Breitenbach 2.0 - EPT

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Load necessary packages

```r
library(tidyverse)
library(patchwork)
library(janitor)
library(SpadeR)
library(vegan)
library(codyn)
library(mobr)
library(iNEXT)
library(readxl)
library(writexl)
```

Load the EPT data

```r
ept <- read_xlsx("Data/Breitenbach_community_data_17.12.2024.xlsx") |>      # read in excel sp
  as_tibble() |>                                                            # Make tibble tabl
  clean_names() |>                                                          # Homogenize colum
  rename_with(~ gsub("^x", "", .x), .cols = matches("^x[0-9]")) |>          # Change column na
  filter(!str_detect(original_name, "Summe")) |>                            # delete rows cont
  filter(order %in% c("Ephemeroptera", "Plecoptera", "Trichoptera")) |>     # Keeps only EPT t
  select(where(~ !is.numeric(.x) || sum(.x) != 0)) |>                       # Removes empty (0
  mutate(trap_new = case_when(                                              # Homogenize trap
    trap %in% c('Haus O') ~ 'O',
    trap %in% c('Haus A', 'A/I') ~ 'A',
    trap %in% c('Haus I') ~ 'I',
    trap %in% c('Haus B', 'B / II', 'B-II-X', 'B/II', 'Haus B/II') ~ 'B',
    trap %in% c('Haus C-IV', 'C / IV', 'C-IV', 'C/IV', 'Haus C', 'Haus C/IV') ~ 'C',
    trap %in% c('Haus III') ~ 'III',
    trap %in% c('Haus D') ~ 'D',
    trap %in% c('Haus E - V', 'E / V', 'E-V', 'E/V', 'Haus E/V') ~ 'E',
    trap %in% c('Haus F - VI', 'F / VI', 'F-VI', 'F-VII', 'F/VI', 'Haus F/VI') ~ 'F',
    trap %in% c('Haus G', 'G-VII', 'G/ VII', 'G/VII', 'Haus G/VII') ~ 'G',
    trap %in% c('Quelle') ~ 'Source',
    TRUE ~ trap)) |>
  filter(!str_detect(trap_new, "D")) |>                                    # delete rows for
  select(-c(taxa_id:trap)) |>                                              # Remove unnecessa
  mutate(sp_name  = validated_name,                                        # Change column na
         trap     = trap_new,                                              # Change column na
         trap     = factor(trap)) |>                                       # make trap a fact
  arrange(trap, family, sp_name) |>                                        # Sort data
  select(-c(validated_name, trap_new, order)) |>                           # Remove unnecessa
  select(trap, sp_name, family, everything()) |>                           # rearrange columr
  print()
```

```
# A tibble: 2,133 x 40
   trap  sp_name  family `1969` `1970` `1971` `1972` `1973` `1974` `1975` `1976`
   <fct> <chr>    <chr>   <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>
 1 A     Apatani~ Apata~      0      0      0      0      0      0      0      0
 2 A     Apatani~ Apata~      0      0      0      0      0      0      0      0
 3 A     Alainit~ Baeti~      0      0      0      0      0      0      0      0
 4 A     Alainit~ Baeti~      0      0      0      0      0      0      0      0
 5 A     Baetis ~ Baeti~      0      0      0      0      0      0      0      0
 6 A     Baetis ~ Baeti~      0      0      0      0      0      0      0      0
 7 A     Baetis ~ Baeti~      0      0      0      0      0      0      0      0
 8 A     Baetis ~ Baeti~      0      0      0      0      0      0      0      0
 9 A     Baetis ~ Baeti~      0      0      0      0      0      0      0      0
10 A     Baetis ~ Baeti~      0      0      0      0      0      0      0      0
# i 2,123 more rows
# i 29 more variables: `1977` <dbl>, `1978` <dbl>, `1979` <dbl>, `1980` <dbl>,
#   `1981` <dbl>, `1982` <dbl>, `1983` <dbl>, `1984` <dbl>, `1985` <dbl>,
#   `1986` <dbl>, `1987` <dbl>, `1988` <dbl>, `1989` <dbl>, `1990` <dbl>,
#   `1991` <dbl>, `1992` <dbl>, `1993` <dbl>, `1994` <dbl>, `1995` <dbl>,
#   `1996` <dbl>, `1997` <dbl>, `1998` <dbl>, `1999` <dbl>, `2000` <dbl>,
#   `2001` <dbl>, `2002` <dbl>, `2003` <dbl>, `2004` <dbl>, `2005` <dbl>
```

Initial data wrangling

```
ept_clean <- ept |>
  group_by(trap,
           sp_name,
           family) |>                                                     # Grouping by tra
  summarise(across(where(is.numeric),
                   ~sum(.x, na.rm = TRUE)),
                   .groups = "drop")

ept_long <- ept_clean |>
  pivot_longer(
    cols = starts_with("19") | starts_with("20"),                         # Specify the yea
    names_to = "year",                                                    # Name column tha
    values_to = "abundance") |>                                           # Name column tha
  mutate(trap_code = paste(trap, year, sep = "_")) |>                     # create new colu
  mutate(year = as.numeric(year)) |>                                      # make year varia
  filter(abundance != 0)  |>                                              # Remove rows whe
  arrange(trap, year)                                                     # Sort data

ept_agg <- ept_long |>
  group_by(sp_name,
           trap) |>                                                       # Group by sp_nam
  summarise(abundance = sum(abundance),
            .groups = "drop") |>                                          # Summarise with
  arrange(trap)                                                           # Sort data

ept_wide <- ept_agg |>
  pivot_wider(names_from  = trap,
              values_from = abundance,
              values_fill = 0,
              values_fn   = sum) |>
  arrange(sp_name)                                                        # Sort data
```

Calculating indices

Chao's indices: species estimation in a single community

```
chaoA_ept      <- ChaoSpecies(ept_wide$A ,"abundance", k = 2, conf = 0.95)            # ept t
chaoB_ept      <- ChaoSpecies(ept_wide$B ,"abundance", k = 2, conf = 0.95)            # ept t
chaoC_ept      <- ChaoSpecies(ept_wide$C ,"abundance", k = 2, conf = 0.95)            # ept t
chaoE_ept      <- ChaoSpecies(ept_wide$E ,"abundance", k = 2, conf = 0.95)            # ept t
chaoF_ept      <- ChaoSpecies(ept_wide$F ,"abundance", k = 2, conf = 0.95)            # ept t
chaoG_ept      <- ChaoSpecies(ept_wide$G ,"abundance", k = 2, conf = 0.95)            # ept t
chaoI_ept      <- ChaoSpecies(ept_wide$I ,"abundance", k = 2, conf = 0.95)            # ept t
chaoIII_ept    <- ChaoSpecies(ept_wide$III ,"abundance", k = 2, conf = 0.95)          # ept t
chaoO_ept      <- ChaoSpecies(ept_wide$O ,"abundance", k = 2, conf = 0.95)            # ept t
```

```
Warning: In this case, it can't estimate the variance of 2nd-order-jackknife estimation
```

Standard community indices + turnover

```
ept_long$ro.ab <- round(ept_long$abundance, digits = 0)                               # Round
TD <- NULL                                                                            # Initia

for (i in unique(ept_long$trap)) {                                                    # Loop f
  sub <- ept_long[ept_long$trap == i, ]                                               # Create
  sub_m <- sub |>
    select(trap_code, sp_name, abundance) |>
    pivot_wider(names_from = sp_name, values_from = abundance, values_fill = 0)
  sub_ta <- sub_m[, -1]                                                               # Remove

  # Calculate diversity indices
  SppRich <- specnumber(sub_ta)                                                       # Specie
  Simp <- diversity(sub_ta, index = "simpson")                                        # Simpso
  Shan <- diversity(sub_ta, index = "shannon")                                        # Shanno
  EvenJ <- Shan / log(SppRich)                                                        # Pielou
  E10 <- Shan / SppRich                                                               # Shanno
  Abund <- rowSums(sub_ta)                                                            # Total
  S_PIE <- calc_PIE(sub_ta, ENS = TRUE)                                               # Effect

  # Calculate species turnover metrics between years
  DATA1_Turnover <- codyn::turnover(sub,
    time.var = "year",
    species.var = "sp_name",
    abundance.var = "abundance",
    replicate.var = NA,
    metric = "total")                                                                # Total
  Turnover <- c("NA", DATA1_Turnover$total)                                          # Add N

  DATA1_Turnover_app <- codyn::turnover(sub,                                         # Speci
    time.var = "year",
    species.var = "sp_name",
    abundance.var = "abundance",
    replicate.var = NA,
    metric = "appearance")
  Turnover_app <- c("NA", DATA1_Turnover_app$appearance)

  DATA1_Turnover_disapp <- codyn::turnover(sub,                                      # Speci
    time.var = "year",
    species.var = "sp_name",
    abundance.var = "abundance",
    replicate.var = NA,
    metric = "disappearance")
  Turnover_disapp <- c("NA", DATA1_Turnover_disapp$disappearance)

  # Prepare data for rarefaction analysis
  sub_m_r <- sub |>
    select(trap_code, sp_name, ro.ab) |>
    pivot_wider(names_from = sp_name,
      values_from = ro.ab,
      values_fill = 0)                                                               # Creat
  sub_ta_r <- sub_m_r[, -1]                                                          # Remov

  # Calculate rarefied species richness
  rare.SppRich <- if (min(rowSums(sub_ta_r)) > 10) {
    rarefy(sub_ta_r, sample = min(rowSums(sub_ta_r)))
  } else {
    rarefy(sub_ta_r, sample = 10)
  }                                                                                  # If mi

  # Combine all calculated metrics into a data frame
  TD.i <- data.frame(sub_m$trap_code,
    SppRich,
    Simp,
    Shan,
    EvenJ,
    E10,
    Abund,
    S_PIE,
    Turnover,
    Turnover_app,
    Turnover_disapp,
    rare.SppRich)

  # Append results to main data frame
  TD <- rbind(TD, TD.i)

  # Clean up temporary variables to avoid conflicts in next iteration
  rm(TD.i, sub_m, sub_ta, sub, SppRich, Simp, Shan, EvenJ, E10, Abund, S_PIE,
    DATA1_Turnover, Turnover, DATA1_Turnover_app, Turnover_app,
    DATA1_Turnover_disapp, Turnover_disapp, sub_m_r, sub_ta_r, rare.SppRich)
}

# Clean up dataframe
TD <- TD |>
  as_tibble() |>                                                                     # Conve
  rename(trap_code = sub_m.trap_code) |>                                             # Fix c
  mutate(trap = gsub("_.*", "", trap_code),                                          # Remov
         year = gsub(".*_", "", trap_code)) |>                                       # Remov
  mutate(across(-c(trap_code, trap), as.numeric)) |>                                 # Conve
  select(trap_code, trap, year, everything()) |>                                     # Reord
  print()
```

```
# A tibble: 117 x 14
   trap_code trap   year SppRich  Simp  Shan EvenJ    E10 Abund S_PIE Turnover
   <chr>     <chr> <dbl>   <dbl> <dbl> <dbl> <dbl>  <dbl> <dbl> <dbl>    <dbl>
 1 A_1983    A      1983      42 0.866 2.43  0.650 0.0578 10727  7.45   NA    
 2 A_1984    A      1984      38 0.841 2.41  0.662 0.0634  9045  6.28    0.298
 3 A_1985    A      1985      41 0.748 2.11  0.567 0.0514 13255  3.96    0.319
 4 A_1986    A      1986      40 0.921 2.79  0.757 0.0698  6628 12.6     0.312
 5 A_1987    A      1987      41 0.923 2.79  0.751 0.0680 10873 12.9     0.312
 6 A_1988    A      1988      38 0.900 2.63  0.723 0.0692 13991  9.97    0.205
 7 A_1989    A      1989      39 0.280 0.828 0.226 0.0212 23568  1.39    0.289
 8 A_1990    A      1990      44 0.607 1.70  0.448 0.0385 15427  2.54    0.196
 9 A_1991    A      1991      39 0.578 1.60  0.436 0.0410 21045  2.37    0.271
10 A_1992    A      1992      37 0.826 2.19  0.608 0.0593 11607  5.74    0.233
```

```
# i 107 more rows
# i 3 more variables: Turnover_app <dbl>, Turnover_disapp <dbl>,
#   rare.SppRich <dbl>
```

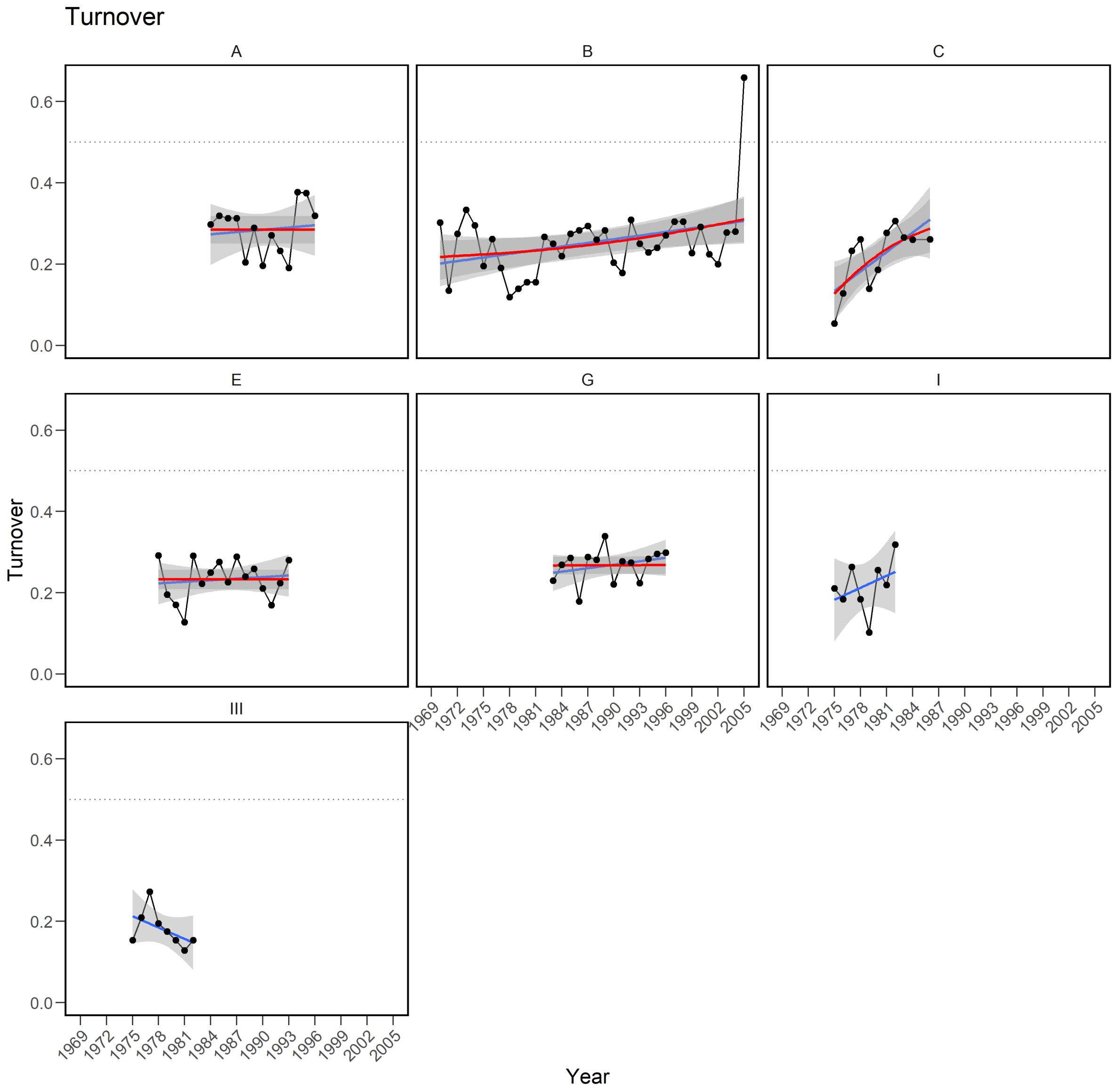
Plotting

Define plotting parameters

```
My_theme <- theme(panel.background = element_blank(),
                  panel.border = element_rect(fill = NA, linewidth = 1.25),
                  strip.background = element_rect(fill = "white",
                                                  color = "white", linewidth = 1.25),
                  legend.position = "bottom",
                  text = element_text(size = 16))
```

Turnover (total) by trap by year

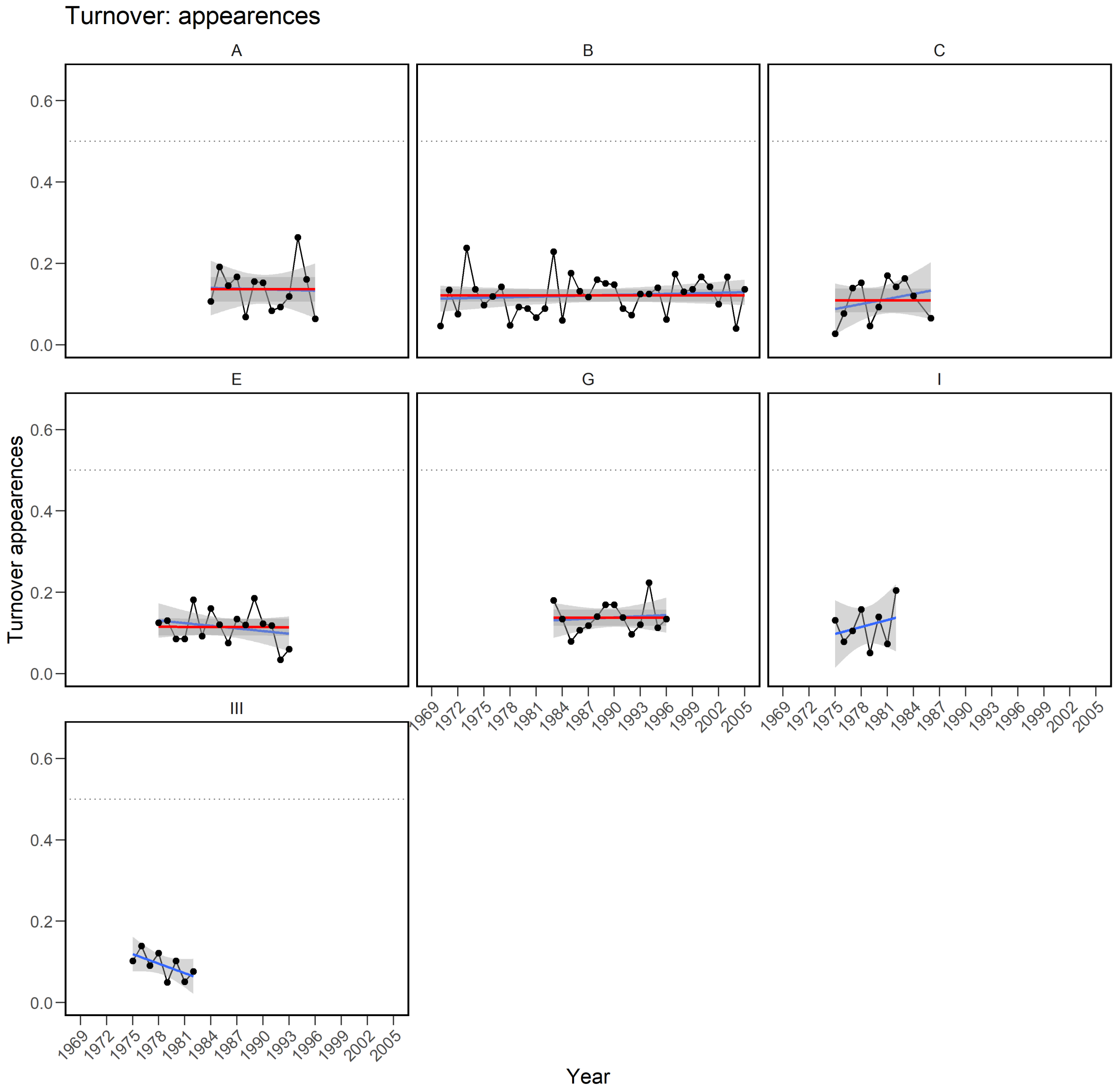
```
ggplot(TD |>
         group_by(trap) |>
         filter(n() > 3),
       aes(x = year, y = Turnover)) +
  geom_line() +
  geom_smooth(method = "lm") +
  geom_smooth(method = "gam", col = "red") +
  geom_point(size = 2) +
  geom_hline(yintercept = 0.5,
             linetype = "dotted",
             color = "grey50",
             size = 0.5) +
  facet_wrap(~trap) +
  scale_x_continuous(breaks = seq(min(TD$year), max(TD$year), by = 3)) +
  scale_y_continuous(limits = c(0, max(TD$Turnover, na.rm = TRUE))) +
  labs(title = "Turnover",
       x = "Year",
       y = "Turnover",
       caption = "Species turnover over time by trap") +
  My_theme +
  My_theme +
  theme(axis.text.x = element_text(angle = 45, hjust = 1),
        axis.ticks.length = unit(0.25, "cm"))
```



Species turnover over time by trap

Turnover (appearances) by trap by year

```r
ggplot(TD |>
         group_by(trap) |>
         filter(n() > 3),
       aes(x = year, y = Turnover_app)) +
  geom_line() +
  geom_smooth(method = "lm") +
  geom_smooth(method = "gam", col = "red") +
  geom_point(size = 2) +
  geom_hline(yintercept = 0.5,
             linetype = "dotted",
             color = "grey50",
             size = 0.5) +
  facet_wrap(~trap) +
  scale_x_continuous(breaks = seq(min(TD$year), max(TD$year), by = 3)) +
  scale_y_continuous(limits = c(0, max(TD$Turnover, na.rm = TRUE))) +
  labs(title = "Turnover: appearences",
       x = "Year",
       y = "Turnover appearences",
       caption = "Species appearences over time by trap") +
  My_theme +
  My_theme +
  theme(axis.text.x = element_text(angle = 45, hjust = 1),
        axis.ticks.length = unit(0.25, "cm"))
```

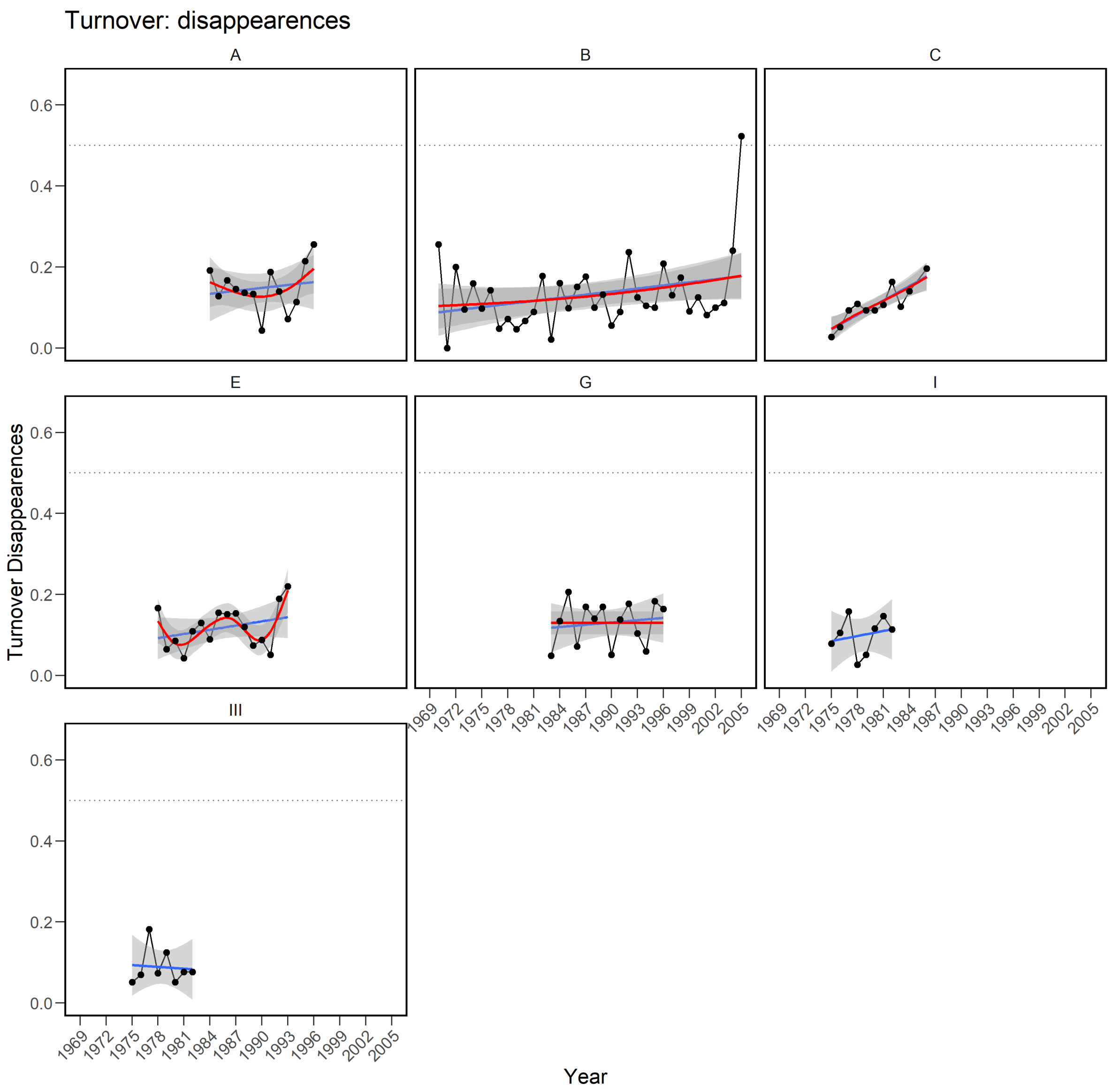


Species appearences over time by trap

Turnover (disappearances) by trap by year

```
ggplot(TD |>
         group_by(trap) |>
         filter(n() > 3),
       aes(x = year, y = Turnover_disapp)) +
  geom_line() +
```

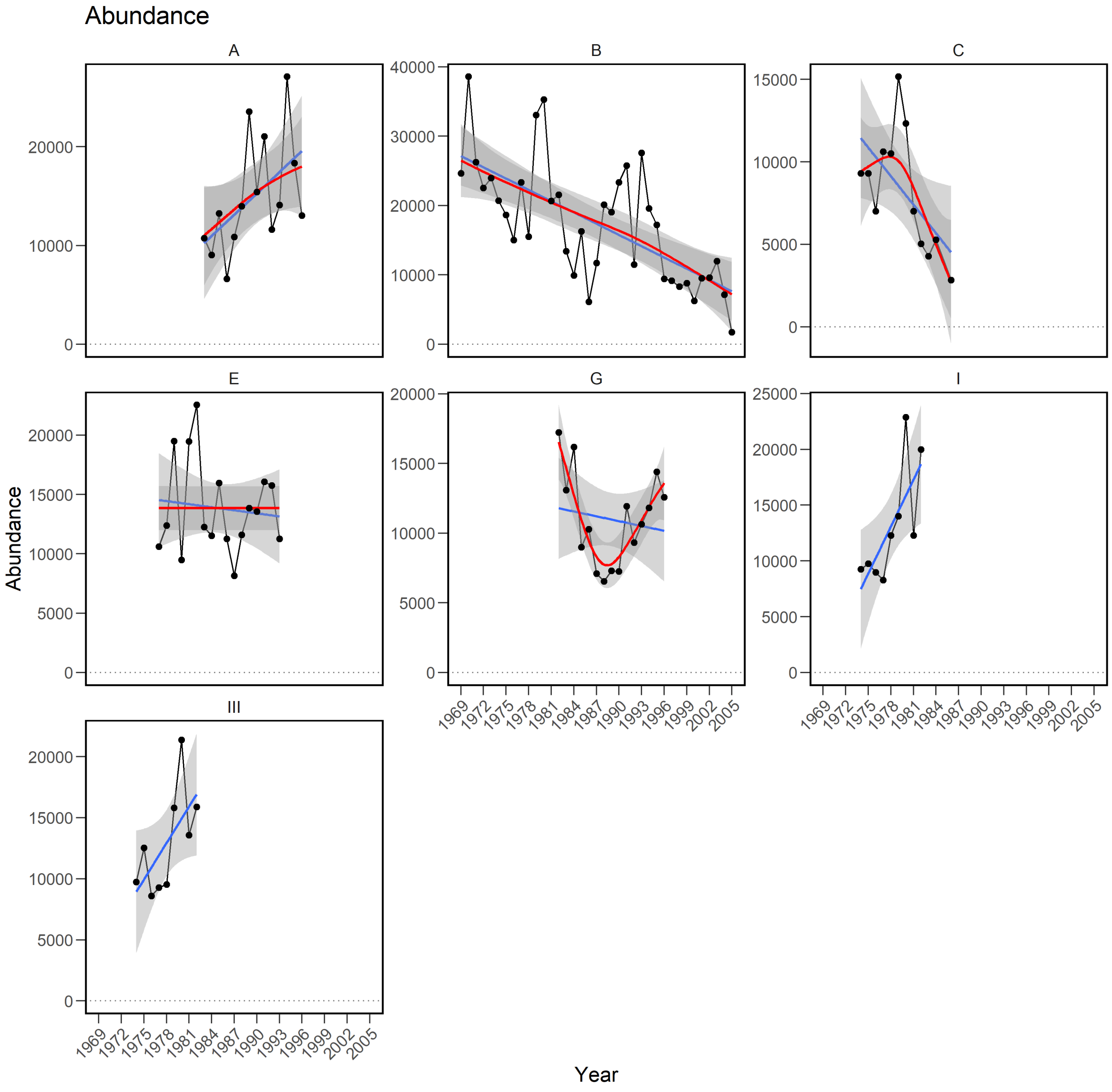
```r
  geom_smooth(method = "lm") +
  geom_smooth(method = "gam", col = "red") +
  geom_point(size = 2) +
  geom_hline(yintercept = 0.5,
             linetype = "dotted",
             color = "grey50",
             size = 0.5) +
  facet_wrap(~trap) +
  scale_x_continuous(breaks = seq(min(TD$year), max(TD$year), by = 3),
                     minor_breaks = seq(min(TD$year), max(TD$year), by = 1)) +
  scale_y_continuous(limits = c(0, max(TD$Turnover, na.rm = TRUE))) +
  labs(title = "Turnover: disappearences",
       x = "Year",
       y = "Turnover Disappearences",
       caption = "Species dissappearences through time by traps") +
  My_theme +
  My_theme +
  theme(axis.text.x = element_text(angle = 45, hjust = 1),
        axis.ticks.length = unit(0.25, "cm"))
```



Species dissappearences through time by traps

Abundance by trap by year

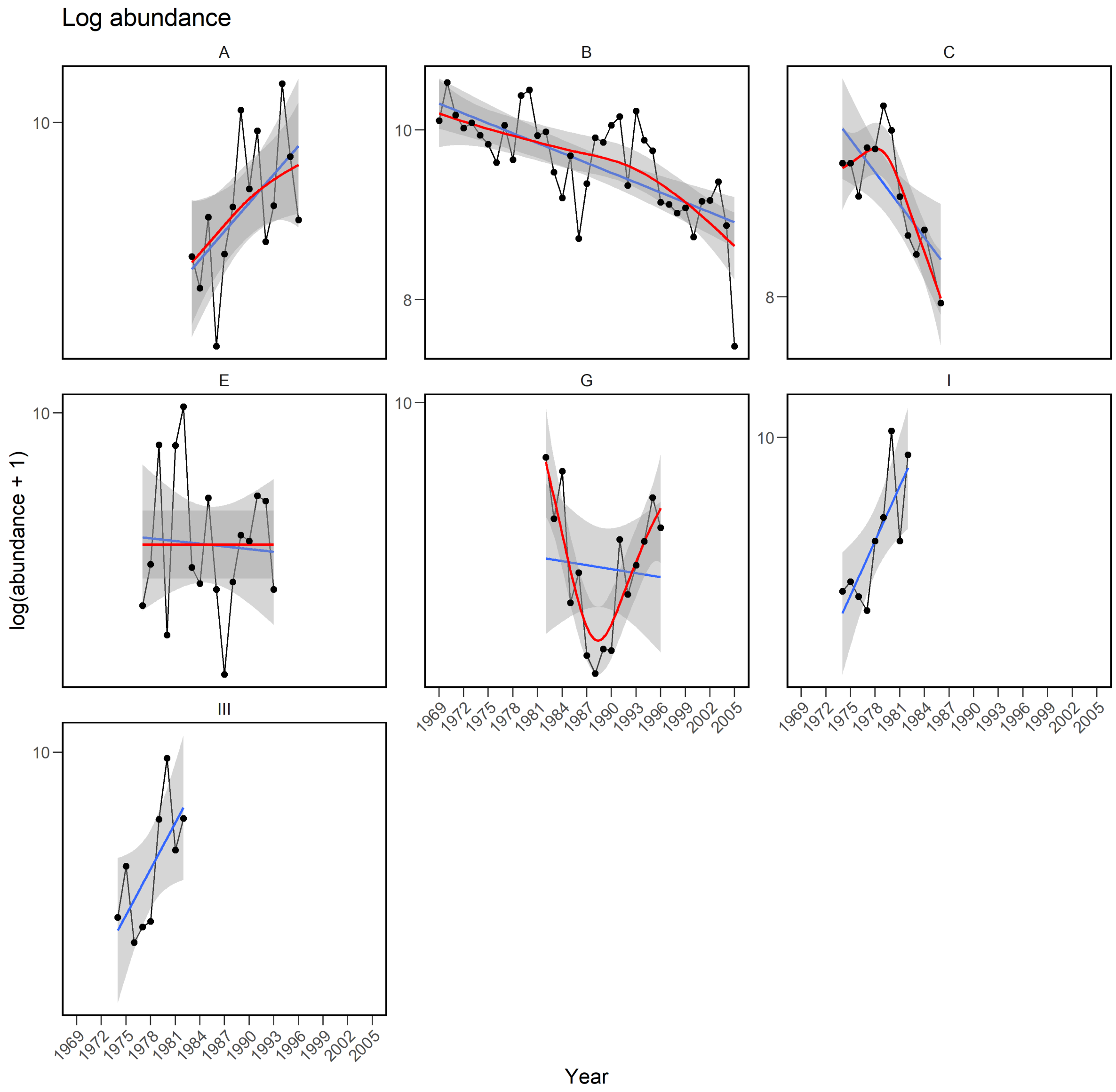
```
ggplot(TD |>
         group_by(trap) |>
         filter(n() > 3),
       aes(x = year, y = Abund)) +
  geom_line() +
  geom_smooth(method = "lm") +
  geom_smooth(method = "gam", col = "red") +
  geom_point(size = 2) +
  geom_hline(yintercept = 0.5,
             linetype = "dotted",
             color = "grey50",
             size = 0.5) +
  facet_wrap(~trap, scales = "free_y") +
  scale_x_continuous(breaks = seq(min(TD$year), max(TD$year), by = 3)) +
  labs(title = "Abundance",
       x = "Year",
       y = "Abundance",
       caption = "Abundance through time by trap") +
  My_theme +
  theme(axis.text.x = element_text(angle = 45, hjust = 1),
        axis.ticks.length = unit(0.25, "cm"))
```



Abundance through time by trap

Log abundance (log10 + 1) by trap by year

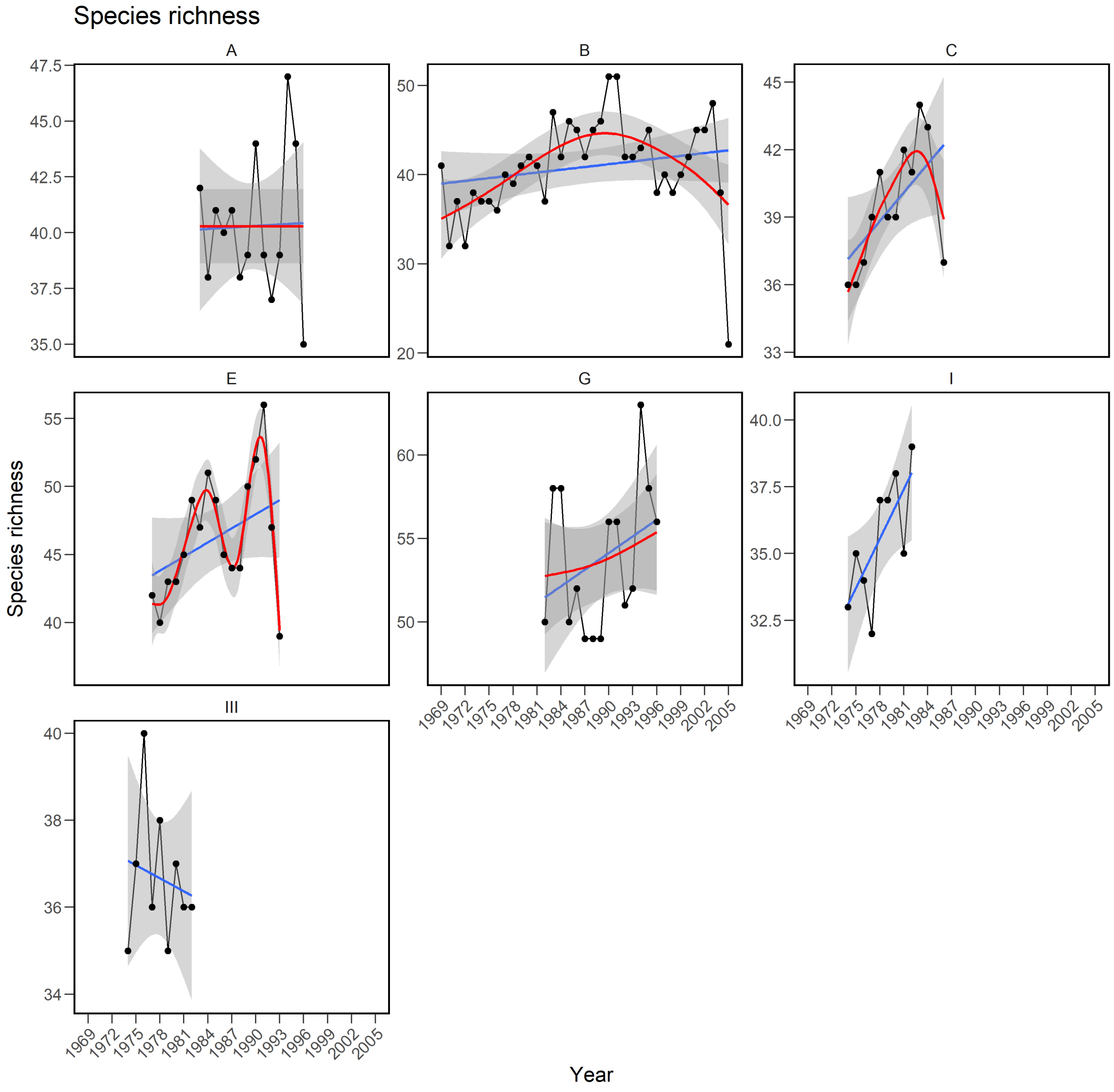
```
ggplot(TD |>
         group_by(trap) |>
         filter(n() > 3),
       aes(x = year, y = log(Abund + 1))) +
  geom_line() +
  geom_smooth(method = "lm") +
  geom_smooth(method = "gam", col = "red") +
  geom_point(size = 2) +
  # geom_hline(yintercept = 0.5,
  #             linetype = "dotted",
  #             color = "grey50",
  #             size = 0.5) +
  facet_wrap(~trap, scales = "free_y") +
  scale_y_continuous(breaks = seq(min(0), max(10), by = 2)) +
  scale_x_continuous(breaks = seq(min(TD$year), max(TD$year), by = 3)) +
  labs(title = "Log abundance",
       x = "Year",
       y = "log(abundance + 1)",
       caption = "Log abundance through time by trap") +
  My_theme +
  theme(axis.text.x = element_text(angle = 45, hjust = 1),
        axis.ticks.length = unit(0.25, "cm"))
```



Log abundance through time by trap

Species richness by trap by year

```
ggplot(TD |>
         group_by(trap) |>
         filter(n() > 3),
       aes(x = year, y = SppRich)) +
  geom_line() +
  geom_smooth(method = "lm") +
  geom_smooth(method = "gam", col = "red") +
  geom_point(size = 2) +
  # geom_hline(yintercept = 0.5,
  #            linetype = "dotted",
  #            color = "grey50",
  #            size = 0.5) +
  facet_wrap(~trap, scales = "free_y") +
  scale_x_continuous(breaks = seq(min(TD$year), max(TD$year), by = 3)) +
  labs(title = "Species richness",
       x = "Year",
       y = "Species richness",
       caption = "Species richness through time by trap") +
  My_theme +
  theme(axis.text.x = element_text(angle = 45, hjust = 1),
        axis.ticks.length = unit(0.25, "cm"))
```

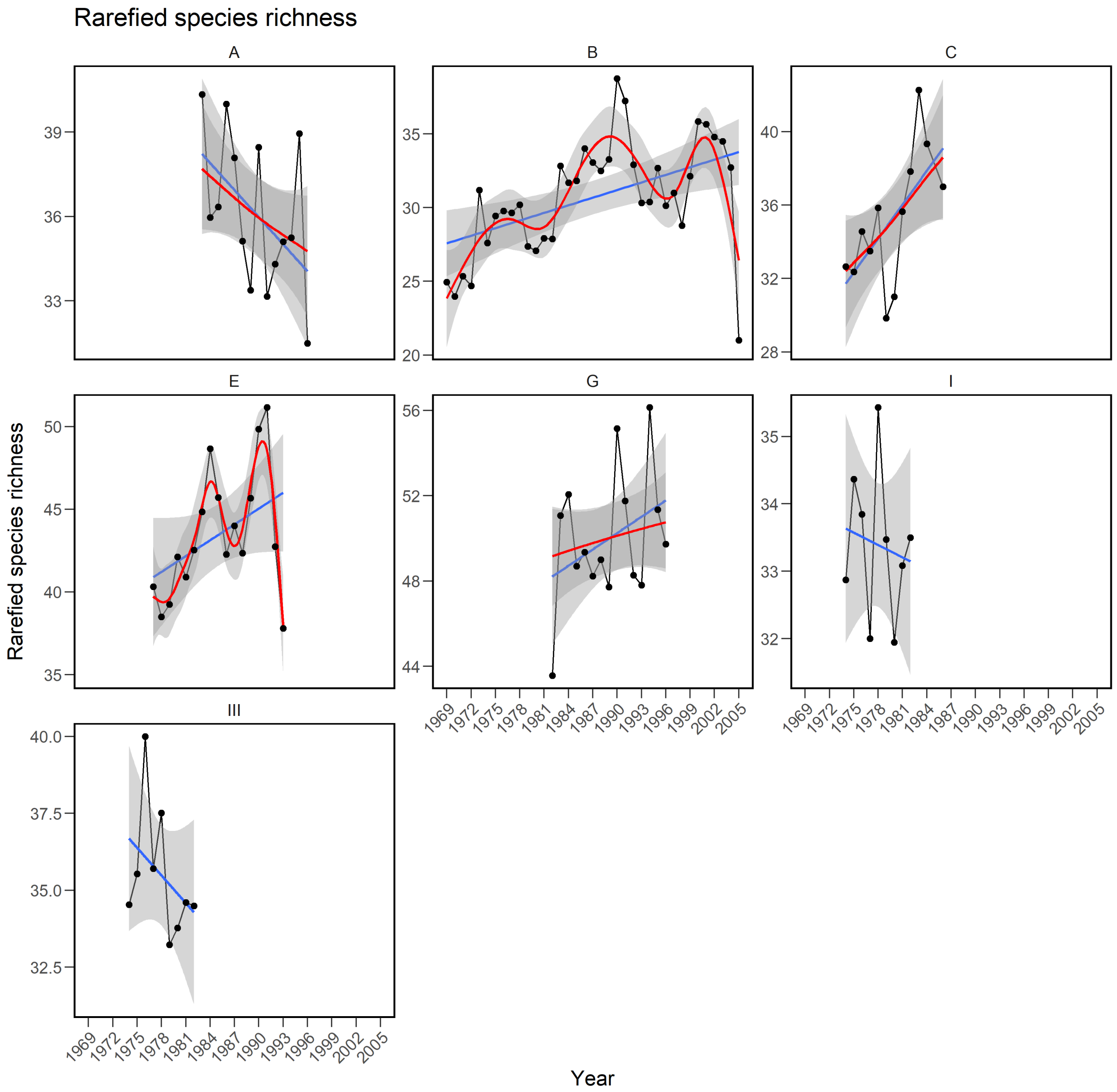


Species richness through time by trap

(Individual-based) rarefied species richness by trap by year

```
ggplot(TD |>
         group_by(trap) |>
         filter(n() > 3),
       aes(x = year, y = rare.SppRich)) +
  geom_line() +
```

```r
geom_smooth(method = "lm") +
geom_smooth(method = "gam", col = "red") +
geom_point(size = 2) +
# geom_hline(yintercept = 0.5,
#            linetype = "dotted",
#            color = "grey50",
#            size = 0.5) +
facet_wrap(~trap, scales = "free_y") +
scale_x_continuous(breaks = seq(min(TD$year), max(TD$year), by = 3)) +
labs(title = "Rarefied species richness",
     x = "Year",
     y = "Rarefied species richness",
     caption = "Rarefied species richness through time by trap") +
My_theme +
theme(axis.text.x = element_text(angle = 45, hjust = 1),
      axis.ticks.length = unit(0.25, "cm"))
```



Rarefied species richness through time by trap

Rarefaction accumulation curves

Calculation of rarefaction curves

```
# ept_wide_red <- ept_wide |>
#   select(-O, -F) |>
#   column_to_rownames(var = "sp_name") |>
#   data.frame() |>
#   print()                                                                              # re
# ept_cum.rare = iNEXT(ept_wide_red, q = 0, datatype = "abundance")                      # ca
# write_rds(ept_cum.rare, "Outputs/rarefaction_ept.rds")                                 # sa
ept_cum.rare <- readRDS("Outputs/rarefaction_ept.rds")                                    # I
```

Check outputs

Basic information

```
ept_cum.rare$DataInfo
```

```
  Assemblage      n S.obs     SC f1 f2 f3 f4 f5 f6 f7 f8 f9 f10
1          A 208785    76 0.9999 15  3  4  2  1  1  2  0  2   1
2          B 643183    90 1.0000 10  6  4  2  4  3  1  1  2   0
3          C  98689    62 0.9999  8  3  1  0  3  3  1  1  0   1
4          E 235327    82 1.0000  9  5  3  4  3  0  1  0  1   2
5          G 164752    98 0.9999 14  8  4  3  0  0  1  1  1   3
6          I 117690    51 1.0000  4  1  2  0  2  0  1  0  2   1
7        III 116367    53 0.9999  9  2  1  0  0  0  0  0  1   0
```

Asymptotic diversity estimates.

```
ept_cum.rare$AsyEst
```

```
   Assemblage         Diversity  Observed  Estimator        s.e.       LCL
1           A  Species richness 76.000000 113.499820 32.38616209 76.000000
2           A Shannon diversity 10.405706  10.408437  0.03385415 10.342084
3           A Simpson diversity  4.672479   4.672561  0.01883733  4.635641
4           B  Species richness 90.000000  98.333320 15.28568549 90.000000
5           B Shannon diversity 13.911444  13.912549  0.02211145 13.869212
6           B Simpson diversity  8.665258   8.665362  0.01815118  8.629786
7           C  Species richness 62.000000  72.666559 11.02675067 62.000000
8           C Shannon diversity 11.487524  11.491853  0.04148104 11.410551
9           C Simpson diversity  6.843397   6.843803  0.02882696  6.787303
10          E  Species richness 82.000000  90.099966 15.85769142 82.000000
11          E Shannon diversity 14.329372  14.332216  0.03172515 14.270035
12          E Simpson diversity  8.771143   8.771433  0.02273724  8.726869
```

```
13          G  Species richness 98.000000 110.249926 11.36512898 98.000000
14          G Shannon diversity 16.870192  16.876113  0.03774784 16.802129
15          G Simpson diversity 11.352314  11.353027  0.02601256 11.302043
16          I  Species richness 51.000000  58.999932  7.64742890 51.000000
17          I Shannon diversity  7.898695   7.900656  0.02933911  7.843153
18          I Simpson diversity  4.698134   4.698282  0.01506555  4.668754
19        III  Species richness 53.000000  73.249826 18.18244064 53.000000
20        III Shannon diversity 10.343251  10.346428  0.03796313 10.272022
21        III Simpson diversity  6.147374   6.147646  0.02672641  6.095263
          UCL
1  176.975532
2   10.474790
3    4.709482
4  128.292713
5   13.955887
6    8.700937
7   94.278593
8   11.573154
9    6.900302
10 121.180470
11  14.394396
12   8.815997
13 132.525169
14  16.950098
15  11.404011
16  73.988617
17   7.958160
18   4.727810
19 108.886755
20  10.420834
21   6.200028
```

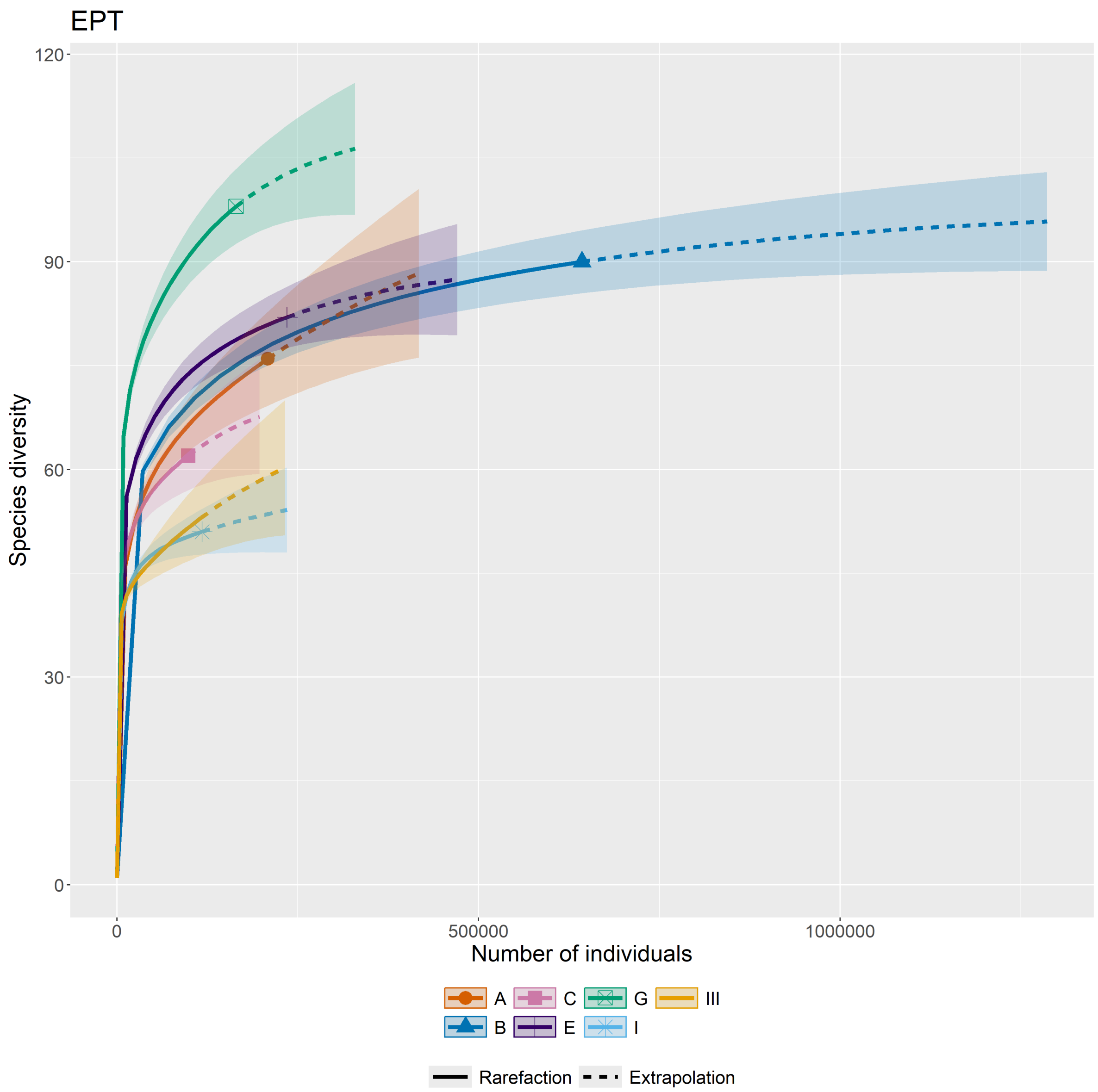
Plotting

Plotting parameters

```
My_theme <- theme(panel.background = element_blank(),
                  panel.border = element_rect(fill = NA, linewidth = 1.25),
                  strip.background = element_rect(fill = "white",
                                                  color = "white", linewidth = 1.25),
                  legend.position = "right",
                  text = element_text(size = 16),
                  axis.text.x = element_text(angle = 45, hjust = 1))
```

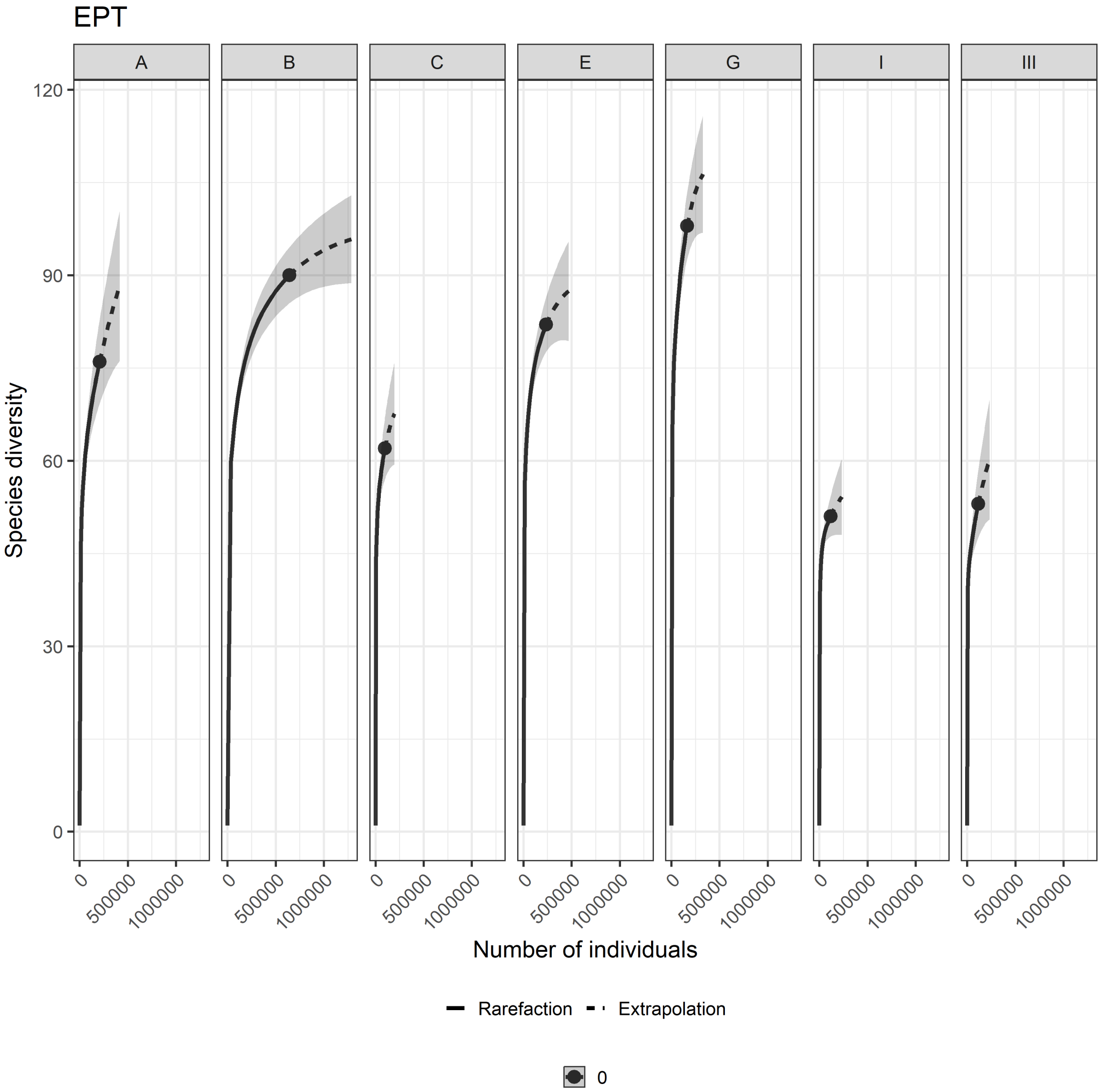
All accumulation curves in one plot

```
options(scipen = 999) # Increase penalty to avoid scientific notation
ept_p <- ggiNEXT(ept_cum.rare, type = 1, color.var = "Assemblage")
ept_p <- ept_p + ggtitle("EPT")
ept_p <- ept_p + theme(legend.position = "bottom")
ept_p
```



Accumulation curves in separate plots

```
options(scipen = 999) # Increase penalty to avoid scientific notation
ept_p1 <- ggiNEXT(ept_cum.rare, facet.var = "Assemblage", grey = T)
ept_p1 <- ept_p1 + ggtitle("EPT")
ept_p1 <- ept_p1 + theme(axis.text.x = element_text(angle = 45, hjust = 1), legend.position =
ept_p1
```


EPT
A
B
C
E
G
I
III
120
90
60
30
0
Species diversity
0
500000
1000000
Number of individuals
Rarefaction
Extrapolation
0