Butterfly Monitoring and Analyses

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Preface

This project aims to collate documentation of methods used to analyze and work with Butterfly Monitoring Schemes (BMS) data. We focus on methods used to analyze count data associated with Pollard transects that represent the core of the eBMS database.

NOTE - this book project is a work in progress that only started.

Reto Schmucki, July 2024

Part I

Counting Butterflies

Butterfly Monitoring

Content under construction

Part II

From Counts to FLight Curves

Data Analyses and Methods

Biodiversity monitoring plays a crucial role in generating metrics and knowledge to improve our understanding of the status and trends of biodiversity. By integrating new information with existing knowledge, as limited as it may be, we can update our understanding and thereby improve our ability to inform action and support decision-making. Analysis of monitoring data can take various forms, from simple data exploration to the development of complex statistical models. Regardless of the level of complexity, the main goal of analysis remains the same - to derive relevant information from the data to improve our understanding.

Data Generation processes and biases

There are several methods for extracting information from monitoring data, and each method is based on a set of assumptions. A fundamental assumption for any monitoring program is that the data are only representative of the sampled population. Depending on how the data are collected, the sample may accurately represent the population of interest, or it may be biased and provide only a skewed representation of the population. It is important to understand how the specific sampling protocol may affect the representativeness of the data and what potential biases should be considered when analyzing the data. To develop robust monitoring methods and analyze the incoming data appropriately, it is important to understand the data generation process and how the monitoring protocol may affect the data and the information it contains. The life cycle of butterflies, for example, influences the number of adult individuals in a particular place at a particular time. The seasonality of the emergence process leads to a temporal pattern in the observed and recorded data and it is important to be aware of this systematic component when analyzing the data. Systematic variations can also be associated with variations in the sampling effort such as in the area sampled, the time spent recording or the experience of the recorders. Understanding the influence of both the biological and sampling components on the data generation process that produced the observed dataset is crucial for conceptualizing and developing methods that can disentangle the component of interest while accounting for the systematic structures in the data.

Data Simulation

To better understand the influence of species biology and sampling protocols on data generation, we will rely on data simulation approaches. Data simulation involves generating random data sets based on certain rules and known parameters. It is useful not only to show the outcome of certain ecological and sampling processes and illustrate how they can shape systematic patterns in the data but also to test methods and gain a better understanding of how the statistical models work and where they may fail.

When carefully designed, data simulations can be a powerful tool for testing and validating methods as well as performing sensitivity analyzes to assess their robustness to violations of underlying assumptions. Simulated data sets enable the exploration of model behavior and help to identify their strengths and limitations. In the following sections, we will use data simulations to illustrate and explore the different components of butterfly monitoring data when generated under different scenarios. Using these simulations, we will demonstrate the modeling process and the type of information that can be extracted from the different approaches used to analyze butterfly count data.

Statistical Modelling

From Counts to Models

Butterfly Counts

Simulation of Butterfly Counts

To demonstrate and assess the method used to compute butterfly abundance indices and the Grassland Butterfly Indicator which involves calculating collated abundance indices from multiple sites and estimating the population trend from a set of indicator species, the best option is to use simulated datasets that provide realistic data with known parameters. The simulation approach allows us to assess the methods' performance and enables us to control individual parameters and conduct rigorous sensitivity analysis. This will provide useful insight into the method and enable rigorous assessment of its power and limitations.

```
if(!require("data.table")) install.packages("data.table")
if(!require("ggplot2")) install.packages("ggplot2")
if(!require("devtools")) install.packages("devtools")
if(!require("rbms")) devtools::install_github("RetoSchmucki/rbms")

flc_col <- '#ff8c00'
cnt_col <- '#008b8b'
missing_col <- '#8b0000'
GAM_col <- '#483d8b'
```

Simulation Tool for Butterflies and Other Phenologies

In the first case, we will simulate counts for one site for one year (e.g. 2023), using a Gaussian curve to depict the shape of adult butterflies' seasonal phenology (activity curve). We will use the function `timeseries_sim()` from the R package `butterflyGamSims` developed by Collin Edwards (see Edwards et al. 2023), available on GitHub. This function will allow us to generate butterfly counts for one or multiple sites (iterations), using a specific shape, position (peak), period, sampling process and initial abundance. For multi-year time series, we can also define a growth rate (temporal trend).

```
set.seed(13276)

if(!require("butterflyGamSims")) devtools::install_github("cbedwards/butterflyGamSim

btfl_data <- timeseries_sim(nsims=1,
                year = c(2023),
                doy.samples = seq(from=1, to=365, by=1),
                abund.type = "exp",
                activity.type = "gauss",
                sample.type = "pois",
                sim.parms = list(growth.rate = 0,
                                 init.size = 500,
                                 act.mean = 175,
                                 act.sd = 15)
                )
```

The object produced by the `timeseries_sim()` function contains 1) a `data.frame` NAME$timeseries with the time series and 2) a `data.frame` NAME$parms with the parameters used for the simulation. In the parameters, you will find the population growth rate (`growth.rate`), the initial population size (`init. size`) measure in number of individuals expected over the season, the peak of the activity curve (`act.mean`) measured in days and the width of the activity curve (`act.sd`) that is measured in standard deviation. Note that not all sampling parameters used for the simulation are included in the parms object; the `activity.type` (the distribution function used to define the activity curve), the `sample.type` (the sampling process used to sample random counts along the activity curve) and the `abund.type` (the type of the growth rate, deterministic or with a log-normal process error) are missing.

Simulate Data Sampling Process

With the `timeseries_sim()` function above, we simulated a regular time series of butterfly counts where the actual number of active butterfly of each day are draw from a Poisson distribution with a given expectation defined by the activity curve along a day-of-year vector j following the probability density of a normal distribution (Gaussian) with mean equal to the peak day μ (`act.mean`) and a standard deviation α (`act.sd`). Because the integral of the probability density distribution (area under the curve) sum to 1, we can multiply the density by the abundance to retrieve a vector of expected abundance for each day-of-year, λ_j.

$$\lambda_j = abundance * \frac{1}{\alpha\sqrt{2\pi}} \exp\left(-\frac{1}{2}\left(\frac{(j-\mu)}{\alpha}\right)^2\right)$$

From the activity curve, we can use the `rpois()` function in R to draw a random value from a Poisson distribution, representing the count of events for day j, where $n = 1$ and the mean is specified by expected value λ at day j.

$$y_j = rpois(n, \lambda_j)$$

From this simulation, we have generated the ecological process for the butterfly counts, for a given abundance distributed over a specific phenology defined by a Gaussian curve with a peak (mean) and a breath (standard deviation).

```
library(knitr)
kable(btfl_data$timeseries[c(1:3,160:163,250:253),])
```

Table 1: Butterfly Simmulation Data

	years	doy	count	act	abund.true	onset.true	median.true	end.true	fp.true	sim.id
1	2023	1	0	0.0000000	500	155.8	175	194.2	38.4	1
2	2023	2	0	0.0000000	500	155.8	175	194.2	38.4	1
3	2023	3	0	0.0000000	500	155.8	175	194.2	38.4	1
160	2023	160	9	8.0656908	500	155.8	175	194.2	38.4	1
161	2023	161	11	8.6025942	500	155.8	175	194.2	38.4	1
162	2023	162	10	9.1345489	500	155.8	175	194.2	38.4	1
163	2023	163	5	9.6563851	500	155.8	175	194.2	38.4	1
250	2023	250	0	0.0000496	500	155.8	175	194.2	38.4	1
251	2023	251	0	0.0000354	500	155.8	175	194.2	38.4	1
252	2023	252	0	0.0000252	500	155.8	175	194.2	38.4	1
253	2023	253	0	0.0000179	500	155.8	175	194.2	38.4	1

The additional structure resulting from the monitoring protocol (observation process) can now be added to the simulated time series and replicate a specific protocol. In this first case, we will simulate a protocol with weekly visits and include some missing counts for weeks when the minimal monitoring conditions were not met or the observer was absent. For this, we will write some new R functions. The first function will define the start and end of the monitoring season and sample one monitoring day per week over the season. Then we will write functions to simulate a certain level of missing weekly visits within the season. The likelihood of missing weeks tends to be higher at the beginning and the end of the season and lower in the middle. Let's start with the first function that defines the monitoring season and resamples one day of the simulated time series every week. We will name the function `sim2bms()` as it aligns the simulated time series to the protocol of a specific Butterfly Monitoring Scheme (BMS). The function needs the time series, and additional arguments to define the year that we want to extract `yearKeep`, if the time series must be resampled

weekly `weeklySample`, which day should be used for the weekly resampling `weekdayKeep` (this can be a vector of days, e.g. c(2,3,4,5), or a specific day), and finally the monitoring season `monitoringSeason` which correspond to a vector of months, e.g c(4,5,6,7,8,9) represent a season starting in April and ending in September. Note that this function will also add some new variables such as the date, the ISO week number and the day of the week.

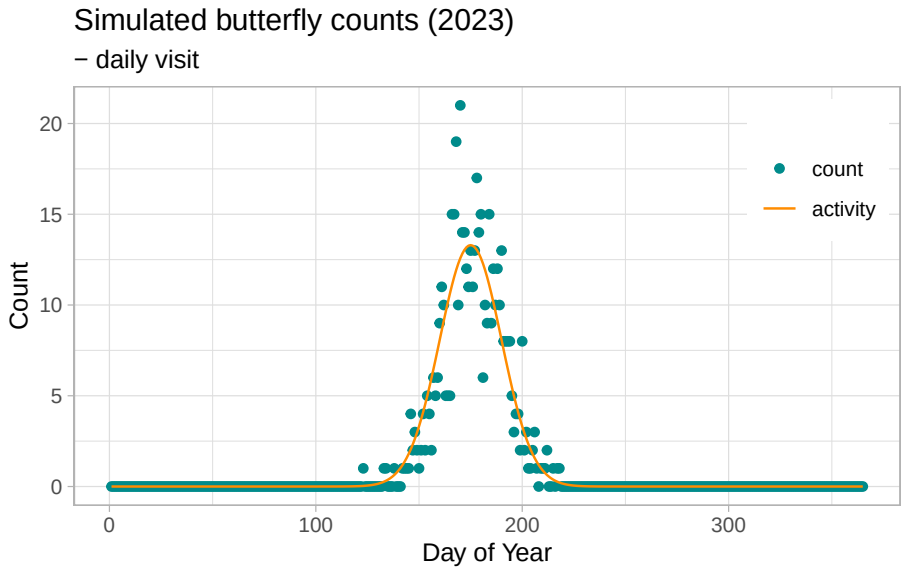
```
# data: Time series resulting from the simulation generated for 365 days
# weeklySample: TRUE or FALSE; should the daily count in the time series be resample
# weekdayKeep: vector of days c(1,2,..., 7) to be sampled from for the weekly count.
# contains c(2,3,4), the sampling process will be restricted to Tuesday, Wednesday
# monitoringSeason: vector of months that define the monitoring season (e.g. April

sim2bms <- function(data, yearKeep = NULL, weeklySample = FALSE, weekdayKeep = NULL,

                  btfl_ts <- data.table::data.table(data)[, site_id := paste0("site_
                  if(!is.null(yearKeep)){
                        btfl_ts <- btfl_ts[years %in% yearKeep, ]
                  }
                  btfl_ts[ , date := as.Date(doy, origin = paste0(years, "-01-01"))-
                  btfl_ts[ , week := isoweek(date)]
                  btfl_ts[month(date) != 1 | week < 50, weekday := rowid(week), by =
                  if(isTRUE(weeklySample)){
                        if(!is.null(weekdayKeep)){
                              btfl_ts <- btfl_ts[weekday %in% weekdayKeep, ]
                        }
                        btfl_ts <- btfl_ts[btfl_ts[,.I[sample(.N, 1)], by = .(week,
                  }
                  if(!is.null(monitoringSeason)){
                  btfl_ts <- btfl_ts[month(date) %in% monitoringSeason, ]
                  }
            return(btfl_ts)
            }
```

We can apply this function to retrieve a specific year of the simulated time series and add some new variables, leaving all other parameters empty. With the same function, we can also resample weekly counts (e.g. one day from c(2:5)) and restrict the time series to a specific monitoring season (e.g. c(4:9)).

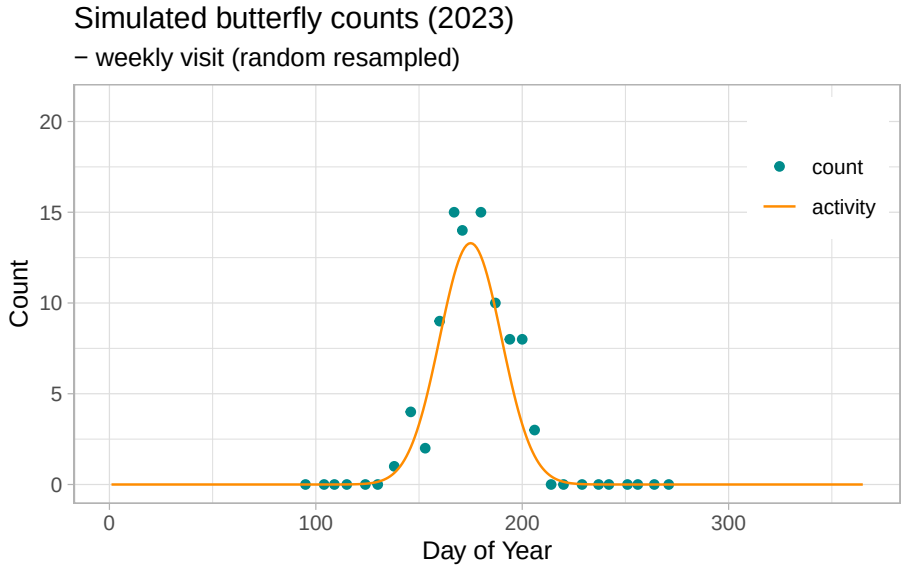
```
set.seed(13276)
y <- c(2023)

btfl_ts <- sim2bms(data = btfl_data$timeseries, yearKeep = y)
btfl_fig1 <- ggplot() +
```

```
                  geom_point(data=btfl_ts, aes(x=doy, y=count, colour = "count")) +
                  geom_line(data = btfl_ts,
                  aes(x = doy, y = act, colour = "activity")) +
                  xlim(1,365) + ylim(0, max(btfl_ts$count, btfl_ts$act)) +
                  scale_colour_manual("",
                        breaks = c("count", "activity"),
                        values = c(cnt_col, flc_col)) +
                  theme_light() +
                  theme(legend.position = "inside", legend.position.inside = c(0.9, 0.8)) +
                  labs(title = paste0("Simulated butterfly counts (", y,")"),
                       subtitle = "- daily visit",
                       x = "Day of Year",
                       y = "Count")

btfl_week_smpl <- sim2bms(data = btfl_data$timeseries, yearKeep = y,
                    weeklySample = TRUE,
                    weekdayKeep = c(2:5),
                    monitoringSeason = c(4:9))
btfl_fig2 <- ggplot() +
                  geom_point(data=btfl_week_smpl, aes(x=doy, y=count, colour = "count")) +
                  geom_line(data = btfl_ts,
                  aes(x = doy, y = act, colour = "activity")) +
                  xlim(1,365) + ylim(0, max(btfl_ts$count, btfl_ts$act)) +
                  scale_colour_manual("",
                        breaks = c("count", "activity"),
                        values = c(cnt_col, flc_col)) +
                  theme_light() +
                  theme(legend.position = "inside", legend.position.inside = c(0.9, 0.8)) +
                  labs(title = paste0("Simulated butterfly counts (", y,")"),
                       subtitle = "- weekly visit (random resampled)",
                       x = "Day of Year",
                       y = "Count")

btfl_fig1
btfl_fig2
```

In the example above, the activity curve represented by the line has a Gaussian shape and counts presented by the points along the curve are independent random samples from a Poisson distribution. Because we sampled a count value for 365 days (day-of-year; doy), the counts are representative of the population of active adult butterflies as if the site was visited every. This implies that a proportion of butterflies are counted more than one day as their lifespan exceeds one day. On Pollard transect, this is how butterfly counts are likely to be counted and reported, but with a different frequency as visits are generally weekly, fortnightly, or even monthly. We can replicate this value by resampling


Simulated butterfly counts (2023)
− daily visit
Count
Day of Year
count
activity
0
5
10
15
20
0
100
200
300

(a) a)


Simulated butterfly counts (2023)
− weekly visit (random resampled)
Count
Day of Year
count
activity
0
5
10
15
20
0
100
200
300

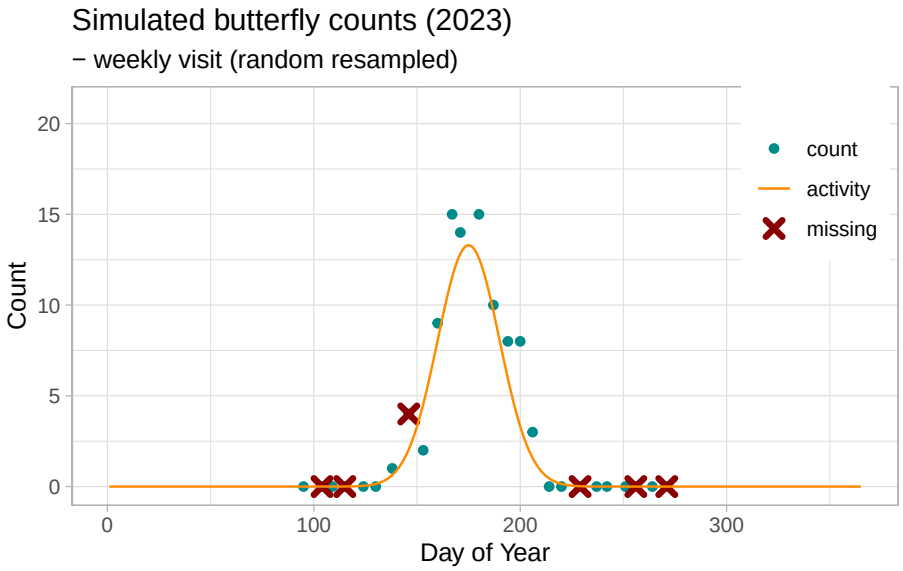
(a) b)

the daily count weekly.

From the weekly visits, counts outside of the monitoring period will not be informed, in many cases these are 'zeros' as we expect the monitoring season to align with butterflies' activity. Some other weeks might be missing from the time series, potentially due to unsuitable weather conditions for monitoring or the recorder's availability. We can inform and exclude the missing visits by resampling a subset of the weekly counts.

```
missing_prob <- function(data, mu=NULL, alpha = 5, theta = 0.3){
                              x_ <- seq_len(nrow(data))
                              mu_ <- ifelse(is.null(mu), length(x_) / 2, mu)
                              std_ <- sqrt(mu_ / theta)
                              y_ <- abs((alpha * exp((-(x_ - mu_)^2) / std_^2)) - alpha) + alp
                              yn_ <- y_ / (sum(y_))
                        return(yn_)
                  }

sample_missing <- function(data, propMissing = 0.25){

            missing.prob <- data.table::data.table()
            for(i in data[, unique(years)]){
                  for(j in data[, unique(site_id)]){
                  missing.prob <- rbind(missing.prob, missing_prob(data[years == i & site_id =
                  }
            }

            missing.week <- data[sample(seq_len(.N), round(propMissing * .N), prob = unlist(mi

      return(missing.week)
}

btfl_week_missing <- sample_missing(data = btfl_week_smpl, propMissing = 0.25)

btfl_fig3 <- ggplot() +
                geom_point(data=btfl_week_smpl, aes(x=doy, y=count, colour = "count")) +
                geom_point(data=btfl_week_missing, aes(x=doy, y=count, colour = "missing"),
                           shape=4, size=2, stroke=2) +
                geom_line(data = btfl_ts,
                aes(x = doy, y = act, colour = "activity")) +
                xlim(1,365) + ylim(0, max(btfl_ts$count, btfl_ts$act)) +
                scale_colour_manual("",
                      breaks = c("count", "activity", "missing"),
                      values = c(cnt_col, flc_col, missing_col)) +
                theme_light() +
```

```
                theme(legend.position = "inside", legend.position.inside = c(0.9, 0.
                labs(title = paste0("Simulated butterfly counts (", y,")"),
                     subtitle = "- weekly visit (random resampled)",
                     x = "Day of Year",
                     y = "Count")
btfl_fig3
```



Generalized Additive Models with rbms

We will use the simulation to test the GAM method implemented in the R package rbms. Because recorders only report the number of observed butterflies, zeros are generally not reported but can be derived from the visit dates.

Organising BMS count data

```
visit_sim <- btfl_week_smpl[!date %in% btfl_week_missing$date, .(site_id, date, cour
count_sim <- visit_sim[count>=1,][, species := "sp1"]

names(visit_sim) <- toupper(names(visit_sim))
names(count_sim) <- toupper(names(count_sim))

ts_date <- rbms::ts_dwmy_table(InitYear = 2023, LastYear = 2023, WeekDay1 = 'monday'

ts_season <- rbms::ts_monit_season(ts_date,
```

```
                        StartMonth = 4,
                        EndMonth = 9,
                        StartDay = 1,
                        EndDay = NULL,
                        CompltSeason = TRUE,
                        Anchor = TRUE,
                        AnchorLength = 2,
                        AnchorLag = 2,
                        TimeUnit = 'd')

ts_season_visit <- rbms::ts_monit_site(ts_season, visit_sim)

ts_season_count <- rbms::ts_monit_count_site(ts_season_visit, count_sim, sp = "sp1")
```

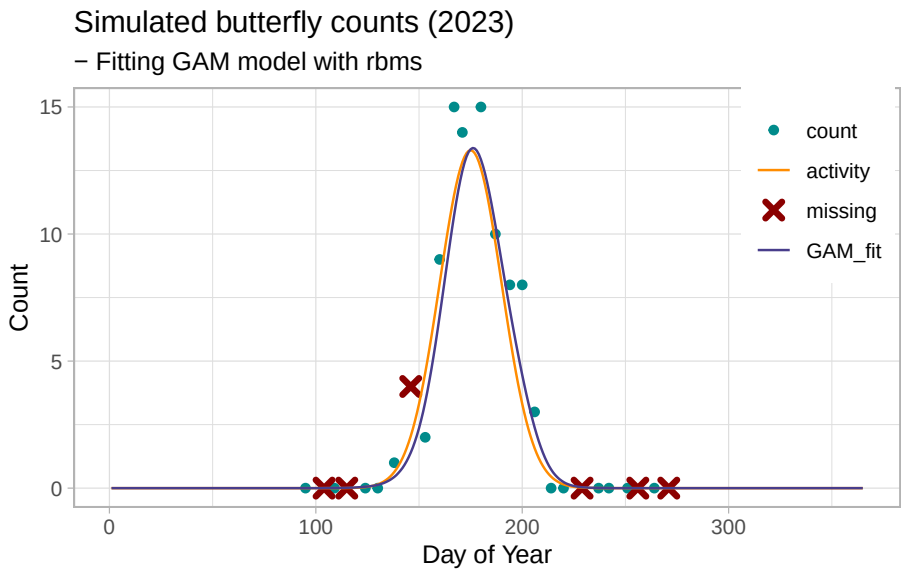
Fitting a GAM to Butterfly Counts

```
ts_flight_curve <- rbms::flight_curve(ts_season_count,
                        NbrSample = 300,
                        MinVisit = 5,
                        MinOccur = 3,
                        MinNbrSite = 1,
                        MaxTrial = 4,
                        GamFamily = 'nb',
                        SpeedGam = FALSE,
                        CompltSeason = TRUE,
                        SelectYear = NULL,
                        TimeUnit = 'd')
```

The flight curve computed by the `rbms::flight_curve()` function is stored in the …$pheno object where the days of year are stored under the variable `trimDAYNO` and the standardized flight curve under the variable `NM`. The `NM` variable is scaled to an Area Under the Curve (AUC) that sum to 1. To compare the flight curve derived from the GAM with the activity curve used for the simulation, we must rescale them to the same AUC, in other words, we must rescale the activity curve to have an AUC of 1 or rescale the `NM` to the population size used for the simulation. Here we will rescale the `NM` to match the simulation population size, this will allow us to display the curves and the counts on the same plot with the correct scale.

```
pheno <- ts_flight_curve$pheno

btfl_fig4 <- ggplot() +
                geom_point(data=ts_season_count[ANCHOR == 0 & !is.na(COUNT), ], aes(x=DAY_SINC
```

```
                  geom_point(data=btfl_week_missing, aes(x=doy, y=count, colour = "mis
                             shape=4, size=2, stroke=2) +
                  geom_line(data = btfl_ts, aes(x = doy, y = act, colour = "activity")
                  geom_line(data = pheno,
                      aes(x = trimDAYNO, y = btfl_ts[,unique(abund.true)]*NM, colour =
                  xlim(1,365) + ylim(0, max(btfl_ts$act,
                                            pheno$NM*btfl_ts[,unique(abund.true)],
                                            btfl_week_missing$count,
                                            ts_season_count[!is.na(COUNT), COUNT] )) +
                  scale_colour_manual("",
                        breaks = c("count", "activity", "missing", "GAM_fit"),
                        values = c(cnt_col, flc_col, missing_col, GAM_col)) +
                  theme_light() +
                  theme(legend.position = "inside", legend.position.inside = c(0.9, 0.
                  labs(title = paste0("Simulated butterfly counts (", y,")"),
                       subtitle = "- Fitting GAM model with rbms",
                       x = "Day of Year",
                       y = "Count")
btfl_fig4
```



To compare the fitted curve with the activity curve, we should use a standard AUC of 1 to enable a fair comparison between models fitted to different population sizes. Using the standardized activity curve and the GAM-generated flight curve (`NM`), we can calculate the Root Mean Squared Error (RMSE) to estimate the goodness of fit of the flight curve generated with the rbms package.

$$RMSE = \sqrt{\frac{1}{n}\sum_{i=1}^{n}(y_i - \tilde{y}_i)}$$

where y_i is the `NM` value at time i and $\tilde{y}_i$ the value from the standardized activity curve at time i, from day 1 to n of the monitoring season.

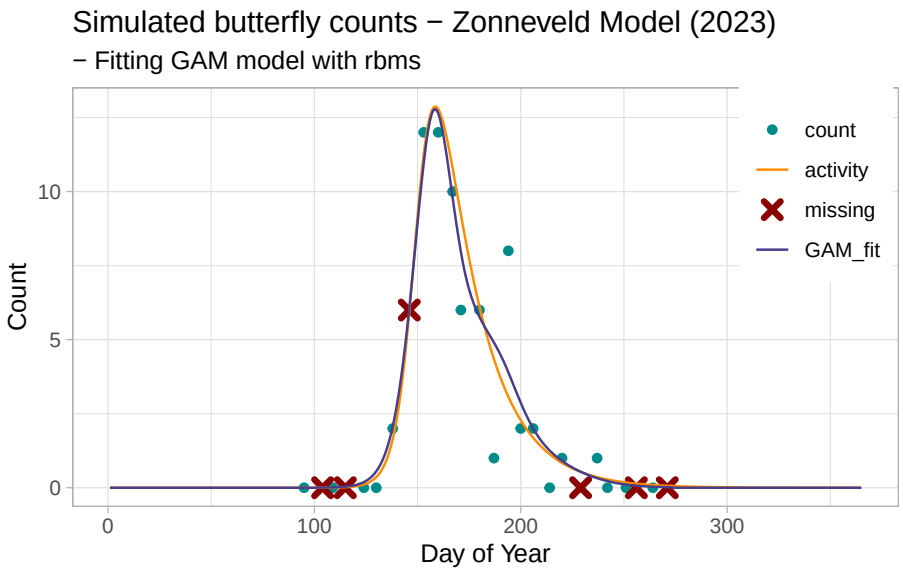
Non Gaussian flight curve

The same procedure can be applied to flight curves having more complex shapes. Here we will generate a time series of butterfly counts drawn from a known flight curve (adult activity), using simulation from a Zonneveld model.

```
btfl_data_zn <- timeseries_sim(nsims=1,
                year = c(2023),
                doy.samples = seq(from=1, to=365, by=1),
                abund.type = "exp",
                activity.type = "zon",
                sample.type = "pois",
                sim.parms = list(growth.rate = 0,
                                 init.size = 500,
                                 act.mean = 175,
                                 act.sd = 15,
                                 #theta = 5,
                                 zon.theta = 50,
                                 t0 = 100,
                                 beta = 5,
                                 alpha = 0.05)
                )


set.seed(13276)
btfl_ts <- sim2bms(data = btfl_data_zn$timeseries, yearKeep = y)

btfl_week_smpl <- sim2bms(data = btfl_data_zn$timeseries, yearKeep = y,
                  weeklySample = TRUE,
                  weekdayKeep = c(2:5),
                  monitoringSeason = c(4:9))

btfl_week_missing <- sample_missing(data = btfl_week_smpl, propMissing = 0.25)

visit_sim <- btfl_week_smpl[!date %in% btfl_week_missing$date, .(site_id, date, count)]
count_sim <- visit_sim[count>=1,][, species := "sp1"]
```

```
names(visit_sim) <- toupper(names(visit_sim))
names(count_sim) <- toupper(names(count_sim))

ts_date <- rbms::ts_dwmy_table(InitYear = 2023, LastYear = 2023, WeekDay1 = 'monday'

ts_season <- rbms::ts_monit_season(ts_date,
                        StartMonth = 4,
                        EndMonth = 9,
                        StartDay = 1,
                        EndDay = NULL,
                        CompltSeason = TRUE,
                        Anchor = TRUE,
                        AnchorLength = 2,
                        AnchorLag = 2,
                        TimeUnit = 'd')

ts_season_visit <- rbms::ts_monit_site(ts_season, visit_sim)

ts_season_count <- rbms::ts_monit_count_site(ts_season_visit, count_sim, sp = "sp1")

# mod_k <- "COUNT ~ s(DAY_SINCE, bs =\"cr\", k = 5) + factor(SITE_ID)"

ts_flight_curve <- rbms::flight_curve(ts_season_count,
                        NbrSample = 300,
                        MinVisit = 5,
                        MinOccur = 3,
                        MinNbrSite = 1,
                        MaxTrial = 4,
                        GamFamily = 'nb',
                        SpeedGam = FALSE,
                        CompltSeason = TRUE,
                        SelectYear = NULL,
                        #mod_form = mod_k,
                        TimeUnit = 'd')

pheno <- ts_flight_curve$pheno

btfl_fig5 <- ggplot() +
                geom_point(data=ts_season_count[ANCHOR == 0 & !is.na(COUNT), ], aes(
                geom_point(data=btfl_week_missing, aes(x=doy, y=count, colour = "mis
                            shape=4, size=2, stroke=2) +
                geom_line(data = btfl_ts, aes(x = doy, y = act, colour = "activity")
                geom_line(data = pheno, aes(x = trimDAYNO, y = btfl_ts[,unique(abund
                xlim(1,365) + ylim(0, max(btfl_ts$act,
```

```
                                          pheno$NM*btfl_ts[,unique(abund.true)],
                                          btfl_week_missing$count,
                                          ts_season_count[!is.na(COUNT), COUNT] )) +
                  scale_colour_manual("",
                        breaks = c("count", "activity", "missing", "GAM_fit"),
                        values = c(cnt_col, flc_col, missing_col, GAM_col)) +
                  theme_light() +
                  theme(legend.position = "inside", legend.position.inside = c(0.9, 0.8)) +
                  labs(title = paste0("Simulated butterfly counts - Zonneveld Model (", y,")"),
                       subtitle = "- Fitting GAM model with rbms",
                       x = "Day of Year",
                       y = "Count")
btfl_fig5
```



Simple trend case

In the first scenario, we will apply the method to a simple case where we have one univoltine species that is monitored over 15 years across 100 sites where the populations follow the same trend with a known growth rate.

Part III

Bibliography

References

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