The package contains three functions that clean the data of any unwanted experiments. Firstly, data containing trials of the species White-rumped shama and Zebra dove are removed due to low sampling effort. Secondly, data containing trials not equal to 15 minutes are removed due to low sampling effort. Lastly, a generalized linear mixed model is applied to the data.

- > library(CAXA)
- > library(lme4)
- > library(dplyr)
- > data("cax\_data")
- > ## Remove all experiments with wrsh or zedo as track species
- > cax\_data\_1 <- Remove.WRSH.ZEDO(cax\_data)
- # A tibble: 573 x 12
- # Groups: experiment [73]

experiment track.order track.spp track.type track.length breeding.season <fctr> <fctr> <chr> <chr> <int> <int> 1 1 1 control con 15 1 2 2 1 control con 15 1 3 3 control 15 1 1 con 4 1 4 control 15 con 5 5 60 1 rvbu treat 2 6 1 control con 15 7 2 2 15 control con 1 8 2 3 control con 15 1 9 2 4 control 15 1 con 10 5 15 jawe treat

- # ... with 563 more rows, and 6 more variables: native.plant <int>, jawe <int>,
  # rble <int>, rvbu <int>, rwbu <int>, other <int>
- > ## Keep only experiments with all trials of track lengths equal to 15 minutes
  > cax\_data\_2 <- Keep.15.Tracks(cax\_data\_1)</pre>
- # A tibble: 448 x 12
- # Groups: experiment [56]

	1	_	_			
	experiment	track.order	track.spp	<pre>track.type</pre>	${\tt track.length}$	breeding.season
	<fctr></fctr>	<fctr></fctr>	<chr></chr>	<chr></chr>	<int></int>	<int></int>
1	13	1	control	con	15	0
2	13	2	control	con	15	0
3	13	3	control	con	15	0
4	13	4	control	con	15	0
5	13	5	rvbu	treat	15	0
6	13	6	<pre>jawe.rble</pre>	treat	15	0
7	13	7	rwbu	treat	15	0
8	13	8	rble	treat	15	0
9	15	1	control	con	15	0
10	15	2	control	con	15	0

```
# ... with 438 more rows, and 6 more variables: native.plant <int>, jawe <int>,
   rble <int>, rvbu <int>, rwbu <int>, other <int>
> ## Apply a generalized linear mixed model with a binomial distribution
> ## For each glmm have bird species as response variable; track species, breeding season, a
> GLMM.Bin(cax_data_2)
Generalized linear mixed model fit by maximum likelihood (Laplace
 Approximation) [glmerMod]
Family: binomial (logit)
Formula:
species ~ track.spp + breeding.season + native.plant + (1 | track.order)
  Data: cax_data_2
    AIC
             BIC
                   logLik deviance df.resid
    498
             535
                     -240
                               480
                                        439
Scaled residuals:
   Min 1Q Median
                            3Q
-2.3400 -0.5263 -0.4832 0.4631 2.1722
Random effects:
Groups
           Name
                       Variance Std.Dev.
track.order (Intercept) 0.01191 0.1091
Number of obs: 448, groups: track.order, 8
Fixed effects:
                  Estimate Std. Error z value Pr(>|z|)
                             0.2805 -4.589 4.46e-06 ***
(Intercept)
                   -1.2871
                    2.9869
                               0.4133 7.226 4.96e-13 ***
track.sppjawe
                           0.6680 4.632 3.63e-06 ***
track.sppjawe.rble 3.0937
track.spprble
                              0.3783 3.407 0.000658 ***
                   1.2887
track.spprvbu
                   1.1971
                               0.3240 3.695 0.000220 ***
                               0.3705 0.656 0.511997
track.spprwbu
                   0.2429
                           0.2302 -0.580 0.562028
breeding.season
                   -0.1335
native.plant
                   -0.0773
                              0.2610 -0.296 0.767146
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Correlation of Fixed Effects:
           (Intr) trck.sppj trck.. trck.spprb trck.spprv trck.spprw brdng.
track.sppjw -0.212
trck.sppjw. -0.275 0.106
trck.spprbl -0.257 0.217
                             0.143
trck.spprvb -0.334 0.261
                             0.147 0.271
trck.spprwb -0.316 0.217
                             0.155 0.260
                                              0.278
```