Using DFAclust to analyse bird indices

Load R package

```r
library(DFAclust)
#> Le chargement a nécessité le package : TMB
#> Le chargement a nécessité le package : RcppEigen
```

Empirical data: preparing data from raw monitoring data

The following empirical example corresponds to the empirical analysis in the paper related to this R package. Preparation of the data from the raw data are not in the scope of the package, this is why required packages have to be loaded first. The user can skip this part as the ready-to-use data are already available in the package (i.e. start the vignette at *Empirical data: analysing data*).

Load additionnal R packages

```r

require(stringr)
#> Le chargement a nécessité le package : stringr
require(rnaturalearth)
#> Le chargement a nécessité le package : rnaturalearth
require(sp)
#> Le chargement a nécessité le package : sp
require(ggplot2)
#> Le chargement a nécessité le package : ggplot2
require(reshape2)
#> Le chargement a nécessité le package : reshape2
require(plyr)
#> Le chargement a nécessité le package : plyr
require(dplyr)
#> Le chargement a nécessité le package : dplyr
#>
#> Attachement du package : 'dplyr'
#> Les objets suivants sont masqués depuis 'package:plyr':
#>
#>     arrange, count, desc, failwith, id, mutate, rename, summarise,
#>     summarize
#> Les objets suivants sont masqués depuis 'package:stats':
#>
#>     filter, lag
#> Les objets suivants sont masqués depuis 'package:base':
#>
#>     intersect, setdiff, setequal, union
require(emmeans)
#> Le chargement a nécessité le package : emmeans
require(arm)
#> Le chargement a nécessité le package : arm
#> Le chargement a nécessité le package : MASS
#>
#> Attachement du package : 'MASS'
#> L'objet suivant est masqué depuis 'package:dplyr':
#>
#>     select
#> Le chargement a nécessité le package : Matrix
#> Le chargement a nécessité le package : lme4
#>
#> arm (Version 1.13-1, built: 2022-8-25)
#> Working directory is /home/stanislas/Documents/Gitlab_dossier/DFAclust/vignettes
require(see)
#> Le chargement a nécessité le package : see
```

Load and prepare data

Bird data

Download and extract data

Breeding bird data for Sweden can be download from https://www.gbif.org/occurrence/download?dataset_key=91fa1a0d-a208-40aa-8a6e-f2c0beb9b253 (an free account is necessary). Type of download: Darwin Core Archive. This will provide you a text file: “occurrence.txt”.

```
bird_se_raw <- read.csv("raw_data/occurrence.txt", header = T, sep="\t")
```

Subselecting and preparing data

We select columns and row of interest (i.e. birds).

```
bird_se_clean <- bird_se_raw[bird_se_raw$class=="Aves",c("class","order","family",
        "genus","species",

        "specificEpithet","infraspecificEpithet","taxonRank",

        "organismQuantity","decimalLatitude","decimalLongitude",

        "day","month","year","taxonKey","speciesKey","countryCode",

        "level1Gid","level2Gid","iucnRedListCategory")]
```

We add a code by species from species name and check for duplicate in species’ code. The link between species name and species name code is stored in a specific dataset `species_data`.

```
species_data <- data.frame(name_long = unique(bird_se_clean$species[bird_se_clean$taxonRank !=
        "GENUS"]))

species_data$code_sp <- paste0(toupper(substr(species_data$name_long, 1, 3)),
                               toupper(substr(sub(".* ", "", species_data$name_long), 1, 3)))

species_data$code_sp[species_data$name_long=="Corvus corax"] <- "CORCOX"

species_data$code_sp[species_data$name_long=="Phylloscopus trochilus"] <- "PHYTRU"

species_data$code_sp[species_data$name_long=="Saxicola rubicola"] <- "SAXRUI"

species_data$code_sp[species_data$name_long=="Sterna paradisaea"] <- "STEPAD"

species_data$genus <- sub(" .*", "", species_data$name_long)

species_data$species <- sub(".* ", "", species_data$name_long)

bird_se_clean <- merge(bird_se_clean, species_data[,c("code_sp", "name_long")],
                                by.x = c("species"), by.y = c("name_long"), all.x = T)

species_data$class <- bird_se_clean$class[match(species_data$code_sp, bird_se_clean$code_sp)]

species_data$order <- bird_se_clean$order[match(species_data$code_sp, bird_se_clean$code_sp)]

species_data$family <- bird_se_clean$family[match(species_data$code_sp, bird_se_clean$code_sp)]

species_data$iucnRedListCategory <-
        bird_se_clean$iucnRedListCategory[match(species_data$code_sp, bird_se_clean$code_sp)]
```

Geographical coordinates and routes

We prepare a specific dataset for coordinates of monitored routes by linking route numbers to their coordinates.

```
route_data <- paste0(bird_se_clean$decimalLatitude, sep="_", bird_se_clean$decimalLongitude)

route_data <- data.frame(code_route = paste0("R",str_pad(1:length(unique(route_data)), 3, pad =
        "0")),
                          coordinate_chr = unique(route_data))

route_data$lat <- as.numeric(sub("_.*", "", route_data$coordinate_chr))

route_data$lon <- as.numeric(sub(".*_", "", route_data$coordinate_chr))
```

We can then display route location on the map.

```
worldmap <- ne_countries(scale = 'medium', type = 'countries',returnclass = 'sf')

sweden_map_wgs84 <- worldmap[worldmap$sovereign=="Sweden",]

sweden_map_moll <- sf::st_transform(sweden_map_wgs84, "+proj=moll")

sweden_map_swe <- sf::st_transform(sweden_map_wgs84, "+init=epsg:3006")

route_data_coord <- route_data

coordinates(route_data_coord) <- ~lon+lat

proj4string(route_data_coord) <- CRS("+proj=longlat +datum=WGS84")

route_data_coord <- spTransform(route_data_coord, CRSobj = "+proj=moll")

route_data_moll <- as.data.frame(coordinates(route_data_coord))

route_data_moll$code_route <- route_data_coord$code_route

route_data_coord <- spTransform(route_data_coord, CRSobj = "+init=epsg:3006")

route_data_swe <- as.data.frame(coordinates(route_data_coord))

route_data_swe$code_route <- route_data_coord$code_route

ggplot() + geom_sf(data=sweden_map_swe) +
  geom_tile(data = route_data_swe, aes(x=lon, y=lat), width=25000, height=25000, alpha=0.5) +
  theme_void() + coord_sf(datum=NA)
```

We aggregate all the projections into on dataset.

```
route_data <- merge(route_data, route_data_moll, by="code_route", all=T)

route_data <- merge(route_data, route_data_swe, by="code_route", all=T)

names(route_data)[3:8] <- c("lat_wgs", "lon_wgs", "lon_moll", "lat_moll", "lon_swe", "lat_swe")

route_data$coordinate_chr <- NULL
```

We finally associate routes and coordinates with the main dataset on bird occurrence.

```
bird_se_clean <- merge(bird_se_clean, route_data[,c("code_route", "lat_wgs", "lon_wgs")],
                        by.x = c("decimalLatitude", "decimalLongitude"), by.y = c("lat_wgs",
        "lon_wgs"), all.x = T)

route_data$level1Gid <- bird_se_clean$level1Gid[match(route_data$code_route,
        bird_se_clean$code_route)]

route_data$level2Gid <- bird_se_clean$level2Gid[match(route_data$code_route,
        bird_se_clean$code_route)]
```

Finalise bird dataset

We need to incorporate 0s in the dataset when, a given year, a species was not present while the route was monitored.

```
bird_se_clean_tot <- dcast(bird_se_clean, countryCode+code_route+year~code_sp,
                           fun.aggregate = sum, value.var="organismQuantity")

bird_se <- melt(bird_se_clean_tot, id.vars = c("countryCode", "code_route", "year"))

names(bird_se)[4:5] <- c("code_sp", "abund")

bird_se$code_sp <- as.character(bird_se$code_sp)

bird_se <- bird_se[bird_se$code_sp!="NA",]
```

We add information on geographical coordinate and taxa in the final dataset `bird_se`.

```
bird_se <- merge(bird_se, route_data, by="code_route", all.x = T)

bird_se$order <- species_data$order[match(bird_se$code_sp, species_data$code_sp)]

bird_se$family <- species_data$family[match(bird_se$code_sp, species_data$code_sp)]

bird_se$genus <- species_data$genus[match(bird_se$code_sp, species_data$code_sp)]

bird_se$species <- species_data$species[match(bird_se$code_sp, species_data$code_sp)]

bird_se$name_long <- species_data$name_long[match(bird_se$code_sp, species_data$code_sp)]

bird_se$iucnRedListCategory <- species_data$iucnRedListCategory[match(bird_se$code_sp,
        species_data$code_sp)]
```

Estimate species time-series

Now that the data are ready, we can estimate species time-series and standard errors of these time-series.

Select period of time

We first remove data from the first two years of the survey (1996 and 1997) because there was a low number of routes monitored in 1996 and 1997.

```
bird_se_1998 <- droplevels(bird_se[bird_se$year>1997,])
```

Compute species time series

As we said above about the additional packages that needed to be loaded, it is not in the scope of this R package to obtain time-series from raw data and the user will normally have usable time-series. So we need to specify here an additional function adapted from the French Breeding Bird Survey analysis https://www.vigienature.fr/sites/vigienature/files/atoms/files/analysestoceps_0.zip) to estimate time-series from bird abundance data.

```
get_ts <- function(data_bird_input){

  # d: data for species i

  d <- droplevels(data_bird_input)

  sp <- levels(as.factor(d$code_sp))

  # number of route followed by year

  nb_route <- tapply(rep(1,nrow(d)),d$year,sum)

  # number of route with species i by year

  nb_route_presence <- tapply(ifelse(d$abund>0,1,0),d$year,sum)

  year <- as.numeric(as.character(levels(as.factor(d$year))))

  firstY <- min(year)

  lastY <- max(year)

  timestep <- length(year)-1

  # table for analysis result

  threshold_occurrence <- 3

  tab_ana <- data.frame(year=rep(year,2),val=c(nb_route,nb_route_presence),LL = NA,UL=NA,
                        catPoint=NA,pval=NA,
                        curve=rep(c("route","presence"),each=length(year)))

  tab_ana$catPoint <- ifelse(tab_ana$val == 0,"0", ifelse(tab_ana$val < threshold_occurrence,
                                                          "inf_threshold",NA))


  # abundance by year

  abund <- tapply(d$abund,d$year,sum)
```

```r
threshold_abundance <- 5

tab_fig <- data.frame(year=year,val=abund,LL = NA,UL=NA,catPoint=NA,pval=NA)

tab_fig$catPoint <- ifelse(tab_fig$val == 0,"0",ifelse(tab_fig$val < threshold_abundance,
                                                       "inf_threshold",NA))

# remove criteria

remove_sp <- FALSE

# if first year empty

if(tab_fig$val[1]==0){remove_sp <- TRUE}

# if four consecutive years empty

ab_vec <- paste(tab_fig$val,collapse="")

if(str_detect(ab_vec, "0000")){remove_sp <- TRUE}

# if less than three consecutive years

ab_vec2 <- paste(sign(tab_fig$val),collapse="")

if(!str_detect(ab_vec2, "111")){remove_sp <- TRUE}

if(anyNA(tab_fig$catPoint) & anyNA(tab_ana$catPoint[tab_ana$curve=="presence"]) &
      remove_sp==F){

  # GLM abundance variation
  glm1 <- glm(abund~as.factor(code_route)+as.factor(year),data=d,family=quasipoisson)

  sglm1 <- summary(glm1)

  # mean-centered values

  con.mat <- diag(length(year)) - 1/length(year)

  colnames(con.mat) <- year # firstY:lastY

  rg <- ref_grid(glm1, nuisance = 'code_route')

  sglm2 <- summary(contrast(rg, as.data.frame(con.mat)))

  # as link function is log, estimates need to be back transformed from sglm1 (first year set
      to 1 and se to 0)

  coef_yr <- tail(matrix(sglm1$coefficients[,1]), timestep)

  coef_yr <- rbind(1, exp(coef_yr))

  error_yr <- tail(matrix(sglm1$coefficients[,2]), timestep)

  error_yr <- rbind(0, error_yr)*coef_yr # approximated se values

  log_error_yr <- tail(matrix(sglm1$coefficients[,2]), timestep)

  log_error_yr <- rbind(0, log_error_yr)

  pval <- c(1,tail(matrix(coefficients(sglm1)[,4]),timestep))
```

```r
# from sglm2 (mean value to 0)

coef_yr_m0 <- exp(sglm2$estimate)

error_yr_m0 <- sglm2$SE*coef_yr_m0 # approximated se values

log_error_yr_m0 <- sglm2$SE

pval_m0 <- sglm2$p.value

# CIs

glm1.sim <- sim(glm1)

ci_inf_sim <- c(1, exp(tail(apply(coef(glm1.sim),2, quantile, .025), timestep)))

ci_sup_sim <- c(1, exp(tail(apply(coef(glm1.sim),2, quantile, .975), timestep)))

thresold_signif <- 0.05

tab_res <- data.frame(year,val=coef_yr,val_m0=coef_yr_m0,
                      LL=ci_inf_sim,UL=ci_sup_sim,
                      catPoint=ifelse(pval<thresold_signif,"significatif",NA),pval)

# cleaning out of range CIs

tab_res$UL <- ifelse(nb_route_presence==0,NA,tab_res$UL)

tab_res$UL <-  ifelse(tab_res$UL == Inf, NA,tab_res$UL)

tab_res$UL <-  ifelse(tab_res$UL > 1.000000e+20, NA,tab_res$UL)

tab_res$UL[1] <- 1

tab_res$val <-  ifelse(tab_res$val > 1.000000e+20,1.000000e+20,tab_res$val)

tab_res$val_m0 <-  ifelse(tab_res$val_m0 > 1.000000e+20,1.000000e+20,tab_res$val_m0)

# overdispersion index
dispAn <- sglm1$deviance/sglm1$null.deviance

# class uncertainity

if(dispAn > 2 | (median(nb_route_presence)<threshold_occurrence &
    median(abund)<threshold_abundance)) catIncert <- "Uncertain" else catIncert <-"Good"

vecLib <-  NULL

if(dispAn > 2 | median(nb_route_presence)<threshold_occurrence) {

  if(median(nb_route_presence)<threshold_occurrence) {

        vecLib <- c(vecLib,"too rare species")

      }

  if(dispAn > 2) {

     vecLib <- c(vecLib,"deviance")
```

```
        }
      }

      reason_uncert <-  paste(vecLib,collapse=" and ")

      # Store results

      tab_tot <- data.frame(code_sp=sp, year = tab_res$year, nb_year=timestep,
                            firstY = firstY, lastY = lastY,
                            relative_abundance = tab_res$val,
                            CI_inf = tab_res$LL, CI_sup = tab_res$UL,
                            Standard_error = error_yr,
                            Log_SE = log_error_yr,
                            p_value = tab_res$pval,
                            relative_abundance_m0 = tab_res$val_m0,
                            Standard_error_m0 = error_yr_m0,
                            Log_SE_m0 = log_error_yr_m0,
                            p_value_m0 = pval_m0, signif = !is.na(tab_res$catPoint),
                            nb_route,nb_route_presence,abundance=abund,
                            mediane_occurrence=median(nb_route_presence),
        mediane_ab=median(abund) ,
                            valid = catIncert, uncertanity_reason = reason_uncert)

    }
    else{
      tab_tot <- data.frame(code_sp=sp, year = year, nb_year=timestep,
                            firstY=firstY, lastY=lastY,
                            relative_abundance=NA,
                            CI_inf = NA, CI_sup = NA,
                            Standard_error = NA,
                            p_value = NA,
                            relative_abundance_m0 = NA,
                            Standard_error_m0 = NA,
                            Log_SE_m0 = NA,
                            p_value_m0 = NA,signif = NA,
                            nb_route,nb_route_presence,abundance=abund,
                            mediane_occurrence=median(nb_route_presence),
        mediane_ab=median(abund) ,
                            valid = NA, uncertanity_reason = NA)
    }

    return(tab_tot)
  }
```

We can now compute time-series between 1998 and 2020 for each species in the Swedish Breeding Bird Survey.

```
ts_bird_se_allcountry <- ddply(bird_se_1998, .(code_sp), .fun=get_ts, .progress="text")
```

We can then check, by plotting the estimated time-series, if they are similar to the one produced by the official institution in charge in Sweden Svensk fageltaxering (https://www.fageltaxering.lu.se/resultat/trender).

```
for(i in 1:length(levels(as.factor(bird_se$code_sp)))){

  sp <- levels(as.factor(ts_bird_se_allcountry$code_sp))[i]

  gp <- ggplot(ts_bird_se_allcountry[ts_bird_se_allcountry$code_sp==sp,],
         aes(year, relative_abundance)) + geom_line() + geom_text(x=2010, y=1, label=sp) +
    geom_line(aes(y=CI_inf), linetype="dashed") +
    geom_line(aes(y=CI_sup), linetype="dashed") +
    ylab("Relative abundance") + xlab("Years") +
    theme_modern()

  print(gp)

}
```

Those data (species time-series, their log standrard errors and species names) are already available in the package. Let's load them.

```
data(ts_bird_se_allcountry)
data(species_data)
```

Empirical data: preparing data from PECBMS national indices

Instead of reconstructing time-series from monitoring data, the user may want to use national indices already processed using TRIM. Here are the step to go from PECBMS national indices to `species_ts_mat` and `species_uncert_ts_mat` used in README.

Load data from PECBMS

```
require(data.table)
#> Le chargement a nécessité le package : data.table
#>
#> Attachement du package : 'data.table'
#> Les objets suivants sont masqués depuis 'package:dplyr':
#>
#>     between, first, last
#> Les objets suivants sont masqués depuis 'package:reshape2':
#>
#>     dcast, melt
require(stringr)
require(dplyr)

# Load national indices

df <- data.table::fread('https://zenodo.org/record/4590199/files/national_indices2017.csv?
        download=1')
```

Prepare data format

```
# Pass from wide to long format

df <- data.table::melt(df, id.vars = c("species","euring_code","scheme","type"))
df <- data.table::dcast(data = df, formula = species + euring_code + scheme + variable ~ type,
        fun.aggregate = sum)
df <- df[,c("euring_code","species","scheme","variable","index","se")]
names(df) <- c("Code","Species","CountryGroup","Year","Index","Index_SE")
df <- droplevels(na.omit(df))
df$Species <- as.factor(df$Species)
df$CountryGroup <- as.factor(df$CountryGroup)
df$Year <- as.numeric(as.character(df$Year))
```

```r
# Get species and country names

S <- levels(df$Species)
C <- levels(df$CountryGroup)

# Update species names

df$Species <- as.character(df$Species)
df$Species[df$Species=="Bonasa bonasia"] <- "Tetrastes bonasia"
df$Species[df$Species=="Carduelis cannabina"] <- "Linaria cannabina"
df$Species[df$Species=="Carduelis chloris"] <- "Chloris chloris"
df$Species[df$Species=="Carduelis flammea"] <- "Acanthis flammea"
df$Species[df$Species=="Carduelis spinus"] <- "Spinus spinus"
df_cornix <- df[df$Species=="Corvus corone+cornix",]
df$Species[df$Species=="Corvus corone+cornix"] <- "Corvus corone"
df_cornix$Species[df_cornix$Species=="Corvus corone+cornix"] <- "Corvus cornix"
df <- rbind(df,df_cornix)
df$Species[df$Species=="Corvus monedula"] <- "Coloeus monedula"
df$Species[df$Species=="Delichon urbica"] <- "Delichon urbicum"
df$Species[df$Species=="Dendrocopos medius"] <- "Dendrocoptes medius"
df$Species[df$Species=="Dendrocopos minor"] <- "Dryobates minor"
df$Species[df$Species=="Hippolais pallida"] <- "Iduna pallida"
df$Species[df$Species=="Hirundo daurica"] <- "Cecropis daurica"
df$Species[df$Species=="Hirundo rupestris"] <- "Ptyonoprogne rupestris"
df$Species[df$Species=="Larus ridibundus"] <- "Chroicocephalus ridibundus"
df$Species[df$Species=="Miliaria calandra"] <- "Emberiza calandra"
df$Species[df$Species=="Parus ater"] <- "Periparus ater"
df$Species[df$Species=="Parus caeruleus"] <- "Cyanistes caeruleus"
df$Species[df$Species=="Parus cristatus"] <- "Lophophanes cristatus"
df$Species[df$Species=="Parus montanus"] <- "Poecile montanus"
df$Species[df$Species=="Parus palustris"] <- "Poecile palustris"
df$Species[df$Species=="Saxicola torquata"] <- "Saxicola torquatus"
df$Species[df$Species=="Serinus citrinella"] <- "Carduelis citrinella"
df$Species[df$Species=="Sylvia cantillans"] <- "Curruca cantillans"
df$Species[df$Species=="Sylvia communis"] <- "Curruca communis"
df$Species[df$Species=="Sylvia curruca"] <- "Curruca curruca"
df$Species[df$Species=="Sylvia hortensis"] <- "Curruca hortensis"
df$Species[df$Species=="Sylvia melanocephala"] <- "Curruca melanocephala"
df$Species[df$Species=="Sylvia melanothorax"] <- "Curruca melanothorax"
df$Species[df$Species=="Sylvia nisoria"] <- "Curruca nisoria"
df$Species[df$Species=="Sylvia undata"] <- "Curruca undata"
df$Species[df$Species=="Tetrao tetrix"] <- "Lyrurus tetrix"
df$Species <- as.factor(df$Species)


# Update species code format

df$Code <- as.character(df$Code)
df$Code <- stringr::str_pad(df$Code, width = 5, pad = "0")
df$Code <- paste0("sp_", df$Code)

species_all <- data.frame(dplyr::summarise(.data=dplyr::group_by(.data=df,Code, Species),
        count=dplyr::n()))
#> `summarise()` has grouped output by 'Code'. You can override using the
#> `.groups` argument.
species_all$count <- NULL

df_all_country <- df
```

```
names(df_all_country)[1] <- names(species_all)[1] <- "code_sp"
names(species_all)[2] <- "name_long"
```

Get data for farmland birds in Czech Republic

```
# Select Czech Republic data

df_all_country_2000 <- droplevels(df_all_country[which(df_all_country$CountryGroup == "Czech
        Republic"),])



# List of species from https://www.tandfonline.com/doi/abs/10.1080/00063657.2015.1048423

species_cze_farm  <- data.frame(name_long=c("Hirundo rustica","Corvus corone","Curruca
        communis","Falco tinnunculus",
                                    "Linaria cannabina","Sturnus vulgaris","Pica
        pica","Carduelis carduelis",
                                    "Chloris chloris","Coloeus monedula","Vanellus
        vanellus","Lanius collurio",
                                    "Emberiza schoeniclus","Alauda arvensis","Passer
        montanus","Streptopelia turtur",
                                    "Saxicola rubetra","Columba palumbus","Emberiza
        citrinella"))

species_cze_farm <- merge(species_cze_farm, species_all, by="name_long", all.x=T)
species_sub <- species_cze_farm <- na.omit(species_cze_farm)

Obs <- df_all_country_2000[df_all_country_2000$Species %in% species_sub$name_long,]
species_sub <- species_cze_farm <- species_cze_farm[species_cze_farm$code_sp %in%
        unique(Obs$code_sp),]

y_farm <- data.table::dcast(Obs[,c("code_sp","Index","Year")],
                code_sp~Year, fun.aggregate = sum, value.var = "Index")

obs_se_farm <- data.table::dcast(Obs[,c("code_sp","Index_SE","Year")],
                     code_sp~Year, fun.aggregate = sum, value.var = "Index_SE")
```

Prepare data format for DFAclust

Remove non numeric columns (here species names)

```
# Dataset for species time-series

data_ts <- y_farm[,c(-1)]

# Dataset for observation error time-series

data_ts_se <- obs_se_farm[,c(-1)]
```

Specify time period

Usually the data are available for a given interval of time and one wants to study them on the same interval or a shorter interval. To obtain mean centered data for the right interval, one has to specify the boundaries (min_year and max_year) of the original interval and the first year of the interval of interest (min_year_sc). Here we choose the recale the interval from 1982-2017 to 2000-2017.

```r
# Get interval boundaries

min_year <- min(as.numeric(colnames(data_ts)))
max_year <- max(as.numeric(colnames(data_ts)))

# Set reference year to rescale

min_year_sc <- 2000
```

Define the rescale function

The national indices from PECBMS have a specific format with a first year value to 100 and the other year expressed as a percentage of the first year and the associated uncertainty. The following function enables mean-centering of the national indices and estimation of the transformed uncertainty. Note however that several hypotheses and approximations are made (delta approximation to transform the uncertainty vector, hypothesis on the uncertainty of the first year of the new interval) and the user must know what he/she is doing here.

```r
# Specify a rescale function for indices not mean centered

rescale_index <- function(index, # numeric vector of length n equal to the original interval
        size, one species time-series from the original interval
                          se, # numeric vector of length n, associated uncertainty time-series
                          ref # logical vector of length n, indicating the years in the new
        interval (TRUE) and only in the original interval (FALSE). Could be specify as
        follows:  min_year:max_year %in% min_year_sc:max_year
                          ) {

  # Identify years with missing values
  missing <- is.na(index)

  # Get the log of abundance indices
  log_index <- log(index[!missing])

  # Rescale uncertainty using the delta approximation
  log_var <- se[!missing]^2 / index[!missing]^2

  # Identify years without missing values
  ref_nmiss <- ref[!missing]

  # Identify first year in the original interval
  first.ix <- which(log_index == log(100) & log_var == 0)

  # Specify the rescaling matrix
  n <- length(log_index)
  M <- diag(1, n) - 1/sum(ref_nmiss) * rep(1,n) %*% t(as.integer(ref_nmiss))

  # Estimate uncertainty for the first year of the new interval. Her we assume variance of
        first year raw log index to be close to the smallest of the remaining indices.

  if(se[first.ix] > 0){
    vy1 <- min(min(log_var[-first.ix])/1.01,log_var[first.ix])
  }else{
    vy1 <- min(log_var[-first.ix])/1.01
  }

  # Mean center indices
  log_index_scaled <- NA + index
  log_index_scaled[!missing] <- M %*% log_index

  # Estimate transformed uncertainty accordingly
  log_index_se <- NA + index
  log_index_se[!missing] <- sqrt(diag(M %*% (diag(log_var  +  vy1 * replace(rep(-1,
        length(log_index)), first.ix, 1))) %*% t(M)))

  scale_index_se <- rbind(log_index = log_index_scaled, se_log = log_index_se)

  return(scale_index_se)

}
```

Mean-centered indices and uncertainty

```
# Rescale species and observation error time-series

data_ts_prov <- as.matrix(data_ts)
data_ts_se_prov <- as.matrix(data_ts_se)

for(i in 1:nrow(data_ts)){

  # Apply the rescale function
  rescale_value <- rescale_index(index = data_ts_prov[i,],
                                 se = data_ts_se_prov[i,],
                                 ref = min_year:max_year %in% min_year_sc:max_year)

  # In DFAclust, the indices are log in core_dfa, they must be provided as non-log input, so
        take the exponential of mean-centered log values.
  data_ts_prov[i,] <- exp(rescale_value[1,])

  # In DFAclust, the uncertainty should correspond to log indices. No need to back transform
        the uncertainty values here.
  data_ts_se_prov[i,] <- rescale_value[2,]
}
```

Interval selection and comparison with `species_ts_mat` from `DFAclust`

```
# Select mean-centered indices for the new interval only

data_ts_prov <- data_ts_prov[,attr(data_ts_prov,"dimnames")[[2]] %in% min_year_sc:max_year]
data_ts_se_prov <- data_ts_se_prov[,attr(data_ts_se_prov,"dimnames")[[2]] %in%
        min_year_sc:max_year]

data_ts <- data_ts_prov
data_ts_se <- data_ts_se_prov

# Rename the rows with species names

row.names(data_ts) <- y_farm$code_sp
row.names(data_ts_se) <- obs_se_farm$code_sp

# Compare data_ts with species_ts_mat used as an example in DFAclust README

all.equal(species_ts_mat,data_ts)
#> [1] TRUE
all.equal(species_uncert_ts_mat,data_ts_se)
#> [1] TRUE
```

Empirical data: analysing data

DFA cluster analysis for Swedish birds

Now that we have time-series and standard errors for each species, we can launch the analysis. If you want to start the vignette here, first load the datasets.

```
data(ts_bird_se_allcountry)
data(species_data)
```

Farmland birds

We will first run the analysis on farmland birds. We therefore select the 15 farmland species.

```
species_sub <- species_farm <-  droplevels(species_data[species_data$code_sp %in% c(
  "FALTIN","VANVAN","ALAARV","HIRRUS","CORFRU",
  "SAXRUB","SYLCOM","ANTPRA","MOTFLA","LANCOL",
  "STUVUL","LINCAN","EMBCIT","EMBHOR","PASMON"),])
```

We then subselect the corresponding time-series and standard errors for farmland birds.

```
Obs <- ts_bird_se_allcountry[ts_bird_se_allcountry$code_sp %in% species_sub$code_sp,]
```

We finally produce a dataset of species time-series `y_farm_ts` and a dataset of standard errors `obs_se_farm_ts`.

```
y_farm <- dcast(Obs[,c("code_sp","relative_abundance_m0","year")],
           code_sp~year, fun.aggregate = sum, value.var = "relative_abundance_m0")
#> Warning in dcast(Obs[, c("code_sp", "relative_abundance_m0", "year")],
#> code_sp ~ : The dcast generic in data.table has been passed a data.frame
#> and will attempt to redirect to the reshape2::dcast; please note that
#> reshape2 is deprecated, and this redirection is now deprecated as well.
#> Please do this redirection yourself like reshape2::dcast(Obs[, c("code_sp",
#> "relative_abundance_m0", "year")]). In the next version, this warning will
#> become an error.

obs_se_farm <- dcast(Obs[,c("code_sp","Log_SE_m0","year")],
             code_sp~year, fun.aggregate = sum, value.var = "Log_SE_m0")
#> Warning in dcast(Obs[, c("code_sp", "Log_SE_m0", "year")], code_sp ~ year, :
#> The dcast generic in data.table has been passed a data.frame and will attempt
#> to redirect to the reshape2::dcast; please note that reshape2 is deprecated, and
#> this redirection is now deprecated as well. Please do this redirection yourself
#> like reshape2::dcast(Obs[, c("code_sp", "Log_SE_m0", "year")]). In the next
#> version, this warning will become an error.

y_farm_ts <- as.matrix(y_farm[,2:ncol(y_farm)]) # species time series

y_uncert_ts <- as.matrix(obs_se_farm[,2:ncol(obs_se_farm)]) # standard error on time series

rownames(y_farm_ts) <- rownames(y_uncert_ts) <- y_farm$code_sp # add species names as row names
```

We can now run the `prepare_data` function. This function allows the user to log-transform the standard errors if they are not and check if there are missing values in standard error input. It also handles zeros in time-series by replacing zeros by a percentage of the reference year value (1 % by default). `perc_replace` correspond to the proportion of the average index value used to replace zeros in species time-series with `0.01` as default value (1 %). It can also transform the observation error time-series to get their log values if they are initially not in log values (in that case set `se_log` to `TRUE`).

```
data_ready_dfa <- prepare_data(data_ts = y_farm_ts,data_ts_se = y_uncert_ts, se_log = TRUE,
        perc_replace = 0.01)
```

Then the `fit_dfa` function to launch the DFA analysis. Note that, here, we know the number of latent trends `nfac`=3 (by running this function with `nfac`=0), so we specify it which shortens the computation. In general the user will not know the optimal number for `nfac` and in that case, set `nfac`=0 (which is the default) to look for it between `mintrend` and `maxtrend`. `center_option` allows to handle time-series centered according to the first year (`center_option` = 0) or mean-centred, which is the default (`center_option` = 1). `control` is a `list` of control options for `MakeADFun()` (default is list()).

```
dfa_result <- fit_dfa(data_ts = data_ready_dfa$data_ts,data_ts_se = data_ready_dfa$data_ts_se,
        min_year = data_ready_dfa$min_year, max_year = data_ready_dfa$max_year,
        species_name_ordre = data_ready_dfa$species_name_ordre, species_sub = species_farm,
        nfac = 3, mintrend = 1, maxtrend = 5, AIC = TRUE, center_option = 1, silent = TRUE,
        control = list())
#> NLMINB   BFGS NLMINB   BFGS NLMINB   BFGS
#>      0      0      0      0      0      0
#>    NLMINB       BFGS     NLMINB       BFGS     NLMINB       BFGS
#> -232.2488 -232.2488 -232.2488 -232.2488 -232.2488 -232.2488
#>       NLMINB         BFGS       NLMINB         BFGS       NLMINB         BFGS
#> 4.951064e-04 2.954483e-05 5.047746e-04 1.259253e-05 1.542756e-04 1.450338e-04
#> AIC:  -350.497564098778
```

Once the latent trend are estimated, the clustering analysis can be performed using the function `cluster_dfa`.

```
cluster_result <- cluster_dfa(data_dfa = dfa_result, species_sub = species_farm, nboot = 500)
```

And finally the `plot_dfa_result` function to get the results of the whole analysis.

```
dfa_result_plot_farm <- plot_dfa_result(data_dfa = dfa_result, sdRep = cluster_result$sdRep,
        species_sub = species_farm, group_dfa = cluster_result$group_dfa, min_year =
        data_ready_dfa$min_year, species_name_ordre = data_ready_dfa$species_name_ordre)
#> Using name_long as id variables
```

Woodland birds

Before showing the results for farmland birds, we will now run the analysis on woodland birds. We therefore select the 26 woodland species.

```
species_sub <- species_forest <- droplevels(species_data[species_data$code_sp %in% c(
   "ACCNIS","TETBON","TRIOCH","COLOEN","DRYMAR",
  "DRYMIN","NUCCAR","GARGLA","PERATE","LOPCRI","POEPAL","POEMON",
  "SITEUR","CERFAM","TURVIS","PHOPHO","PHYCOL","PHYSIB","REGREG","FICHYP","FICALB",
  "ANTTRI","COCCOC","SPISPI","PYRPYR","EMBRUS"),])
```

We then subselect the corresponding time-series and standard errors for woodland birds.

```
Obs <- ts_bird_se_allcountry[ts_bird_se_allcountry$code_sp %in% species_sub$code_sp,]
```

We finally produce a dataset of species time-series `y_forest` and a dataset of standard errors `obs_se_forest`.

```
y_forest <- dcast(Obs[,c("code_sp","relative_abundance_m0","year")],
            code_sp~year, fun.aggregate = sum, value.var = "relative_abundance_m0")
#> Warning in dcast(Obs[, c("code_sp", "relative_abundance_m0", "year")],
#> code_sp ~ : The dcast generic in data.table has been passed a data.frame
#> and will attempt to redirect to the reshape2::dcast; please note that
#> reshape2 is deprecated, and this redirection is now deprecated as well.
#> Please do this redirection yourself like reshape2::dcast(Obs[, c("code_sp",
#> "relative_abundance_m0", "year")]). In the next version, this warning will
#> become an error.

obs_se_forest <- dcast(Obs[,c("code_sp","Log_SE_m0","year")],
                 code_sp~year, fun.aggregate = sum, value.var = "Log_SE_m0")
#> Warning in dcast(Obs[, c("code_sp", "Log_SE_m0", "year")], code_sp ~ year, :
#> The dcast generic in data.table has been passed a data.frame and will attempt
#> to redirect to the reshape2::dcast; please note that reshape2 is deprecated, and
#> this redirection is now deprecated as well. Please do this redirection yourself
#> like reshape2::dcast(Obs[, c("code_sp", "Log_SE_m0", "year")]). In the next
#> version, this warning will become an error.

y_forest_ts <- as.matrix(y_forest[,2:ncol(y_forest)]) # species time series

y_uncert_ts <- as.matrix(obs_se_forest[,2:ncol(obs_se_forest)]) # standard error on time series

rownames(y_forest_ts) <- rownames(y_uncert_ts) <- y_forest$code_sp # add species names as row
        names
```

We can now run the `prepare_data` function.

```
data_ready_dfa <- prepare_data(data_ts = y_forest_ts,data_ts_se = y_uncert_ts, se_log = TRUE,
        perc_replace = 0.01)
```

Then the `fit_dfa` function to launch the DFA analysis. Note that, as for farmland birds, we know the number of latent trends `nfac`=4 (by running this function with `nfac`=0), so we specify it which shortens the computation. In general the user will not know the optimal number for `nfac` and in that case, set `nfac`=0 (which is the default) to look for it.

```
dfa_result <- fit_dfa(data_ts = data_ready_dfa$data_ts,data_ts_se = data_ready_dfa$data_ts_se,
        min_year = data_ready_dfa$min_year, max_year = data_ready_dfa$max_year,
        species_name_ordre = data_ready_dfa$species_name_ordre, species_sub = species_forest,
        nfac = 4, mintrend = 1, maxtrend = 5, AIC = TRUE, center_option = 1, silent = TRUE,
        control = list())
#> NLMINB   BFGS NLMINB   BFGS NLMINB   BFGS
#>      0      0      0      0      0      0
#>    NLMINB      BFGS    NLMINB      BFGS    NLMINB      BFGS
#> -327.4038 -327.4038 -327.4038 -327.4038 -327.4038 -327.4038
#>       NLMINB         BFGS       NLMINB         BFGS       NLMINB         BFGS
#> 6.234733e-04 9.409873e-05 3.669179e-04 5.673957e-05 1.912420e-04 6.884552e-05
#> AIC:  -406.80762263983
```

Then the `cluster_dfa` function to launch the clustering analysis. To make the analysis faster `nboot` is set to 100. By default it is 500.

```
cluster_result <- cluster_dfa(data_dfa = dfa_result, species_sub = species_forest, nboot = 100)
```

And finally the `plot_dfa_result` function to get the results of the whole analysis.

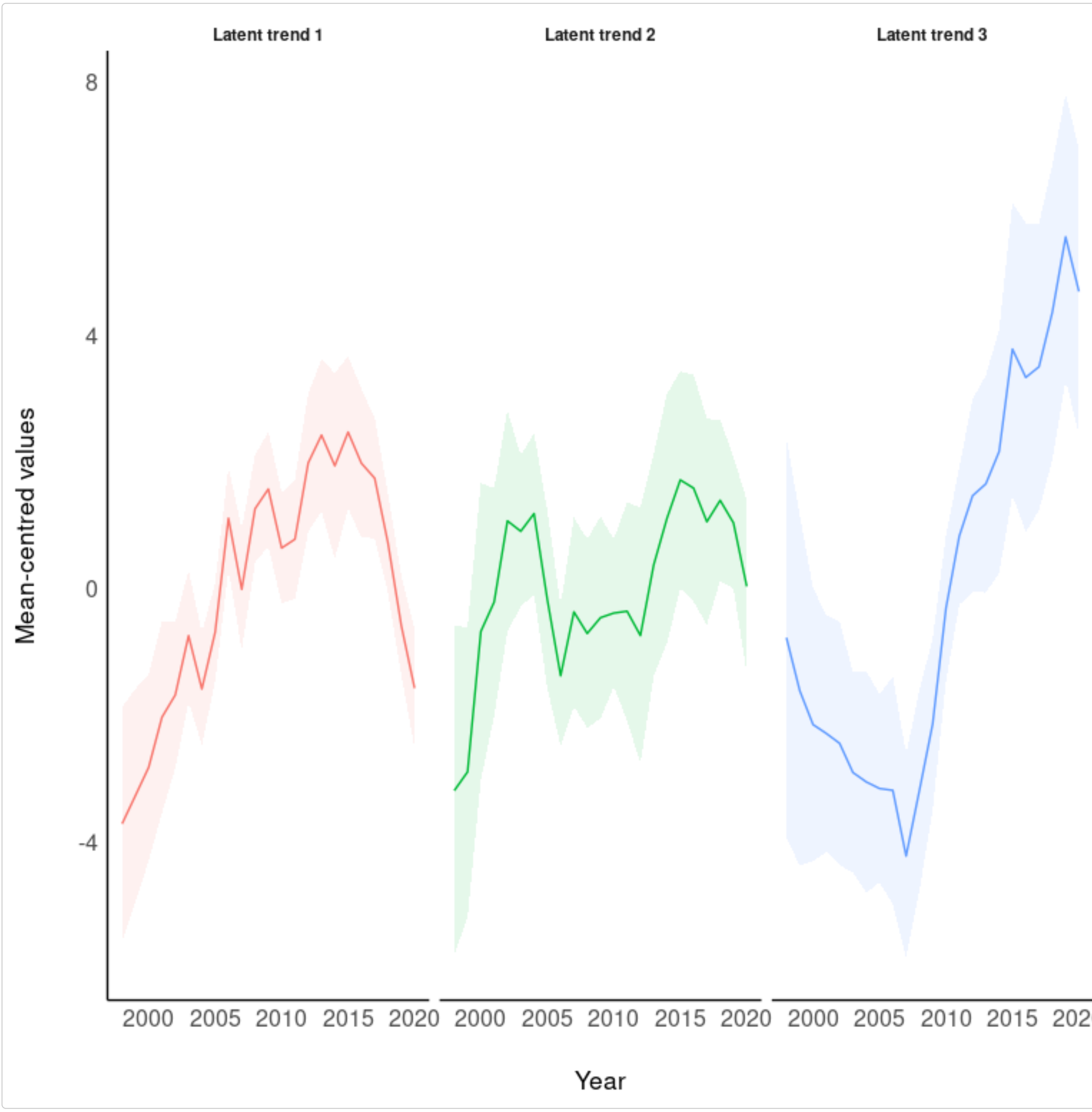
```
dfa_result_plot_forest <- plot_dfa_result(data_dfa = dfa_result, sdRep = cluster_result$sdRep,
        species_sub = species_forest, group_dfa = cluster_result$group_dfa, min_year =
        data_ready_dfa$min_year, species_name_ordre = data_ready_dfa$species_name_ordre)
#> Using name_long as id variables
```

Display results

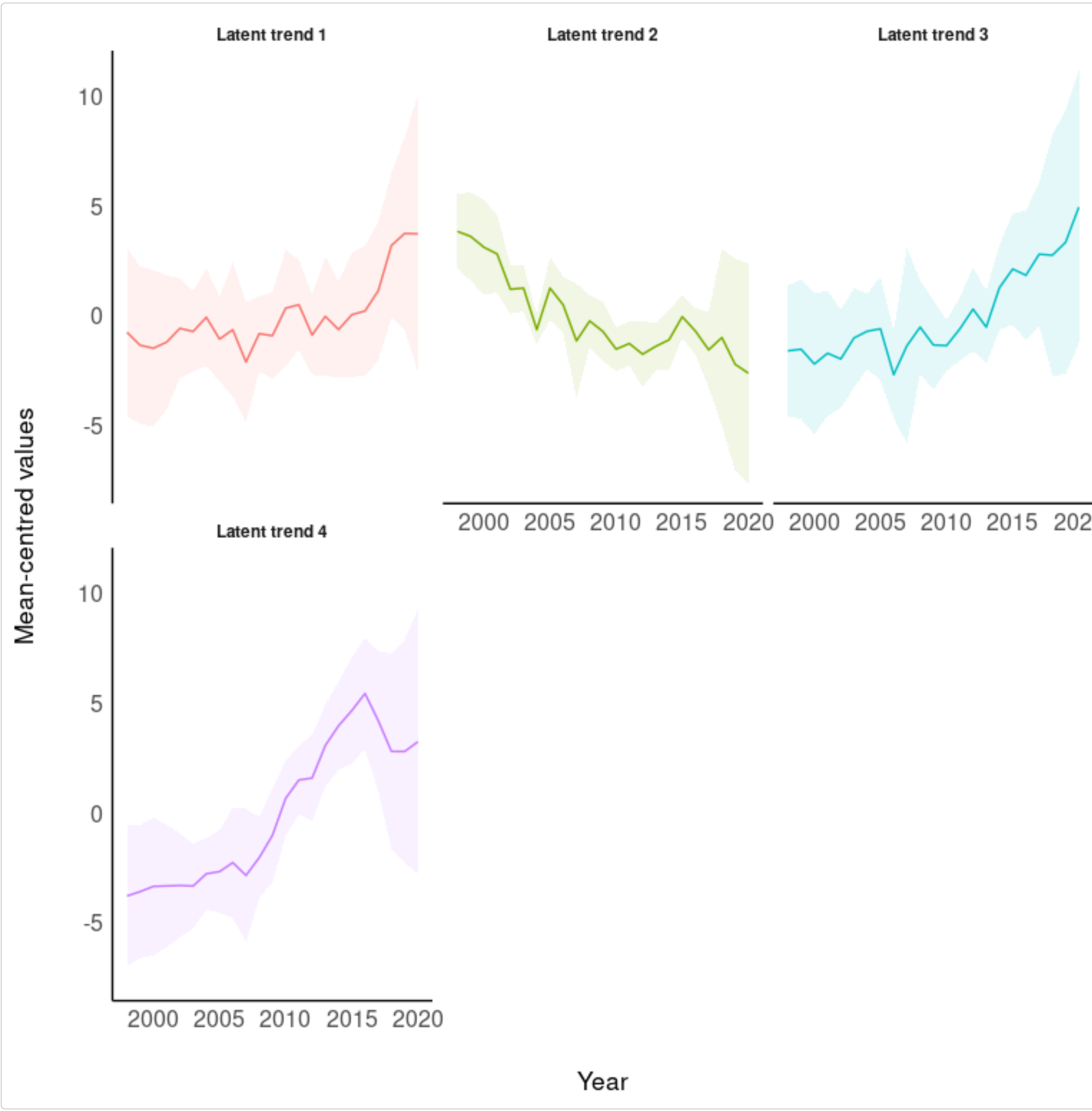
We now can look at the tree tools of the toolbox that are the main results for farmland and woodland birds.

Tool 1: Latent trends

```
dfa_result_plot_farm$plot_tr
```

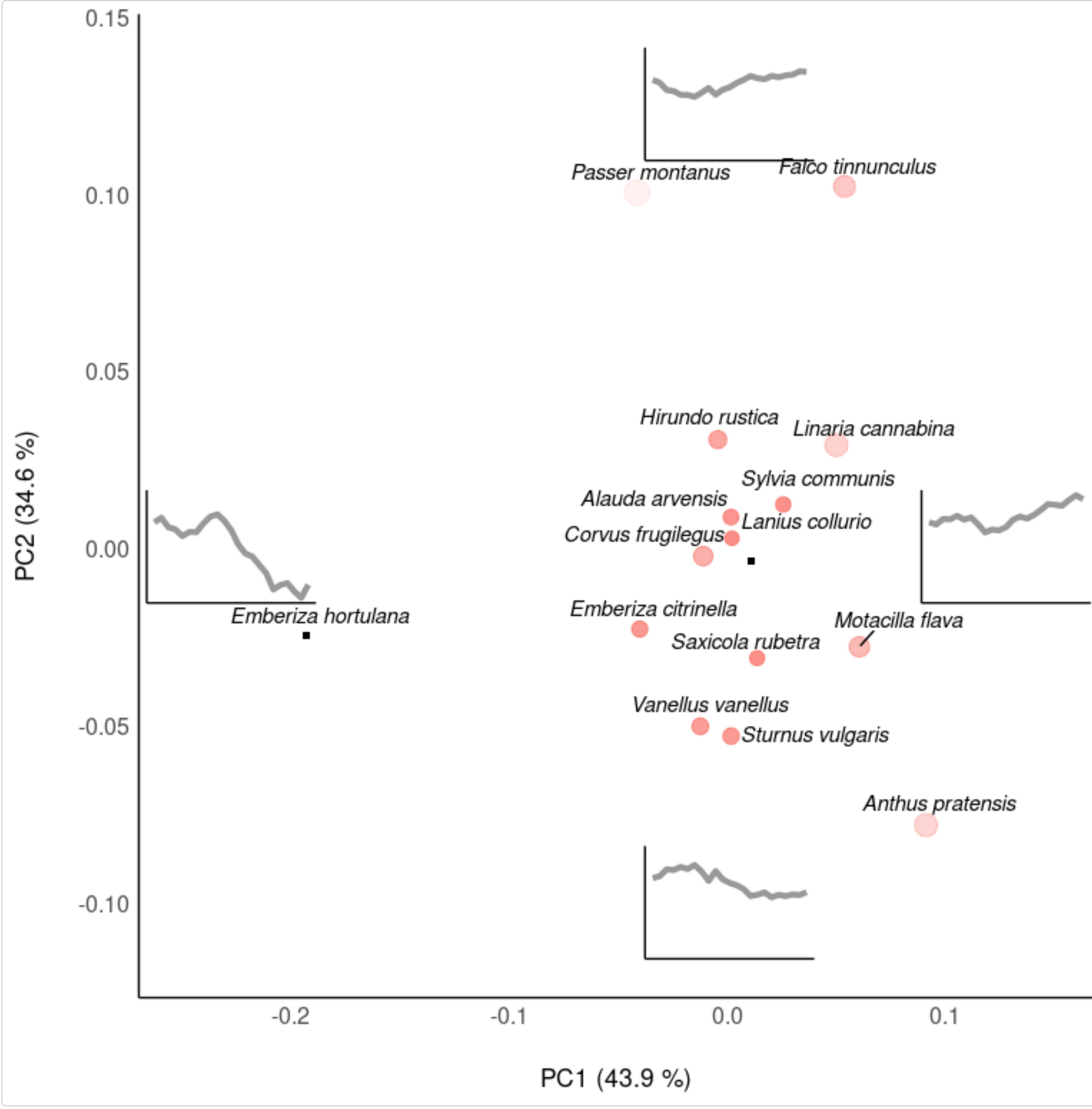


```
dfa_result_plot_forest$plot_tr
```

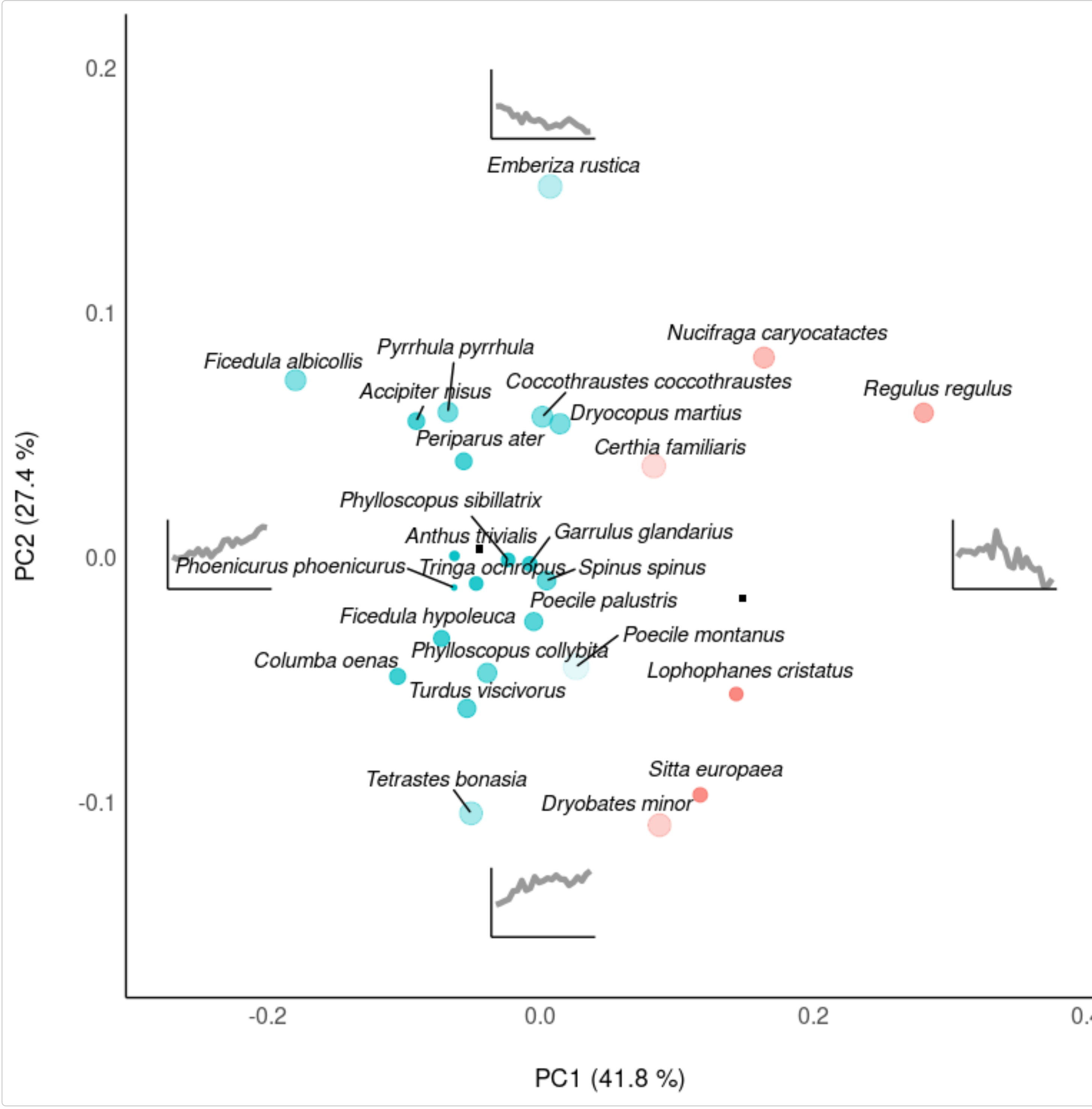


Tools 2 and 3: Ordination and clusters

```
dfa_result_plot_farm$plot_sp_group[[1]]
```



```
dfa_result_plot_forest$plot_sp_group[[1]]
```



0.2
0.1
0.0
-0.1
-0.2
0.0
0.2
PC2 (27.4 %)
PC1 (41.8 %)
Emberiza rustica
Nucifraga caryocatactes
Ficedula albicollis
Pyrrhula pyrrhula
Accipiter nisus
Coccothraustes coccothraustes
Regulus regulus
Dryocopus martius
Periparus ater
Certhia familiaris
Phylloscopus sibillatrix
Anthus trivialis
Garrulus glandarius
Phoenicurus phoenicurus
Tringa ochropus
Spinus spinus
Poecile palustris
Ficedula hypoleuca
Poecile montanus
Columba oenas
Phylloscopus collybita
Lophophanes cristatus
Turdus viscivorus
Tetrastes bonasia
Sitta europaea
Dryobates minor