

# opticut: likelihood based optimal partitioning for indicator species analysis

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## Introduction

Identifying and monitoring indicator species has long been considered a cost-effective way of tracking environmental change or the status of the biota. Examples include the characterization of vegetation types (Chytry et al. 2002), degradation of ecosystems (McGeoch & Chown 1988), or signalling cryptic or rare species (Halme et al. 2009). Throughout these examples, a key attribute of indicator species (also referred to as character or differential species) is that they have strong associations with the environmental variables that they are supposed to indicate.

Approaches to quantify the degree of environmental associations for species (indicator value) traditionally falls into three major types of approaches:

1. contingency table based measures (De Caceres & Legendre 2009);
2. analysis of variance (ANOVA; Wildi & Feldmeyer-Christe 2013); and
3. the widely used non-parametric IndVal method (Dufrene & Legendre 1997).

While the different approaches have strong appeal and applications, they do not always meet the challenges presented by ecological data.

Ecological data come in different forms: binary, ordinal, count, abundance, or presence only data. Some of these data types are suitable for a particular approach, while some formats need ‘tweaking’. For example, binarizing abundance or count data for contingency tables leads to information loss. ANOVA, on the other hand, implies normality and homoscedastic errors, which might not always be satisfied by 0/1, ordinal, skewed, or percent cover data. Finally, randomization test for the IndVal approach requires count data, which renders hypothesis testing difficult if not impossible for continuous or ordinal data.

Another staple of observation field studies is the presence of modifying or confounding variables, or the presence of systematic biases (variable sampling effort, imperfect detectability, sample selection bias). Ignoring these effects can lead to erroneous indicator species analysis (Zettler et al. 2013). Controlling for these effects can improve the assessment of species-environment relationships, thus lead to better evaluation of indicator species.

To address these limitations, Kemencei et al. (2014) proposed a model-based indicator species analysis that accounted for the effects of modifying variables, and non-independence in the data due to paired sampling design. This model-based approach has been generalized and made available in the `opticut` R extension package. The `opticut` package offers computationally efficient and extensible algorithms for finding indicator species, tools for exploring and visualizing the results, and quantifying uncertainties. This manual showcases the functionality of the package.

## Install

The `opticut` R package can be installed from the Comprehensive R Archive Network (CRAN) as:

```
install.packages("opticut")
```

Install development version from GitHub:

```
library(devtools)
install_github("psolymos/opticut")
```

User visible changes in the package are listed in the [NEWS](#) file.

## Report a problem

Use the [issue tracker](#) to report a problem.

## License

[GPL-2](#)

## Loading the package

To get started, open R and load the **opticut** package as:

```
library(opticut)
```

```
## Loading required package: pbapply
```

```
## opticut 0.0-9      2016-10-30
```

## Partitioning

Optimal partitioning (optimal cut, or in short: opticut) is found for each species independent of each other. We make observations ( $y_i$ ) of possibly multiple species at  $i = 1, \dots, n$  sites. Now let us consider a discrete site descriptor ( $g_i$ ) with  $K$  levels or strata ( $K > 2$ ). This stratification might come from remotely sensed or other geospatial information, field measurements, or from multivariate clustering. We can use  $g_i$  to create  $m = 1, \dots, M$  possible binary partitions based on coding one or more levels as 1s and the rest with 0s. We denote any such possible partition as  $z^{(m)}$ . The total number of binary partitions is  $M = 2^{K-1} - 1$ , not counting cases when 0s or 1s are completely missing (which is the null model). The opticut method, as opposed to for example IndVal method is invariant to the coding of 0s and 1s in  $z^{(m)}$ . This means that complementary cases, such as  $z^{(m)}$  and  $1 - z^{(m)}$ , are treated as interchangeable. The opticut package provides utility functions to create and check binary partitions from multi-level vectors (`kComb`, `allComb`, `checkComb`).

## Manipulating partitions

Finding all combinations does not require a model or observed responses. It only takes a classification vector with  $K > 1$  strata. The `kComb` function returns a ‘contrast’ matrix corresponding to all possible binary partitions of the factor with  $K$  levels:

```
kComb(k = 2)
```

```
##      [,1]
## [1,]    1
## [2,]    0
```

```
kComb(k = 3)
```

```
##      [,1] [,2] [,3]
## [1,]    1    0    0
## [2,]    0    1    0
## [3,]    0    0    1
```

```
kComb(k = 4)
```

```
##      [,1] [,2] [,3] [,4] [,5] [,6] [,7]
## [1,]    1    0    0    0    1    1    1
## [2,]    0    1    0    0    1    0    0
## [3,]    0    0    1    0    0    1    0
## [4,]    0    0    0    1    0    0    1
```

allComb takes a classification vector with at least 2 levels and returns a model matrix with binary partitions. checkComb checks if combinations are unique and non-complementary (misfits are returned as attributes):

```
## finding all combinations
```

```
(f <- rep(LETTERS[1:4], each=2))
```

```
## [1] "A" "A" "B" "B" "C" "C" "D" "D"
```

```
(mc <- allComb(f, collapse = "_"))
```

```
##   A B C D A_B A_C A_D
## A 1 0 0 0    1    1    1
## A 1 0 0 0    1    1    1
## B 0 1 0 0    1    0    0
## B 0 1 0 0    1    0    0
## C 0 0 1 0    0    1    0
## C 0 0 1 0    0    1    0
## D 0 0 0 1    0    0    1
## D 0 0 0 1    0    0    1
## attr("collapse")
## [1] "_"
## attr("comb")
## [1] "all"
```

```
## checking for complementary entries
```

```
checkComb(mc) # TRUE
```

```
## [1] TRUE
```

```
## attr("comp")
```

```
##      i j
```

```
## attr("same")
```

```
##      i j
```

```
## adding complementary entries to the matrix
```

```
mc2 <- cbind(z = 1 - mc[,1], mc[,c(1:ncol(mc), 1)])
```

```
colnames(mc2) <- 1:ncol(mc2)
```

```
mc2

##   1 2 3 4 5 6 7 8 9
## A 0 1 0 0 0 1 1 1 1
## A 0 1 0 0 0 1 1 1 1
## B 1 0 1 0 0 1 0 0 0
## B 1 0 1 0 0 1 0 0 0
## C 1 0 0 1 0 0 1 0 0
## C 1 0 0 1 0 0 1 0 0
## D 1 0 0 0 1 0 0 1 0
## D 1 0 0 0 1 0 0 1 0
```

```
checkComb(mc2) # FALSE
```

```
## [1] FALSE
## attr("comp")
##      i j
## [1,] 1 2
## [2,] 1 9
## attr("same")
##      i j
## [1,] 9 2
```

## Choosing a parametric model

A suitable parametric (or semi-parametric) model can be chosen to describe the relationship between the observations for a single species and the site descriptors. The choice of the parametric model depends on the nature of the observations and the goals of the study. The systematic component of the model (also called the linear predictor),  $f(\mu_i) = \beta_0^{(m)} + \beta_1^{(m)} z_i^{(m)} + \sum_{j=1}^p \alpha_j^{(m)} x_{ij}$ , is linked to the random component of the model through the link function  $f$ . The expected value is given by the inverse link function:  $E[Y_i] = \mu_i = f^{-1}(\beta_0^{(m)} + \beta_1^{(m)} z_i^{(m)} + \sum_{j=1}^p \alpha_j^{(m)} x_{ij})$ . Expected values can then be estimated for each partition. The symbol  $x_{ij}$  denotes other site descriptors ( $j = 1, \dots, p$ ; number of predictors besides  $g_i$ ) that can take discrete or continuous values. These variables might describe variation in the observations not fully explained by the partitions, e.g. due to spatially uneven distribution, differences in sampling effort, or environmental variables interfering with the observation process.

We can estimate the parameters in the linear predictor (and possibly other “nuisance” factors such as variance components in mixed effects models) and calculate expected values. The probability density function for the model  $P(Y_i = y_i | z_i^{(m)}, x_{ij}, \theta)$  is used to find the maximum likelihood estimates (MLE) of the model parameters  $\hat{\theta}^{(m)} = (\hat{\beta}_0^{(m)}, \hat{\beta}_1^{(m)}, \hat{\alpha}_1^{(m)}, \dots, \hat{\alpha}_p^{(m)})$  that jointly maximize the log-likelihood function. The log-likelihood function evaluated at the MLE is  $l(\hat{\theta}^{(m)}; y)$ .

The opticut package has several built-in distributions that can be specified through the `dist` argument. Currently available distributions:

- "gaussian": real valued continuous observations, e.g. biomass;
- "poisson": Poisson count data;
- "binomial": presence-absence type data;

- "negbin": overdispersed Negative Binomial count data;
- "beta": continuous response in the unit interval, e.g. percent cover;
- "zip", "zip2": zero-inflated Poisson counts (partitioning in count model: "zip", or in zero model: "zip2");
- "zinb", "zinb2": zero-inflated Negative Binomial counts (partitioning in count model: "zinb", or in zero model: "zinb2");
- "ordered": response measured on ordinal scale, e.g. ordinal vegetation cover (only available for single species because ordinal levels often do not match across different species thus leading to different intercept terms);
- "rsf", "rspf": presence-only data using resource selection and resource selection probability functions (only available for single species because used distribution is unique for all species thus multiple species cannot be combined in a single input matrix).

Other distributions can be specified by user-defined functions as explained later in the manual.

## All combinations

Fitting the model to all the  $M$  candidate binary partitions leads to a set of log-likelihood values. One can compare the log-likelihood values  $l(\hat{\theta}^{(m)}; y)$  to the log-likelihood value based on the null model  $l(\hat{\theta}^{(0)}; y)$ . We define the null model the same way as the other  $M$  models but without the binary partition:  $\beta_1^{(m)} = 0$ . The log of the likelihood ratio between the  $M$  candidate models and the null model can be calculated as  $l(\hat{\theta}^{(m)}; y) - l(\hat{\theta}^{(0)}; y)$ .

The best-supported model  $m'$  and the corresponding binary partition  $z^{(m')}$  is the model with the highest log-likelihood ratio value  $l(\hat{\theta}^{(m')}; y)$ . Model weights are calculated as  $w_m = \exp\{l(\hat{\theta}^{(m)}; y) - l(\hat{\theta}^{(m')}; y)\} / \sum_{m=1}^M \exp\{l(\hat{\theta}^{(m)}; y) - l(\hat{\theta}^{(m')}; y)\}$ . These weights sum to 1 and indicate asymptotic probabilities of finding the same best partition when the sampling is replicated. The concentration of asymptotic probabilities among the models can be expressed through the Simpson index  $H = \sum_{m=1}^M w_m^2$ . High values of  $H$  indicate high concentration of the model weights for one or few model out of the total number of models compared (Kemencei et al. 2014).

The opticut package provides the `opticut1` function to fit a chosen parametric model to a set of binary partitions and the summary returns the model output for each candidate partition with log likelihood ratios and model weights.

```
## stratification
g <- c(1,1,1,1, 2,2,2,2, 3,3,3,3)
## abundance
y <- c(0,0,3,0, 2,3,0,5, 5,6,3,4)
mods <- opticut1(Y = y, Z = allComb(g), dist = "gaussian")
mods

## Univariate opticut results, comb = all, dist = gaussian
## I = 0.8932; w = 0.5742; H = 0.4926; logL_null = -25.93
##
## Best supported models with logLR >= 2:
##   assoc      I    mu0  mu1 logLR      w
## 3    ++ 0.8932 1.625 4.50 3.233 0.5742
## 1    -- 0.8798 3.500 0.75 2.879 0.4031
```

```
## 3 binary splits (1 model not shown)
```

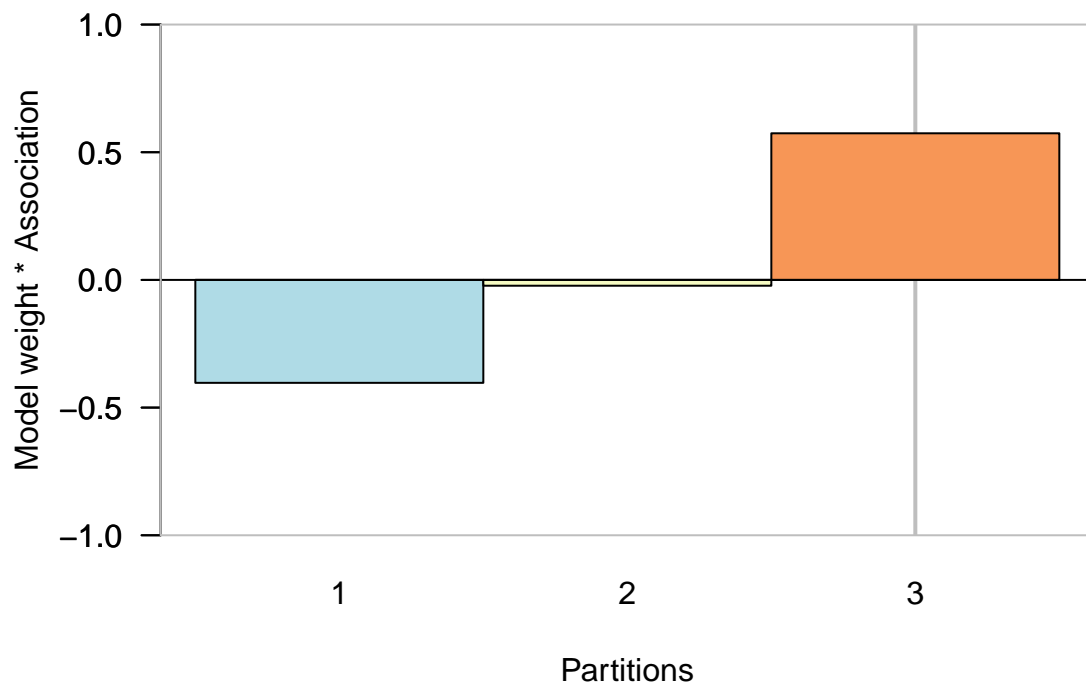
Not all the models are printed, only the ones where the log likelihood ratio (`logLR`) value is  $\geq 2$  by default. We can change this by explicitly defining the `cut` argument in the `print` method (or by setting the `cut` global option via `ocoptions`, as explained later):

```
print(mods, cut = -Inf)
```

```
## Univariate opticut results, comb = all, dist = gaussian
## I = 0.8932; w = 0.5742; H = 0.4926; logL_null = -25.93
##
## Best supported models with logLR >= -Inf:
##   assoc      I  mu0 mu1  logLR      w
## 3    ++ 0.89319 1.625 4.50 3.232629 0.57415
## 1    -- 0.87983 3.500 0.75 2.878892 0.40309
## 2     - 0.06242 2.625 2.50 0.004726 0.02276
## 3 binary splits
```

Model support across the partitions can be visualized by the model weight plot (`wplot`):

```
wplot(mods, cut = -Inf)
```



The `opticut` function can take matrices or a model formula as its input, and repeats the procedure done by `opticut1` for multiple species in a community matrix. The summary shows the best-supported model for each species. It is the preferred way of specifying the model for single species as well. Single species results are part of the `$species` element of the output object:

```
(oc <- opticut(y, strata = g, comb = "all", dist = "gaussian"))
```

```
## Multivariate opticut results, comb = all, dist = gaussian
##
## Call:
```

```
## opticut.default(Y = y, strata = g, dist = "gaussian", comb = "all")
##
## 1 species, 3 binary splits
```

```
summary(oc)
```

```
## Multivariate opticut results, comb = all, dist = gaussian
##
## Call:
## opticut.default(Y = y, strata = g, dist = "gaussian", comb = "all")
##
## Best supported model with logLR >= 2:
##      split assoc      I  mu0 mu1 logLR      w
## Sp 1      3    ++ 0.8932 1.625 4.5 3.233 0.5742
## 3 binary splits
```

```
oc$species
```

```
## $`Sp 1`
## Univariate opticut results, comb = all, dist = gaussian
## I = 0.8932; w = 0.5742; H = 0.4926; logL_null = -25.93
##
## Best supported models with logLR >= 2:
##   assoc      I  mu0 mu1 logLR      w
## 3    ++ 0.8932 1.625 4.50 3.233 0.5742
## 1    -- 0.8798 3.500 0.75 2.879 0.4031
## 3 binary splits (1 model not shown)
```

The use of the `opticut1` function is generally discouraged: some of the internal checks are not guaranteed to flag issues when the formula-to-model-matrix translation is side-stepped (this is what is happening when the modifier variables are supplied as `X` argument in `opticut1`). Use the `opticut` with a single species instead, as shown above.

## Indicator value

Once a model is fit to a given binary partition, we can quantify the indicator value for the species. The indicator value denoted by  $I^{(m)}$  describes the contrast between the two subset of the data represented by the binary partition  $z^{(m)}$ . We define indicator value as a scaled version of the  $\beta_1^{(m)}$  coefficient estimate:  $I^{(m)} = |\tanh(c\beta_1^{(m)})|$ , where  $c = 0.5$ . The hyperbolic tangent function is used as an inverse Fisher transformation to scale real valued coefficients into the  $[-1, 1]$  range. The absolute value then results in a  $[0, 1]$  range for the indicator value.

The  $c$  is a scaling constant that modifies the shape of the function. We chose 0.5 as the default value that allows the indicator value to change more gradually according to our experience with real-world data sets. The  $c = 0.5$  setting is also identical to an inverse logistic function transformed into the  $[-1, 1]$  range.

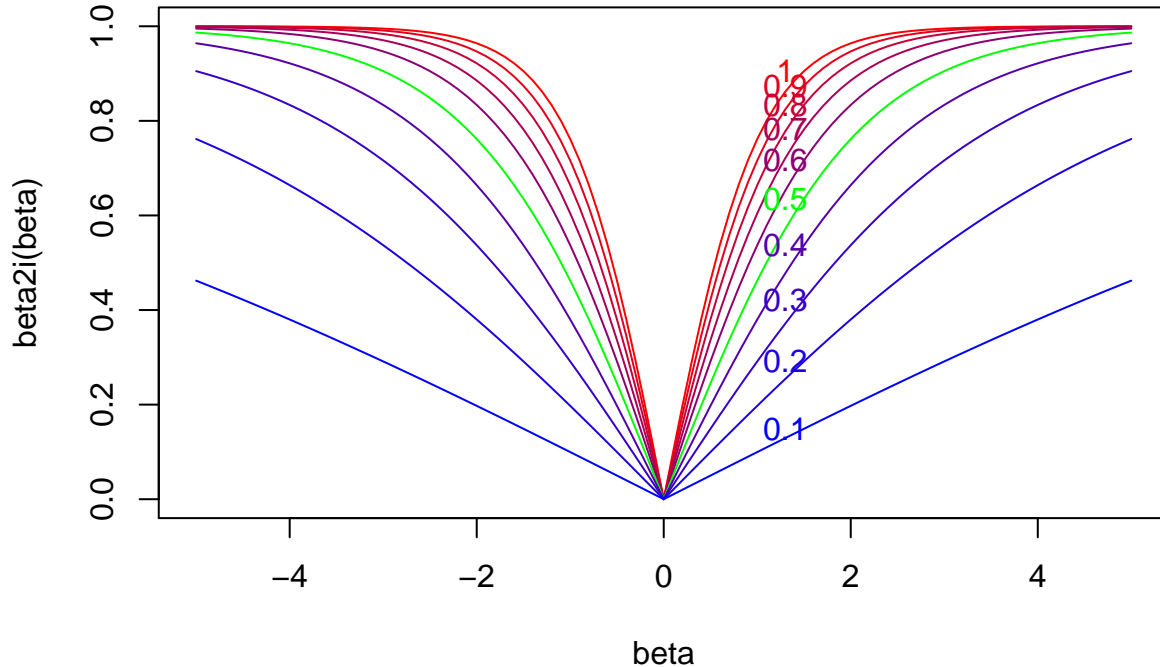
The `beta2i` function is used internally to calculate the indicator value. Here we show the effect of the scaling constant  $c$  on the shape of the function, the default  $c = 0.5$  is in green:



```

beta <- seq(-5, 5, 0.1)
Col <- occcolors(c("red", "blue"))(10)
Col[6] <- "#00FF00"
plot(beta, beta2i(beta), type = "n")
s <- seq(1, 0.1, -0.1)
for (i in 1:10) {
  lines(beta, beta2i(beta, scale = s[i]), col = Col[i])
  text(1.5 - 0.2, beta2i(1.5, scale = s[i]), s[i], col = Col[i])
}

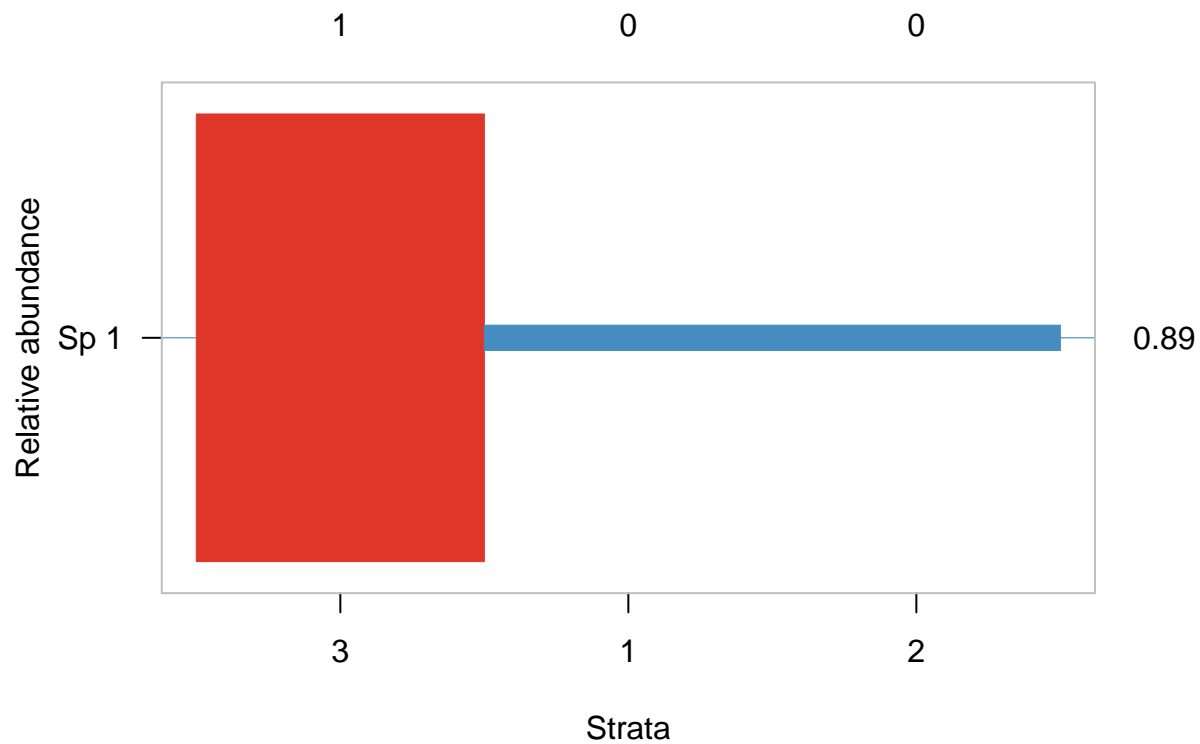
```



An alternative way to define the indicator value would be taking the relative difference between the expected values for the 0 and 1 stratum in  $z^{(m)}$ . This, however, depends on the response scale and the baseline values chosen for possible modifying effects.

Our definition of indicator value is on the linear predictor scale and is more readily compared across species without respect to their relative abundance and values of other modifying factors. Note however, that the meaning of the indicator value might be quite different for studies using different parametric models: it is a difference in the Gaussian case, multiplier in log-linear models, change in log-odds in logistic or ordinal regression. The indicator value given a binary partition is returned by the model summaries, and used in visualization:

```
plot(oc)
```



Use the `options` function to change the default `scale (c)` setting.

## User defined combinations

It is possible to

```
comb <- cbind(
  A = c(rep(1, 4), rep(0, 8)),
  B = c(rep(0, 4), rep(1, 4), rep(0, 4)))
comb
```

```
##      A B
## [1,] 1 0
## [2,] 1 0
## [3,] 1 0
## [4,] 1 0
## [5,] 0 1
## [6,] 0 1
## [7,] 0 1
## [8,] 0 1
## [9,] 0 0
## [10,] 0 0
## [11,] 0 0
## [12,] 0 0
```

```
print(opticut1(Y = y, Z = comb, dist = "gaussian"), cut = -Inf)
```

```
## Univariate opticut results, comb = NA, dist = gaussian
```

```
## I = 0.8798; w = 0.9466; H = 0.8988; logL_null = -25.93
##
## Best supported models with logLR >= -Inf:
##   assoc      I    mu0  mu1    logLR      w
## A    -- 0.87983 3.500 0.75 2.878892 0.94655
## B    - 0.06242 2.625 2.50 0.004726 0.05345
## 2 binary splits
```

If the user happen to define complementary partitions, an error message is thrown:

```
comb <- cbind(comb, 1-comb)
colnames(comb) <- LETTERS[1:4]
comb
```

```
##      A B C D
## [1,] 1 0 0 1
## [2,] 1 0 0 1
## [3,] 1 0 0 1
## [4,] 1 0 0 1
## [5,] 0 1 1 0
## [6,] 0 1 1 0
## [7,] 0 1 1 0
## [8,] 0 1 1 0
## [9,] 0 0 1 1
## [10,] 0 0 1 1
## [11,] 0 0 1 1
## [12,] 0 0 1 1
```

```
try(opticut1(Y = y, Z = comb, dist = "gaussian"))
checkComb(comb)
```

```
## [1] FALSE
## attr(,"comp")
##      i j
## [1,] 1 3
## [2,] 2 4
## attr(,"same")
##      i j
```

The global option `check_comb` can be set to override this default behaviour, although there is no real point in duplicating reparametrized but otherwise identical models:

```
op <- ocoptions(check_comb = FALSE, cut = -Inf)
opticut1(Y = y, Z = comb, dist = "gaussian")
```

```
## Univariate opticut results, comb = NA, dist = gaussian
## I = 0.8798; w = 0.4733; H = 0.4494; logL_null = -25.93
##
## Best supported models with logLR >= -Inf:
##   assoc      I    mu0  mu1    logLR      w
## A    -- 0.87983 3.500 0.750 2.878892 0.47328
```

```
## C    ++ 0.87983 0.750 3.500 2.878892 0.47328
## B    - 0.06242 2.625 2.500 0.004726 0.02672
## D    + 0.06242 2.500 2.625 0.004726 0.02672
## 4 binary splits
ocoptions(op)
```

## Rank based combinations

The IndVal method requires the algorithm to evaluate  $2^K - 1$  binary partitions. Our opticut approach is parametrization invariant with respect to coding the levels in the binary partitions (it affects the intercept term but not the contrast or the log likelihood ratio). This effectively halves the number of partitions we need to compare ( $2^{K-1} - 1$ , `comb = "all"` in opticut). Still, the number of partitions increases according to powers of 2. Here we propose an approach that increases linearly with  $K$ . This algorithm is based on sorting all the  $K$  partitions in  $g$  according to increasing order of the linear predictor estimates for  $K$  coefficients (as opposed to estimating 2 coefficients for a binary partition). The logic follows from the fact that the optimal binary partitioning tries to find the best split in terms of likelihood ratio with lower estimates on one side, and higher estimates on the other side of the split. As a consequence, we only need to try  $K - 1$  binary partitions to find the optimal  $z^{(m')}$ . This algorithm is implemented in the `rankComb` function that is called by opticut with the argument `comb = "rank"`.

The function `rankComb` evaluates a model with a  $K$ -level factor and returns a corresponding partitioning matrix. Attributes hold the estimates for the  $K$  levels:

```
rankComb(Y = y, Z = as.factor(g), dist = "gaussian", collapse = "_")

##    3 2_3
## 1 0  0
## 1 0  0
## 1 0  0
## 1 0  0
## 2 0  1
## 2 0  1
## 2 0  1
## 2 0  1
## 3 1  1
## 3 1  1
## 3 1  1
## 3 1  1
## attr("est")
##    1    2    3
## 0.75 2.50 4.50
## attr("collapse")
## [1] "_"
## attr("comb")
## [1] "rank"
```

The `collapse` argument can be important to make partitions more distinguishable. The global

option is " " that can be modified via the `options` function. It can cause problems when the the collapse character is part of the factor levels used for  $g$ . The `fix_levels` function comes handy for fixing these levels. The function replaces the `collapse` character to something else:

```
getOption("options")$collapse

## [1] " "

fix_levels(as.factor(c("A b", "C d")), sep=":")

## [1] A:b C:d
## Levels: A:b C:d

fix_levels(as.factor(c("A b", "C d")), sep="")

## [1] Ab Cd
## Levels: Ab Cd
```

There is an overhead of fitting the model to calculate the ranking first. But computing efficiencies can be still high compared to all partitions. As a consequence of the ranking process, we do not have summaries for all the possible binary partitions, only for the top candidates. Moreover, the partitions produced for each species might not be identical. Therefore the model weights ( $w$ ) and Simpson index ( $H$ ) have different interpretation and cannot be that easily compared across species, unless the model weights are highly concentrated for the top models. In this case, the sum of weights for the missing models becomes negligible. Another consequence of the ranking process is that  $\beta_1^{(m)}$  estimates are always positive. In the case of comparing all the partitions, the full set of partitions is fixed for all species, and some respond positively while others respond negatively to the same binary variable in terms of the  $\beta_1^{(m)}$  values. Thus it is required to store the sign of the relationship as part of the summary.

The `comb = "rank"` is the default setting in `opticut`. It is clear that the 2 approaches lead to identical best partitions. Only the model weights ( $w$ ) are different:

```
summary(opticut(y, strata = g, comb = "all", dist = "gaussian"))

## Multivariate opticut results, comb = all, dist = gaussian
##
## Call:
## opticut.default(Y = y, strata = g, dist = "gaussian", comb = "all")
##
## Best supported model with logLR >= 2:
##      split assoc      I    mu0 mu1 logLR      w
## Sp 1      3    ++ 0.8932 1.625 4.5 3.233 0.5742
## 3 binary splits

summary(opticut(y, strata = g, comb = "rank", dist = "gaussian"))

## Multivariate opticut results, comb = rank, dist = gaussian
##
## Call:
## opticut.default(Y = y, strata = g, dist = "gaussian", comb = "rank")
##
```

```
## Best supported model with logLR >= 2:
##      split assoc      I    mu0 mu1 logLR      w
## Sp 1      3      ++ 0.8932 1.625 4.5 3.233 0.5875
## 2 binary splits
```

Here is how the ranking info is turned into binary partitions internally:

```
## simulate some data
set.seed(1234)
n <- 200
x0 <- sample(1:4, n, TRUE)
x1 <- ifelse(x0 %in% 1:2, 1, 0)
x2 <- rnorm(n, 0.5, 1)
lam <- exp(0.5 + 0.5*x1 + -0.2*x2)
Y <- rpois(n, lam)

## binary partitions
head(rc <- rankComb(Y, model.matrix(~x2), as.factor(x0), dist="poisson"))
```

```
##      2 1 2 1 2 4
## 1 0      1      1
## 3 0      0      0
## 3 0      0      0
## 3 0      0      0
## 4 0      0      1
## 3 0      0      0
```

```
attr(rc, "est") # expected values in factor levels
```

```
##      1      2      3      4
## 2.644132 2.650397 1.738868 1.738892
```

```
aggregate(exp(0.5 + 0.5*x1), list(x0=x0), mean) # true values
```

```
##      x0      x
## 1  1 2.718282
## 2  2 2.718282
## 3  3 1.648721
## 4  4 1.648721
```

```
## simple example
oComb(1:4, "+")
```

```
##      1 1+2 1+2+3
## 1 1      1      1
## 2 0      1      1
## 3 0      0      1
## 4 0      0      0
```

```
## using estimates
oComb(attr(rc, "est"))
```

```
##   3 3 4 1 3 4
## 1 0  0  1
## 2 0  0  0
## 3 1  1  1
## 4 0  1  1
```

## Partitioning for multiple species

The `opticut` function can take matrices or a model formula as its input, and repeats the procedure done by `opticut1` for multiple species in a community matrix. The summary shows the best-supported model for each species, in this case based on a Poisson count model (`dist = "poisson"`). The `plot` method uses the indicator value (`I` in the summary) to represent the contrast between the two strata of the best supported binary partition:

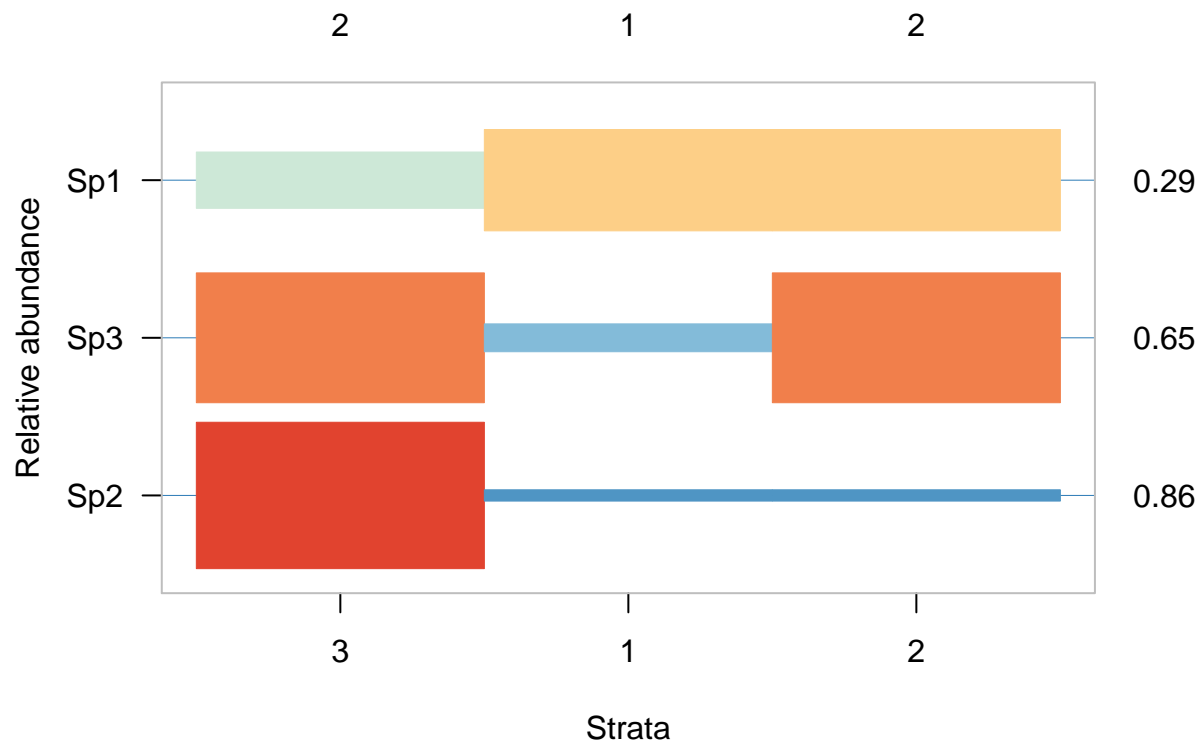
```
## stratification
g <- c(1,1,1,1, 2,2,2,2, 3,3,3,3)

## community matrix
y <- cbind(
  Sp1=c(4,6,3,5, 5,6,3,4, 4,1,3,2),
  Sp2=c(0,0,0,0, 1,0,0,1, 4,2,3,4),
  Sp3=c(0,0,3,0, 2,3,0,5, 5,6,3,4))

oc <- opticut(formula = y ~ 1, strata = g, dist = "poisson", comb = "all")
summary(oc)

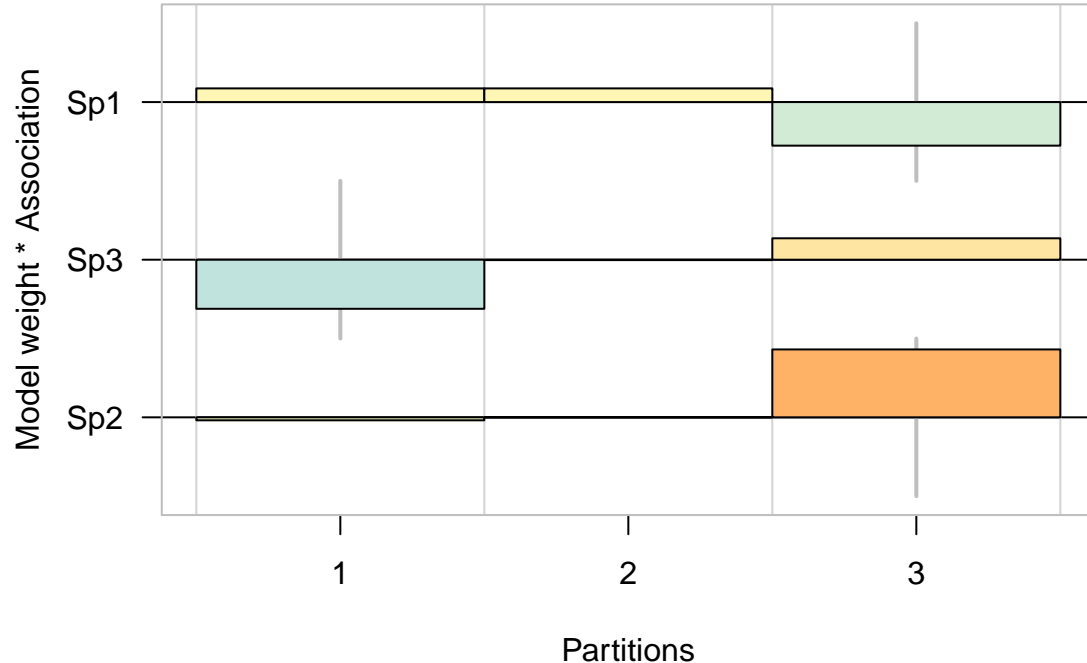
## Multivariate opticut results, comb = all, dist = poisson
##
## Call:
## opticut.formula(formula = y ~ 1, strata = g, dist = "poisson",
##   comb = "all")
##
## Best supported models with logLR >= 2:
##   split assoc      I mu0 mu1 logLR      w
## Sp3     1    -- 0.6471 3.50 0.75 4.793 0.6922
## Sp2     3   +++ 0.8571 0.25 3.25 9.203 0.9573
## 3 binary splits
## 1 species not shown

plot(oc, cut = -Inf)
```



Model support across the partitions can be visualized by the model weight plot (`wplot`).

```
wplot(oc, cut = -Inf)
```



Note that the `wplot` uses 'splits' (binary partitions) whereas `plot` uses the  $K$  levels. Therefore, `wplot` does not work for multiple species when `comb = "rank"`. In this case the splits can be different across the species, whereas `comb = "all"` uses the same pre-defined partitions across all species.



Compare the "all" and "rank" based combinations: same best partitions putting aside complementarity

```
op <- ocoptions(cut = -Inf)
summary(opticut(formula = y ~ 1, strata = g, dist = "poisson", comb = "all"))

## Multivariate opticut results, comb = all, dist = poisson
##
## Call:
## opticut.formula(formula = y ~ 1, strata = g, dist = "poisson",
##   comb = "all")
##
## Best supported models with logLR >= -Inf:
##   split assoc      I mu0 mu1 logLR      w
## Sp1      3      - 0.2857 4.50 2.50 1.498 0.6144
## Sp3      1     -- 0.6471 3.50 0.75 4.793 0.6922
## Sp2      3    +++ 0.8571 0.25 3.25 9.203 0.9573
## 3 binary splits

summary(opticut(formula = y ~ 1, strata = g, dist = "poisson", comb = "rank"))

## Multivariate opticut results, comb = rank, dist = poisson
##
## Call:
## opticut.formula(formula = y ~ 1, strata = g, dist = "poisson",
##   comb = "rank")
##
## Best supported models with logLR >= -Inf:
##   split assoc      I mu0 mu1 logLR      w
## Sp1   1 2      + 0.2857 2.50 4.50 1.498 0.7611
## Sp3   2 3     ++ 0.6471 0.75 3.50 4.793 0.6962
## Sp2    3    +++ 0.8571 0.25 3.25 9.203 0.9577
## 2 binary splits

ocoptions(op)
```

## Accessing models and partitions

The `bestmodel` method returns the best-supported model for further model diagnostics and prediction, the `getMLE` prints out the estimated coefficients and the variance-covariance matrix:

```
mods <- bestmodel(oc)
mods

## $Sp1
##
## Call: stats::glm(formula = Y ~ . - 1, family = Family, data = XX)
##
## Coefficients:
##      V1      Z1
```

```

## 1.5041 -0.5878
##
## Degrees of Freedom: 12 Total (i.e. Null); 10 Residual
## Null Deviance: 63.01
## Residual Deviance: 4.39 AIC: 46.05
##
## $Sp2
##
## Call: stats::glm(formula = Y ~ . - 1, family = Family, data = XX)
##
## Coefficients:
## V1 Z1
## -1.386 2.565
##
## Degrees of Freedom: 12 Total (i.e. Null); 10 Residual
## Null Deviance: 25.54
## Residual Deviance: 6.445 AIC: 26.58
##
## $Sp3
##
## Call: stats::glm(formula = Y ~ . - 1, family = Family, data = XX)
##
## Coefficients:
## V1 Z1
## 1.253 -1.540
##
## Degrees of Freedom: 12 Total (i.e. Null); 10 Residual
## Null Deviance: 49.33
## Residual Deviance: 18.9 AIC: 48.37
## explore further
str(predict(mods[[1]]))

## Named num [1:12] 1.5 1.5 1.5 1.5 1.5 ...
## - attr(*, "names")= chr [1:12] "1" "2" "3" "4" ...
confint(mods[[1]])

## Waiting for profiling to be done...

## 2.5 % 97.5 %
## V1 1.158610 1.81387284
## Z1 -1.343213 0.07397014

## MLE and variance-covariance matrix (species 1)
getMLE(oc, which = 1)

## $coef
## V1 Z1
## 1.5040774 -0.5877867
##

```

```
## $vcov
##           V1           Z1
## V1  0.02777777 -0.02777777
## Z1 -0.02777777  0.12777667
##
## $dist
## [1] "poisson"
```

The `bestpart` method returns the binary partition for the best-supported model:

```
bestpart(oc)
```

```
##   Sp1 Sp2 Sp3
## 1   0   0   1
## 1   0   0   1
## 1   0   0   1
## 1   0   0   1
## 2   0   0   0
## 2   0   0   0
## 2   0   0   0
## 2   0   0   0
## 3   1   1   0
## 3   1   1   0
## 3   1   1   0
## 3   1   1   0
```

## Quantifying uncertainty

Uncertainty in the estimated coefficients and uncertainty in the derived indicator value for the best-supported model ( $I^{(m')}$ ) is quantified based on the estimate of the Hessian matrix assuming asymptotic normality of the MLE. The distribution of  $I^{(m')}$  in this case is based on parametric bootstrap. This approach (`type = "asyp"` in `uncertainty`) is suitable when asymptotic normality assumption is reasonable, i.e. sample size is large. For small sample situations, a parametric bootstrap algorithm is implemented (`type = "boot"`) to estimate uncertainty in  $I^{(m')}$ . The summary contains lower and upper confidence limits (for a given error rate) representing the asymptotic or bootstrap distribution (based on  $B$  number of iterations) given the fixed partition for the best model,  $z^{(m')}$ .

The output is summarized, the `$uncertainty` component contains individual species results:

```
g <- c(1,1,1,1, 2,2,2,2, 3,3,3,3)

y <- cbind(
  Sp1=c(4,6,3,5, 5,6,3,4, 4,1,3,2),
  Sp2=c(0,0,0,0, 1,0,0,1, 4,2,3,4),
  Sp3=c(0,0,3,0, 2,3,0,5, 5,6,3,4))

oc <- opticut(formula = y ~ 1, strata = g, dist = "poisson")

uc <- uncertainty(oc, type = "asyp", B = 999)
```

```
summary(uc)
```

```
## Multivariate opticut uncertainty results
```

```
## type = asymp, B = 999, level = 0.95
```

```
##
```

```
##      split R      I      Lower      Upper
```

```
## Sp1    1 2 1 0.2819 0.01915 0.5611
```

```
## Sp3    2 3 1 0.6120 0.23287 0.8668
```

```
## Sp2    3 1 0.8280 0.51930 0.9662
```

```
uc$uncertainty
```

```
## $Sp1
```

```
## Univariate opticut uncertainty results, type = asymp, B = 999
```

```
##
```

```
##      best      I      mu0      mu1
```

```
## 1 2:1000  Min.    :0.0005819  Min.    :1.043  Min.    :2.684
```

```
##          1st Qu.:0.1705304  1st Qu.:2.051  1st Qu.:3.996
```

```
##          Median :0.2813414  Median :2.506  Median :4.479
```

```
##          Mean   :0.2818717  Mean    :2.630  Mean    :4.546
```

```
##          3rd Qu.:0.3888490  3rd Qu.:3.056  3rd Qu.:5.003
```

```
##          Max.   :0.7179702  Max.    :7.440  Max.    :7.081
```

```
##
```

```
## $Sp2
```

```
## Univariate opticut uncertainty results, type = asymp, B = 999
```

```
##
```

```
##      best      I      mu0      mu1
```

```
## 3:1000  Min.    :0.1822  Min.    :0.02765  Min.    :1.342
```

```
##          1st Qu.:0.7750  1st Qu.:0.15502  1st Qu.:2.714
```

```
##          Median :0.8621  Median :0.23968  Median :3.267
```

```
##          Mean   :0.8280  Mean    :0.31351  Mean    :3.396
```

```
##          3rd Qu.:0.9138  3rd Qu.:0.40962  3rd Qu.:3.939
```

```
##          Max.   :0.9824  Max.    :2.06166  Max.    :7.864
```

```
##
```

```
## $Sp3
```

```
## Univariate opticut uncertainty results, type = asymp, B = 999
```

```
##
```

```
##      best      I      mu0      mu1
```

```
## 2 3:1000  Min.    :0.03062  Min.    :0.1238  Min.    :1.768
```

```
##          1st Qu.:0.50640  1st Qu.:0.5115  1st Qu.:3.078
```

```
##          Median :0.64176  Median :0.7602  Median :3.496
```

```
##          Mean   :0.61203  Mean    :0.8888  Mean    :3.539
```

```
##          3rd Qu.:0.74693  3rd Qu.:1.1265  3rd Qu.:3.947
```

```
##          Max.   :0.93269  Max.    :4.0788  Max.    :6.218
```

The bootstrap can be difficult for small sample sizes, strata can go completely missing:

```
try(uc <- uncertainty(oc, type = "boot", B = 99))
```

A general requirement for the bootstrap approach ("boot" and "multi") is that the bootstrap samples contain observations from each stratum. We recommend having at least 5 observations per strata. Possible problems with missing partitions in small data sets can be remedied by supplying pre-defined indices for resampling, for example, based on jackknife (leave-one-out) approach. The resampling scheme can be customized for such needs. Use the `check_strata` function:

```
B <- sapply(1:length(g), function(i) which((1:length(g)) != i))
check_strata(oc, B) # check representation

## [1] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## attr(,"nx")
## [1] 3
## attr(,"nmat")
## [1] 3 3 3 3 3 3 3 3 3 3 3 3

summary(uncertainty(oc, type = "boot", B = B))
```

```
## Multivariate opticut uncertainty results
## type = boot, B = 12, level = 0.95
##
##      split R      I Lower Upper
## Sp1   1 2 1 0.2866 0.2167 0.3644
## Sp3   2 3 1 0.6523 0.5556 0.9053
## Sp2    3 1 0.8572 0.8384 0.9158
```

The reliability of the best partition can also be assessed using the setting `type = "multi"` (as in *multiple* models). In this case, the model partitions are re-evaluated for each bootstrap sample. Model uncertainty is assessed as the number of times a partition is supported out of the  $B$  bootstrap runs. The reliability ( $R$ ) metric in the summary is the proportion for the most frequently supported partition. The corresponding indicator value and confidence interval is conditional on this most commonly supported partition.

```
summary(uncertainty(oc, type = "multi", B = B))

## Multivariate opticut uncertainty results
## type = multi, B = 12, level = 0.95
##
##      split      R      I Lower Upper
## Sp1   1 2 1.0000 0.2866 0.2167 0.3644
## Sp3   2 3 0.6923 0.6872 0.6174 0.9368
## Sp2    3 1.0000 0.8572 0.8384 0.9158
```

## Distributions

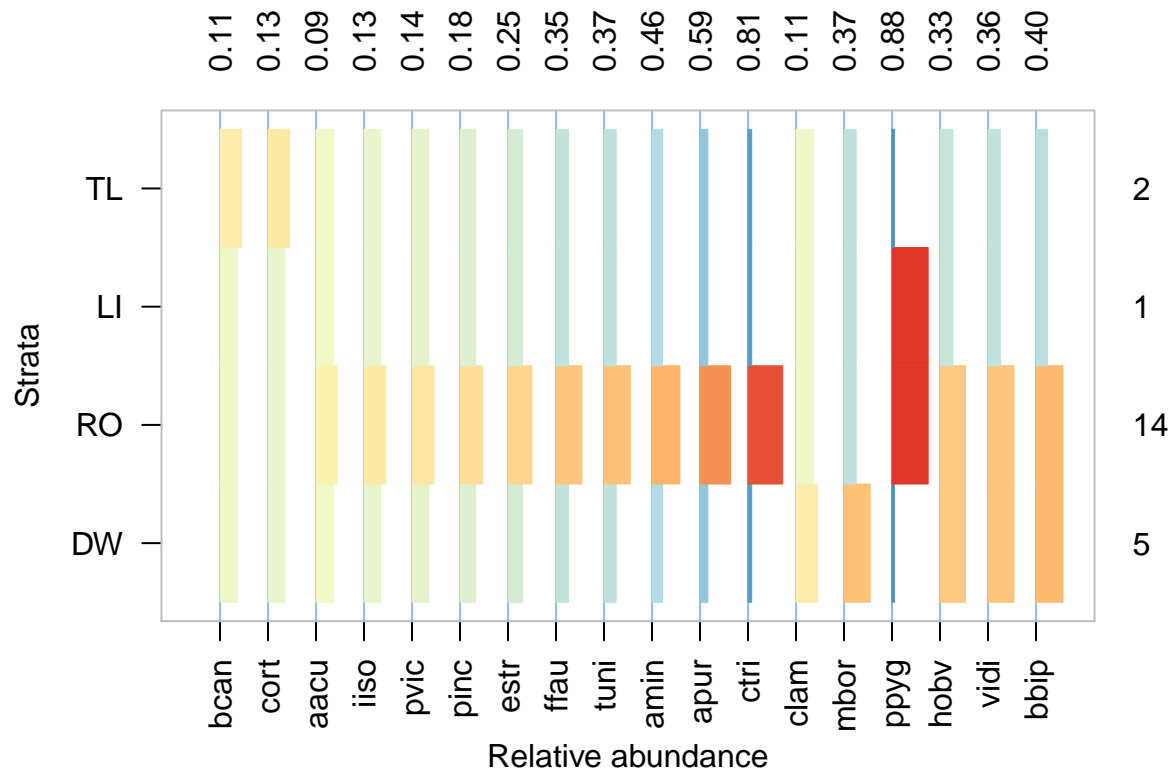
For most distributions, we will use the `dolina` data set that is part of the **opticut** package. It is a comprehensive and micro-scale land snail data set from 16 dolines of the Aggtelek Karst Area, Hungary. Data set containing land snail counts as described in Kemecei et al. 2014.

```
data(dolina)
## stratum as ordinal
dolina$samp$stratum <- as.integer(dolina$samp$stratum)
## filter species to speed up things a bit
Y <- dolina$xtab[,colSums(dolina$xtab > 0) >= 20]
```

## Gaussian

```
dol <- opticut(Y ~ stratum + lmoist + method, data=dolina$samp,
  strata=dolina$samp$mhab, dist="gaussian")
summary(dol)

## Multivariate opticut results, comb = rank, dist = gaussian
##
## Call:
## opticut.formula(formula = Y ~ stratum + lmoist + method, data = dolina$samp,
##   strata = dolina$samp$mhab, dist = "gaussian")
##
## Best supported models with logLR >= 2:
##      split assoc      I      mu0      mu1  logLR      w
## dper DW RO    +++ 0.5988  3.03383 4.4165  9.238 0.6600
## bbip DW RO    +++ 0.4028  0.11875 0.9727 26.906 0.5892
## vidi DW RO    +++ 0.3552  0.64966 1.3925 10.360 0.9866
## hobv DW RO    +++ 0.3297 -0.07760 0.6074 23.017 0.6582
## ppyg LI RO    ++ 0.8822  4.47006 7.2414  4.533 0.8833
## mbor  DW    +++ 0.3662 -0.17269 0.5952 25.555 1.0000
## clam  DW    ++ 0.1078  0.12200 0.3385  5.527 0.8665
## ctri  RO    +++ 0.8063 -0.37944 1.8531  9.223 0.9954
## apur  RO    +++ 0.5912  1.82422 3.1831  9.096 0.9754
## amin  RO    +++ 0.4560  2.17491 3.1595  9.546 0.5919
## tuni  RO    +++ 0.3683  1.01426 1.7872 21.063 1.0000
## ffau  RO    +++ 0.3480  0.02962 0.7560 30.899 1.0000
## estr  RO    +++ 0.2462  0.23962 0.7423 21.892 1.0000
## pinc  RO    +++ 0.1836  0.26944 0.6409 20.890 0.9924
## pvic  RO    ++ 0.1431  0.36807 0.6562  7.107 0.7323
## iiso  RO    +++ 0.1274  0.06840 0.3245 25.005 1.0000
## cort  TL    +++ 0.1321 -0.03773 0.2280 21.583 0.9921
## bcan  TL    +++ 0.1086  0.11177 0.3298 12.425 0.9988
## 3 binary splits
## 1 species not shown
## vertical plot orientation
plot(dol, horizontal=FALSE, pos=1, upper=0.8)
```



## Poisson and Negative Binomial

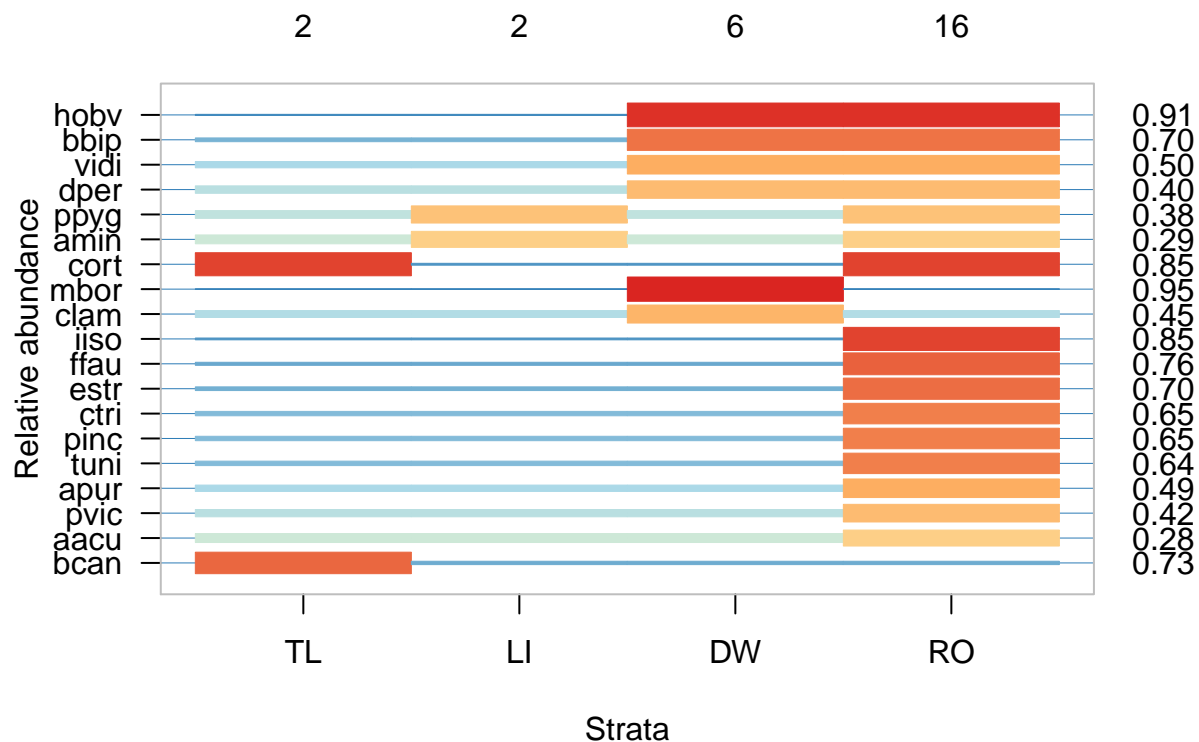
```
dol <- opticut(Y ~ stratum + lmoist + method, data=dolina$samp,
  strata=dolina$samp$mhab, dist="poisson")
summary(dol)
```

```
## Multivariate opticut results, comb = rank, dist = poisson
##
## Call:
## opticut.formula(formula = Y ~ stratum + lmoist + method, data = dolina$samp,
##   strata = dolina$samp$mhab, dist = "poisson")
##
## Best supported models with logLR >= 2:
##   split assoc      I      mu0      mu1    logLR      w
## hobv DW RO    +++ 0.9083 0.0384393 0.80014 75.633 1.0000
## bbip DW RO    +++ 0.6986 0.1843710 1.03897 63.376 1.0000
## vidi DW RO    +++ 0.4955 0.7994519 2.36967 38.141 1.0000
## dper DW RO    +++ 0.4029 4.5082800 10.59304 54.686 0.8816
## ppyg LI RO    +++ 0.3758 3.0963391 6.82425 100.632 1.0000
## amin LI RO    +++ 0.2884 2.1715347 3.93142 22.048 0.7260
## cort TL RO    +++ 0.8506 0.0212887 0.26361 22.532 0.4901
## mbor DW    +++ 0.9489 0.0004436 0.01693 80.850 1.0000
## clam DW    ++ 0.4461 0.1125752 0.29391 7.122 0.6114
## iiso RO    +++ 0.8545 0.0504103 0.64254 21.695 1.0000
```

```
## ffau    R0    +++ 0.7557 0.1043986 0.75035 49.352 1.0000
## estr    R0    +++ 0.7050 0.1853057 1.07085 29.952 1.0000
## ctri    R0    +++ 0.6495 0.2931486 1.37962 124.868 1.0000
## pinc    R0    +++ 0.6476 0.2513583 1.17509 19.970 0.8020
## tuni    R0    +++ 0.6418 2.3448978 10.74959 42.793 1.0000
## apur    R0    +++ 0.4897 2.6442605 7.72006 53.488 1.0000
## pvic    R0    +++ 0.4150 0.4325312 1.04624 9.007 0.6502
## aacu    R0    ++ 0.2821 0.6989512 1.24819 3.741 0.4915
## bcan    TL    +++ 0.7292 0.1594665 1.01806 15.246 0.9958
## 3 binary splits
```

```
## horizontal plot orientation
```

```
plot(dol)
```



Because `opticut` uses the `stats::glm` function to fit the Poisson model, it accepts other arguments, e.g. offsets. Let's subset the `dolina` data set for the litter sampling method ("Q"). Pool the abundances in each of the 16 dolines by microhabitat types. By doing this, we make sampling effort uneven. Litter microhabitat was sampled along a North-South transect (7 locations), whereas the other three strata (rock, live trees, dead wood) were sampled at 3 random locations in each dolina.

```
DQ <- dolina$samp[dolina$samp$method == "Q",]
DQ$dol_mhab <- paste0(DQ$dolina, "_", DQ$mhab)
head(DQ)
```

```
##      sample dolina microhab mhab method aspect stratum lmoist lthick
## 10A1Q   10A1     10  litter  LI      Q southern      4     1.0    2.0
## 10A2Q   10A2     10  litter  LI      Q southern      3     1.0    2.5
## 10A3Q   10A3     10  litter  LI      Q southern      2     1.0    3.0
```



```
## 10A4Q    10A4      10  litter  LI      Q      flat      1      1.5    0.5
## 10A5Q    10A5      10  litter  LI      Q northern    2      1.0    1.5
## 10A6Q    10A6      10  litter  LI      Q northern    3      1.0    3.0
##          dol_mhab
## 10A1Q      10_LI
## 10A2Q      10_LI
## 10A3Q      10_LI
## 10A4Q      10_LI
## 10A5Q      10_LI
## 10A6Q      10_LI
```

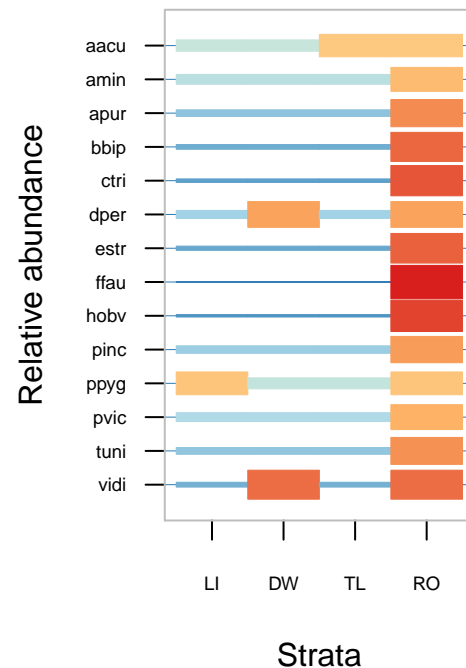
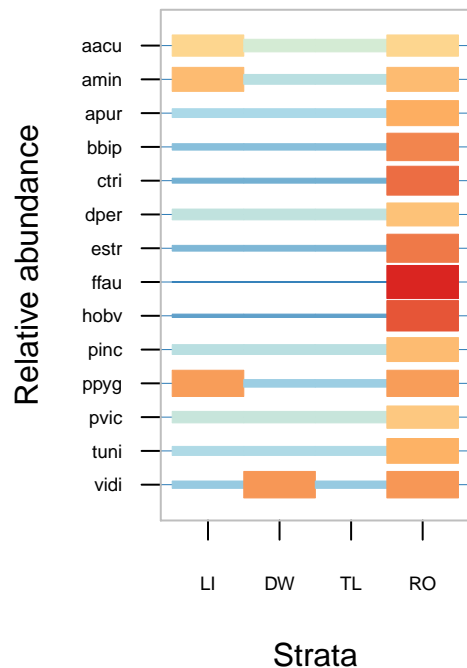
```
YQ <- dolina$xtab[dolina$samp$method == "Q",]
YQ <- YQ[,colSums(YQ > 0) >= 20]
YQ <- mefa4::groupSums(YQ, 1, DQ$dol_mhab)
DQ <- mefa4::nonDuplicated(DQ, dol_mhab, TRUE)
```

Let's compare the results of ignoring sampling effort differences with a case when we use sampling effort as offset. Offsets are defined as  $\log(7)$  or  $\log(3)$  representing the sampling volume differences (more debris searched leads to more snails found). Using offsets results in less species that is associated with litter:

```
op <- ooptions(collapse="_", sort=FALSE, cut=-Inf)
dol0 <- opticut(YQ, strata=DQ$mhab, dist="poisson")
off <- ifelse(DQ$mhab == "LI", log(7), log(3))
dol1 <- opticut(YQ, strata=DQ$mhab, dist="poisson", offset=off)
table(wo_offset=summary(dol0)$summary$split,
      with_offset=summary(dol1)$summary$split)
```

```
##          with_offset
## wo_offset DW_RO LI_RO RO TL_RO
##    DW_RO    1     0  0    0
##    LI_RO    0     1  1    1
##    RO      1     0  9    0
```

```
options(op)
opar <- par(mfrow=c(1,2))
plot(dol0, show_I=FALSE, show_S=FALSE, sort=FALSE, cex.axis=0.6)
plot(dol1, show_I=FALSE, show_S=FALSE, sort=FALSE, cex.axis=0.6)
```



```
par(opar)
```

The Negative Binomial model can be quite picky, as it gives an error somewhere in the middle of the process:

```
try(dol <- opticut(Y ~ stratum + lmoist + method, data=dolina$samp,
  strata=dolina$samp$mhab, dist="negbin"))
```

```
## Warning: step size truncated due to divergence
```

Changing the try\_error global option will allow the process to go on after catching the error:

```
op <- ooptions(try_error = TRUE)
dol <- opticut(Y ~ stratum + lmoist + method, data=dolina$samp,
  strata=dolina$samp$mhab, dist="negbin")
```

```
## Warning: step size truncated due to divergence
```

```
## Warning in opticut.default(Y = Y, X = X, strata = strata, dist = dist, comb
## = comb, : Bad news: opticut failed for 1 out of 19 species.
```

```
dol$failed
```

```
## [1] "mbor"
```

```
options(op)
```

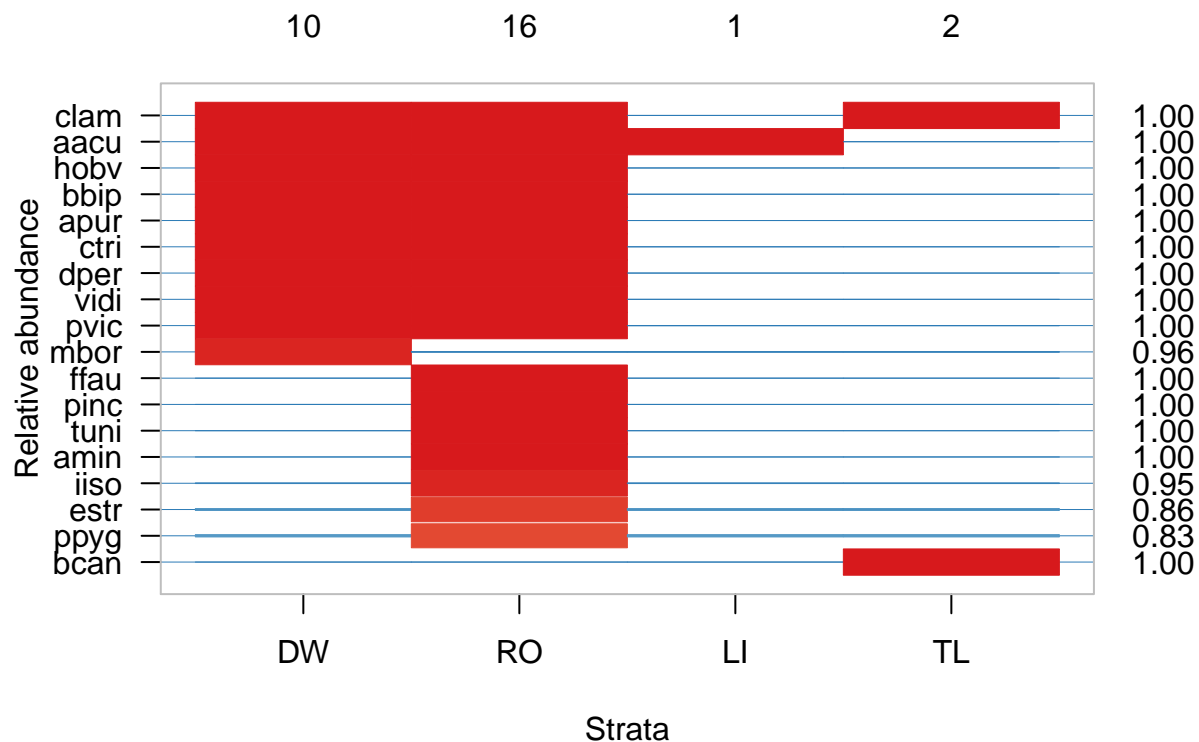
It failed for the "mbor" (*Macrogastra borealis*) species, which is now excluded from the output.

## Zero-inflated distributions

The Zero-inflated Negative Binomial implementation in the **pscl** package seems more robust, no error messages. We use the `dist = "zinb2"` option so that we test for optimal partitioning in the zero-inflation (ZI) component. Using a mixture distribution can be important if 0s can occur not only as a result of the ZI component, but due to low abundance in the count distribution (Poisson or Negative Binomial). Differentiating among these different types of zeros is not possible by binarizing the data and using logistic regression.

In the case of "zip2" and "zinb2" distributions, the coefficients refer to the probability of non-zero, so that positive and negative effects are properly identified (as opposed to "zip" and "zinb" where the ZI coefficients refer to probability of zero):

```
dol <- opticut(Y ~ stratum + lmoist + method, data=dolina$samp,  
  strata=dolina$samp$mhab, dist="zinb2")  
plot(dol)
```



## Binomial, Beta distribution and ordinal data

Stratigraphy example using Beta distribution:

```
library(rioja)
```

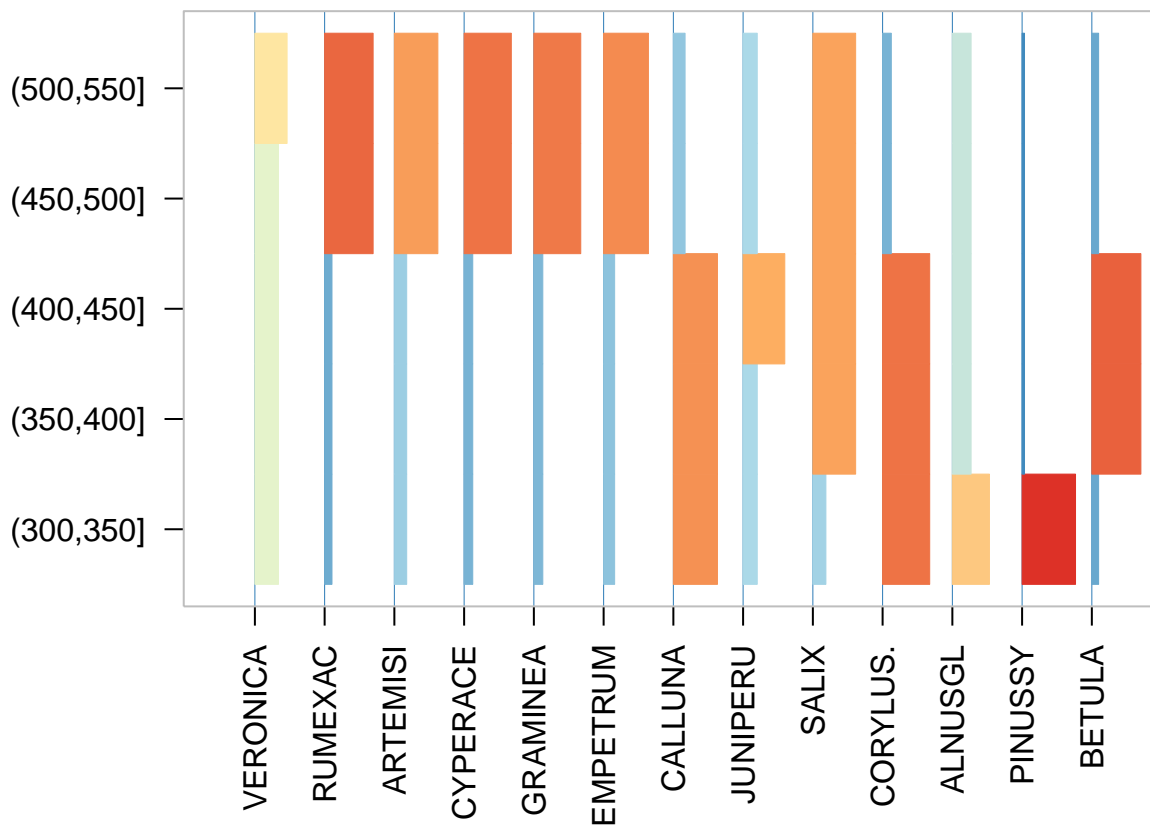
```
## This is rioja 0.9-9
```

```
data(aber)  
strat.plot(aber$spec, aber$ages$Depth, scale.percent=TRUE, y.rev=TRUE)
```



```
## PINUSSY (300,350] +++ 0.9142 0.083196
## ALNUSGL (300,350] ++ 0.3289 0.002089
## JUNIPERU (400,450] ++ 0.4933 0.025317
##          mu1 logLR w
## SALIX 0.044639 8.393 0.5344
## CORYLUS. 0.096616 17.133 0.9940
## CALLUNA 0.019421 12.719 0.5430
## BETULA 0.568254 27.575 1.0000
## RUMEXAC 0.095248 15.892 0.9888
## CYPERACE 0.080857 24.351 1.0000
## GRAMINEA 0.131311 21.569 0.9914
## EMPETRUM 0.079641 10.171 0.6500
## ARTEMISI 0.145790 7.025 0.9708
## PINUSSY 0.669499 26.667 1.0000
## ALNUSGL 0.004128 2.081 0.4201
## JUNIPERU 0.071110 4.017 0.6459
## 4 binary splits
## 1 species not shown
```

```
plot(a, sort=FALSE, horizontal=FALSE, pos=1, upper=0.8,
     show_I=FALSE, show_S=FALSE, mar=c(6,6,1,1), xlab="", ylab="")
```

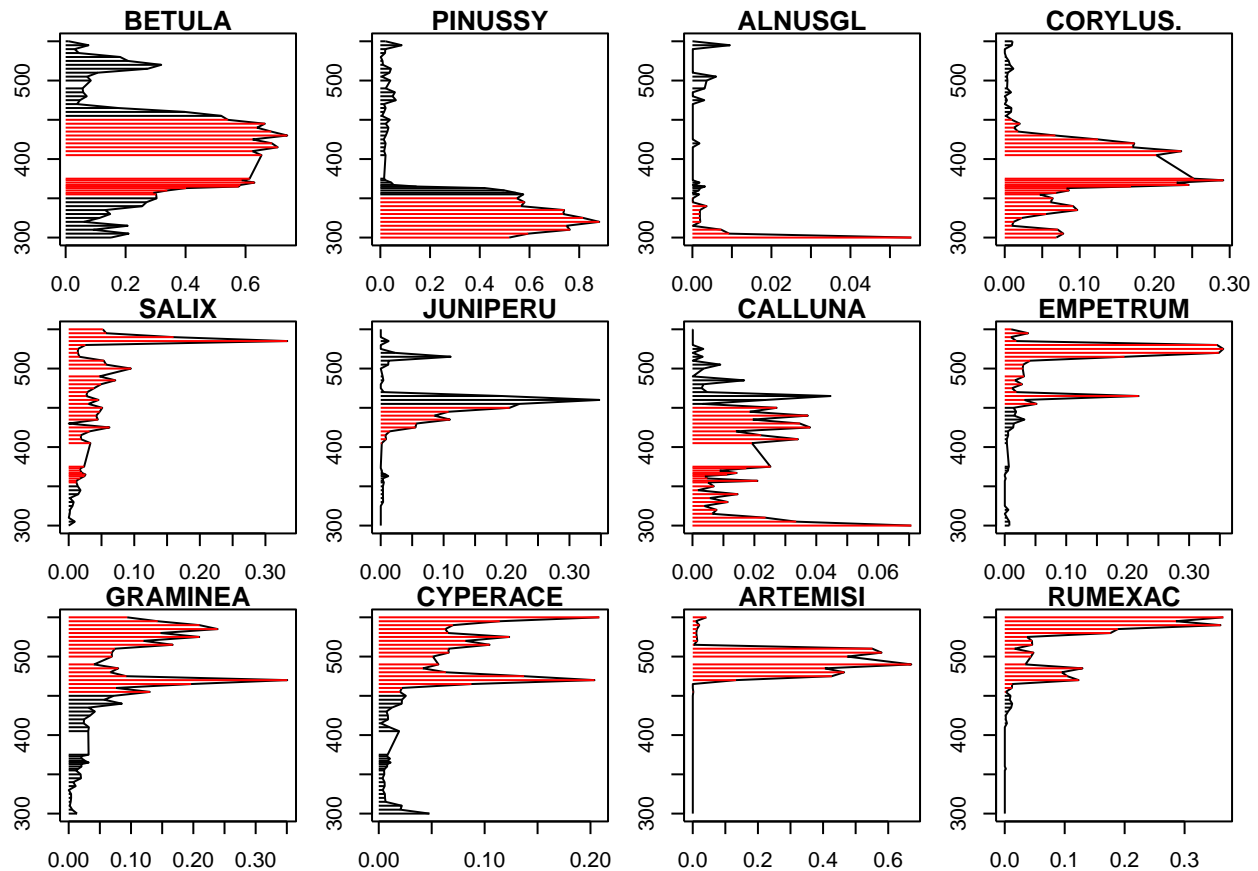


```
bp <- bestpart(a)
opar <- par(mfrow=c(3,4), mar=c(2,2,1,1))
for (i in 1:12) {
```

```

plot(ab[,i], aber$ages$Depth, type="l", ann=FALSE)
segments(x0=rep(0, nrow(ab)), y0=aber$ages$Depth, x1=ab[,i],
         col=ifelse(bp[,i] > 0, 2, 1))
title(main=colnames(ab)[i])
}

```



```

par(opar)

```

```

op <- ocoptions(try_error=TRUE)
library(optpart)

data(shoshsite)
data(shoshveg)

elev <- cut(shoshsite$elevation, breaks=c(0, 7200, 8000, 9000, 20000))
levels(elev) <- c("low","mid1","mid2", "high")

sveg <- as.matrix(shoshveg)
sveg[sveg > 0] <- 1
o <- opticut(sveg ~ 1, strata=elev, dist="binomial")
plot(o, sort=1)

```

```

sveg <- as.matrix(shoshveg)
sveg <- sveg[,colSums(sveg>0) >= 50]
table(sveg)
sveg[sveg==0] <- 0.001
sveg[sveg==0.1] <- 0.01
sveg[sveg==0.5] <- 0.05
sveg[sveg==1] <- 0.15
sveg[sveg==2] <- 0.25
sveg[sveg==3] <- 0.35
sveg[sveg==4] <- 0.45
sveg[sveg==5] <- 0.55
sveg[sveg==6] <- 0.65
sveg[sveg==7] <- 0.75
sveg[sveg==8] <- 0.8
table(sveg)
o2 <- opticut(sveg ~ 1, strata=elev, dist="beta")
plot(o2, sort=1)

## ZI-Beta
zi_beta_fun <- function(Y, X, linkinv, ...) {
  kx <- ncol(X)
  id1 <- Y > 0
  id0 <- !id1
  nll_ZIB_ML <- function(parms) {
    mu <- plogis(X %*% parms[1:kx])
    gamma <- exp(parms[kx + 1]) # precision
    phi <- plogis(parms[kx+2])
    alpha <- mu * gamma
    beta <- (1 - mu) * gamma
    loglik0 <- log(phi)
    loglik1 <- log(1 - phi) + suppressWarnings(dbeta(Y,
      alpha, beta, log = TRUE))
    loglik <- sum(loglik0[id0]) + sum(loglik1[id1])
    if (!is.finite(loglik) || is.na(loglik))
      loglik <- -.Machine$double.xmax^(1/3)
    -loglik
  }
  Yv <- Y
  Yv[Y <= 0.001] <- 0.001
  ini <- c(coef(betareg::betareg(Yv ~ .-1, data=X)), zi=-5)
  X <- as.matrix(X)
  res <- optim(ini, nll_ZIB_ML, ...)
  list(coef=res$par,
    logLik=-res$value,
    linkinv=binomial("logit")$linkinv)
}
sveg <- as.matrix(shoshveg)

```

```

sveg <- sveg[,colSums(sveg>0) >= 50]
table(sveg)
#sveg[sveg==0] <- 0.001
sveg[sveg==0.1] <- 0.01
sveg[sveg==0.5] <- 0.05
sveg[sveg==1] <- 0.15
sveg[sveg==2] <- 0.25
sveg[sveg==3] <- 0.35
sveg[sveg==4] <- 0.45
sveg[sveg==5] <- 0.55
sveg[sveg==6] <- 0.65
sveg[sveg==7] <- 0.75
sveg[sveg==8] <- 0.8
table(sveg)

o2 <- opticut(sveg ~ 1, strata=elev, dist=zi_beta_fun)
plot(o2, sort=1)

y <- as.matrix(varespec / 100)
range(y[y>0])
y <- y[,apply(y, 2, max) > 0.05]
zi_beta_fun(y[,3], data.frame(matrix(1, nrow(y), 1)))
opticut1(y[,1], matrix(1, nrow(y), 1), varechem$grazing, dist=zi_beta_fun)

sveg2 <- as.matrix(shoshveg)
sveg2[sveg2 > 0] <- 1
sveg2 <- sveg2[,colnames(sveg)]
o3 <- opticut(sveg2 ~ 1, strata=elev, dist="binomial")
plot(o3, sort=1)

sveg2 <- as.matrix(shoshveg)
sveg2[sveg2 > 0] <- 1
sveg2 <- sveg2[,colnames(sveg)]

Y <- shoshveg$ASTMIS
table(Y)
o4 <- opticut(Y ~ 1, strata=elev, dist="ordered")
o4$species

## check for modifier variable
ocoptions(op)

```

Link functions and uncertainty:

```

## dolina example
data(dolina)
## stratum as ordinal
dolina$samp$stratum <- as.integer(dolina$samp$stratum)

```



```

## filter species to speed up things a bit
Y <- ifelse(dolina$xtab[,colSums(dolina$xtab > 0) >= 20] > 0, 1, 0)
## opticut results, note the cloglog link function
dol <- opticut(Y ~ stratum + lmoist + method, data=dolina$samp,
  strata=dolina$samp$mhab, dist="binomial:cloglog")

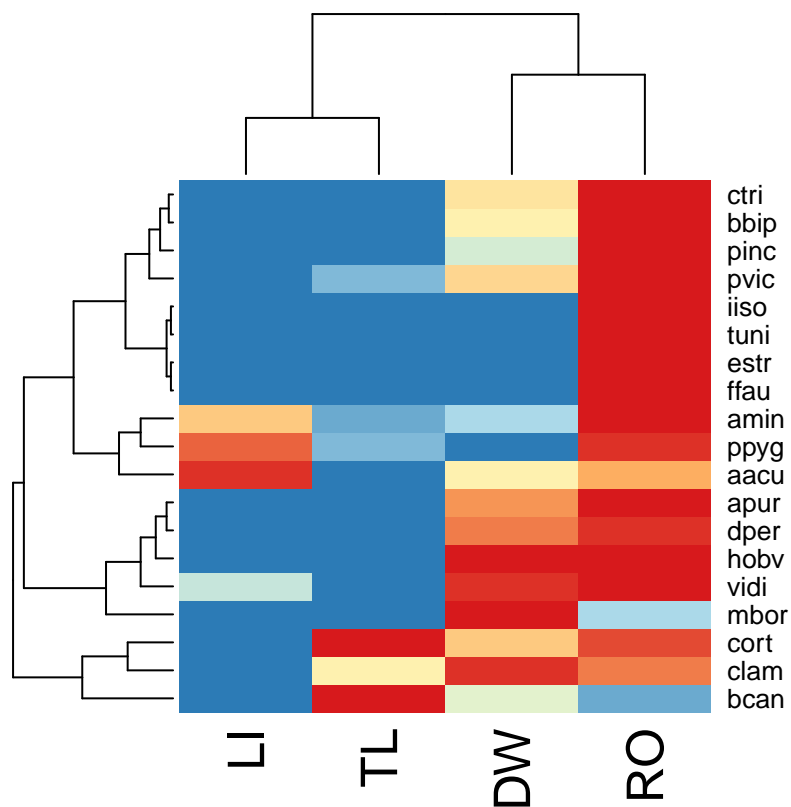
## parallel computing for uncertainty
ucdol <- uncertainty(dol, type="multi", B=25)

bestpart(ucdol)

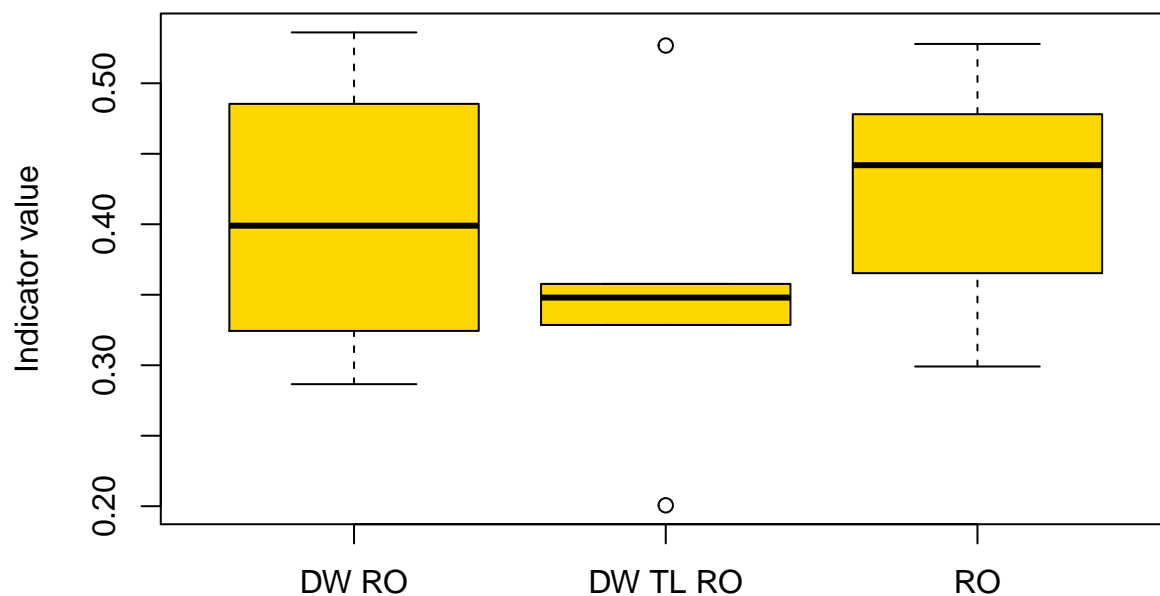
##          aacu      amin      apur      bbip      bcan      clam      cort
## LI 0.92307692 0.6538462 0.03846154 0.0000000 0.0000000 0.0000000 0.0000000
## DW 0.53846154 0.2692308 0.76923077 0.5384615 0.4230769 0.9230769 0.6538462
## TL 0.03846154 0.1538462 0.03846154 0.0000000 1.0000000 0.5384615 1.0000000
## RD 0.73076923 1.0000000 0.96153846 1.0000000 0.1538462 0.8076923 0.8846154
##          ctri      dper      estr ffau      hobv      iiso      mbor
## LI 0.00000000 0.00000000 0.00000000 0 0.0000000 0.03846154 0.00000000
## DW 0.57692308 0.80769231 0.00000000 0 1.0000000 0.03846154 1.00000000
## TL 0.03846154 0.03846154 0.03846154 0 0.0000000 0.00000000 0.03846154
## RD 1.00000000 0.92307692 1.00000000 1 0.9615385 1.00000000 0.26923077
##          pinc      ppyg      pvic      tuni      vidi
## LI 0.00000000 0.8461538 0.00000000 0.03846154 0.3461538
## DW 0.3846154 0.0000000 0.6153846 0.00000000 0.9230769
## TL 0.0000000 0.1923077 0.1923077 0.00000000 0.0000000
## RD 1.0000000 0.9230769 1.0000000 1.00000000 1.0000000

heatmap(t(bestpart(ucdol)), scale="none", col=occolours()(25),
  distfun=function(x) dist(x, "manhattan"))

```



```
## See how indicator value changes with different partitions
with(ucdol$uncertainty[["pvic"]],
  boxplot(I ~ best, col="gold", ylab="Indicator value"))
```



## Presence-only (use-availability) data

```
library(ResourceSelection)
data(goats)
slp <- cut(goats$SLOPE,c(-1, 20, 30, 40, 50, 90))
table(slp, goats$STATUS)
o <- opticut(STATUS ~ ELEVATION, data=goats, strata=slp, dist="rsf")
o <- opticut(goats$STATUS, strata=slp, dist="rsf")
o$species
plot(o, sort=FALSE)
```

## Customizing the distribution

```
## dolina example
data(dolina)
## stratum as ordinal
dolina$samp$stratum <- as.integer(dolina$samp$stratum)
## filter species to speed up things a bit
Y <- dolina$xtab[,colSums(dolina$xtab > 0) >= 20]

## we may want to expand the Zero-inflation component in a ZIP model
## see how the return value needs to be structured
fun <- function(Y, X, linkinv, zi_term, ...) {
  X <- as.matrix(X)
  mod <- pscl::zeroinfl(Y ~ X-1 | zi_term, dist = "poisson", ...)
  list(coef=coef(mod),
        logLik=logLik(mod),
        linkinv=mod$linkinv)
}
Xdol <- model.matrix(~ stratum + lmoist + method, data=dolina$samp)
## this fits the null model (i.e. no partitions added)
fun(Y[, "amin"], Xdol, zi_term=dolina$samp$method)

## $coef
## count_X(Intercept)      count_Xstratum      count_Xlmoist
##           1.30243481          -0.14266929           0.02460366
##      count_XmethodT    zero_(Intercept)    zero_zi_termT
##          -0.64335270          -0.56590398           0.61664601
##
## $logLik
## 'log Lik.' -788.9897 (df=6)
##
## $linkinv
## function (eta)
## .Call(C_logit_linkinv, eta)
## <environment: namespace:stats>
```

```
## now we can use dist=fun
opticut1(Y[, "amin"], Xdol, Z=dolina$samp$mhab,
         dist=fun, zi_term=dolina$samp$method)

## Univariate opticut results, comb = rank, dist = fun
## I = 0.2652; w = 0.9849; H = 0.9703; logL_null = -789
##
## Best supported models with logLR >= 2:
##      assoc      I      mu0      mu1  logLR      w
## LI RO      +++ 0.2652 0.7754 0.8560 15.370 9.849e-01
## RO      +++ 0.2358 0.7941 0.8618 11.189 1.505e-02
## LI DW RO  ++ 0.2036 0.7409 0.8121  5.328 4.286e-05
## 3 binary splits

dol2 <- opticut(Y ~ stratum + lmoist + method, data=dolina$samp,
               strata=dolina$samp$mhab, dist=fun, zi_term=dolina$samp$method)
summary(dol2)

## Multivariate opticut results, comb = rank, dist = fun
##
## Call:
## opticut.formula(formula = Y ~ stratum + lmoist + method, data = dolina$samp,
##      strata = dolina$samp$mhab, dist = fun, zi_term = dolina$samp$method)
##
## Best supported models with logLR >= 2:
##      split assoc      I      mu0      mu1  logLR      w
## cort DW TL RO      +++ 1.0000 7.247e-10 0.1302 19.933 0.6502
## hobv  DW RO      +++ 0.9117 9.715e-02 0.6996 49.368 1.0000
## bbip  DW RO      +++ 0.7037 3.155e-01 0.7260 45.369 1.0000
## vidi  DW RO      +++ 0.4519 6.570e-01 0.8353 19.411 1.0000
## ctri  LI RO      +++ 0.3951 5.638e-01 0.7488 27.661 1.0000
## amin  LI RO      +++ 0.2652 7.754e-01 0.8560 15.370 0.9849
## ppyg  LI RO      +++ 0.2518 8.781e-01 0.9234 41.925 1.0000
## aacu  TL RO      ++ 0.3969 5.375e-01 0.7291  6.650 0.9738
## mbor   DW      +++ 0.9423 4.190e-01 0.9605 23.691 0.9803
## clam  DW      ++ 0.4736 3.755e-01 0.6273  5.582 0.7947
## iiso   RO      +++ 0.8562 1.757e-01 0.7334 17.176 0.9998
## ffau   RO      +++ 0.7118 1.149e-01 0.4355 20.143 0.9475
## pinc   RO      +++ 0.6322 2.465e-01 0.5921 14.673 0.5292
## estr   RO      +++ 0.6316 2.133e-01 0.5457 14.059 0.9903
## tuni   RO      +++ 0.4617 8.441e-01 0.9363 13.350 0.9996
## apur   RO      +++ 0.4326 7.859e-01 0.9026 37.612 0.9844
## pvic   RO      ++ 0.4205 5.499e-01 0.7497  7.165 0.4985
## dper   RO      +++ 0.3616 9.152e-01 0.9584 37.337 0.5118
## bcan   TL      +++ 0.7402 3.854e-01 0.8077 11.543 0.9844
## 3 binary splits
```

## Mixed-effects models (LMM, GLMM)

Here is an example using mixed models and the package **lme4**:

```
library(lme4)

## Loading required package: Matrix

set.seed(1234)
n <- 200
x0 <- sample(1:4, n, TRUE)
x1 <- ifelse(x0 %in% 1:2, 1, 0)
x2 <- rnorm(n, 0.5, 1)
ee <- rnorm(n/5)
g <- rep(1:5, each=n/5)
lam1 <- exp(0.5 + 0.5*x1 + -0.2*x2 + ee[g])
Y1 <- rpois(n, lam1)

X <- model.matrix(~x2)
Z <- allComb(x0)

lmefun <- function(Y, X, linkinv, gr, ...) {
  X <- as.matrix(X)
  m <- glmer(Y ~ X-1 + (1|gr), family=poisson("log"), ...)
  list(coef=fixef(m),
       logLik=logLik(m),
       linkinv=family(m)$linkinv)
}

lmefun(Y1, X, gr=g)

## $coef
## X(Intercept)          Xx2
##    0.6880337   -0.1899153
##
## $logLik
## 'log Lik.' -345.1799 (df=3)
##
## $linkinv
## function (eta)
## pmax(exp(eta), .Machine$double.eps)
## <environment: namespace:stats>

opticut1(Y1, X, Z, dist=lmefun, gr=g)

## Univariate opticut results, comb = all, dist = lmefun
## I = 0.2518; w = 0.9985; H = 0.997; logL_null = -345.2
##
## Best supported models with logLR >= 2:
##      assoc      I    mu0    mu1  logLR      w
## 1 2    +++ 0.2518 1.480 2.476 13.582 0.9984969
```

```
## 1      ++ 0.2120 1.745 2.683 6.864 0.0012072
## 4      -- 0.1792 2.168 1.509 4.739 0.0001441
## 3      -- 0.1805 2.134 1.482 4.620 0.0001279
## 2      ++ 0.1242 1.858 2.386 2.813 0.0000210
## 7 binary splits (2 models not shown)
```

## Generalized additive models (GAM)

```
library(mgcv)
```

```
## Loading required package: nlme
##
## Attaching package: 'nlme'
## The following object is masked from 'package:lme4':
##
##      lmList
## This is mgcv 1.8-15. For overview type 'help("mgcv-package")'.
```

```
library(detect)
```

```
## Loading required package: Formula
## Loading required package: stats4
## detect 0.4-0      2016-03-02
```

```
data(oven)
oven$veg <- factor(NA, c("agr", "open", "decid", "conif", "mix"))
oven$veg[oven$pforest < 0.5] <- "open"
oven$veg[oven$pagri > 0.5 & oven$pforest < 0.5] <- "agr"
oven$veg[oven$pforest >= 0.5] <- "mix"
oven$veg[oven$pforest >= 0.5 & oven$pdecid >= 0.8] <- "decid"
oven$veg[oven$pforest >= 0.5 & oven$pdecid < 0.2] <- "conif"
table(oven$veg, useNA="always")
```

```
##
##   agr  open decid conif  mix  <NA>
##   530   33   78   30  220     0
```

```
oven$xlat <- scale(oven$lat)
oven$xlong <- scale(oven$long)
gamfun <- function(Y, X, linkinv, Data, ...) {
  X <- as.matrix(X)
  m <- mgcv::gam(Y ~ X-1 + s(xlat) + s(xlong), Data, ...)
  list(coef=coef(m),
        logLik=logLik(m),
        linkinv=family(m)$linkinv)
}
```

```

x <- ifelse(oven$veg=="agr",1,0)
X <- model.matrix(~x)
gamfun(oven$count, X, Data=oven, family=poisson)

## $coef
## X(Intercept)          Xx      s(xlat).1      s(xlat).2      s(xlat).3
## -0.306661304 -1.382449156 -0.555089095 -0.890381109  0.306380012
##      s(xlat).4      s(xlat).5      s(xlat).6      s(xlat).7      s(xlat).8
##  1.122776013  0.132117780 -0.052077672  0.036702449 -3.041886993
##      s(xlat).9      s(xlong).1      s(xlong).2      s(xlong).3      s(xlong).4
##  0.955525315 -1.090347031  1.922368963 -0.004724731 -0.428722334
##      s(xlong).5      s(xlong).6      s(xlong).7      s(xlong).8      s(xlong).9
##  0.369410432  0.241421901 -0.228281375 -0.857581486  0.995878919
##
## $logLik
## 'log Lik.' -730.8404 (df=16.34444)
##
## $linkinv
## function (eta)
## pmax(exp(eta), .Machine$double.eps)
## <environment: namespace:stats>

print(opticut1(oven$count, X=X[,1,drop=FALSE], oven$veg, dist=gamfun,
  Data=oven, family=poisson), cut=-Inf)

## Univariate opticut results, comb = rank, dist = gamfun
## I = 0.5988; w = 0.9985; H = 0.997; logL_null = -777.7
##
## Best supported models with logLR >= -Inf:
##
##          assoc      I      mu0      mu1 logLR      w
## open decid conif mix +++ 0.5988 0.1847 0.7359 46.906 9.985e-01
## decid conif mix      +++ 0.5801 0.2049 0.7712 40.373 1.451e-03
## decid mix            +++ 0.5211 0.2298 0.7298 37.182 5.973e-05
## decid                ++ 0.2455 0.3462 0.5714  6.942 4.396e-18
## 4 binary splits

o <- opticut(count ~ 1, oven, strata=veg, dist=gamfun, Data=oven, family=poisson)
summary(o)

## Multivariate opticut results, comb = rank, dist = gamfun
##
## Call:
## opticut.formula(formula = count ~ 1, data = oven, strata = veg,
##   dist = gamfun, Data = oven, family = poisson)
##
## Best supported model with logLR >= 2:
##
##          split assoc      I      mu0      mu1 logLR      w
## Sp 1 open decid conif mix +++ 0.5988 0.1847 0.7359 46.91 0.9985
## 4 binary splits

```

```

o <- opticut(count ~ 1, oven, strata=veg, dist="poisson")
summary(o)

## Multivariate opticut results, comb = rank, dist = poisson
##
## Call:
## opticut.formula(formula = count ~ 1, data = oven, strata = veg,
##   dist = "poisson")
##
## Best supported model with logLR >= 2:
##               split assoc      I    mu0    mu1 logLR      w
## Sp 1 open decid conif mix   +++ 0.6903 0.1868 1.019 142.7 0.9998
## 4 binary splits

oven$pa <- ifelse(oven$count > 0, 1, 0)
o <- opticut(pa ~ 1, oven, strata=veg, dist=gamfun, Data=oven, family=binomial)
summary(o)

## Multivariate opticut results, comb = rank, dist = gamfun
##
## Call:
## opticut.formula(formula = pa ~ 1, data = oven, strata = veg,
##   dist = gamfun, Data = oven, family = binomial)
##
## Best supported model with logLR >= 2:
##               split assoc      I    mu0    mu1 logLR      w
## Sp 1 open decid conif mix   +++ 0.6982 0.1421 0.4824 28.84 0.919
## 4 binary splits

o <- opticut(pa ~ 1, oven, strata=veg, dist="binomial")
summary(o)

## Multivariate opticut results, comb = rank, dist = binomial
##
## Call:
## opticut.formula(formula = pa ~ 1, data = oven, strata = veg,
##   dist = "binomial")
##
## Best supported model with logLR >= 2:
##               split assoc      I    mu0    mu1 logLR      w
## Sp 1 open decid conif mix   +++ 0.7582 0.1377 0.5374 82.37 0.6569
## 4 binary splits

```

## N-mixture models

A single-visit based N-mixture is an example where detection error is estimated. Let us compare results based on naive GLM and N-mixture:



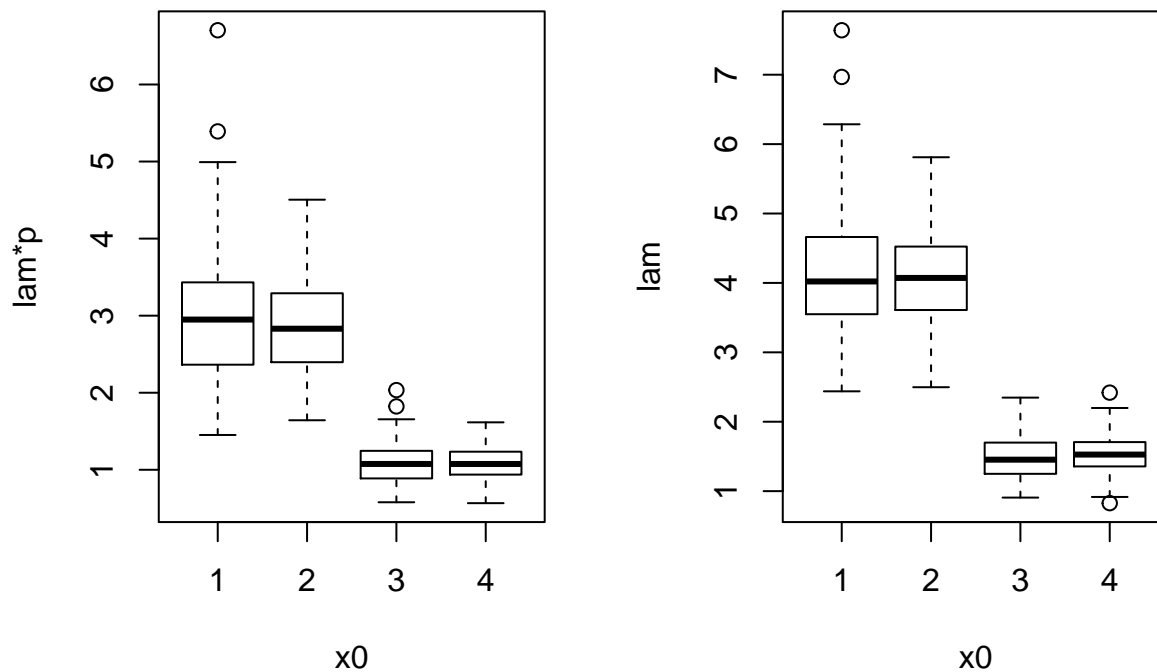
```

library(detect)
set.seed(2345)
n <- 500
x0 <- sample(1:4, n, TRUE)
x1 <- ifelse(x0 %in% 1:2, 1, 0)
x2 <- rnorm(n, 0.5, 1)
x3 <- runif(n, 0, 1)
lam <- exp(0.5 + 1*x1 + -0.2*x2)
p <- plogis(2 + -2*x3)
Y <- rpois(n, lam*p)

X <- model.matrix(~x2)

op <- par(mfrow=c(1,2))
boxplot((lam*p) ~ x0, ylab="lam*p", xlab="x0")
boxplot(lam ~ x0, ylab="lam", xlab="x0")

```



```

par(op)

svfun <- function(Y, X, linkinv, ...) {
  X <- as.matrix(X)
  m <- svabu(Y ~ X-1 | x3, ...)
  list(coef=coef(m, "sta"),
       logLik=logLik(m),
       linkinv=poisson()$linkinv)
}

svfun(Y, X)

```

```
## $coef
```

```
## X(Intercept)          Xx2
##      1.6746855      -0.2458261
##
## $logLik
## 'log Lik.' -884.583 (df=5)
##
## $linkinv
## function (eta)
## pmax(exp(eta), .Machine$double.eps)
## <environment: namespace:stats>

## naive GLM
print(opticut1(Y, X, as.factor(x0), dist="poisson"), cut=-Inf)

## Univariate opticut results, comb = rank, dist = poisson
## I = 0.474; w = 1; H = 1; logL_null = -930
##
## Best supported models with logLR >= -Inf:
##      assoc      I    mu0    mu1  logLR      w
## 1 2      +++ 0.4740 1.139 3.193 115.16 1.000e+00
## 1 2 4      +++ 0.4082 1.078 2.566  52.38 5.383e-28
## 2      +++ 0.2842 1.808 3.243  38.04 3.211e-34
## 3 binary splits

## N-mixture
print(opticut1(Y, X, as.factor(x0), dist=svfun), cut=-Inf)

## Univariate opticut results, comb = rank, dist = svfun
## I = 0.4873; w = 1; H = 0.9999; logL_null = -884.6
##
## Best supported models with logLR >= -Inf:
##      assoc      I    mu0    mu1  logLR      w
## 1 2      +++ 0.4873 2.409 6.989 26.239 1.000e+00
## 1 2 3      +++ 0.4303 1.936 4.859 15.787 2.888e-05
## 2      ++ 0.2475 4.142 6.866  3.284 1.073e-10
## 3 binary splits
```

## Package options

### High performance computing

```
data(dolina)
dolina$samp$stratum <- as.integer(dolina$samp$stratum)
Y <- ifelse(dolina$xtab > 0, 1, 0)
dol <- opticut(Y ~ stratum + lmoist + method, data=dolina$samp,
  strata=dolina$samp$mhab, dist="binomial")
```

```

## parallel computing comparisons
library(parallel)
cl <- makeCluster(2)

## sequential, all combinations ( $2^{(K-1)} - 1$ )
system.time(opticut(Y ~ stratum + lmoist + method, data=dolina$samp,
  strata=dolina$samp$mhab, dist="binomial", comb="all", cl=NULL))

##    user    system elapsed
##  1.789    0.005    1.797

## sequential, rank based combinations ( $K - 1$ )
system.time(opticut(Y ~ stratum + lmoist + method, data=dolina$samp,
  strata=dolina$samp$mhab, dist="binomial", comb="rank", cl=NULL))

##    user    system elapsed
##  1.131    0.003    1.135

## parallel, all combinations ( $2^{(K-1)} - 1$ )
system.time(opticut(Y ~ stratum + lmoist + method, data=dolina$samp,
  strata=dolina$samp$mhab, dist="binomial", comb="all", cl=cl))

##    user    system elapsed
##   0.012    0.002    2.036

## parallel, rank based combinations ( $K - 1$ )
system.time(opticut(Y ~ stratum + lmoist + method, data=dolina$samp,
  strata=dolina$samp$mhab, dist="binomial", comb="rank", cl=cl))

##    user    system elapsed
##   0.010    0.002    0.723

## compare timings for uncertainty calculations
system.time(uncertainty(dol, type="asympt", B=999))

##    user    system elapsed
##   0.703    0.002    0.706

system.time(uncertainty(dol, type="asympt", B=999, cl=cl))

##    user    system elapsed
##   0.024    0.004    0.464

system.time(uncertainty(dol, type="boot", B=4))

##    user    system elapsed
##   2.277    0.007    2.289

system.time(uncertainty(dol, type="boot", B=4, cl=cl))

##    user    system elapsed
##   0.024    0.002    1.390

```

```

system.time(uncertainty(dol, type="multi", B=4))

##    user  system elapsed
##   6.367    0.017    6.398

system.time(uncertainty(dol, type="multi", B=4, cl=cl))

##    user  system elapsed
##   0.023    0.002    3.819

stopCluster(cl)

```

## Global options

The `ocoptions` function provides a convenient way of handling options related to the **opticut** package. The function takes arguments in `<tag> = <value>` form, or a list of tagged values. The tags must come from the parameters described below. When parameters are set by `ocoptions`, their former values are returned in an invisible named list. Such a list can be passed as an argument to `ocoptions` to restore the parameter values. Tags are the following:

- `collapse`: character value to be used when merging factor levels, the default is " ".
- `cut`: log likelihood ratio value, model/species with lower values are excluded from summaries and plots, the default is 2.
- `sort`: logical value indicating if species/partitions should be meaningfully sorted, the default is TRUE. It can take numeric value when only species (1) or partitions (2) are to be sorted (1:2 is equivalent to TRUE, while any other numeric value is equivalent to FALSE).
- `theme`: the color theme to be used based on `occolors`, the default is "br".
- `check_comb`: check the design matrices for complementary partitions using `checkComb`, the default is TRUE.
- `try_error`: if `opticut` should try to exclude species where the models failed (TRUE), the default is to stop when an error is encountered (FALSE).
- `scale`: the scaling factor used to calculate indicator value (I) based on the estimated coefficient (b):  $I = \text{abs}(\tanh(b \cdot \text{scale}))$ , the default is 0.5.

```

## simple example from Legendre 2013
## Indicator Species: Computation, in
## Encyclopedia of Biodiversity, Volume 4
## http://dx.doi.org/10.1016/B978-0-12-384719-5.00430-5
gr <- as.factor(paste0("X", rep(1:5, each=5)))
spp <- cbind(Species1=rep(c(4,6,5,3,2), each=5),
             Species2=c(rep(c(8,4,6), each=5), 4,4,2, rep(0,7)),
             Species3=rep(c(18,2,0,0,0), each=5))
rownames(spp) <- gr

## current settings
str(ocoptions()) # these give identical answers

## List of 7
## $ collapse : chr " "

```

```

## $ cut      : num 2
## $ sort     : logi TRUE
## $ theme    : chr "br"
## $ check_comb: logi TRUE
## $ try_error : logi FALSE
## $ scale    : num 0.5

str(getOption("coptions"))

## List of 7
## $ collapse : chr " "
## $ cut      : num 2
## $ sort     : logi TRUE
## $ theme    : chr "br"
## $ check_comb: logi TRUE
## $ try_error : logi FALSE
## $ scale    : num 0.5

summary(ocall <- opticut(spp ~ 1, strata=gr, dist="gaussian", comb="all"))

## Multivariate opticut results, comb = all, dist = gaussian
##
## Call:
## opticut.formula(formula = spp ~ 1, strata = gr, dist = "gaussian",
##   comb = "all")
##
## Best supported models with logLR >= 2:
##      split assoc      I mu0  mu1 logLR      w
## Species2 X1 X3   +++ 0.9866 2.0  7.0 14.82 0.4995
## Species1 X2 X3   +++ 0.8483 3.0  5.5 17.33 0.4999
## Species3  X1   +++ 1.0000 0.5 18.0 55.19 1.0000
## 15 binary splits

## resetting pboptions and checking new settings
ocop <- ocoptions(collapse="+", sort=FALSE)
str(ocoptions())

## List of 7
## $ collapse : chr "+"
## $ cut      : num 2
## $ sort     : logi FALSE
## $ theme    : chr "br"
## $ check_comb: logi TRUE
## $ try_error : logi FALSE
## $ scale    : num 0.5

## running again with new settings
summary(ocall <- opticut(spp ~ 1, strata=gr, dist="gaussian", comb="all"))

## Multivariate opticut results, comb = all, dist = gaussian
##

```

```
## Call:
## opticut.formula(formula = spp ~ 1, strata = gr, dist = "gaussian",
##   comb = "all")
##
## Best supported models with logLR >= 2:
##           split assoc      I mu0  mu1 logLR      w
## Species1 X2+X3   +++ 0.8483 3.0   5.5 17.33 0.4999
## Species2 X1+X3   +++ 0.9866 2.0   7.0 14.82 0.4995
## Species3   X1   +++ 1.0000 0.5  18.0 55.19 1.0000
## 15 binary splits
## resetting original
ocoptions(ocop)
str(ocoptions())

## List of 7
## $ collapse : chr " "
## $ cut       : num 2
## $ sort      : logi TRUE
## $ theme     : chr "br"
## $ check_comb: logi TRUE
## $ try_error : logi FALSE
## $ scale     : num 0.5
```

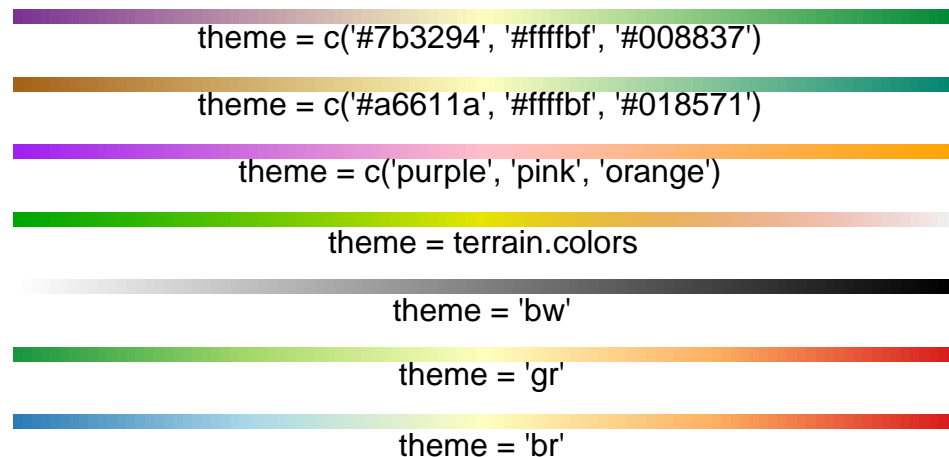
## Color themes

The **opticut** package uses color themes for plotting and provides a convenient way of setting color palettes via the `occolours` function. The function takes a single `theme` argument and returns a function as in `colorRampPalette`.

The `theme` argument can be a character value, character vector, or a function used to interpolate the colors. The built-in values are "br" (blue-red divergent palette, colorblind safe), "gr" (green-red divergent palette), "bw" (black and white). Hexadecimal values for the built-in palettes are taken from <http://colorbrewer2.org>.

```
plot(1:100, rep(2, 100), pch = 15,
     ylim = c(0, 21), axes = FALSE, ann = FALSE,
     col = occolours()(100)) # default 'bg'
text(50, 1, "theme = 'br'")
points(1:100, rep(5, 100), pch = 15,
       col=occolours("gr")(100))
text(50, 4, "theme = 'gr'")
points(1:100, rep(8, 100), pch = 15,
       col=occolours("bw")(100))
text(50, 7, "theme = 'bw'")
points(1:100, rep(11, 100), pch = 15,
       col=occolours(terrain.colors)(100))
text(50, 10, "theme = terrain.colors")
points(1:100, rep(14, 100), pch = 15,
```

```
col=occolours(c("purple", "pink", "orange"))(100))
text(50, 13, "theme = c('purple', 'pink', 'orange')")
points(1:100, rep(17, 100), pch = 15,
       col=occolours(c("#a6611a", "#ffffbf", "#018571"))(100))
text(50, 16, "theme = c('#a6611a', '#ffffbf', '#018571')")
points(1:100, rep(20, 100), pch = 15,
       col=occolours(c("#7b3294", "#ffffbf", "#008837"))(100))
text(50, 19, "theme = c('#7b3294', '#ffffbf', '#008837')")
```



## Progress bar

The expected completion time of extensive calculations and the progress is shown by the progress bar via the **pbapply** package. Default options with **opticut** are:

```
str(pboptions())
```

```
## List of 10
## $ type      : chr "none"
## $ char      : chr "[=-]"
## $ txt.width : num 50
## $ gui.width : num 300
## $ style     : num 6
## $ initial   : num 0
## $ title     : chr "R progress bar"
## $ label     : chr ""
## $ nout      : int 100
## $ min_time  : num 2
```

See `?pboptions` for a description of these options. Use `pboptions(type = "none")` to turn off the progress bar in interactive R sessions. The progress bar is automatically turned off during non-interactive sessions.

## Dynamic documents

**opticut** object summaries come with an `as.data.frame` method that can be used to turn the summary into a data frame, which is what for example the `kable` function from **knitr** package expects. This way, formatting the output is much facilitated, and the user does not have to dig into the structure of the summary object.

The GitHub repository has a minimal [Rmarkdown](#) example to demonstrate how to format **opticut** objects for best effects: [Rmd](#) source, knitted [PDF](#).

```
library(knitr)

y <- cbind(
  Sp1=c(4,6,3,5, 5,6,3,4, 4,1,3,2),
  Sp2=c(0,0,0,0, 1,0,0,1, 4,2,3,4),
  Sp3=c(0,0,3,0, 2,3,0,5, 5,6,3,4))
g <- c(1,1,1,1, 2,2,2,2, 3,3,3,3)
oc <- opticut(formula = y ~ 1, strata = g, dist = "poisson")
uc <- uncertainty(oc, type = "asympt", B = 999)

print(kable(as.data.frame(oc), digits=3))

##
##
##      split  assoc      I    mu0    mu1    logLR      w
## ---- -
## Sp3  2 3    ++    0.647  0.75  3.50  4.793  0.696
## Sp2   3    +++    0.857  0.25  3.25  9.203  0.958

print(kable(oc$species[[1]][,c(1,2,4,5,8,9,10)], digits=3))

##
##
##      assoc      I    mu0    mu1    logL    logLR      w
## ---- -
## 1      1  0.125  3.5  4.5  -22.185  0.339  0.239
## 1 2    1  0.286  2.5  4.5  -21.026  1.498  0.761

print(kable(as.data.frame(uc), digits=3))

##
##
##      split    R      I    Lower    Upper
## ---- -
## Sp1  1 2      1  0.277  0.024  0.564
## Sp3  2 3      1  0.622  0.204  0.880
## Sp2  3      1  0.824  0.496  0.962
```

The `kable` output is rendered as nice tables (without the `print` part):



```
kable(as.data.frame(oc), digits=3)
```

	split	assoc	I	mu0	mu1	logLR	w
Sp3	2 3	++	0.647	0.75	3.50	4.793	0.696
Sp2	3	+++	0.857	0.25	3.25	9.203	0.958

```
kable(oc$species[[1]][,c(1,2,4,5,8,9,10)], digits=3)
```

	assoc	I	mu0	mu1	logL	logLR	w
1	1	0.125	3.5	4.5	-22.185	0.339	0.239
1 2	1	0.286	2.5	4.5	-21.026	1.498	0.761

```
kable(as.data.frame(uc), digits=3)
```

	split	R	I	Lower	Upper
Sp1	1 2	1	0.277	0.024	0.564
Sp3	2 3	1	0.622	0.204	0.880
Sp2	3	1	0.824	0.496	0.962

## Summary

The likelihood-based optimal partitioning framework implemented in the **opticut** R package provides a compelling alternative to other available R packages (**indicspecies**, De Caceres & Legendre 2009; **labdsv** and **optpart**, Roberts 2016a, 2016b; **vegan**, Oksanen et al. 2016), especially when the type of data or the presence of modifying effects call for an alternative approach.

The package comes with many parametric models included for binary, count, abundance, percent cover, ordinal, and presence-only data, and the approach can be extended to more complex situations, such as mixed models, additive models. The **opticut** package leverages other R packages (**MASS**, Venables & Ripley 2002; **betareg**, Cribari-Neto & Zeileis 2010; **pscl**, Zeileis et al. 2008; **ResourceSelection**, Lele et al. 2016) for fitting parametric models. The approach can be extended to linear and generalized linear mixed models (LMM, GLMM; see Kemencei et al. 2014), generalized additive models, N-mixture models.

Computing times are shortened by the application of efficient algorithms and through high performance computing options. The **opticut** package provides progress bars with estimated remaining time for long-running evaluations (through the **pbapply** package, Solymos & Zawadzki 2016), natively supports several parallel back-ends (multicore machines, computing clusters, forking; through the **parallel** package, R Core Team 2016) to speed calculations up, and provides options and methods for dynamic report generation (coercion methods and color themes). Functions in the package can be customized and extended to meet the needs under a wide range of real-world situations.

Please cite the **opticut** package in scholarly publications as:

Peter Solymos and Ermias T. Azeria (2016). `opticut`: Likelihood Based Optimal Partitioning for Indicator Species Analysis. R package version . <https://github.com/psolymos/opticut>

Use `citation("opticut")` for an up-to-date citation.

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