

# Overview of Unmarked: An R Package for the Analysis of Wildlife Data

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## Abstract

Unmarked aims to be a complete environment for the statistical analysis of wildlife data. Currently, the focus is on 2-level hierarchical models that separately model a latent state and an observation process. Unmarked uses S4 classes to help the user both explore their data and analyze in a transparent manner.

## 1 Overview of unmarked

Occupancy and abundance data are often associated with metadata related to the design of the study. For example, in distance sampling, the study design (line- or point-transect), distance class break points, transect lengths, and units of measurement need to be accounted for in the analysis. Unmarked uses S4 classes to store data and metadata in a way that allows for easy data manipulation, summarization, and model specification. Table 1 lists the currently implemented models and their associated fitting functions and data classes.

Each data class can be created with a call to the constructor function of the same name as described in the examples below.

## 2 Typical unmarked session

The first step is to import the data into R. This can be accomplished with either a call to the appropriate type of `unmarkedFrame`:

```
> library(unmarked)
> wt <- read.csv(system.file("csv", "widewt.csv", package = "unmarked"))
> head(wt)
  site y.1 y.2 y.3      elev      forest   length   date.1
1    1  0  0  0 -1.1729446 -1.156228147 1.824549 -1.761481
2    2  0  0  0 -1.1265010 -0.501483710 1.629241 -2.904339
3    3  0  0  0 -0.1976283 -0.101362109 1.458615 -1.690053
4    4  0  0  0 -0.1047411  0.007761963 1.686399 -2.190053
5    5  0  0  0 -1.0336137 -1.192602838 1.280934 -1.832910
6    6  0  0  0 -0.8478392  0.917129237 1.808289 -2.618624
      date.2   date.3   ivel.1   ivel.2   ivel.3
1  0.3099471 1.3813757 -0.5060353 -0.5060353 -0.5060353
2 -1.0471958 0.5956614 -0.9336151 -0.9907486 -1.1621491
3 -0.4757672 1.4528042 -1.1355754 -1.3388644 -1.6099164
```

Model	Fitting Function	Data	Citation
Occupancy	occu	unmarkedFrameOccu	[2]
Royle-Nichols	occuRN	unmarkedFrameOccu	[5]
Point Count	pcount	unmarkedFramePCount	[4]
Distance-sampling	distsamp	unmarkedFrameDS	[6]
Arbitrary multinomial-Poisson	multinomPois	unmarkedFrameMPois	[3]
Colonization-extinction	colect	unmarkedMultFrame	[1]

Table 1: Models handled by unmarked.

```

4 -0.6900529 1.2385185 -0.8193481 -0.9272669 -1.1970640
5 0.1670899 1.3813757 0.6375563 0.8803737 1.0422520
6 0.1670899 1.3813757 -1.3288666 -1.0422624 -0.8989603
> y <- wt[, 2:4]
> siteCovs <- wt[, c("elev", "forest", "length")]
> obsCovs <- reshape(wt[, c("date.1", "date.2", "date.3",
    "ivel.1", "ivel.2", "ivel.3")], varying = 1:6, direction = "long")
> obsCovs <- obsCovs[order(obsCovs$id, obsCovs$time), c(2:3)]
> wt <- unmarkedFrameOccu(y = y, siteCovs = siteCovs, obsCovs = obsCovs)
> summary(wt)
unmarkedFrame Object

```

```

237 sites
Maximum number of observations per site: 3
Mean number of observations per site: 2.81
Sites with at least one detection: 79

```

```

Tabulation of y observations:
  0    1 <NA>
483 182   46

```

```

Site-level covariates:
      elev      forest      length
Min.   :-1.436125  Min.   :-1.265e+00  Min.   :0.1823
1st Qu.: -0.940726  1st Qu.: -9.744e-01  1st Qu.: 1.4351
Median : -0.166666  Median : -6.499e-02  Median : 1.6094
Mean    : 0.007612  Mean    : 8.798e-05  Mean    : 1.5924
3rd Qu.: 0.994425  3rd Qu.: 8.080e-01  3rd Qu.: 1.7750
Max.    : 2.434177  Max.    : 2.299e+00  Max.    : 2.2407

```

```

Observation-level covariates:
      date      ivel
Min.   :-2.9043386  Min.   :-1.753e+00
1st Qu.: -1.1186243  1st Qu.: -6.660e-01
Median : -0.1186243  Median : -1.395e-01
Mean    : -0.0002173  Mean    : -3.008e-11
3rd Qu.: 1.3099471  3rd Qu.: 5.493e-01
Max.    : 3.8099471  Max.    : 5.980e+00
NA's    : 42.0000000  NA's    : 4.600e+01

```

or by using the convenience function `csvToUMF`:

```

> wt <- csvToUMF(system.file("csv", "widewt.csv", package = "unmarked"),
  long = FALSE, type = "unmarkedFrameOccu")

```

If not all sites have the same numbers of observations, then manual importation of data in long format can be tricky. `csvToUMF` seamlessly handles this situation.

```

> pcru <- csvToUMF(system.file("csv", "frog2001pcru.csv",
  package = "unmarked"), long = TRUE, type = "unmarkedFrameOccu")
> summary(pcru)
unmarkedFrame Object

```

```

130 sites
Maximum number of observations per site: 3
Mean number of observations per site: 2.59
Sites with at least one detection: 96

```

```

Tabulation of y observations:
  0    1    2    3 <NA>
197  25  28  87  53

```

Observation-level covariates:

MinAfterSunset	Wind	Sky	Temperature
Min. : -21.00	Min. : 0.0000	Min. : 0.0000	Min. : 4.00
1st Qu.: 66.00	1st Qu.: 0.0000	1st Qu.: 0.0000	1st Qu.: 13.00
Median : 97.00	Median : 1.0000	Median : 0.0000	Median : 17.50
Mean : 97.57	Mean : 0.8813	Mean : 0.4837	Mean : 16.61
3rd Qu.: 126.00	3rd Qu.: 2.0000	3rd Qu.: 1.0000	3rd Qu.: 20.60
Max. : 228.00	Max. : 3.0000	Max. : 5.0000	Max. : 28.00
NA's : 53.00	NA's : 53.0000	NA's : 53.0000	NA's : 53.00

JulianDate
Min. : 72.0
1st Qu.: 95.0
Median : 123.0
Mean : 127.4
3rd Qu.: 159.0
Max. : 179.0
NA's : 53.0

To help stabilize the numerical optimization algorithm, we recommend standardizing the covariates.

```
> obsCovs(pcrU) <- scale(obsCovs(pcrU))
```

Occupancy models can then be fit with the `occu()` function:

```
> fm1 <- occu(~1 ~ 1, pcrU)
> fm2 <- occu(~MinAfterSunset + Temperature ~ 1, pcrU)
> summary(fm1)
```

Call:

```
occu(formula = ~1 ~ 1, data = pcrU)
```

Occupancy (logit-scale):

Estimate	SE	z	P(> z )
2.95	1.44	2.05	0.04

Detection (logit-scale):

Estimate	SE	z	P(> z )
-0.249	0.170	-1.47	0.142

AIC: 461.0986

Sample size: 130

optim convergence code: 0

optim iterations: 22

Bootstrap iterations: 0

```
> summary(fm2)
```

Call:

```
occu(formula = ~MinAfterSunset + Temperature ~ 1, data = pcrU)
```

Occupancy (logit-scale):

Estimate	SE	z	P(> z )
1.54	0.292	5.26	1.42e-07

Detection (logit-scale):

	Estimate	SE	z	P(> z )
(Intercept)	0.2098	0.206	1.017	3.09e-01
MinAfterSunset	-0.0855	0.160	-0.536	5.92e-01
Temperature	-1.8936	0.291	-6.508	7.60e-11

AIC: 357.0791

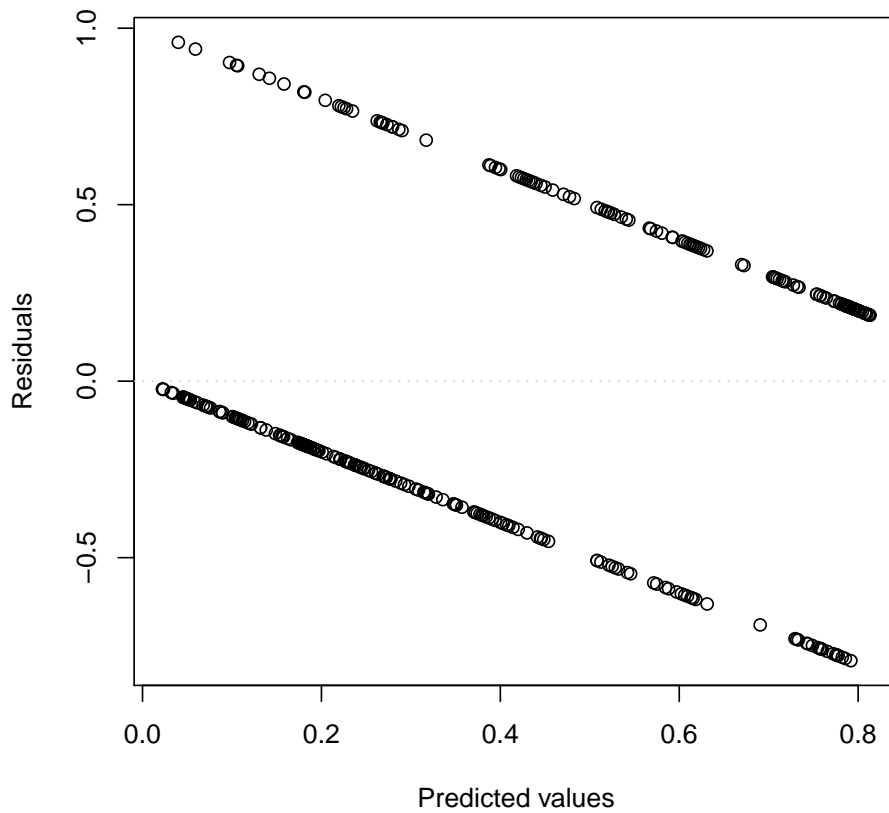
Sample size: 130

optim convergence code: 0

optim iterations: 21

Bootstrap iterations: 0

```
> plot(fm2)
```



Here, we have specified that the detection process is modeled with the `MinAfterSunset` and `Temperature` covariates. No covariates are specified for occupancy here. See `?occu` for more details.

Unmarked fitting functions return `unmarkedFit` objects which can be queried to investigate the model fit. Variables can be back-transformed to the unconstrained scale using `backTransform`. Standard errors are computed using the delta method.

```
> backTransform(fm2, "state")
```

Backtransformed linear combination(s) of Occupancy estimate(s)

Estimate	SE LinComb	(Intercept)
0.823	0.0425	1.54

Transformation: logistic

Because the detection component was modeled with covariates, covariate coefficients must be specified to back-transform. Here, we request the probability of detection given a site is occupied and all covariates are set to 0.

```
> backTransform(linearComb(fm2, coefficients = c(1, 0,
0), type = "det"))
```

Backtransformed linear combination(s) of Detection estimate(s)

Estimate	SE LinComb	(Intercept)	MinAfterSunset	Temperature
0.552	0.051	0.210	1	0

Transformation: logistic

A `predict` method also exists.

```

> newData <- data.frame(MinAfterSunset = 0, Temperature = -2:2)
> predict(fm2, type = "det", newdata = newData, appendData = TRUE)
      Predicted      SE MinAfterSunset Temperature
1 0.98196076 0.01266193          0          -2
2 0.89123189 0.04248804          0          -1
3 0.55225129 0.05102660          0           0
4 0.15658708 0.03298276          0           1
5 0.02718682 0.01326263          0           2

```

Confidence intervals are requested with `confint`, using either the asymptotic normal approximation or profiling.

```

> confint(fm2, type = "det")
              0.025      0.975
(Intercept) -0.1946872  0.6142292
MinAfterSunset -0.3985642  0.2274722
Temperature  -2.4638797 -1.3233511
> confint(fm2, type = "det", method = "profile")
Profiling parameter 1 of 3 ... done.
Profiling parameter 2 of 3 ... done.
Profiling parameter 3 of 3 ... done.
              0.025      0.975
p(Int)          -0.1929210  0.6208837
p(MinAfterSunset) -0.4044794  0.2244221
p(Temperature)   -2.5189984 -1.3789261

```

Model selection and multi-model inference can be implemented after organizing models using the `fitList` function.

```

> fms <- fitList(NULL = fm1, TimeTemp = fm2)
> modSel(fms, nullmod = "Null")
      model    n nPars    AIC deltaAIC    AICwt    Rsq cumlAICwt
1 TimeTemp 130     4 357.08     0.00 1.0000e+00 0.58243      1
2 Null      130     2 461.10    104.02 2.5849e-23 0.00000      1
> predict(fms, type = "det", newdata = newData, appendData = TRUE)
      Predicted      SE MinAfterSunset Temperature
1 0.98196076 0.01266193          0          -2
2 0.89123189 0.04248804          0          -1
3 0.55225129 0.05102660          0           0
4 0.15658708 0.03298276          0           1
5 0.02718682 0.01326263          0           2

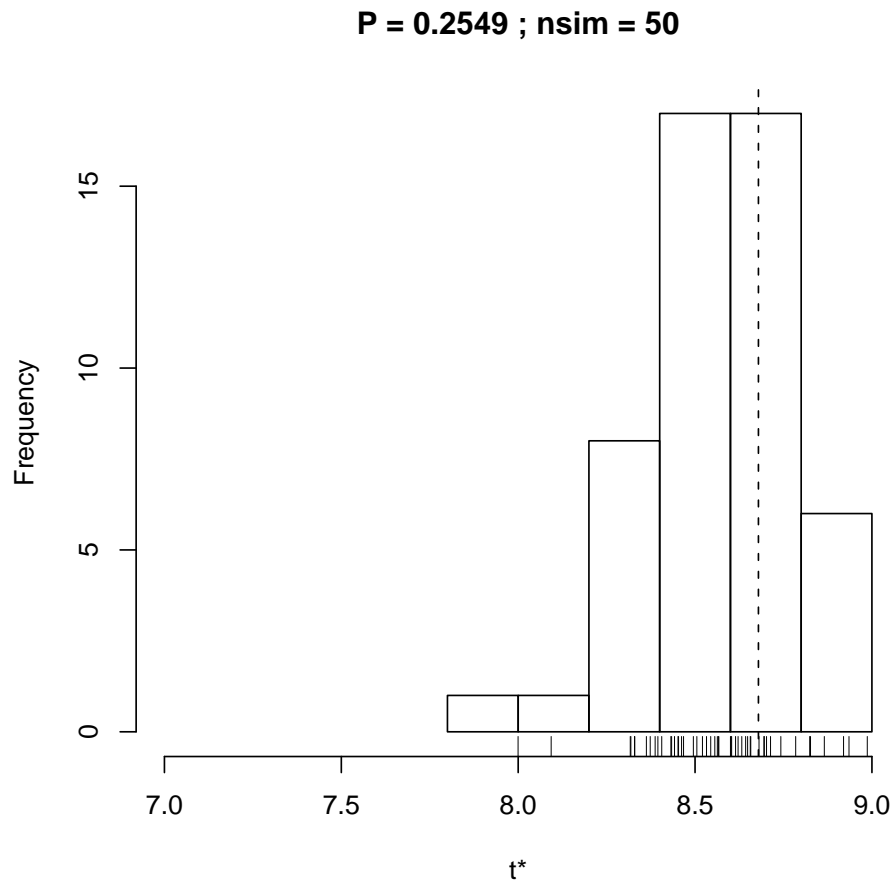
```

Parametric bootstrapping can be used to check the adequacy of model fit.

```

> pcru.pb <- parboot(fm2, nsim = 50, report = 5)
t0 = 8.679173
8.8, 8.3, 8.9, 8.7, 8
8.8, 8.6, 8.3, 8.5, 8.4
8.6, 8.6, 8.7, 8.5, 8.6
8.3, 8.7, 8.5, 8.5, 8.5
8.6, 8.5, 9, 8.4, 8.3
8.6, 8.8, 8.8, 8.5, 8.7
8.9, 8.5, 8.3, 8.5, 8.7
8.4, 9, 8.5, 8.4, 8.7
8.3, 8.3, 8.6, 8.4, 8.6
8.4, 8.3, 8.5, 8.7, 8.6
> plot(pcru.pb)

```



This example suggests an adequate fit.

## References

- [1] Darryl I. MacKenzie, James D. Nichols, James E. Hines, Melinda G. Knutson, and Alan B. Franklin. Estimating site occupancy, colonization, and local extinction when a species is detected imperfectly. *Ecology*, 84(8):2200–2207, 2003.
- [2] Darryl I. MacKenzie, James D. Nichols, G. B. Lachman, S. Droege, J. A. Royle, and C. A. Langtimm. Estimating site occupancy rates when detection probabilities are less than one. *Ecology*, 83(8):2248–2255, 2002.
- [3] J. A. Royle. Generalized estimators of avian abundance from count survey data. *Animal Biodiversity and Conservation*, 27(1):375–386, 2004.
- [4] J. A. Royle. N-mixture models for estimating population size from spatially replicated counts. *Biometrics*, 60(1):108–115, 2004.
- [5] J. A. Royle and J. D. Nichols. Estimating abundance from repeated presence-absence data or point counts. *Ecology*, 84(3):777–790, 2003.
- [6] JA Royle, DK Dawson, and S. Bates. Modeling abundance effects in distance sampling. *Ecology*, 85(6):1591–1597, 2004.