

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

Ian Fiske and Richard Chandler

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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

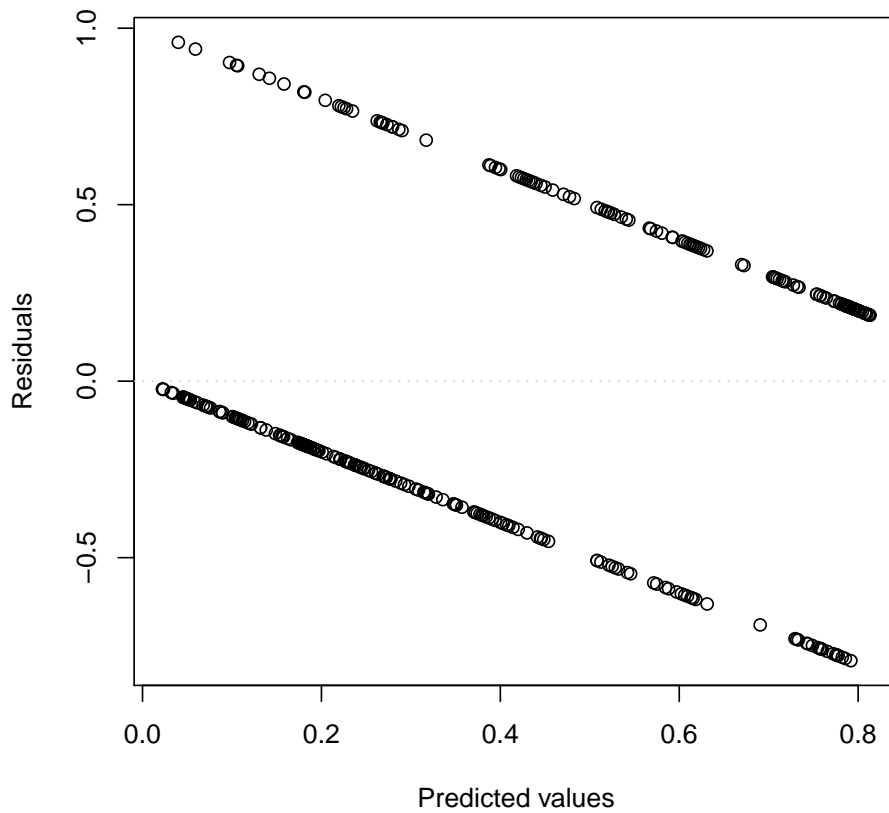
Sample size: 130

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

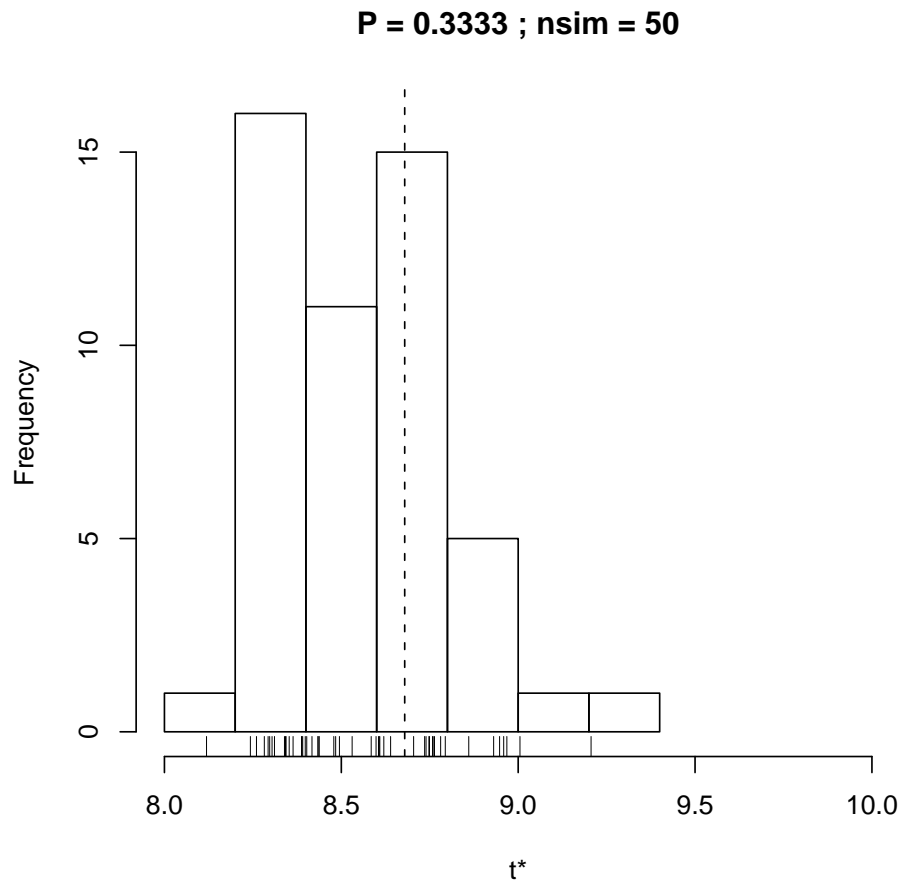
```

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, 8.8, 8.2, 8.5, 8.7
8.7, 8.5, 8.7, 8.7, 8.3
8.5, 8.9, 8.8, 8.6, 8.6
8.2, 8.5, 8.2, 8.7, 8.5
8.6, 8.3, 8.6, 8.7, 8.3
8.1, 8.7, 8.2, 8.7, 8.6
8.7, 8.7, 8.6, 8.5, 8.3
8.9, 8.6, 8.6, 8.9, 8.7
8.6, 8.7, 8.6, 8.4, 8.6
8.3, 8.6, 8.5, 8.4, 8.5
> 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.