sparta - Species Presence/Absence R Trends Analyses

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Contents

1 Introduction

Sparta provides a range of tools for analysing trends in species occurrence data and is based on the work presented in Isaac et al (2014). The data that is used in these method is 'what where and when'. The 'what' is typically a species name. 'Where' is the location of the observation, sometimes referred to as the site. This is typically a 1km, 2km or 10km grid square but could also be a none regular location such as field sites or counties. 'When' is the time when an observation is made, and the requirements differ between methods. Some methods require a date while others require you to aggregate dates into time periods for comparison.

All of the methods described here require multi species data. This is because they use information across all species to assess biases.

In this vignette we will run through the methods and show how they can be used in reproducible examples.

1.1 Installation

Installing the package is easy and can be done from CRAN. Alternatively the development version can be installed from GitHub.

NOTE: JAGS must be installed before the R package installation will work. JAGS can be found here - http://sourceforge.net/projects/mcmc-jags/files/JAGS/

```r
# Install the package from CRAN
# THIS WILL WORK ONLY AFTER THE PACKAGE IS PUBLISHED
install.packages('sparta')

# Or install the development version from GitHub
library(devtools)
install_github('biologicalrecordscentre/sparta')
```

```r
# Once installed, load the package
library(sparta)
```

```
## Loading required package: lme4
## Loading required package: Matrix
## Loading required package: Rcpp
```

The functions in sparta cover a range of tasks. Primarily they are focused on analysing trends in species occurrence data while accounting for biases (see Isaac et al, 2014). In this vignette we step through these functions and others so that you can understand how the package works. If you have any questions you can find the package maintainers email address using `maintainer('sparta')`, and if you have issues or bugs you can report them here

2 Modelling methods

2.1 Create some example data

Clearly when you are using sparta you will want to use your own data, however perhaps you are only at the planning stage of your project? This code shows you how to create some example data so that you can try out sparta's functionality.

```r
# Create data
n <- 8000 # size of dataset
nyr <- 50 # number of years in data
nSamples <- 200 # set number of dates
nSites <- 100 # set number of sites
set.seed(125) # set a random seed

# Create somes dates
first <- as.Date(strptime("1950/01/01", "%Y/%m/%d"))
last <- as.Date(strptime(paste(1950+(nyr-1),"/12/31", sep=''), "%Y/%m/%d"))
dt <- last-first
rDates <- first + (runif(nSamples)*dt)

# taxa are set semi-randomly
taxa_probabilities <- seq(from = 0.1, to = 0.7, length.out = 26)
taxa <- sample(letters, size = n, TRUE, prob = taxa_probabilities)

# sites are visited semi-randomly
site_probabilities <- seq(from = 0.1, to = 0.7, length.out = nSites)
site <- sample(paste('A', 1:nSites, sep=''), size = n, TRUE, prob = site_probabilities)

# the date of visit is selected semi-randomly from those created earlier
time_probabilities <- seq(from = 0.1, to = 0.7, length.out = nSamples)
time_period <- sample(rDates, size = n, TRUE, prob = time_probabilities)

myData <- data.frame(taxa, site, time_period)

# Let's have a look at the my example data
head(myData)
```

```
##   taxa site time_period
## 1    r  A51  1970-01-14
## 2    v  A87  1980-09-29
## 3    e  A56  1996-04-14
## 4    z  A28  1959-01-16
## 5    r  A77  1970-09-21
## 6    x  A48  1990-02-25
```

In general this is the format of data you will need for all of the functions in sparta. The taxa and site columns should be characters and the time_period column should ideally be a date but can in some cases be a numeric.

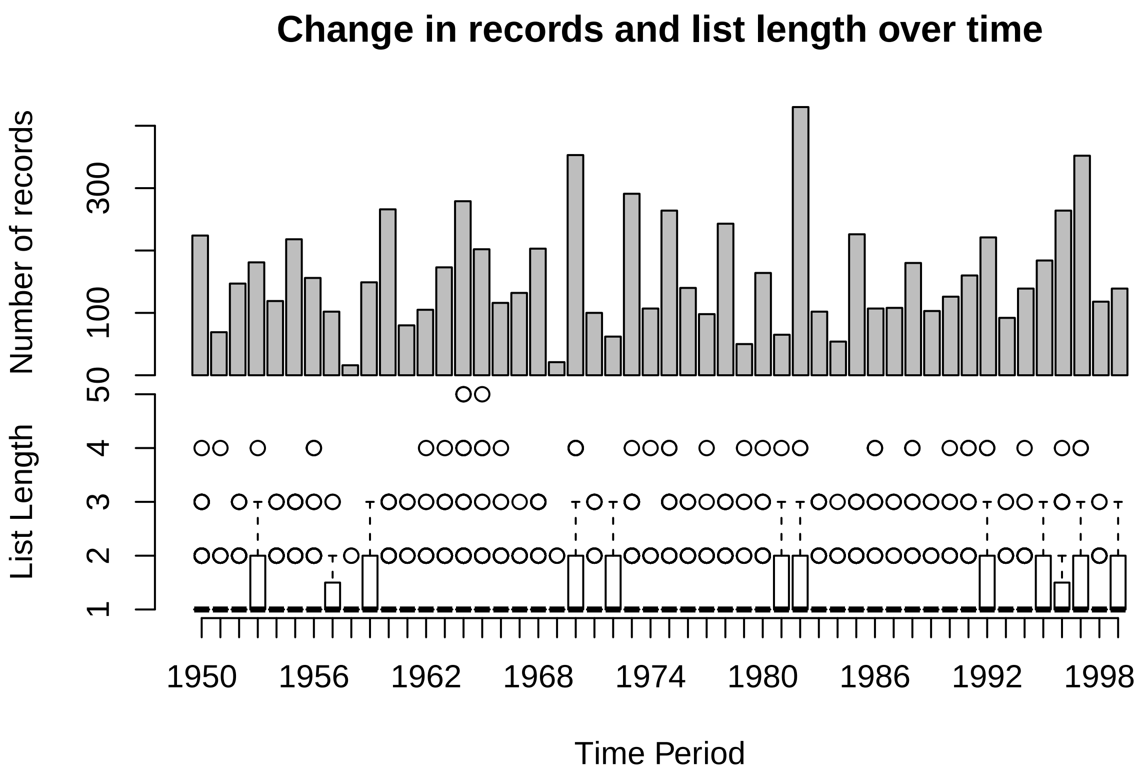
There are many sources of wildlife observation data including GBIF (Global Biodiversity Information Facility) and the NBN gateway (National Biodiversity Network). Both of these repositories have R packages that will allow you to download this type of data straight into your R session (see rgbif and rnbn for details)

2.2 Assessing the quality of data

It can be useful to have a look at your data before you do any analyses. For example it is important to understand the biases in your data. The function `dataDiagnostics` is designed to help with this.

```
# Run some data diagnostics on our data
results <- dataDiagnostics(taxa = myData$taxa,
                           site = myData$site,
                           time_period = myData$time_period,
                           progress_bar = FALSE)
```

```
## Warning in errorChecks(taxa = taxa, site = site, time_period =
## time_period): 94 out of 8000 observations will be removed as duplicates
```



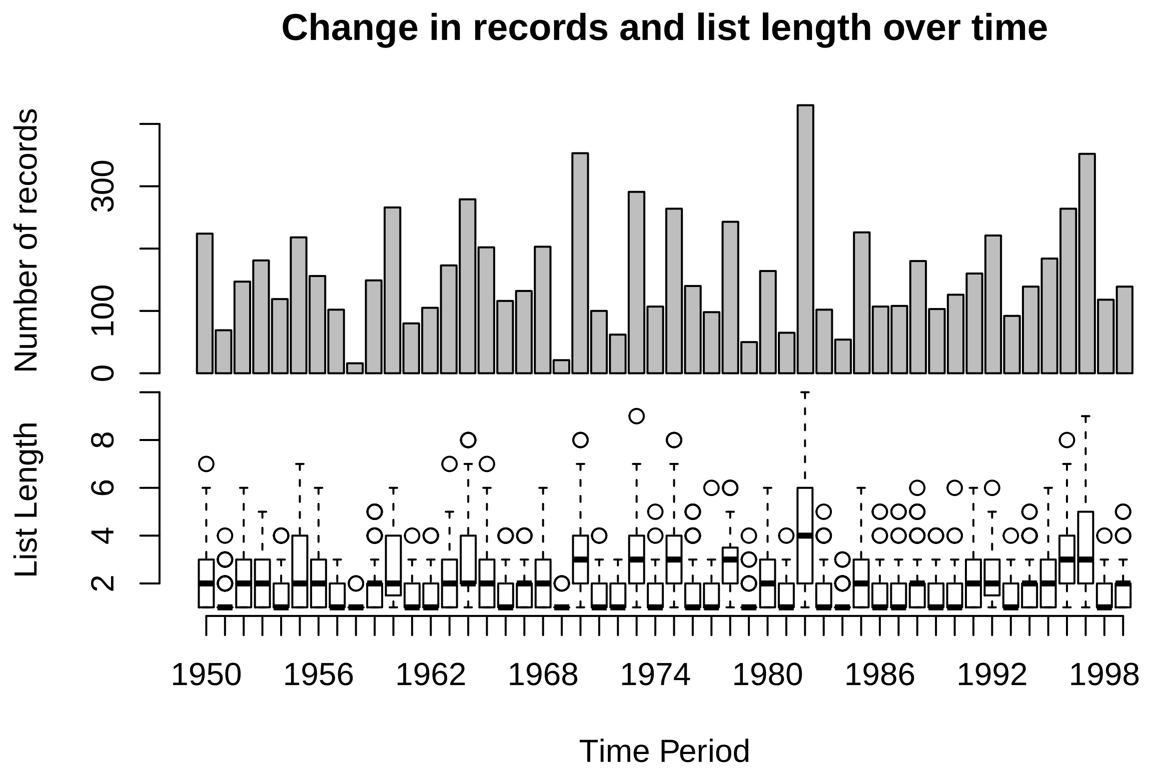
```
## ## Linear model outputs ##
##
## There is no detectable change in the number of records over time:
##
##                  Estimate   Std. Error    t value  Pr(>|t|)
## (Intercept) -894.8997359 1710.0719088 -0.5233112 0.6031654
## time_period    0.5342617    0.8660553  0.6168910 0.5402219
##
##
## There is no detectable change in list lengths over time:
##
```

```
##                   Estimate   Std. Error    z value     Pr(>|z|)
## (Intercept) 2.390402e-01 1.208657e-02 19.7773477 4.665954e-87
## time_period 1.098369e-06 2.135956e-06  0.5142282 6.070924e-01
```

The plot produced shows the number of records for each year in the top plot and the average list length in a box plot at the bottom. List length is the number of taxa observed on a visit to a site, where a visit is taken to be a unique combination of 'where' and 'when'. A trend in the number of observations across time is not uncommon and a formal test for such a trend is performed in the form of a linear model. Trends in the number of records over time are handled by all of the methods presented in sparta in a variety of different ways. Trends in list length are tested in the same manner, and both are returned to the console. A in list length can cause some methods such as the reporting rate methods to fail (see 'LessEffortPerVisit' scenario in Isaac et al (2014)) Unsurprisingly, since this is a random dataset, we have no trend in either the number of records or list length over time. This function also works if we have a numeric for time period such as the year

```
# Run some data diagnostics on our data, now time_period
# is set to be a year
results <- dataDiagnostics(taxa = myData$taxa,
                           site = myData$site,
                           time_period = as.numeric(format(myData$time_period, '%Y')),
                           progress_bar = FALSE)
```

```
## Warning in errorChecks(taxa = taxa, site = site, time_period =
## time_period): 419 out of 8000 observations will be removed as duplicates
```



```
## ## Linear model outputs ##
```

```
##
## There is no detectable change in the number of records over time:
##
##                  Estimate   Std. Error    t value  Pr(>|t|)
## (Intercept) -894.8997359 1710.0719088 -0.5233112 0.6031654
## time_period    0.5342617    0.8660553  0.6168910 0.5402219
##
##
## There is no detectable change in list lengths over time:
##
##                   Estimate   Std. Error    z value  Pr(>|z|)
## (Intercept) -0.6465523185 1.5554513917 -0.4156686 0.6776525
## time_period  0.0007201245 0.0007874907  0.9144546 0.3604780
```

If we want to view these results in more detail we can interrogate the object `results`

```
# See what is in results..
names(results)
```

```
## [1] "RecordsPerYear"  "VisitListLength" "modelRecs"       "modelList"
```

```
# Let's have a look at the details
head(results$RecordsPerYear)
```

```
## RecordsPerYear
## 1950 1951 1952 1953 1954 1955
##  224   69  147  181  119  218
```

```
head(results$VisitListLength)
```

```
##   time_period site listLength
## 1        1950 A100          3
## 2        1950  A11          1
## 3        1950  A12          2
## 4        1950  A13          1
## 5        1950  A15          1
## 6        1950  A16          2
```

```
summary(results$modelRecs)
```

```
##
## Call:
## glm(formula = count ~ time_period, data = mData)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -136.06   -59.03   -22.40    50.51   265.99
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -894.8997  1710.0719  -0.523    0.603
## time_period    0.5343     0.8661   0.617    0.540
##
## (Dispersion parameter for gaussian family taken to be 7809.915)
##
##     Null deviance: 377848  on 49  degrees of freedom
## Residual deviance: 374876  on 48  degrees of freedom
## AIC: 594.01
##
## Number of Fisher Scoring iterations: 2
```

```
summary(results$modelList)
```

```
##
## Call:
## glm(formula = listLength ~ time_period, family = "poisson", data = space_time)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -0.9132  -0.8866  -0.1309   0.5260   3.8475
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.6465523  1.5554514  -0.416    0.678
## time_period  0.0007201  0.0007875   0.914    0.360
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 2737.1  on 3489  degrees of freedom
## Residual deviance: 2736.3  on 3488  degrees of freedom
## AIC: 11607
##
## Number of Fisher Scoring iterations: 5
```

2.3 Telfer

Telfer's change index is designed to assess the relative change in range size of species between two time periods (Telfer et al, 2002). This is a simple method that is robust but has low power to detect trends where they exist. While this method is designed to compare two time period sparta can take many time periods and will complete all pairwise comparisons.

Our data is not quite in the correct format for Telfer since it is used to compare time periods but our `time_period` column is a date. We can fix this by using the `date2timeperiod` function.

```
## Create a new column for the time period
# First define my time periods
time_periods <- data.frame(start = c(1950, 1960, 1970, 1980, 1990),
                           end = c(1959, 1969, 1979, 1989, 1999))

time_periods
```

```
##   start  end
## 1  1950 1959
## 2  1960 1969
## 3  1970 1979
## 4  1980 1989
## 5  1990 1999
```

```
# Now use these to assign my dates to time periods
myData$tp <- date2timeperiod(myData$time_period, time_periods)

head(myData)
```

```
##   taxa site time_period tp
## 1    r  A51  1970-01-14  3
## 2    v  A87  1980-09-29  4
## 3    e  A56  1996-04-14  5
## 4    z  A28  1959-01-16  1
## 5    r  A77  1970-09-21  3
## 6    x  A48  1990-02-25  5
```

As you can see our new column indicates which time period each date falls into with 1 being the earliest time period, 2 being the second and so on. This function will also work if instead of a single date for each record you have a date range

```
## Create a dataset where we have date ranges
Date_range <- data.frame(startdate = myData$time_period,
                         enddate = (myData$time_period + 600))

head(Date_range)
```

```
##    startdate    enddate
## 1 1970-01-14 1971-09-06
## 2 1980-09-29 1982-05-22
## 3 1996-04-14 1997-12-05
## 4 1959-01-16 1960-09-07
## 5 1970-09-21 1972-05-13
## 6 1990-02-25 1991-10-18
```

```
# Now assign my date ranges to time periods
Date_range$time_period <- date2timeperiod(Date_range, time_periods)

head(Date_range)
```

```
##    startdate    enddate time_period
## 1 1970-01-14 1971-09-06           3
## 2 1980-09-29 1982-05-22           4
## 3 1996-04-14 1997-12-05           5
## 4 1959-01-16 1960-09-07          NA
## 5 1970-09-21 1972-05-13           3
## 6 1990-02-25 1991-10-18           5
```

As you can see in this example when a date range spans the boundaries of your time periods NA is returned.

Now we have our data in the right format we can use the `telfer` function to analyse the data. The Telfer index for each species is the standardized residual from a linear regression across all species and is a measure of relative change only as the average real trend across species is obscured (Isaac et al (2014); Telfer et al, 2002).Telfer is used for comparing two time periods and if you have more than this the `telfer` function will all pair-wise comparisons.

```
# Here is our data
head(myData)
```

```
##   taxa site time_period tp
## 1    r  A51  1970-01-14  3
## 2    v  A87  1980-09-29  4
## 3    e  A56  1996-04-14  5
## 4    z  A28  1959-01-16  1
## 5    r  A77  1970-09-21  3
## 6    x  A48  1990-02-25  5
```

```
telfer_results <- telfer(taxa = myData$taxa,
                         site = myData$site,
                         time_period = myData$tp,
                         minSite = 2)
```

```
## Warning in errorChecks(taxa = taxa, site = site, time_period =
## time_period, : 2541 out of 8000 observations will be removed as duplicates
```

We get a warning message indicating that a large number of rows are being removed as duplicates. This occurs since we are now aggregating records into time periods and therefore creating a large number of duplicates.

The results give the change index for each species (rows) in each of the pairwise comparisons of time periods (columns).

```
head(telfer_results)
```

```
##   taxa  Telfer_1_2   Telfer_1_3 Telfer_1_4 Telfer_1_5 Telfer_2_3
## 1    a -0.67842545 -1.744577671 -1.8073843 -0.7000801 -1.8352888
## 2    b -0.90368128 -0.841219630 -0.8697828 -1.5449132 -0.5139840
## 3    c  0.96096754 -0.008737329  0.2181534  0.3726534 -0.7254485
## 4    d  0.79744179 -0.558165922  0.3848417  1.6642357 -1.1759409
## 5    e -0.01856808  0.490523483 -1.0901348 -1.6500473  0.3450083
## 6    f -0.80201507 -0.412461197 -1.0846426  0.3817399  0.1657078
##   Telfer_2_4 Telfer_2_5 Telfer_3_4 Telfer_3_5 Telfer_4_5
## 1 -2.1097232 -0.4557972 -1.1728237  0.8437536  1.4880569
## 2 -0.6234749 -0.8326960 -0.3171487 -1.1756988 -0.8995878
## 3 -0.3891040 -0.3595835  0.3549603 -0.2184517 -0.3834038
## 4 -0.1875890  0.5294236  1.2663488  1.3562488  0.6466352
## 5 -1.1254544 -1.7153826 -1.8881411 -2.1972910 -1.0810351
## 6 -0.5122655  0.8827473 -0.8383498  0.4662370  1.3111555
```

2.4 Reporting Rate Models

The reporting rates models in sparta are all either GLMs or GLMMs with year as a continuous covariate but are flexible, giving the user a number of options for their analyses. These options include the addition of covariates to account for biases in the data including a random site effect and fixed effect of list length.

In Isaac et al (2014) it was shown that reporting rate models can be susceptible to type 1 errors under certain scenarios and that with site and list length covariates the models performed better when the data were bias. These methods were found to out perform simple methods like Telfer.

The common feature among these models is that the quantity under consideration is the ‘probability of being recorded’. When binomial models are used (as is the default), it’s the ‘probability for an average visit’ for the Bernoulli version it is the probability of being recorded per time period.

2.4.1 Data selection

Before undertaking modelling the data can be subset in an effort to remove data that may introduce bias. Model sub-setting was found to reduce power in Isaac et al (2014) but can partially deal with uneven sampling of site. This process can also be used with other methods and is not solely applicable to the reporting rate models.

The first function allows you to subset your data by list length. This works out, for each combination of ‘where’ and ‘when’ (a visit), the number of species observed (list length). Any records that to not come from a list that meets your list length criteria are then dropped.

```
# Select only records which occur on lists of length 2 or more
myDataL <- siteSelectionMinL(taxa = myData$taxa,
                             site = myData$site,
                             time_period = myData$time_period,
                             minL = 2)
```

```
## Warning in errorChecks(taxa, site, time_period): 94 out of 8000
## observations will be removed as duplicates
```

```
head(myDataL)
```

```
##   taxa site time_period
## 1    u   A1  1952-11-16
## 2    n   A1  1952-11-16
## 3    x   A1  1960-06-06
## 4    s   A1  1960-06-06
## 5    x   A1  1999-08-03
## 6    d   A1  1999-08-03
```

```
# We now have a much smaller dataset after subsetting
nrow(myData)
```

```
## [1] 8000
```

```
nrow(myDataL)
```

```
## [1] 3082
```

We are also able to subset by the number of times a site is sampled. The function `siteSelectionMinTP` does this. When time_period is a date, as in this case, minTP is minimum number of years a site must be sampled in for it be included in the subset.

```
# Select only data from sites sampled in at least 10 years
myDataTP <- siteSelectionMinTP(taxa = myData$taxa,
                               site = myData$site,
                               time_period = myData$time_period,
                               minTP = 10)
```

```
## Warning in errorChecks(taxa, site, time_period): 94 out of 8000
## observations will be removed as duplicates
```

```
head(myDataTP)
```

```
##   taxa site time_period
## 1    r  A51  1970-01-14
## 2    v  A87  1980-09-29
## 3    e  A56  1996-04-14
## 4    z  A28  1959-01-16
## 5    r  A77  1970-09-21
## 6    x  A48  1990-02-25
```

```
# Here we have only lost a small number rows, this is because
# many sites in our data are visited in a lot of years. Those
# rows that have been removed are duplicates
nrow(myData)
```

```
## [1] 8000
```

```
nrow(myDataTP)
```

```
## [1] 7906
```

As you can see in the above example minTP specifies the number of years a site must be sampled in order to be included. However, our dataset is very well sampled so we might be interested in another measure of time. For example, you might want only sites that have been observed in at least 60 months. Let's see how this could be done.

```
# We need to create a new column to represent unique months
# this could also be any unit of time you wanted (week, decade, etc.)

# This line returns a unique character for each month
unique_Months <- format(myData$time_period, "%B_%Y")
head(unique_Months)
```

```
## [1] "January_1970"   "September_1980" "April_1996"     "January_1959"
## [5] "September_1970" "February_1990"
```

```
# Week could be done like this, see ?strptime for more details
unique_Weeks <- format(myData$time_period, "%U_%Y")
head(unique_Weeks)
```

```
## [1] "02_1970" "39_1980" "15_1996" "02_1959" "38_1970" "08_1990"
```

```r
# Now lets subset to records found on 60 months or more
myData60Months <- siteSelectionMinTP(taxa = myData$taxa,
                                     site = myData$site,
                                     time_period = unique_Months,
                                     minTP = 60)
```

```
## Warning in errorChecks(taxa, site, time_period): 129 out of 8000
## observations will be removed as duplicates
```

```r
head(myData60Months)
```

```
##   taxa site    time_period
## 1    r  A51   January_1970
## 2    v  A87 September_1980
## 3    e  A56     April_1996
## 5    r  A77 September_1970
## 6    x  A48  February_1990
## 7    t  A59   January_1981
```

```r
# We could merge this back with our original data if
# we need to retain the full dates
myData60Months <- merge(myData60Months, myData$time_period,
                        all.x = TRUE, all.y = FALSE,
                        by = "row.names")
head(myData60Months)
```

```
##   Row.names taxa site  time_period          y
## 1         1    r  A51 January_1970 1970-01-14
## 2        10    w  A81    June_1982 1982-06-19
## 3       100    v  A91 January_1996 1996-01-29
## 4      1000    h  A94     May_1990 1981-01-17
## 5      1001    m  A73   March_1999 1990-05-18
## 6      1002    b  A59    July_1997 1999-03-05
```

```r
nrow(myData)
```

```
## [1] 8000
```

```r
nrow(myData60Months)
```

```
## [1] 5289
```

Following the method in Roy et al (2012) we can combine these two functions to subset both by the length of lists and by the number of years that sites are sampled. This has been wrapped up in to the function `siteSelection` which takes all the arguments of the previous two functions plus the argument `LFirst` which indicates whether the data should be subset by list length first (`TRUE`) or second (`FALSE`).

```r
# Subset our data as above but in one go
myDataSubset  <- siteSelection(taxa = myData$taxa,
                               site = myData$site,
                               time_period = myData$time_period,
                               minL = 2,
                               minTP = 10,
                               LFirst = TRUE)
```

```
## Warning in errorChecks(taxa, site, time_period): 94 out of 8000
## observations will be removed as duplicates
```

```r
head(myDataSubset)
```

```
##    taxa site time_period
## 11    y A100  1950-01-04
## 12    k A100  1950-01-04
## 13    l A100  1954-01-30
## 14    o A100  1954-01-30
## 15    s A100  1954-01-30
## 16    m A100  1956-02-02
```

```r
nrow(myDataSubset)
```

```
## [1] 2587
```

2.4.2 Running Reporting Rate Models

Once you have subset your data using the above functions (or perhaps not at all) the reporting rate models can be applied using the function `reportingRateModel`. This function offers flexibility in the model you wish to fit, allowing the user to specify whether list length and site should be used as covariates, whether over-dispersion should be used, and whether the family should be binomial or Bernoulli. A number of these variants are presented in Isaac et al (2014). While multi-species data is required it is not nessecary to model all species. In fact you can save a significant amount of time by only modelling hte species you are interested in.

```r
# Run the reporting rate model using list length as a fixed effect and
# site as a random effect. Here we only model a few species.
system.time({
RR_out <- reportingRateModel(taxa = myData$taxa,
                             site = myData$site,
                             time_period = myData$time_period,
                             list_length = TRUE,
                             site_effect = TRUE,
                             species_to_include = c('e','u','r','o','t','a','s'),
                             overdispersion = FALSE,
                             family = 'Bernoulli',
                             print_progress = TRUE)
})
```

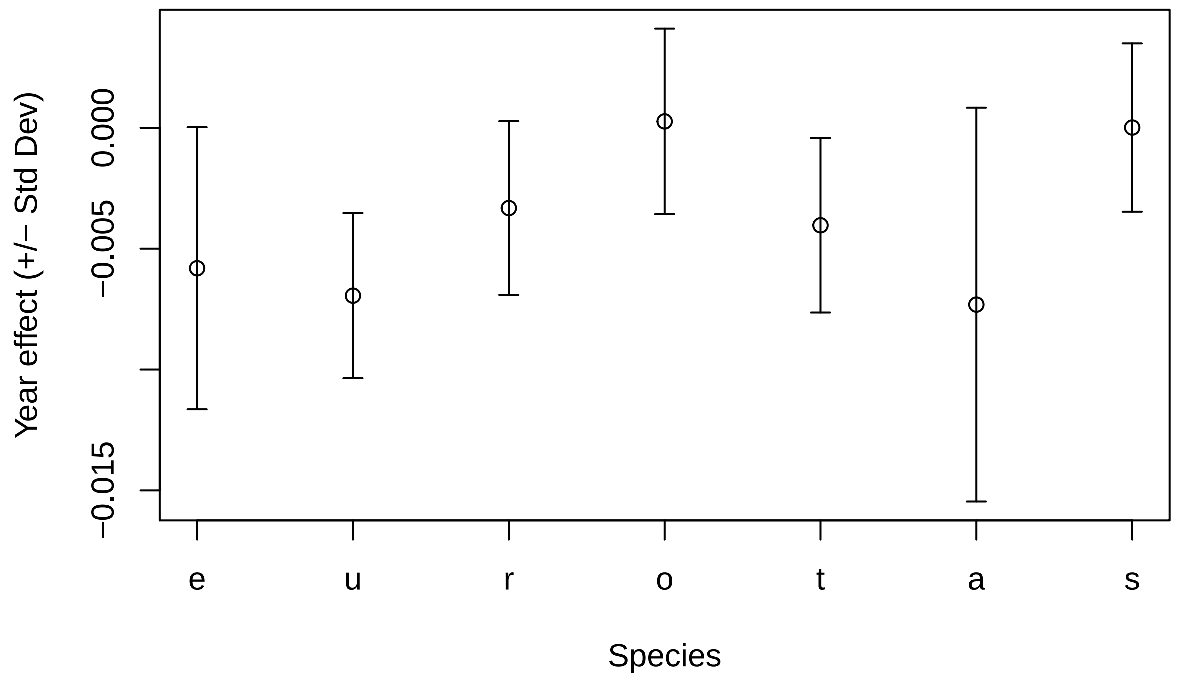
```
## Warning in errorChecks(taxa = taxa, site = site, time_period =
## time_period, : 94 out of 8000 observations will be removed as duplicates
## Modelling e - Species 1 of 7
## Modelling u - Species 2 of 7
## Modelling r - Species 3 of 7
## Modelling o - Species 4 of 7
## Modelling t - Species 5 of 7
## Modelling a - Species 6 of 7
## Modelling s - Species 7 of 7
```

```
##    user  system elapsed
##   10.96    0.04   11.13
```

```
# Let's have a look at the data that is returned
str(RR_out)
```

```
## 'data.frame':    7 obs. of  14 variables:
##  $ species_name       : Factor w/ 7 levels "e","u","r","o",..: 1 2 3 4 5 6 7
##  $ intercept.estimate : num  -4.53 -3.52 -3.32 -3.63 -3.68 ...
##  $ year.estimate      : num  -0.005811 -0.006944 -0.003321 0.000264 -0.004033 ...
##  $ listlength.estimate: num  0.574 0.702 0.472 0.572 0.717 ...
##  $ intercept.stderror : num  0.185 0.113 0.123 0.129 0.116 ...
##  $ year.stderror      : num  0.00583 0.00342 0.00359 0.00384 0.00361 ...
##  $ listlength.stderror: num  0.1092 0.0659 0.0754 0.0759 0.0683 ...
##  $ intercept.zvalue   : num  -24.5 -31.3 -27.1 -28.2 -31.6 ...
##  $ year.zvalue        : num  -0.9961 -2.0324 -0.9244 0.0688 -1.1177 ...
##  $ listlength.zvalue  : num  5.25 10.65 6.26 7.54 10.49 ...
##  $ intercept.pvalue   : num  2.34e-132 1.58e-214 6.06e-162 1.07e-174 3.78e-219 ...
##  $ year.pvalue        : num  0.3192 0.0421 0.3553 0.9452 0.2637 ...
##  $ listlength.pvalue  : num  1.51e-07 1.68e-26 3.76e-10 4.78e-14 9.57e-26 ...
##  $ observations       : num  144 450 398 346 398 73 426
##  - attr(*, "intercept_year")= num 1974
##  - attr(*, "min_year")= num -24.5
##  - attr(*, "max_year")= num 24.5
##  - attr(*, "nVisits")= int 6211
##  - attr(*, "model_formula")= chr "taxa ~ year + listLength + (1|site)"
```

```
# We could plot these to see the species trends
with(RR_out,
     # Plot graph
     {plot(x = 1:7, y = year.estimate,
           ylim = range(c(year.estimate - year.stderror,
                          year.estimate + year.stderror)),
           ylab = 'Year effect (+/- Std Dev)',
           xlab = 'Species',
           xaxt = "n")
     # Add x-axis with species names
     axis(1, at = 1:7, labels = species_name)
     # Add the error bars
     arrows(1:7, year.estimate - year.stderror,
            1:7, year.estimate + year.stderror,
            length = 0.05, angle = 90, code = 3)}
     )
```



The returned object is a data frame with one row per species. Each column gives information on an element of the model output including covariate estimates, standard errors and p-values. This object also has some attributes giving the year that was chosen as the intercept, the number of visits in the dataset and the model formula used.

These models can take a long time to run when your data set is larg or you have a large number of species to model. To make this faster it is possible to parallelise this process across species which can significantly improve your run times. Here is an example of how we would parallelise the above example using hte R package snowfall.

```r
# Load in snowfall
library(snowfall)
```

```
## Loading required package: snow
```

```r
# I have 4 cpus on my PC so I set cpus to 4
# when I initialise the cluster
sfInit(parallel = TRUE, cpus = 4)
```

```
## Warning in searchCommandline(parallel, cpus = cpus, type = type,
## socketHosts = socketHosts, : Unknown option on commandline:
## rmarkdown::render('W:/PYWELL_SHARED/Pywell Projects/BRC/Tom August/R
## Packages/Trend analyses/sparta/vignette/sparta_vignette.Rmd', encoding
```

```
## R Version:  R version 3.2.0 (2015-04-16)
## snowfall 1.84-6 initialized (using snow 0.3-13): parallel execution on 4 CPUs.
```

```r
# Export my data to the cluster
sfExport('myData')

# I create a function that takes a species name and runs my models
RR_mod_function <- function(taxa_name){

  library(sparta)

  RR_out <- reportingRateModel(species_to_include = taxa_name,
                               taxa = myData$taxa,
                               site = myData$site,
                               time_period = myData$time_period,
                               list_length = TRUE,
                               site_effect = TRUE,
                               overdispersion = FALSE,
                               family = 'Bernoulli',
                               print_progress = FALSE)
}

# I then run this in parallel
system.time({
para_out <- sfClusterApplyLB(c('e','u','r','o','t','a','s'), RR_mod_function)
})
```

```
##    user  system elapsed
##    0.00    0.00    7.07
```

```r
# Name each element of this output by the species
RR_out_combined <- do.call(rbind, para_out)

# Stop the cluster
sfStop()
```

```
##
## Stopping cluster
```

```r
# You'll see the output is the same as when we did it serially but the
# time taken is shorter. Using a cluster computer with many more than
# 4 cores can greatly reduce run time.
str(RR_out_combined)
```

```
## 'data.frame':    7 obs. of  14 variables:
##  $ species_name       : Factor w/ 7 levels "e","u","r","o",..: 1 2 3 4 5 6 7
##  $ intercept.estimate : num  -4.53 -3.52 -3.32 -3.63 -3.68 ...
##  $ year.estimate      : num  -0.005811 -0.006944 -0.003321 0.000264 -0.004033 ...
##  $ listlength.estimate: num  0.574 0.702 0.472 0.572 0.717 ...
##  $ intercept.stderror : num  0.185 0.113 0.123 0.129 0.116 ...
##  $ year.stderror      : num  0.00583 0.00342 0.00359 0.00384 0.00361 ...
##  $ listlength.stderror: num  0.1092 0.0659 0.0754 0.0759 0.0683 ...
##  $ intercept.zvalue   : num  -24.5 -31.3 -27.1 -28.2 -31.6 ...
##  $ year.zvalue        : num  -0.9961 -2.0324 -0.9244 0.0688 -1.1177 ...
##  $ listlength.zvalue  : num  5.25 10.65 6.26 7.54 10.49 ...
##  $ intercept.pvalue   : num  2.34e-132 1.58e-214 6.06e-162 1.07e-174 3.78e-219 ...
##  $ year.pvalue        : num  0.3192 0.0421 0.3553 0.9452 0.2637 ...
##  $ listlength.pvalue  : num  1.51e-07 1.68e-26 3.76e-10 4.78e-14 9.57e-26 ...
##  $ observations       : num  144 450 398 346 398 73 426
##  - attr(*, "intercept_year")= num 1974
##  - attr(*, "min_year")= num -24.5
##  - attr(*, "max_year")= num 24.5
##  - attr(*, "nVisits")= int 6211
##  - attr(*, "model_formula")= chr "taxa ~ year + listLength + (1|site)"
```

Using these functions it is possible to recreate the 'Well-sampled sites' method that is presented in Roy et al (2012) and Thomas et al (2015). This is made available in the function `WSS` which is a simple wrapper around `siteSelection` and `reportingratemodel`. In this variant the data is subset by list length and the number of years each site was sampled before being run in a GLMM with site as a random effect.

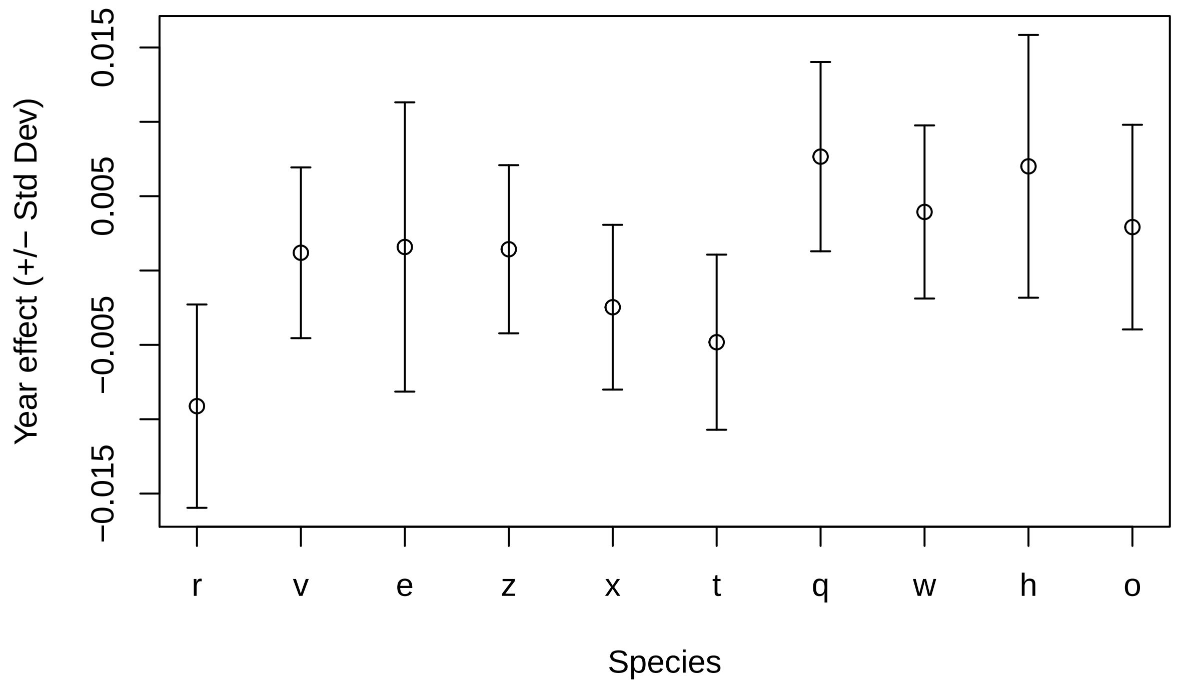
```
# Run our data through the well-sampled sites function
# This time we run all species
WSS_out <- WSS(taxa = myData$taxa,
               site = myData$site,
               time_period = myData$time_period,
               minL = 2,
               minTP = 10,
               print_progress = FALSE)
```

```
## Warning in errorChecks(taxa, site, time_period): 94 out of 8000
## observations will be removed as duplicates
```

```
# The data is returned in the same format as from reportingRateModel
str(WSS_out)
```

```
## 'data.frame':    26 obs. of  10 variables:
##  $ species_name      : Factor w/ 26 levels "r","v","e","z",..: 1 2 3 4 5 6 7 8 9 10 ...
##  $ intercept.estimate: num  -2.29 -1.85 -3.17 -1.81 -1.75 ...
##  $ year.estimate     : num  -0.00912 0.0012 0.00158 0.00143 -0.00247 ...
##  $ intercept.stderror: num  0.1021 0.0861 0.1875 0.0848 0.0829 ...
##  $ year.stderror     : num  0.00684 0.00574 0.00973 0.00565 0.00554 ...
##  $ intercept.zvalue  : num  -22.4 -21.5 -16.9 -21.3 -21.1 ...
##  $ year.zvalue       : num  -1.334 0.208 0.163 0.253 -0.446 ...
##  $ intercept.pvalue  : num  1.70e-111 1.66e-102 6.55e-64 6.87e-101 1.06e-98 ...
##  $ year.pvalue       : num  0.182 0.835 0.871 0.8 0.656 ...
##  $ observations      : num  106 157 50 163 171 148 125 155 61 104 ...
##  - attr(*, "intercept_year")= num 1974
##  - attr(*, "min_year")= num -24.5
##  - attr(*, "max_year")= num 24.5
##  - attr(*, "nVisits")= int 1155
##  - attr(*, "model_formula")= chr "cbind(successes, failures) ~ year + (1|site)"
##  - attr(*, "minL")= num 2
##  - attr(*, "minTP")= num 10
```

```
# We can plot these and see that we get different results to our
# previous analysis since this time the method includes subsetting
with(WSS_out[1:10,],
     # Plot graph
     {plot(x = 1:10, y = year.estimate,
           ylim = range(c(year.estimate - year.stderror,
                          year.estimate + year.stderror)),
           ylab = 'Year effect (+/- Std Dev)',
           xlab = 'Species',
           xaxt="n")
     # Add x-axis with species names
     axis(1, at=1:10, labels = species_name[1:10])
     # Add the error bars
     arrows(1:10, year.estimate - year.stderror,
            1:10, year.estimate + year.stderror,
            length=0.05, angle=90, code=3)}
     )
```



2.5 Occupancy models

Occupancy models were found by Isaac et al (2014) to be one of the best tools for analysing species occurrence data typical of citizen science projects, being both robust and powerful. This method models the occupancy process separately from the detection process, but we will not go in to the details of the model here since there is a growing literature about occupancy models, how and when they should be used. Here we focus on how the occupancy model discussed in Isaac et al 2014 is implemented in `sparta`.

This function works in a very similar fashion to that of the previous functions we have discussed. The data it takes is 'What, where, when' as in other functions, however here we have the option to specify which species we wish to model. This feature has been added as occupancy models are computationally intensive. The parameters of the function allow you control over the number of iterations, burnin, thinning, the number of chains, the seed and for advanced users there is also the possibility to pass in your own BUGS script.

```
# Here is our data
str(myData)
```

```
## 'data.frame':    8000 obs. of  4 variables:
##  $ taxa       : Factor w/ 26 levels "a","b","c","d",..: 18 22 5 26 18 24 20 24 17 23 ...
##  $ site       : Factor w/ 100 levels "A1","A10","A100",..: 48 87 53 22 76 44 56 66 92 81 ...
##  $ time_period: Date, format: "1970-01-14" "1980-09-29" ...
##  $ tp         : int  3 4 5 1 3 5 4 1 5 4 ...
```

```
# Run an occupancy model for three species
# Here we use very small number of iterations
# to avoid a long run time
system.time({
occ_out <- occDetModel(taxa = myData$taxa,
                       site = myData$site,
                       time_period = myData$time_period,
                       species_list = c('a','b','c','d'),
                       write_results = FALSE,
                       n_iterations = 200,
                       burnin = 15,
                       n_chains = 3,
                       thinning = 3,
                       seed = 123)
})
```

```
## Warning in errorChecks(taxa = taxa, site = site, time_period =
## time_period): 94 out of 8000 observations will be removed as duplicates
```

```
##
## ###
## Modeling a - 1 of 4 taxa
```

```
## module glm loaded
```

```
## Compiling model graph
##    Resolving undeclared variables
##    Allocating nodes
##    Graph Size: 64272
##
## Initializing model
##
##
## ###
## Modeling b - 2 of 4 taxa
## Compiling model graph
##    Resolving undeclared variables
##    Allocating nodes
##    Graph Size: 64306
##
## Initializing model
##
##
## ###
## Modeling c - 3 of 4 taxa
## Compiling model graph
##    Resolving undeclared variables
##    Allocating nodes
##    Graph Size: 64308
##
## Initializing model
##
##
## ###
## Modeling d - 4 of 4 taxa
## Compiling model graph
##    Resolving undeclared variables
##    Allocating nodes
##    Graph Size: 64328
##
## Initializing model
```

```
##    user  system elapsed
##   73.08    0.06   74.30
```

```
# Lets look at the results
## The object returned is a list with one element for each species
names(occ_out)
```

```
## [1] "a" "b" "c" "d"
```

```
# Each of these is an object of class 'occDet'
class(occ_out$a)
```

```
## [1] "occDet"
```

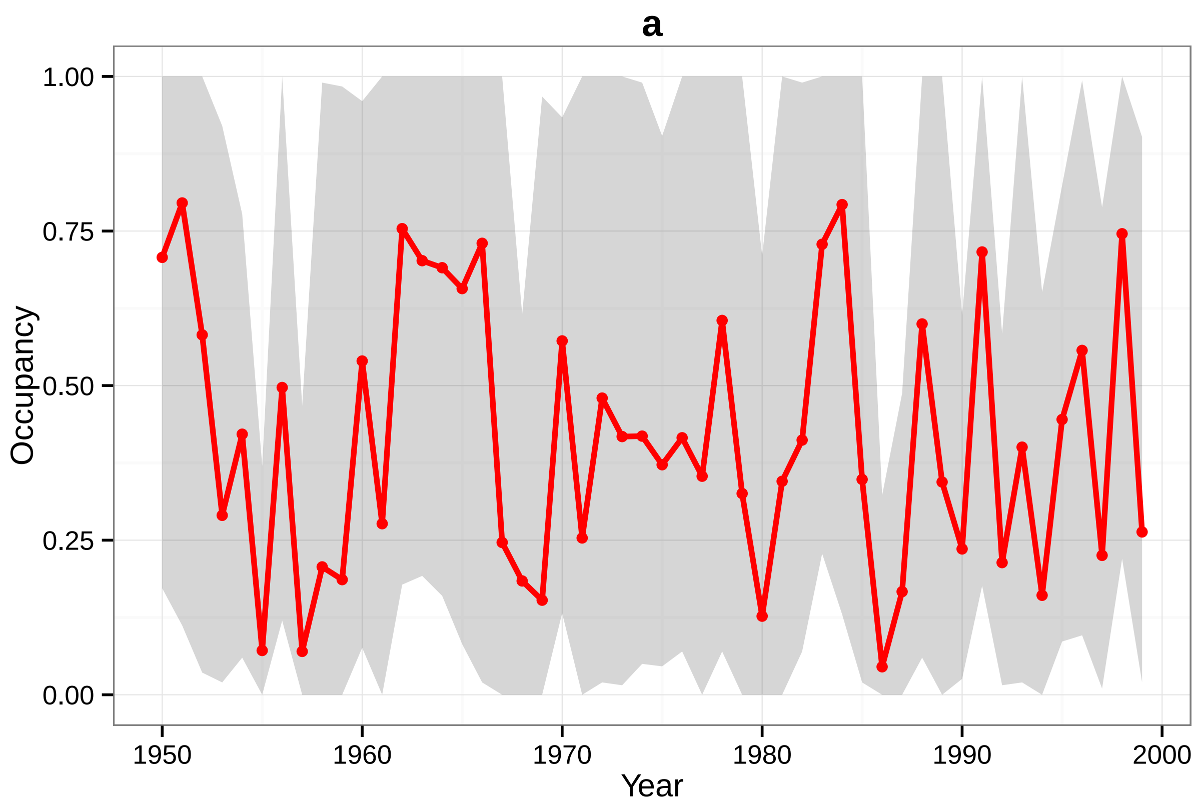
```
# Inside these elements is the information of interest
names(occ_out$a)
```

```
## [1] "model"              "BUGSoutput"         "parameters.to.save"
## [4] "model.file"         "n.iter"             "DIC"
## [7] "SPP_NAME"           "min_year"           "max_year"
```

```
# Of particular interest to many users will be the summary
# data in the BUGSoutput
head(occ_out$a$BUGSoutput$summary)
```

```
##                    mean         sd        2.5%          25%         50%
## LL.p          0.2691009  0.3102804  -0.3519707   0.04895419   0.2556833
## deviance    649.7160858 51.1319847 544.5524433 614.12892478 666.5255290
## fit         281.9522389 89.1997805 190.9883913 219.13112637 247.9393552
## fit.new     283.9149866 90.5760094 185.6004878 217.89008520 254.7165849
## mean_early    0.3701971  0.1718789   0.1274588   0.25082920   0.3516627
## mean_late     0.4114516  0.1241131   0.1808044   0.35083037   0.4000000
##                     75%       97.5%     Rhat n.eff
## LL.p          0.4929832   0.8780177 0.993288   190
## deviance    688.2839296 710.7614446 1.031683    64
## fit         316.7603165 499.9895976 1.009975   120
## fit.new     319.0321333 504.5251365 1.006007   160
## mean_early    0.4283236   0.7837351 1.841981     5
## mean_late     0.4591644   0.7623305 1.295740    12
```

```
# We have included a plotting feature for objects of class
# occDet which provides a useful visualisation of the trend
# in occupancy over time
plot(occ_out$a)
```



He we have run a small example but in reality these models are usually run for many thousands of iterations, making the analysis of more than a handful of species impractical. For those with access to the necessary facilities it is possible to parallelise across species. To do this we use a pair of functions that are used internally by `occDetModel`. These are `formatOccData` which is used to format our occurrence data into the format needed by JAGS, and `occDetFunc`, the function which undertakes the modelling.

```
# First format our data
formattedOccData <- formatOccData(taxa = myData$taxa,
                                  site = myData$site,
                                  time_period = myData$time_period)
```

```
## Warning in errorChecks(taxa = taxa, site = site, time_period =
## time_period): 94 out of 8000 observations will be removed as duplicates
```

```
# This is a list of two elements
names(formattedOccData)
```

```
## [1] "spp_vis"    "occDetdata"
```

`formatOccData` returns a list of length 2; the first element 'spp_vis' is a data.frame with visit (unique combination of site and time period) in the first column and taxa for all the following columns. Values in taxa columns are either TRUE or FALSE depending on whether they were observed on that visit.

```
# Lets have a look at spp_vis
head(formattedOccData$spp_vis[,1:5])
```

```
##             visit     a     b     c     d
## 1 A1001950-01-04 FALSE FALSE FALSE FALSE
## 2 A1001950-11-01  TRUE FALSE FALSE FALSE
## 3 A1001951-08-25 FALSE FALSE FALSE FALSE
## 4 A1001951-11-03 FALSE FALSE FALSE FALSE
## 5 A1001952-02-07 FALSE FALSE FALSE FALSE
## 6 A1001953-02-22 FALSE FALSE FALSE FALSE
```

The second element ('occDetData') is a data frame giving the site, list length (the number of species observed on a visit) and year for each visit.

```
# Lets have a look at occDetData
head(formattedOccData$occDetdata)
```

```
##             visit site L year
## 1 A1001950-01-04 A100 2 1950
## 3 A1001950-11-01 A100 1 1950
## 4 A1001951-08-25 A100 1 1951
## 5 A1001951-11-03 A100 1 1951
## 6 A1001952-02-07 A100 1 1952
## 7 A1001953-02-22 A100 1 1953
```

With our data in the correct format this can now go into the modelling function

```
# Use the occupancy modelling function to parrellise the process
# Here we are going to use the package snowfall
library(snowfall)

# I have 4 cpus on my PC so I set cpus to 4
# when I initialise the cluster
sfInit(parallel = TRUE, cpus = 4)
```

```
## Warning in searchCommandline(parallel, cpus = cpus, type = type,
## socketHosts = socketHosts, : Unknown option on commandline:
## rmarkdown::render('W:/PYWELL_SHARED/Pywell Projects/BRC/Tom August/R
## Packages/Trend analyses/sparta/vignette/sparta_vignette.Rmd', encoding

## snowfall 1.84-6 initialized (using snow 0.3-13): parallel execution on 4 CPUs.
```

```
# Export my data to the cluster
sfExport('formattedOccData')

# I create a function that takes a species name and runs my model
occ_mod_function <- function(taxa_name){

  library(sparta)

  occ_out <- occDetFunc(taxa_name = taxa_name,
                        n_iterations = 200,
                        burnin = 15,
                        occDetdata = formattedOccData$occDetdata,
                        spp_vis = formattedOccData$spp_vis,
                        write_results = FALSE,
                        seed = 123)
}

# I then run this in parallel
system.time({
para_out <- sfClusterApplyLB(c('a','b','c','d'), occ_mod_function)
})
```

```
##    user  system elapsed
##    0.02    0.02   29.81
```

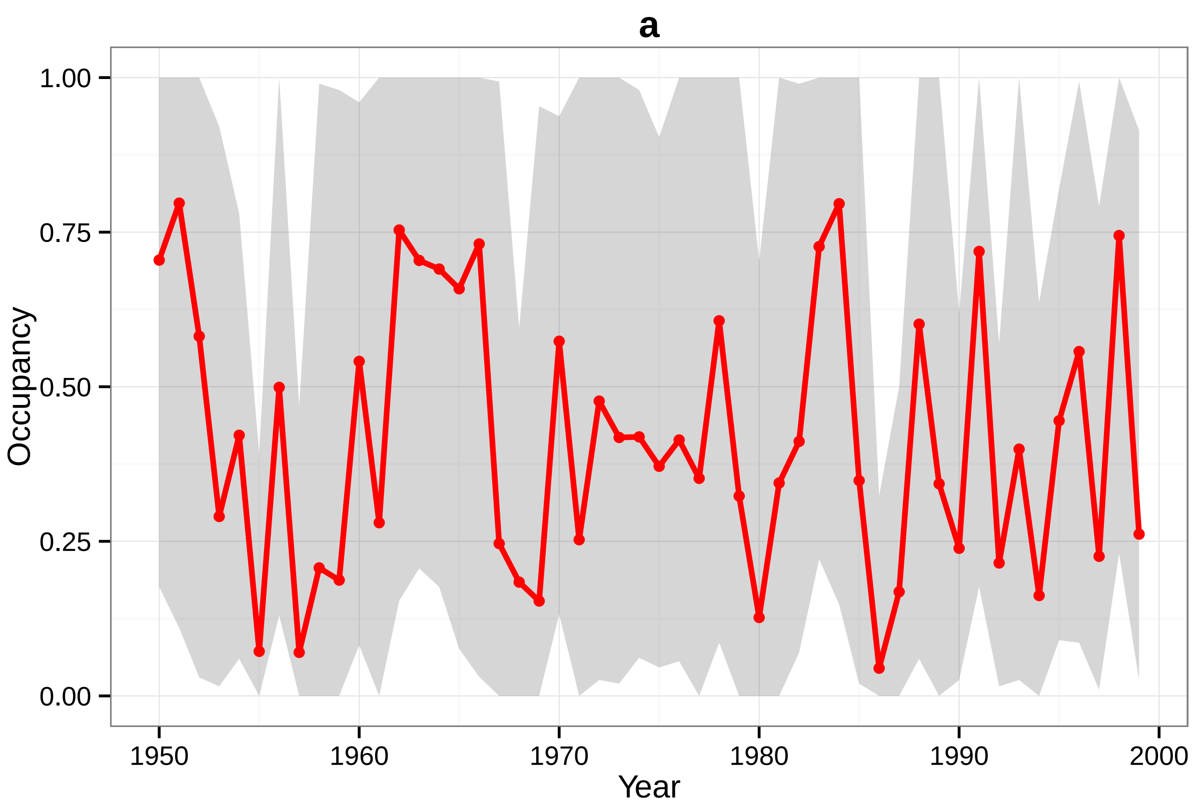
```
# Name each element of this output by the species
for(i in  1:length(para_out)) names(para_out)[i] <- para_out[[i]]$SPP_NAM

# Stop the cluster
sfStop()
```

```
##
## Stopping cluster
```

```
# This takes about half the time of the
# serial version we ran earlier, and the resulting object
# is the same (since we set the random seed to be the same
# in each)
head(para_out$a$BUGSoutput$summary)
```

```
##                  mean         sd       2.5%          25%         50%
## LL.p        0.2691009  0.3102804 -0.3519707   0.04895419   0.2556833
## deviance  649.7160858 51.1319847 544.5524433 614.12892478 666.5255290
## fit       281.9522389 89.1997805 190.9883913 219.13112637 247.9393552
## fit.new   283.9149866 90.5760094 185.6004878 217.89008520 254.7165849
## mean_early    0.3708781  0.1715081   0.1307932   0.25000000   0.3466667
## mean_late     0.4106272  0.1219015   0.1887431   0.35000000   0.3966667
##                     75%       97.5%     Rhat n.eff
## LL.p          0.4929832   0.8780177 0.993288   190
## deviance    688.2839296 710.7614446 1.031683    64
## fit         316.7603165 499.9895976 1.009975   120
## fit.new     319.0321333 504.5251365 1.006007   160
## mean_early    0.4349904   0.7779150 1.853765     5
## mean_late     0.4533333   0.7547538 1.302426    11
```

```r
plot(para_out$a)
```



This same approach can be used on cluster computers, which can have hundreds of processors, to dramatically reduce run times.

2.6 Frescalo

The frescalo method is outlined in Hill (2012) and is a means to account for both spatial and temporal bias. This method was shown by Isaac et al (2014) to be a good method for data that is aggregated into time periods such as when comparing atlases. The frescalo method is run using a .exe, you will need to download this file by visiting this link - https://github.com/BiologicalRecordsCentre/frescalo. Once you have downloaded the .exe make a note of the directory you have placed it in, we will need that in a moment.

Again we will assume that your data is in a 'what, where, when' format similar to that we used in the previous method:

```
head(myData)
```

```
##   taxa site time_period tp
## 1    r  A51  1970-01-14  3
## 2    v  A87  1980-09-29  4
## 3    e  A56  1996-04-14  5
## 4    z  A28  1959-01-16  1
## 5    r  A77  1970-09-21  3
## 6    x  A48  1990-02-25  5
```

Frescalo's requirements in terms of data structure and types is a little different to that we have seen in other functions. Firstly the entire data.frame is passed in as an argument called `Data`, and the column names of your various elements (taxa, site, etc) are given as other arguments. Secondly frescalo requires that the 'when' component is either a column of year or two columns, one of 'start date' and one of 'end date'. Our data as presented above does not fit into this format so first we must reformat it. In our situation the simplest thing to do is to add a column giving the year. Since frescalo aggregates across time periods (often decades or greater) this loss of temporal resolution is not an issue.

```
# Add a year column
myData$year <- as.numeric(format(myData$time_period, '%Y'))
head(myData)
```

```
##   taxa site time_period tp year
## 1    r  A51  1970-01-14  3 1970
## 2    v  A87  1980-09-29  4 1980
## 3    e  A56  1996-04-14  5 1996
## 4    z  A28  1959-01-16  1 1959
## 5    r  A77  1970-09-21  3 1970
## 6    x  A48  1990-02-25  5 1990
```

Now we have our data in the correct format for frescalo there is one other major component we need, a weights file. You can find out more about the weights file and what it is used for in the original paper (Hill, 2012). In short the weights file outlines the similarity between sites in your dataset. This information is used to weight the analysis of each site accordingly. If you are undertaking this analysis in the UK at 10km square resolution there are some built in weights files you can use. Some of these weights files use the UK landcover map instead of floristic similarity (as used in Hill (2012)). You can find out more about these in the frescalo help file.

For the sake of demonstration let us assume that you do not have a weights file for your analysis, or that you want to create your own. To create a weights file you need two things, a measure of physical distance between your sites and a measure of similarity. In the original paper this similarity measure was floristic similarity, but it could also be habitat similarity or whatever is relevant for the taxa you are studying. In this example I have a table of distances and of land cover proportions at each site

```
# Here is the distance table
head(myDistances)
```

```
##     x   y     dist
## 1 A51 A51    0.000
## 2 A87 A51 4074.258
## 3 A56 A51 6595.711
## 4 A28 A51 1531.943
## 5 A77 A51 5732.942
## 6 A48 A51 2394.873
```

```
# Here is our habitat data
head(myHabitatData)
```

```
##   site grassland  woodland  heathland      urban freshwater
## 1  A51 0.1169123 0.1084992 0.28376157 0.37312774 0.11769919
## 2  A87 0.1781151 0.1307214 0.35258119 0.26223604 0.07634632
## 3  A56 0.2359391 0.1263644 0.25898930 0.13490734 0.24379991
## 4  A28 0.3100922 0.1373896 0.20870313 0.28659095 0.05722412
## 5  A77 0.2034073 0.4897063 0.05368464 0.01677132 0.23643036
## 6  A48 0.2397599 0.1046128 0.34250853 0.13055663 0.18256221
```

```
# With our distance and habitat tables in hand we can
# use the createWeights function to build our weights file
# I have changed the defualts of dist_sub and sim_sub since
# we have a very small example dataset of only 50 sites
myWeights <- createWeights(distances = myDistances,
                           attributes = myHabitatData,
                           dist_sub = 20,
                           sim_sub = 10)
```

```
## Creating similarity distance table...Complete
## Creating weights file...
## 0%
## 10%
## 20%
## 30%
## 40%
## 50%
## 60%
## 70%
## 80%
## 90%
## 100%
## Complete
```

```
head(myWeights)
```

```
##   target neighbour weight
## 1    A51        A2 0.0311
## 2    A51       A47 0.1150
## 3    A51       A49 0.0012
## 4    A51       A51 1.0000
## 5    A51       A53 0.0160
## 6    A51       A62 0.2687
```

The `createWeights` function follows the procedure outlined in Hill (2012) for creating weights and more information can be found in the help file of the function. With our data and weights file we are now ready to proceed with frescalo. As with other functions frescalo can take a range of additional arguments which you can see by entering `?frescalo` at the console, here we will do a minimal example.

```
# First we need to enter the location where we placed the .exe
# In my case I saved it to my documents folder
myFrescaloPath <- 'C:/Users/tomaug/Documents/Frescalo_3a_windows.exe'

# I then want to set up the time periods I want to analyse
# Here I say I want to compare 1980-89 to 1990-99
myTimePeriods <- data.frame(start = c(1980, 1990), end = c(1989, 1999))
head(myTimePeriods)
```

```
##   start  end
## 1  1980 1989
## 2  1990 1999
```

```
# I also need to specify where I want my results to be saved
# I'm going to save it in a folder in my working directory
myFolder <- '~/myFolder'

# Simple run of frescalo
frescalo_results <- frescalo(Data = myData,
                             frespath = myFrescaloPath,
                             time_periods = myTimePeriods,
                             site_col = 'site',
                             sp_col = 'taxa',
                             year = 'year',
                             Fres_weights = myWeights,
                             sinkdir = myFolder)
```

```
##
## SAVING DATA TO FRESCALO WORKING DIRECTORY
## ********************
##
##
## RUNNING FRESCALO
## ********************

## Warning in run_fresc_file(fres_data = Data, output_dir = fresoutput,
## frescalo_path = frespath, : Your value of phi (0.74) is smaller than the
## 98.5 percentile of input phi (0.89). It is reccommended your phi be similar
## to this value. For more information see Hill (2011) reference in frescalo
## help file

## Building Species List - Complete
## Outputting Species Results
##  Species 1 of 26 - a - 25/06/2015 13:28:03
##  Species 2 of 26 - b - 25/06/2015 13:28:03
##  Species 3 of 26 - c - 25/06/2015 13:28:03
##  Species 4 of 26 - d - 25/06/2015 13:28:03
##  Species 5 of 26 - e - 25/06/2015 13:28:03
##  Species 6 of 26 - f - 25/06/2015 13:28:03
##  Species 7 of 26 - g - 25/06/2015 13:28:03
##  Species 8 of 26 - h - 25/06/2015 13:28:03
##  Species 9 of 26 - i - 25/06/2015 13:28:03
##  Species 10 of 26 - j - 25/06/2015 13:28:03
##  Species 11 of 26 - k - 25/06/2015 13:28:03
##  Species 12 of 26 - l - 25/06/2015 13:28:03
##  Species 13 of 26 - m - 25/06/2015 13:28:03
##  Species 14 of 26 - n - 25/06/2015 13:28:03
##  Species 15 of 26 - o - 25/06/2015 13:28:03
##  Species 16 of 26 - p - 25/06/2015 13:28:03
##  Species 17 of 26 - q - 25/06/2015 13:28:03
##  Species 18 of 26 - r - 25/06/2015 13:28:03
##  Species 19 of 26 - s - 25/06/2015 13:28:03
##  Species 20 of 26 - t - 25/06/2015 13:28:03
##  Species 21 of 26 - u - 25/06/2015 13:28:03
##  Species 22 of 26 - v - 25/06/2015 13:28:03
##  Species 23 of 26 - w - 25/06/2015 13:28:03
##  Species 24 of 26 - x - 25/06/2015 13:28:03
##  Species 25 of 26 - y - 25/06/2015 13:28:03
##  Species 26 of 26 - z - 25/06/2015 13:28:03
## [1] "frescalo complete"
```

We get a warning from this analysis that our value of phi is too low. In this case this is because our simulated data suggests every species is found on every site in our time periods. This is a little unrealistic but should you get a similar warning with your data you might want to consult Hill (2012) and change your input value of phi.

The object that is returned (`frescalo_results` in my case) is an object of class `frescalo`. this means there are a couple of special methods we can use with it.

```
# Using 'summary' gives a quick overview of our data
# This can be useful to double check that your data was read in correctly
summary(frescalo_results)
```

```
##  Actual numbers in data
##      Number of samples           100
##      Number of species            26
##      Number of time periods        2
##      Number of observations     2239
##      Neighbourhood weights      1000
##      Benchmark exclusions          0
##      Filter locations included     0
```

```
# Using 'print' we get a preview of the results
print(frescalo_results)
```

```
##
## Preview of $paths - file paths to frescalo log, stats, freq, trend .csv files:
##
## [1] "~/myFolder/frescalo_150625/Output/Log.txt"
## [2] "~/myFolder/frescalo_150625/Output/Stats.csv"
## [3] "~/myFolder/frescalo_150625/Output/Freq.csv"
## [4] "~/myFolder/frescalo_150625/Output/Trend.csv"
## [5] "~/myFolder/frescalo_150625/Output/Freq_quickload.txt"
##
##
```

```
## Preview of $trend - trends file, giving the tfactor value for each species at each time period:
##
##   Species   Time TFactor StDev  X Xspt Xest N.0.00 N.0.98
## 1       a 1984.5   0.544 0.201  8    8    8     92      0
## 2       a 1994.5   1.143 0.302 17   17   17     92      0
## 3       j 1984.5   1.372 0.237 46   45   45    100      0
## 4       j 1994.5   0.702 0.133 35   35   35    100      1
## 5       k 1984.5   0.961 0.167 44   43   43    100      0
## 6       k 1994.5   0.816 0.144 46   45   45    100      5
##
##
## Preview of $stat - statistics for each hectad in the analysis:
##
##   Location Loc_no No_spp Phi_in Alpha Wgt_n2 Phi_out Spnum_in Spnum_out
## 1       A1      1     11  0.815  0.66   1.58    0.74     11.5       9.8
## 2      A10      2     13  0.717  1.14   3.77    0.74     14.9      15.7
## 3     A100      3     18  0.828  0.58   3.01    0.74     18.1      14.9
## 4      A11      4     16  0.847  0.49   1.81    0.74     16.9      13.3
## 5      A12      5     11  0.718  1.15   3.22    0.74     14.5      15.3
## 6      A13      6      8  0.681  1.32   3.88    0.74     14.5      16.4
##   Iter
## 1   15
## 2    5
## 3    8
## 4    9
## 5    3
## 6    8
##
##
## Preview of $freq - rescaled frequencies for each location and species:
##
##   Location Species Pres   Freq  Freq1 SDFrq1 Rank Rank1
## 1       A1       v    1 0.9778 0.9177 0.1372    1 0.102
## 2       A1       k    1 0.9722 0.9046 0.1494    2 0.204
## 3       A1       w    1 0.9634 0.8856 0.1659    3 0.305
## 4       A1       y    1 0.9563 0.8715 0.1776    4 0.407
## 5       A1       x    1 0.9412 0.8440 0.1992    5 0.509
## 6       A1       e    1 0.8965 0.7740 0.2491    6 0.611
##
##
## Preview of $log - log file:
##
##     Number of species            26
##     Number of time periods        2
##     Number of observations     2239
##     Neighbourhood weights      1000
##     Benchmark exclusions          0
##     Filter locations included     0
##
##
##  98.5 percentile of input phi  0.89
##  Target value of phi           0.74
##
##
```

```
##
##
## Preview of $lm_stats - trends in tfactor over time:
##
##    SPECIES NAME       b          a b_std_err b_tval b_pval a_std_err
## 1       S1    a  0.0599 -118.32755        NA     NA     NA        NA
## 12      S2    b  0.0021   -3.27645        NA     NA     NA        NA
## 20      S3    c  0.0045   -8.04525        NA     NA     NA        NA
## 21      S4    d  0.0365  -71.60625        NA     NA     NA        NA
## 22      S5    e -0.0046    9.96270        NA     NA     NA        NA
## 23      S6    f  0.0326  -63.82470        NA     NA     NA        NA
##    a_tval a_pval adj_r2 r2 F_val F_num_df F_den_df   Ymin   Ymax
## 1      NA     NA     NA  1    NA        1        0 1984.5 1994.5
## 12     NA     NA     NA  1    NA        1        0 1984.5 1994.5
## 20     NA     NA     NA  1    NA        1        0 1984.5 1994.5
## 21     NA     NA     NA  1    NA        1        0 1984.5 1994.5
## 22     NA     NA     NA  1    NA        1        0 1984.5 1994.5
## 23     NA     NA     NA  1    NA        1        0 1984.5 1994.5
##          Z_VAL SIG_95
## 1   1.65116558  FALSE
## 12  0.06358704  FALSE
## 20  0.14903522  FALSE
## 21  1.17443512  FALSE
## 22 -0.17104272  FALSE
## 23  1.12652478  FALSE
```

```
# There is a lot of information here and you can read more about
# what these data mean by looking at the frescalo help file
# The files detailed in paths are also in the object returned
frescalo_results$paths
```

```
## [1] "~/myFolder/frescalo_150625/Output/Log.txt"
## [2] "~/myFolder/frescalo_150625/Output/Stats.csv"
## [3] "~/myFolder/frescalo_150625/Output/Freq.csv"
## [4] "~/myFolder/frescalo_150625/Output/Trend.csv"
## [5] "~/myFolder/frescalo_150625/Output/Freq_quickload.txt"
```

```
names(frescalo_results)
```

```
## [1] "paths"    "trend"    "stat"     "freq"     "log"      "lm_stats"
```

```
# However we additionally get some model results in our returned object
# under '$lm_stats'
```

The results from frescalo may seem complex at first and I suggest reading the Value section of the frescalo help file for details. In brief: `frescalo_results$paths` lists the file paths of the raw data files for `$log`, `$stat`, `$freq` and `$trend`, in that order. `frescalo_results$trend` is a data.frame providing the list of time factors (a measure of probability of occurrence relative to benchmark species) for each species-timeperiod. `frescalo_results$stat` is a data.frame giving details about sites such as estimated species richness. `frescalo_results$freq` is a data.frame of the species frequencies, that is the probabilities that a species was present at a certain location. `frescalo_results$log`, a simple report of the console output from the .exe. `frescalo_results$lm_stats` is a data.frame giving the results of a linear regression of Tfactors for each species when more than two time periods are used. If only 2 time periods are used (as in our example) the linear modeling section of this data.frame is filled with NAs and a z-test is performed instead (results are given in the last columns).

```r
# Lets look at some results fo the first three species
frescalo_results$lm_stats[1:3, c('NAME','Z_VAL','SIG_95')]
```

```
##    NAME      Z_VAL SIG_95
## 1     a 1.65116558  FALSE
## 12    b 0.06358704  FALSE
## 20    c 0.14903522  FALSE
```

```r
# None of these have a significant change using a z-test
# Lets look at the raw data
frescalo_results$trend[frescalo_results$trend$Species %in% c('a', 'b', 'c'),
                       c('Species', 'Time', 'TFactor', 'StDev')]
```

```
##    Species   Time TFactor StDev
## 1        a 1984.5   0.544 0.201
## 2        a 1994.5   1.143 0.302
## 23       b 1984.5   0.891 0.237
## 24       b 1994.5   0.912 0.230
## 39       c 1984.5   0.885 0.215
## 40       c 1994.5   0.930 0.212
```

```r
# We can see from these results that the big standard deviations on
# the tfactor values means there is no real difference between the
# two time periods
```

3 References

1. Hill, M.O. (2012) Local frequency as a key to interpreting species occurrence data when recording effort is not known. Methods Ecol. Evol. 3, 195–205
2. Isaac, N.J.B. et al. (2014) Statistics for citizen science: extracting signals of change from noisy ecological data. Methods Ecol. Evol. 5, 1052–1060
3. Roy, H.E. et al. (2012) Invasive alien predator causes rapid declines of native European ladybirds. Divers. Distrib. 18, 717–725
4. Telfer, M.G. et al. (2002) A general method for measuring relative change in range size from biological atlas data. Biol. Conserv. 107, 99–109
5. Thomas, J.A. et al. (2015) Recent trends in UK insects that inhabit early successional stages of ecosystems.