

# Package ‘RAD’

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**Title** Fit RAD models to biological data

**Version** 0.3

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**Description** Fit a variety of models to Rank Abundance Data

**Depends** R (>= 2.10), mvtnorm, MASS

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**License** GPL-2

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fish.data	<i>fish.data</i>
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### Description

fish.data is an example data set to fit models for total abundance (N) and Species Richness (S)

### Details

A much reduced data set from CSIRO voyages in the 1970s

### Authors

Piers Dunstan and Scott Foster

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MDMnMod	<i>MDMnMod</i>
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### Description

MDMnMod

### Usage

```
MDMnMod(MDMn.form, data, ID, dist="MDMn", scale.covar=FALSE, est.var=TRUE, calc.resid=TRUE, trace=TRUE)
```

### Arguments

MDMn.form	an object of class "formula" (or one that can be coerced to that class): a symbolic description of the model to be fitted. Must include both the response and covariates
data	a data frame containing the variables in the formula. Must contain a column with the ordered (most to least) abundances for each site. Covariates must be repeated for each row belonging to a site.
ID	Vector of site identifiers for all observations. For every abundance (row) that comes from a site, the same identifier must be used. The length of ID must equal nrows(data)
dist	one of either multinomial "Mn" or Dirichlet Multinomial "DMN" or Modified Dirichlet Multinomial "MDMn" (default)
scale.covar	Should the model matrix be scaled (TRUE/FALSE)? Useful if models do not converge. Setting this to TRUE will save the column means and sd for later prediction.
est.var	estimate the variance-covariance matrix using newton-raphson
calc.resid	should residuals be calculated?
trace	print model trace

**Details**

Fits a selected distribution to the vector of relative abundances. See Foster and Dunstan 2009 for details.

**Value**

coef	coefficients
vcov	variance-covariance matrix
logl	log-likelihood
AIC	AIC
residuals	model residuals, calculated using PIT
fitted	matrix of fitted values (nij and pij)
mean.X	column means for model matrix if scale.covar is TRUE
sd.X	column sds for model matrix if scale.covar is TRUE
formula	model formula

**Authors**

Piers Dunstan and Scott Foster

**Examples**

```
head(n.data)
## format for the data object
n.data$N.scale <- n.data$N/n.data$area
n.data$S.scale <- n.data$S/n.data$area
nij.form <- nij~1 + N.scale + S.scale + depth + O2_AV + temp_AV
model.nij <- MDMnMod(nij.form, data=n.data, ID=n.data$i, dist="MDMn", scale.covar=TRUE, est.var=FALSE, calc.resi
plot(model.nij$fitted$nij,model.nij$residuals)
plot(log(model.nij$fitted$nij),model.nij$residuals)
```

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n.data

*n.data*


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**Description**

n.data is an example data set to fit models for relative abundance (nij)

**Details**

A much reduced data set from CSIRO voyages in the 1970s

**Authors**

Piers Dunstan and Scott Foster

negBinMod

*negBinMod***Description**

negBinMod fits a negative binomial model to data. Use to fit Total Abundance (Ni)

**Usage**

```
negBinMod(NB.form, data, est.var=TRUE, scale.covar=FALSE , trace=TRUE)
```

**Arguments**

NB.form	an object of class "formula" (or one that can be coerced to that class): a symbolic description of the model to be fitted. An offset in the form <code>offset(log(area sampled))</code> should be included in the model formula to adjust for differences in area sampled between sites.
data	a data frame containing the all variables in the formula including the offset and the response. Each row should be a different site.
scale.covar	Should the model matrix be scaled (TRUE/FALSE)? Useful if models do not converge. Setting this to TRUE will save the column means and sd for later prediction.
est.var	estimate the variance-covariance matrix using newton-raphson
trace	print model trace

**Details**

negBinMod used `glm.nb` (MASS) to get initial parameters & then uses `nlminb` to fit model. Allows calculation of se for overdispersion parameter. Output is otherwise identical to `glm.nb`

**Value**

coef	coefficients
vcov	variance-covariance matrix
logl	log-likelihood
AIC	AIC
residuals	model residuals, calculated using PIT
fitted	fitted values
mean.X	column means for model matrix if scale.covar is TRUE
sd.X	column sds for model matrix if scale.covar is TRUE
formula	model formula

**Authors**

Piers Dunstan and Scott Foster

**Examples**

```
N.form <- N~1 + depth + O2_AV + temp_AV + offset(log(area))
model.N <- negBinMod(N.form,data=fish.data,est.var=TRUE,scale.covar =FALSE)
plot(model.N$fitted,model.N$residuals)
abline(h=0)
```

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predict.MDMnMod	<i>predict</i>
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**Description**

Predict values for the abundances of species 1 to S and the derivative of the RAD curve at species rank 1.

**Usage**

```
## S3 method for class 'MDMnMod'
## S3 method for class 'MDMnMod'
predict(object,new.obs,N=NA,S=NA,...)
```

**Arguments**

object	a fitted model from negBinMod, of class MDMnMod.
new.obs	new covariates used to predict nij. Must contain the same names as in the formula for negBinMod
N	N is the predicted values returned from predict.N
S	S is the predicted values returned from predict.S
...	additional arguments to be passed to predict

**Details**

Uses mvtnorm to obtain new parameters for the glm using calculated variance-covariance matrix, assuming multivariate normal for parameters.

new.obs will be automatically scaled using details in model.nij if scale.covar==TRUE

**Value**

deriv.eta	derivative of the RAD curve at species rank 1
nij	vector of predicted abundances

**Authors**

Piers Dunstan and Scott Foster

**Examples**

```

N.form <- N~1 + depth + O2_AV + temp_AV + offset(log(area))
model.N <- negBinMod(N.form,data=fish.data,est.var=TRUE,scale.covar =FALSE)
fish.data$N.scale <- fish.data$N/fish.data$area
S.form <- S~1 + N.scale + depth + O2_AV + temp_AV + offset(log(area))
model.S <- truncMod(S.form,fish.data$N,data=fish.data,est.var=TRUE,scale.covar=TRUE)
n.data$N.scale <- n.data$N/n.data$area
n.data$S.scale <- n.data$S/n.data$area
nij.form <- nij~1 + N.scale + S.scale + depth + O2_AV + temp_AV
model.nij <- MDMnMod(nij.form, data=n.data, ID=n.data$i, dist="MDMn", scale.covar=TRUE, est.var=TRUE, calc.resid=TRUE)
new.obs <- as.data.frame(t(apply(fish.data,2,mean)))
N.pred <- rep(NA,100)
S.pred <- rep(NA,100)
eta.pred <- rep(NA,100)
for(n in 1:100){
  N.pred[n] <- predict(model.N,new.obs,offset=10)$N
  # insert estimate for N into data frame for it is used, not the original value
  new.obs$N.scale <- N.pred[n]/10
  S.pred[n] <- predict(model.S,new.obs,N.pred[n],offset=10)$S
  new.obs$S.scale <- S.pred[n]/10
  eta.pred[n] <- unlist(predict(model.nij,new.obs,N.pred[n],S.pred[n])$deriv.eta)
}
hist(eta.pred)

```

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predict.negBinMod      *predict*

---

**Description**

Predict values for N and E(N) given a model for N and new covariates.

**Usage**

```

## S3 method for class 'negBinMod'
## S3 method for class 'negBinMod'
predict(object,new.obs,offset=1,...)

```

**Arguments**

object	a fitted model from negBinMod, of class negBinMod.
new.obs	new covariates used to predict N. Must contain the same names as in the formula for negBinMod
offset	Predict sample for an area of this dimension
...	additional arguments to be passed to predict

**Details**

Uses mvtnorm to obtain new parameters for the glm using calculated variance-covariance matrix, assuming multivariate normal for parameters.

new.obs will be automatically scaled using details in model.N if scale.covar==TRUE

**Value**

N	predicted N
expect.N	expected N

**Authors**

Piers Dunstan and Scott Foster

**Examples**

```
N.form <- N~1 + depth + O2_AV + temp_AV + offset(log(area))
model.N <- negBinMod(N.form,data=fish.data,est.var=TRUE,scale.covar =FALSE)
N.pred <- rep(NA,100)
for(n in 1:100) N.pred[n] <- predict(model.N,fish.data[5,],offset=10)$N
hist(N.pred)
```

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predict.truncMod      *predict*

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**Description**

Predict values for S and E(S) given a model for S and new covariates.

**Usage**

```
## S3 method for class 'truncMod'
## S3 method for class 'truncMod'
predict(object,new.obs,N=NA, offset=1,dist="NB",...)
```

**Arguments**

object	a fitted model from truncMod, of class truncMod
new.obs	new covariates used to predict S. Must contain the same names as in the formula for truncMod
N	if S is conditional on N, then N is the predicted values returned from predict.N
offset	offset for sampling
dist	distribution used for S, either negative binomial ("NB") or poisson ("poisson")
...	additional arguments to be passed to predict

**Details**

Uses mvtnorm to obtain new parameters for the glm using calculated variance-covariance matrix, assuming multivariate normal for parameters.

new.obs will be automatically scaled using details in model.S if scale.covar==TRUE

**Value**

S	predicted S
expect.S	expected S

**Authors**

Piers Dunstan and Scott Foster

**Examples**

```
N.form <- N~1 + depth + O2_AV + temp_AV + offset(log(area))
model.N <- negBinMod(N.form,data=fish.data,est.var=TRUE,scale.covar =FALSE)
fish.data$N.scale <- fish.data$N/fish.data$area
S.form <- S~1 + N.scale + depth + O2_AV + temp_AV + offset(log(area))
model.S <- truncMod(S.form,fish.data$N,data=fish.data,est.var=TRUE,scale.covar=TRUE)
new.obs <- as.data.frame(t(apply(fish.data,2,mean)))
N.pred <- rep(NA,100)
S.pred <- rep(NA,100)
for(n in 1:100){
  N.pred[n] <- predict(model.N,new.obs,offset=10)$N
  # insert estimate for N into data frame for it is used, not the original value
  new.obs$N.scale <- N.pred[n]/10
  S.pred[n] <- predict(model.S,new.obs,N.pred[n],offset=10)$S
}
hist(S.pred)
```

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RAD

*RAD*

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**Description**

The package RAD is used to fit models to Rank Abundance Distributions, and predict those distributions using new covariates. Details are provided in Foster and Dunstan (2009) and Dunstan and Foster (some day).

negBinMod fits models for N, truncMod fits models for S and MDMnMod fits models for nij

**References**

Foster, S.D. and Dunstan, P.K. (2009) The Analysis of Biodiversity Using Rank Abundance Distributions. Biometrics DOI: 10.1111/j.1541-0420.2009.01263.x

Dunstan, P.K. and Foster, S.D. (some day) RAD Biodiversity: Prediction of Rank Abundance Distributions from Deep Water Benthic Assemblages.



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truncMod	<i>truncMod</i>
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### Description

truncMod fits a truncated negative binomial model to data. Use to fit Species Richness ( $S_i$ )

### Usage

```
truncMod(trunc.form, trunc.pts, data, dist = 'NB', scale.covar=FALSE, est.var = TRUE, trace = TRUE)
```

### Arguments

trunc.form	an object of class "formula" (or one that can be coerced to that class): a symbolic description of the model to be fitted. An offset in the form <code>offset(log(area sampled))</code> should be included in the model formula to adjust for differences in area sampled between sites.
trunc.pts	A vector of truncation points of model. Must be of length equal to the numbers of rows/sites) of data. Set to N for fitting truncated species richness
data	a data frame containing the variables in the formula including the offset and the response. Each row should be a different site.
dist	one of either NB (negative binomial) or poisson
scale.covar	Should the model matrix be scaled (TRUE/FALSE)? Useful if models do not converge. Setting this to TRUE will save the column means and sd for later prediction.
est.var	estimate the variance-covariance matrix using newton-raphson
trace	print model trace

### Details

truncMod used `glm.nb` (MASS) or `glm` to get initial parameters for untruncated likelihood & then uses `nlminb` to fit truncated model. Allows calculation of se for overdispersion parameter.

### Value

coef	coefficients
vcov	variance-covariance matrix
logl	log-likelihood
AIC	AIC
residuals	model residuals, calculated using PIT
fitted	fitted values
sds	dfdf
sums	model sums
mean.X	column means for model matrix if scale.covar is TRUE
sd.X	column sds for model matrix if scale.covar is TRUE
formula	model formula

**Authors**

Piers Dunstan and Scott Foster

**Examples**

```
fish.data$N.scale <- fish.data$N/fish.data$area
S.form <- S~1 + N.scale + depth + O2_AV + temp_AV + offset(log(area))
model.S <- truncMod(S.form, fish.data$N, data=fish.data, est.var=TRUE, scale.covar=TRUE)
plot(model.S$fitted, model.S$residuals)
abline(h=0)
```

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