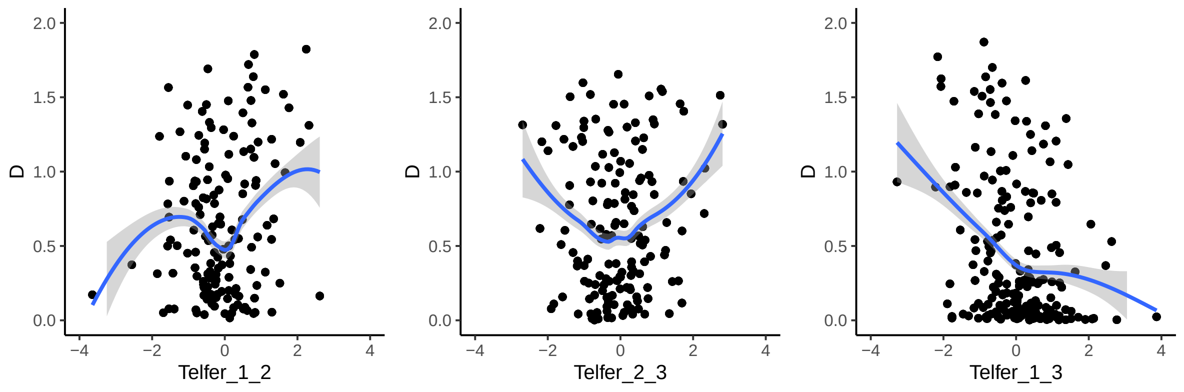
```
# D ~ Telfer Plot ==================================== ####

species_data_new2$D <- species_data_new2$m_AOO
ggp1 <- species_data_new2 %>% filter(tp == 1) %>%
ggplot() +
  geom_point(aes(x = Telfer_1_2, y = D ))+
  geom_smooth(aes(x = Telfer_1_2, y = D ))+
  theme_classic()+
  xlim(-4,4)+
  ylim(0,2)

ggp2 <- species_data_new2 %>% filter(tp == 2) %>%
ggplot() +
  geom_point(aes(x = Telfer_2_3, y = D ))+
  geom_smooth(aes(x = Telfer_2_3, y = D ))+
  theme_classic()+
  xlim(-4,4)+
  ylim(0,2)

ggp3 <- species_data_new2 %>% filter(tp == 3) %>%
ggplot() +
  geom_point(aes(x = Telfer_1_3, y = D ))+
  geom_smooth(aes(x = Telfer_1_3, y = D ))+
  theme_classic()+
  xlim(-4,4)+
  ylim(0,2)

gridExtra::grid.arrange(ggp1,ggp2,ggp3, ncol = 3)
```



0.5.0.2 D ~ log Ratio of AOO

```
# Re-formating the data.. there is probably a smoother way to do it..
species_data_wide1 <- species_data_new2 %>%
  select(verbatim_name, tp, cell_grouping,
         D, b_AOO, AOO, Total_Ncells,
          occupancy_Ncells,
         relative_occupancy_Ncells) %>%
  group_by(verbatim_name, tp) %>%
  distinct() %>%
  filter(tp == 1) %>%
  setNames(paste0('tp1_', names(.))) %>%
  ungroup() %>%
  select(-c(tp1_tp)) %>%
  rename(verbatim_name = tp1_verbatim_name,
         cell_grouping = tp1_cell_grouping)

species_data_wide2 <- species_data_new2 %>%
  select(verbatim_name, tp, cell_grouping,
         D, b_AOO, AOO, Total_Ncells,
          occupancy_Ncells,
         relative_occupancy_Ncells) %>%
  group_by(verbatim_name, tp) %>%
  distinct() %>%
  filter(tp == 2) %>%
  setNames(paste0('tp2_', names(.))) %>%
  ungroup() %>%
  select(-c(tp2_tp)) %>%
  rename(verbatim_name = tp2_verbatim_name,
         cell_grouping = tp2_cell_grouping)

species_data_wide3 <- species_data_new2 %>%
  select(verbatim_name, tp, cell_grouping,
         D, b_AOO, AOO, Total_Ncells,
          occupancy_Ncells,
         relative_occupancy_Ncells) %>%
  group_by(verbatim_name, tp) %>%
  distinct() %>%
  filter(tp == 3) %>%
  setNames(paste0('tp3_', names(.))) %>%
  ungroup() %>%
  select(-c(tp3_tp)) %>%
  rename(verbatim_name = tp3_verbatim_name,
         cell_grouping = tp3_cell_grouping)

# merge back together:
```

```r
temp <- merge(species_data_wide1, species_data_wide2,
            by=intersect(names(species_data_wide1), names(species_data_wide2)))
temp2 <- merge(temp, species_data_wide3,
             by=intersect(names(temp), names(species_data_wide3)))
names_v <- names(temp2[-(1:2)])

# Transform to wide format by cell_grouping
species_data_wide <- temp2 %>%
  pivot_wider(names_from = cell_grouping,
            values_from = all_of(names_v))

species_data_wide <- species_data_wide %>%
  mutate(log_R1 = log(tp2_AOO_cell1grid/tp1_AOO_cell1grid),
         log_R2 = tp2_AOO_cell1grid-tp1_AOO_cell1grid,
         log_R1_3 = log(tp3_AOO_cell1grid/tp1_AOO_cell1grid),
         log_R2_3 = tp3_AOO_cell1grid-tp1_AOO_cell1grid,
         .before = 1) # sort columns to the beginning of the table
```

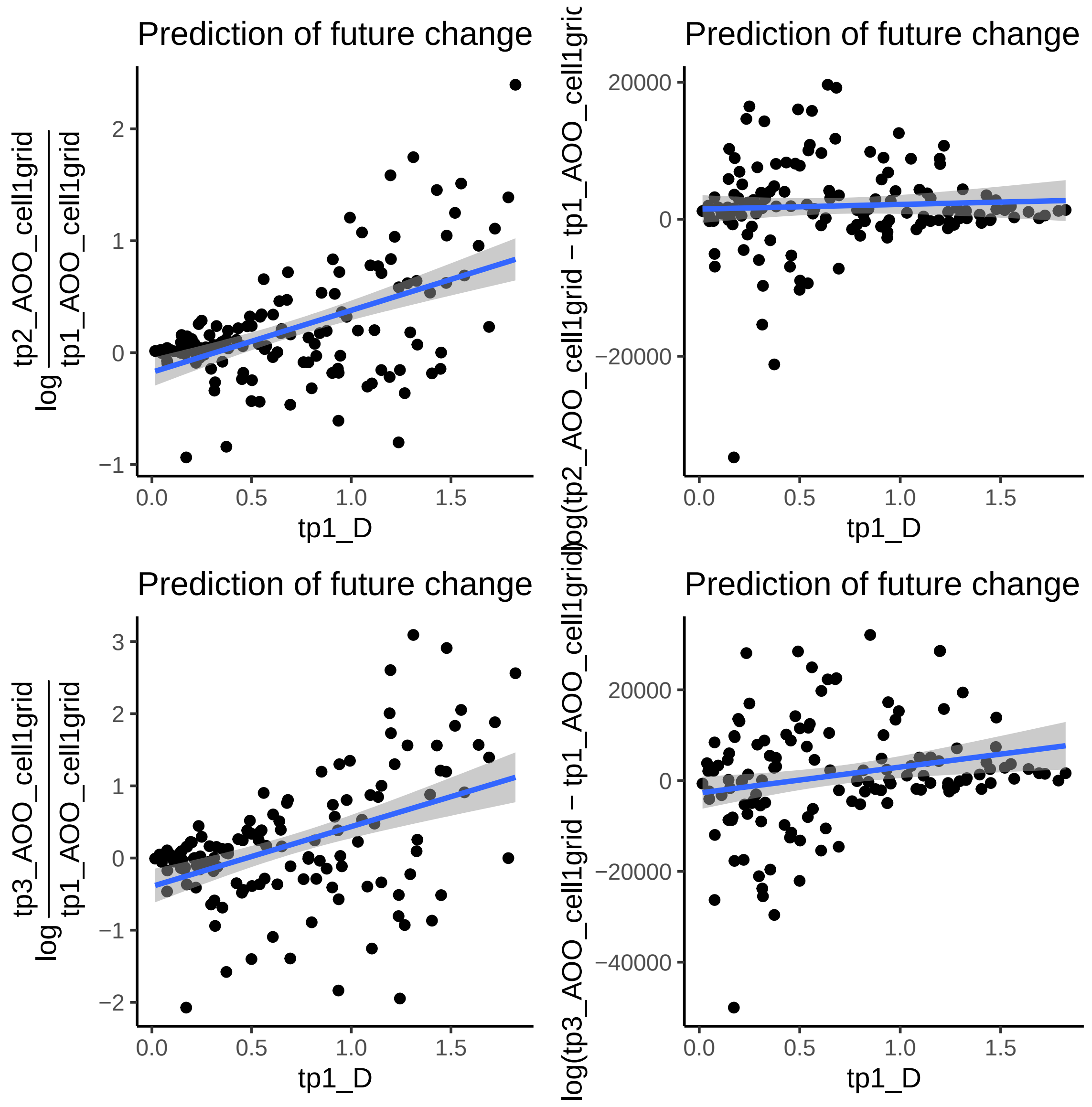
```r
# Plots ================================================================== #
p1 <- species_data_wide %>%
  ggplot(aes(y = log_R1, x =tp1_D_cell1grid))+
  geom_point()+
  ylab(expression("log"~ frac("tp2_AOO_cell1grid", "tp1_AOO_cell1grid")))+
  xlab("tp1_D")+
 geom_smooth(method = "lm", formula = y ~ x, se = T, alpha = 0.5)+
  theme_classic()+
  labs(title = "Prediction of future change")

p2 <- species_data_wide %>%
  ggplot(aes(y = log_R2, x =tp1_D_cell1grid))+
  geom_point()+
  xlab("tp1_D")+
  ylab("log(tp2_AOO_cell1grid - tp1_AOO_cell1grid)")+
  geom_smooth(method = "lm", formula = y ~ x, se = T, alpha = 0.5)+
  theme_classic()+
  labs(title = "Prediction of future change")


p3 <- species_data_wide %>%
  ggplot(aes(y = log_R1_3, x =tp1_D_cell1grid))+
  geom_point()+
  ylab(expression("log"~ frac("tp3_AOO_cell1grid", "tp1_AOO_cell1grid")))+
  xlab("tp1_D")+
 geom_smooth(method = "lm", formula = y ~ x, se = T, alpha = 0.5)+
  theme_classic()+
  labs(title = "Prediction of future change")

p4 <- species_data_wide %>%
  ggplot(aes(y = log_R2_3, x =tp1_D_cell1grid))+
  geom_point()+
  xlab("tp1_D")+
  ylab("log(tp3_AOO_cell1grid - tp1_AOO_cell1grid)")+
  geom_smooth(method = "lm", formula = y ~ x, se = T, alpha = 0.5)+
  theme_classic()+
  labs(title = "Prediction of future change")

gridExtra::grid.arrange(p1,p2,p3,p4)
```



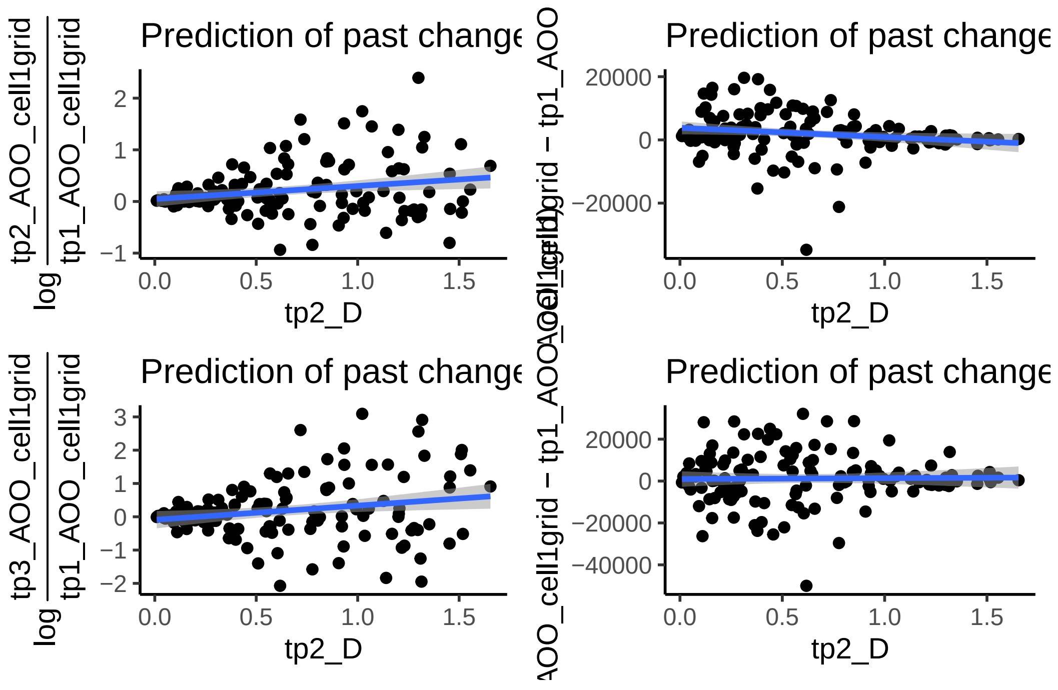
```
p1_2 <- species_data_wide %>%
  ggplot(aes(y = log_R1, x =tp2_D_cell1grid))+
  geom_point()+
  ylab(expression("log"~ frac("tp2_AOO_cell1grid", "tp1_AOO_cell1grid")))+
  xlab("tp2_D")+
 geom_smooth(method = "lm", formula = y ~ x, se = T, alpha = 0.5)+
  theme_classic()+
  labs(title = "Prediction of past change")
```

```r
p2_2 <- species_data_wide %>%
  ggplot(aes(y = log_R2, x =tp2_D_cell1grid))+
  geom_point()+
  xlab("tp2_D")+
  ylab("log(tp2_AOO_cell1grid - tp1_AOO_cell1grid)")+
  geom_smooth(method = "lm", formula = y ~ x, se = T, alpha = 0.5)+
  theme_classic()+
  labs(title = "Prediction of past change")


p3_2 <- species_data_wide %>%
  ggplot(aes(y = log_R1_3, x =tp2_D_cell1grid))+
  geom_point()+
  ylab(expression("log"~ frac("tp3_AOO_cell1grid", "tp1_AOO_cell1grid")))+
  xlab("tp2_D")+
 geom_smooth(method = "lm", formula = y ~ x, se = T, alpha = 0.5)+
  theme_classic()+
  labs(title = "Prediction of past change")

p4_2 <- species_data_wide %>%
  ggplot(aes(y = log_R2_3, x =tp2_D_cell1grid))+
  geom_point()+
  xlab("tp2_D")+
  ylab("log(tp3_AOO_cell1grid - tp1_AOO_cell1grid)")+
  geom_smooth(method = "lm", formula = y ~ x, se = T, alpha = 0.5)+
  theme_classic()+
  labs(title = "Prediction of past change")

gridExtra::grid.arrange(p1_2,p2_2,p3_2,p4_2)
```



Prediction of past change
Prediction of past change
Prediction of past change
Prediction of past change
log tp2_AOO_cell1grid / tp1_AOO_cell1grid
log tp3_AOO_cell1grid / tp1_AOO_cell1grid
tp2_AOO_cell1grid − tp1_AOO_cell1grid
AOO_cell1grid − tp1_AOO_cell1grid
tp2_D
tp2_D
tp2_D
tp2_D