opticut: likelihood based optimal partitioning for indicator species analysis

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1 Introduction

General problem: find where species abundances are high vs. low in a way which leads to optimal classification by maximizing the contrast between the partitions.

Previous attempts: historical review, highlighting IndVal.

Issues with previous attempts:

- summary statistics & Monte Carlo randomization with p-values, no model,
- data types not always compatible with randomization (i.e. decimals),
- confounding effects to classification can impact power,
- assessing the ranking of partitions without inferential statements.

Goals:

- describe a general and extensible approach that addresses the above limitations,
- implement a computationally efficient algorithm,
- tools for exploring the results (i.e. summaries, plots) in a object oriented framework.

2 Theory

2.1 The quest for optimal binary partitioning

Y_i's are observations for a single species from n locations ($i = 1, ..., n$). g_i's are known discrete descriptors of the locations with K levels ($K > 2$). $z^{(m)}$ is a binary reclassification of g taking values (0, 1). The superscript $m = 1, ..., M$ indicates a possible combination of binary reclassification out of the total $M = 2^{K-1} - 1$ total combinations (excluding complements). See below for options for defining binary partitions. There can also be other site descriptors denoted as x_{ij} taking discrete or continuous values ($j = 1, ..., p$; number of predictors).

A suitable parametric model describes the relationship between the observations and the site descriptors through the probability density function $P(Y_i = y_i \mid z_i^{(m)}, x_{ij}, \theta)$ where θ is the vector of model parameters: $\theta = (\beta_0, \beta_1, \alpha_1, ..., \alpha_p)$. The choice of the parametric model depends on the nature of the observations. It can be Gaussian, Binomial, Poisson, ordinal, Beta regression, or zero-inflated models, with a suitable link function (f) for the mean: $f(\eta_i) = \beta_0^{(m)} + \beta_1^{(m)} z_i^{(m)} + \sum_{j=1}^{p} \alpha_j^{(m)} x_{ij}$.

$\widehat{\theta^{(m)}}$ is the maximum likelihood estimate (MLE) of the model parameters given the data and classification m, with corresponding log-likelihood value $l(\widehat{\theta^{(m)}}; y)$. Finding MLEs for all M candidate binary partitions leads to a set of log-likelihood values. One can compare the log-likelihood values to a null model (no binary partition is necessary) where $\beta_1 = 0$ leading to the MLE $\widehat{\theta^{(0)}}$ and corresponding log-likelihood value for the null model: $l(\widehat{\theta^{(0)}}; y)$.

The log-likelihood ratio for each candidate partition can be calculated as $l(\widehat{\theta^{(m)}}; y) - l(\widehat{\theta^{(0)}}; y)$. The best supported binary partition is the model with the highest log-likelihood ratio value.

One way of calculating the indicator value for each candidate partition is based on expected values using the inverse link function as $\mu_0^{(m)} = f^{-1}(\beta_0^{(m)})$ and $\mu_1^{(m)} = f^{-1}(\beta_0^{(m)} + \beta_1^{(m)})$. $I = 1 - min(\mu_0^{(m)}, \mu_1^{(m)})/max(\mu_0^{(m)}, \mu_1^{(m)})$. Where $\mu_0^{(m)} = E[Y_i \mid z_i^{(m)} = 0, x_{ij} = 0]$ and $\mu_1^{(m)} = E[Y_i \mid z_i^{(m)} = 1, x_{ij} = 0]$ are expected values for the observations given the binary partition $z_i^{(m)}$ and at 0 value for all x_{ij}. This approach can be sensitive to the range of values supported by the link function. For example it works nicely with logarithmic or logistic link function where non-negativity of predicted values is ensured by definition. This is, however, not the case for the identity link in the Gaussian case, when negative values can invaludate the indicator value calculations as described above. (This usually happens when confounding variables are not centered and the intercept then reflects that difference as part of the baseline.)

As an alternative, one can use the estimate $\beta_1^{(m)}$ itself to express the contrast between the two strata. This also makes the index more comparable when different link functions are used. We used the hyperbolic tangent function (or inverse Fisher's z transform) to scale the real valued $\beta_1^{(m)}$ into the unit range (0-1): $I = tanh(\mid \beta_1^{(m)} \mid) = \frac{exp(2|\beta_1^{(m)}|)-1}{exp(2|\beta_1^{(m)}|)+1}$. Positive and negative cases are taken as absolute values, so that the index reflects only the contrast between strata, and not the direction of it. Negative value can happen when using all combinations.

2.2 Finding all possible binary partitions

Finding all combinations does not require a model or observed responses. It only takes a classification vector with $K > 1$ partitions.

`kComb` returns a 'contrast' matrix corresponding to all possible binary partitions of the factor with `K` levels. Complements are not counted twice, i.e. (0,0,1,1) is equivalent to (1,1,0,0). The number of such possible combinations is $M = 2^{K-1} - 1$.

Get the package and load it:

```
#devtools::install_github("psolymos/opticut")
#devtools::install("~/repos/opticut")
#devtools::check("~/repos/opticut")
#devtools::build("~/repos/opticut", binary=TRUE)
library(opticut)
```

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

```
## opticut 0.1-2     2016-09-14
```

```
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` this 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).

```
(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"
```

```
checkComb(mc)
```

```
## [1] TRUE
## attr(,"comp")
##      i j
## attr(,"same")
##      i j
```

```
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)
```

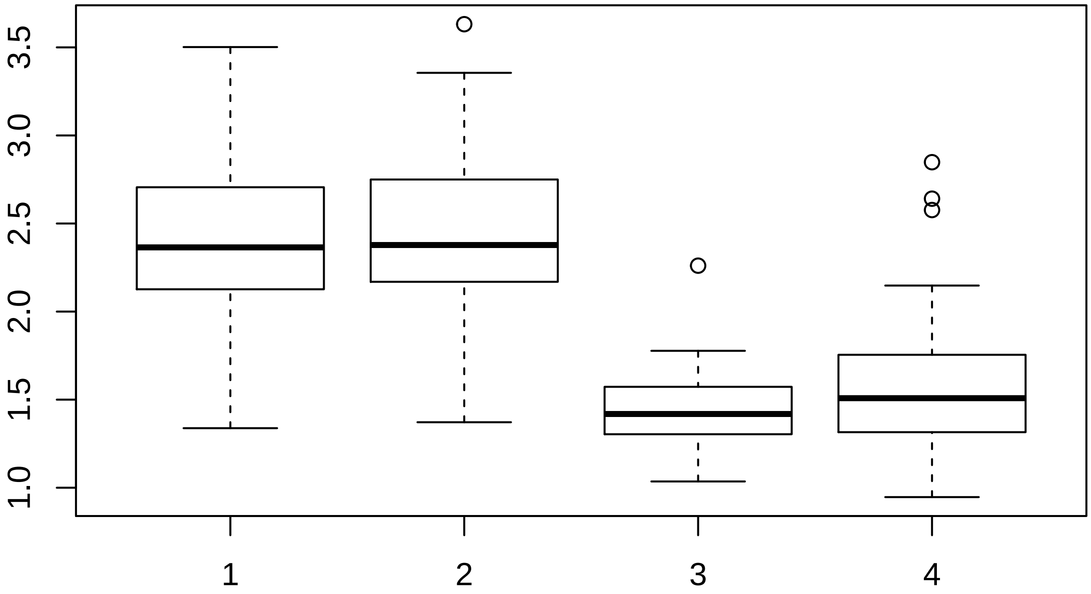
```
## [1] FALSE
## attr(,"comp")
##      i j
## [1,] 1 2
## [2,] 1 9
## attr(,"same")
##      i j
## [1,] 9 2
```

2.3 Poisson count model example

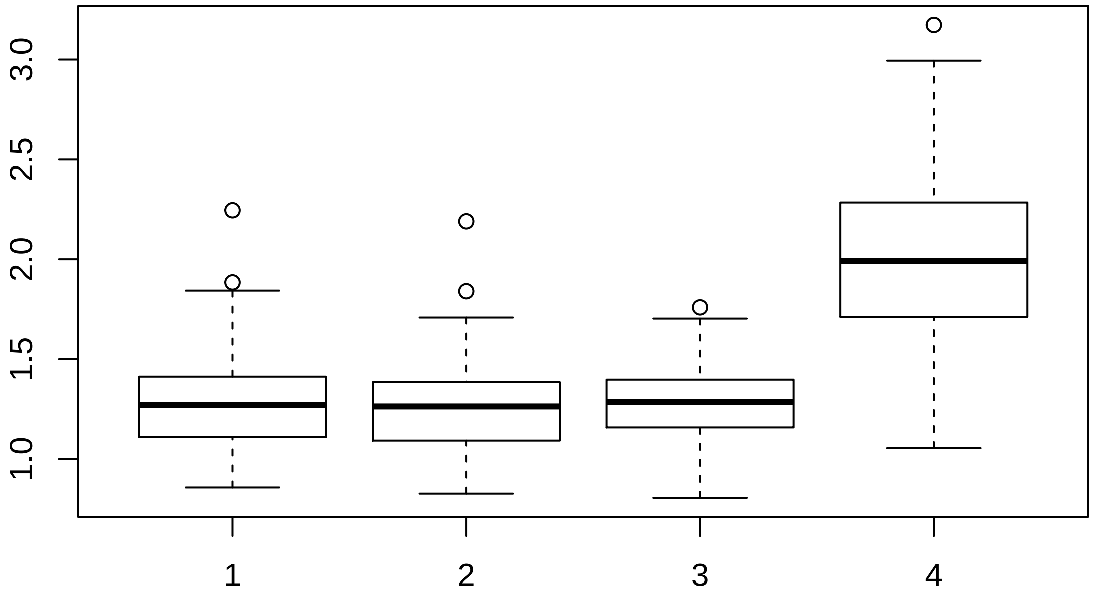
```
set.seed(1234)
n <- 200
x0 <- sample(1:4, n, TRUE)
x1 <- ifelse(x0 %in% 1:2, 1, 0)
x2 <- rnorm(n, 0.5, 1)
table(x0,x1)
```

```
##    x1
## x0   0  1
##   1  0 52
##   2  0 51
##   3 51  0
##   4 46  0
```

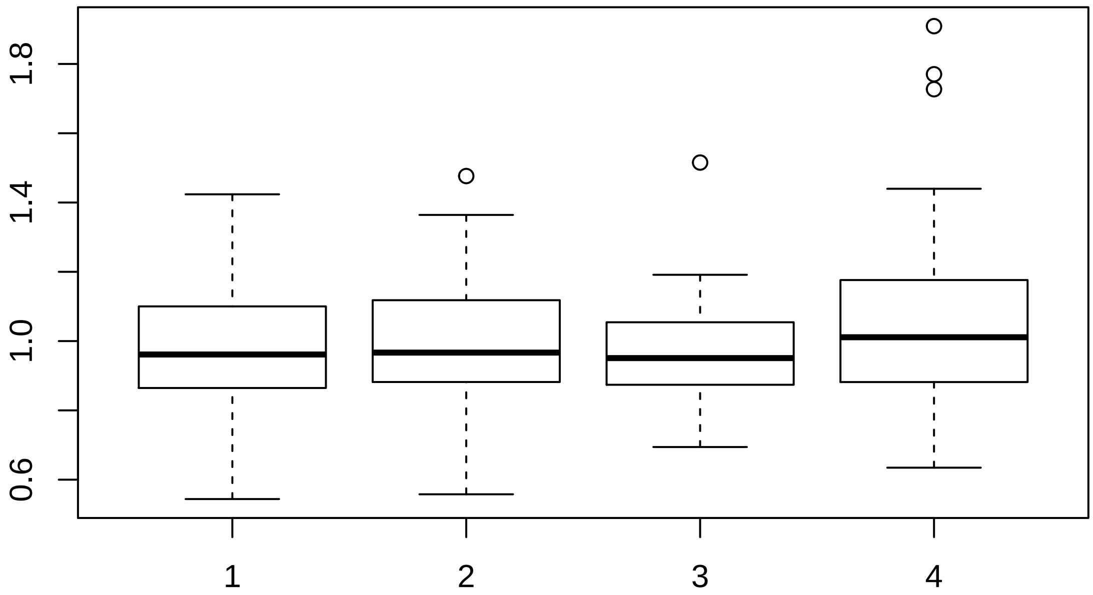
```
lam1 <- exp(0.5 + 0.5*x1 + -0.2*x2)
boxplot(lam1~x0)
```



```
Y1 <- rpois(n, lam1)
lam2 <- exp(0.1 + 0.5*ifelse(x0==4,1,0) + 0.2*x2)
boxplot(lam2~x0)
```



```
Y2 <- rpois(n, lam2)
lam3 <- exp(0.1 + -0.2*x2)
boxplot(lam3~x0)
```



```
Y3 <- rpois(n, lam3)
Y <- cbind(SPP1=Y1, SPP2=Y2, SPP3=Y3)
X <- model.matrix(~x2)
Z <- allComb(x0)
opticut1(Y1, X, Z, dist="poisson")
```

```
## Univariate opticut results, comb = all, dist = poisson
## I = 0.3972; w = 0.9842; H = 0.9687; logL_null = -343.8
##
## Best supported models with logLR >= 2:
```

```
##     assoc      I    mu0    mu1 logLR        w
## 1 2   +++ 0.3972 1.739 2.647 8.396 0.984200
## 3      -- 0.3006 2.337 1.714 3.051 0.004694
## 4      -- 0.3005 2.371 1.739 3.027 0.004583
## 2      ++ 0.2505 2.048 2.645 2.633 0.003092
## 1      ++ 0.2483 2.048 2.639 2.598 0.002987
## 7 binary splits (2 models not shown)
```

```
opticut1(Y2, X, Z, dist="poisson")
```

```
## Univariate opticut results, comb = all, dist = poisson
## I = 0.4326; w = 0.9254; H = 0.8584; logL_null = -315.6
##
## Best supported models with logLR >= 2:
##     assoc      I    mu0    mu1 logLR       w
## 4      ++ 0.4326 1.134 1.803 6.245 0.92545
## 1 3    -- 0.2863 1.486 1.107 3.119 0.04063
## 1 2    -- 0.2342 1.458 1.149 2.064 0.01415
## 7 binary splits (4 models not shown)
```

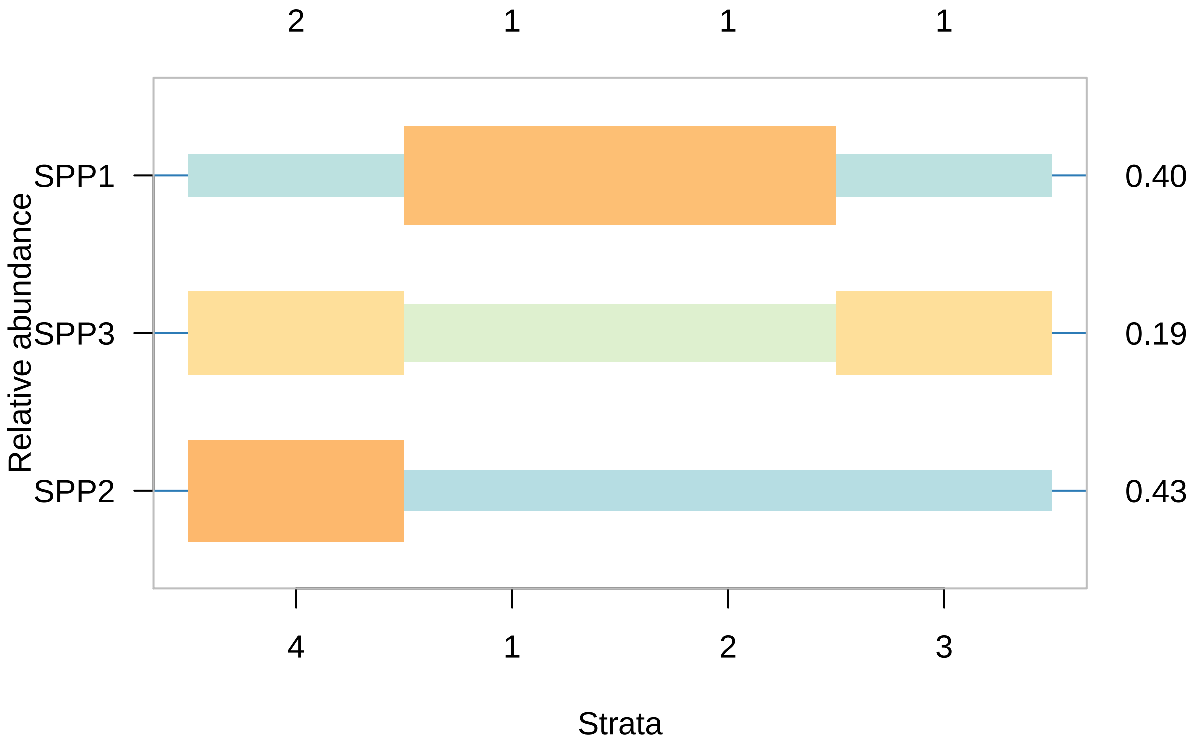
```
opticut1(Y3, X, Z, dist="poisson")
```

```
## Univariate opticut results, comb = all, dist = poisson
## I = 0.1899; w = 0.2205; H = 0.1562; logL_null = -244.4
##
## Best supported model:
##     assoc      I    mu0    mu1 logLR      w
## 1 2     - 0.1899 1.096 0.9047 0.805 0.2205
## 7 binary splits (6 models not shown)
```

```
summary(m <- opticut(Y ~ x2, strata=x0, dist="poisson", comb="all"))
```

```
## Multivariate opticut results, comb = all, dist = poisson
##
## Call:
## opticut(formula = Y ~ x2, strata = x0, dist = "poisson", comb = "all")
##
## Best supported models with logLR >= 2:
##      split assoc      I    mu0    mu1 logLR      w
## SPP1   1 2   +++ 0.3972 1.739 2.647 8.396 0.9842
## SPP2     4    ++ 0.4326 1.134 1.803 6.245 0.9254
## 7 binary splits
## 1 species not shown
```

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



Describe here what is what in the output.

2.4 Not using all possible partitions

Blindly fitting a model to all possible partitions is wasteful use of resources. Instead, one can rank the K partitions based on expected response values $(\mu_1, ..., \mu_k, ..., \mu_K$, where $\mu_k = E[Y_i \mid g_i = k, x_{ij} = 0])$. This way we have to explore only $K - 1$ partitions:

```
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
## attr(,"rank")
## 1 2 3 4
## 1 2 3 4
```

`oComb` return the 'contrast' matrix based on the rank vector as input. Rank 1 means lowest expected value among the partitions.

The function `rankComb` fits the model with multiple $(K > 2)$ factor levels to find out the ranking, and returns a binary classification matrix similarly to `allComb`:

```
head(rc <- rankComb(Y1, 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")
```

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

Note that the ranking varies from species to species, thus it is not possible to supply the resulting matrix as `strata` definition:

```
summary(opticut(Y ~ x2, strata=x0, dist="poisson", comb="rank"))
```

```
## Multivariate opticut results, comb = rank, dist = poisson
##
## Call:
## opticut(formula = Y ~ x2, strata = x0, dist = "poisson", comb = "rank")
##
## Best supported models with logLR >= 2:
##      split assoc      I   mu0   mu1 logLR      w
## SPP1   1 2   +++ 0.3972 1.739 2.647 8.396 0.9922
## SPP2     4    ++ 0.4326 1.134 1.803 6.245 0.9505
## 3 binary splits
## 1 species not shown
```

There is an overhead of fitting the model to calculate the ranking. But computing efficiencies can be still high compared to all partitions when the number of levels (k) is high.

3 Distributions

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"`, `"zinb"`: 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,
- `"rsf"`, `"rspf"`: presence-only data using resource selection and resource selection probability functions.

3.1 Gaussian

```
Y <- rnorm(n, log(lam1) + 10, 0.5)
(mod <- opticut(Y ~ x2, strata=x0, dist="gaussian"))
```

```
## Multivariate opticut results, comb = rank, dist = gaussian
##
## Call:
## opticut(formula = Y ~ x2, strata = x0, dist = "gaussian")
##
## 1 species, 3 binary splits
```

Legendre example

```
gr <- rep(1:5, each=5)
spp <- cbind(Sp1=rep(c(4,6,5,3,2), each=5),
    Sp2=c(rep(c(8,4,6), each=5), 4,4,2, rep(0,7)),
    Sp3=rep(c(18,2,0,0,0), each=5))
rownames(spp) <- gr
spp
```

```
##   Sp1 Sp2 Sp3
## 1   4   8  18
## 1   4   8  18
## 1   4   8  18
## 1   4   8  18
## 1   4   8  18
## 2   6   4   2
## 2   6   4   2
## 2   6   4   2
## 2   6   4   2
## 2   6   4   2
## 3   5   6   0
## 3   5   6   0
## 3   5   6   0
## 3   5   6   0
## 3   5   6   0
## 4   3   4   0
## 4   3   4   0
## 4   3   2   0
## 4   3   0   0
## 4   3   0   0
## 5   2   0   0
## 5   2   0   0
## 5   2   0   0
## 5   2   0   0
## 5   2   0   0
```

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

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

```
## opticut(formula = spp ~ 1, strata = gr, dist = "gaussian", comb = "all")
##
## Best supported models with logLR >= 2:
##     split assoc      I mu0  mu1 logLR      w
## Sp2   1 3   +++ 0.9999 2.0  7.0 14.82 0.4995
## Sp1   2 3   +++ 0.9866 3.0  5.5 17.33 0.4999
## Sp3     1   +++ 1.0000 0.5 18.0 55.19 1.0000
## 15 binary splits
```

```
summary(mod <- opticut(spp ~ 1, strata=gr, dist="gaussian", comb="rank"))
```

```
## Multivariate opticut results, comb = rank, dist = gaussian
##
## Call:
## opticut(formula = spp ~ 1, strata = gr, dist = "gaussian", comb = "rank")
##
## Best supported models with logLR >= 2:
##     split assoc      I mu0  mu1 logLR      w
## Sp2   1 3   +++ 0.9999 2.0  7.0 14.82 0.4996
## Sp1   2 3   +++ 0.9866 3.0  5.5 17.33 0.4999
## Sp3     1   +++ 1.0000 0.5 18.0 55.19 1.0000
## 4 binary splits
```

```
## DeCaceres & Legendre 2013 Oikos example from Fig 1
## Oikos 119: 1674-1684, 2010
## doi: 10.1111/j.1600-0706.2010.18334.x
Y <- c(0, 0, 3, 0, 2, 3, 0, 5, 5, 6, 3, 4)
z <- rep(1:3, each=4)
Z <- allComb(z)
Z <- cbind(Z, 1-Z)
colnames(Z) <- c("1", "2", "3", "2 3", "1 3", "1 2")
Z
```

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

```
try(opticut1(Y, Z=Z))
oc <- ocoptions(check_comb=FALSE, cut=-Inf) # relax the checks
opticut1(Y, Z=Z) # identical results for complementary partitions
```

```
## Univariate opticut results, comb = NA, dist = gaussian
## I = 0.9937; w = 0.2871; H = 0.2463; logL_null = -25.93
##
## Best supported models with logLR >= -Inf:
##     assoc      I   mu0   mu1    logLR       w
## 3      ++ 0.9937 1.625 4.500 3.232629 0.28708
## 1 2    -- 0.9937 4.500 1.625 3.232629 0.28708
## 1      -- 0.9919 3.500 0.750 2.878892 0.20154
## 2 3    ++ 0.9919 0.750 3.500 2.878892 0.20154
## 2       - 0.1244 2.625 2.500 0.004726 0.01138
## 1 3     + 0.1244 2.500 2.625 0.004726 0.01138
## 6 binary splits
```

```
ocoptions(oc) # restore defaults
```

BCI data

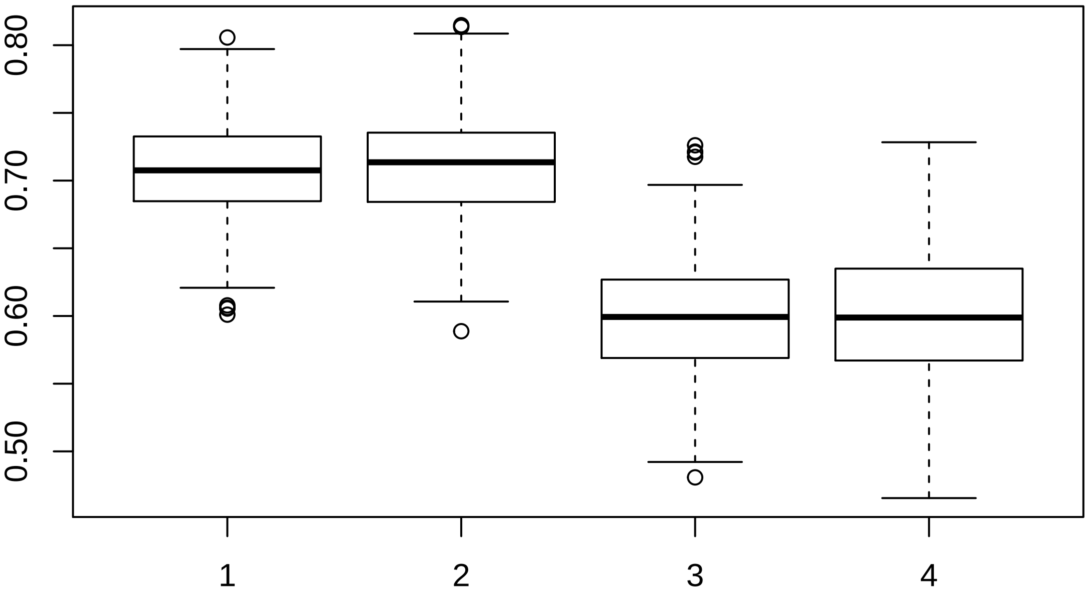
```
library (vegan)
data (BCI)
library (BiodiversityR)  # available from R version 2.15.1, not older!
data (BCI.env)
BCI.soil <- read.delim ('http://www.davidzeleny.net/anadat-r/lib/exe/fetch.php?media=data:bci.soil.txt'
###
BCI.hab <- read.table("http://www.kharms.biology.lsu.edu/TORUS_Habitats.txt",
    sep="\t", header=TRUE)
```

3.2 Binomial

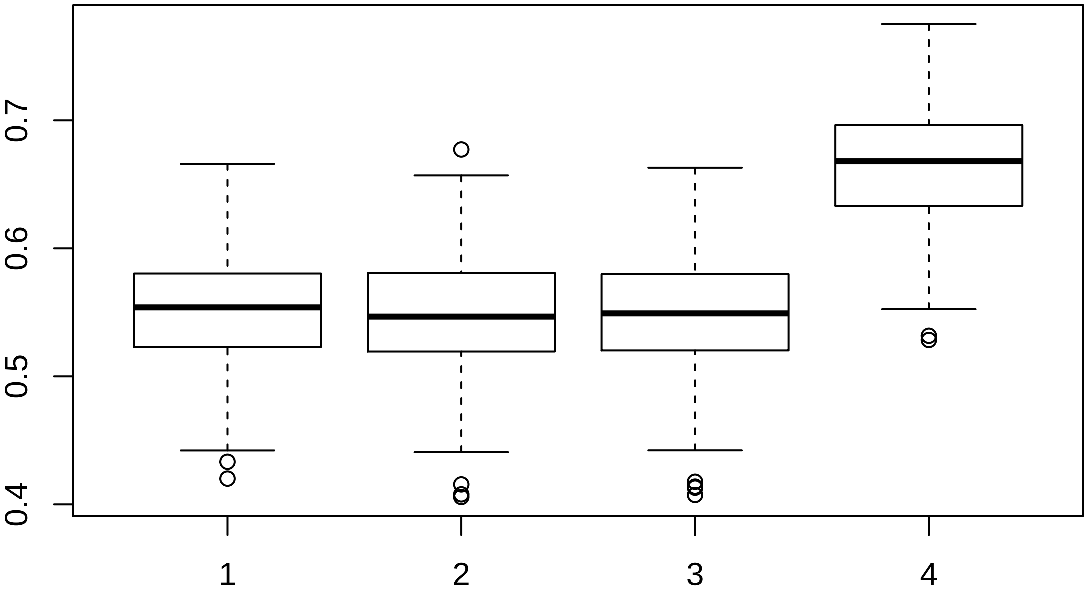
```
set.seed(1234)
n <- 1000
x0 <- sample(1:4, n, TRUE)
x1 <- ifelse(x0 %in% 1:2, 1, 0)
x2 <- rnorm(n, 0.5, 1)
table(x0,x1)
```

```
##    x1
## x0    0   1
##   1   0 240
##   2   0 242
##   3 260   0
##   4 258   0
```

```
p1 <- plogis(0.5 + 0.5*x1 + -0.2*x2)
boxplot(p1~x0)
```



```
Y1 <- rbinom(n, 1, p1)
p2 <- plogis(0.1 + 0.5*ifelse(x0==4,1,0) + 0.2*x2)
boxplot(p2~x0)
```



```
Y2 <- rbinom(n, 1, p2)
Y <- cbind(SPP1=Y1, SPP2=Y2)
X <- model.matrix(~x2)
Z <- allComb(x0)

summary(opticut(Y ~ x2, strata=x0, dist="binomial"))
```

```
## Multivariate opticut results, comb = rank, dist = binomial
##
## Call:
```

```
## opticut(formula = Y ~ x2, strata = x0, dist = "binomial")
##
## Best supported models with logLR >= 2:
##      split assoc      I    mu0    mu1 logLR      w
## SPP1   1 2    ++ 0.4656 0.6301 0.7383 6.954 0.9222
## SPP2     4    ++ 0.4416 0.5415 0.6549 5.046 0.6378
## 3 binary splits
```

3.3 Poisson: Mite data set – high performance computing

See computing time diffs and plotting options.

```r
library(vegan)
```

```
## Loading required package: permute
```

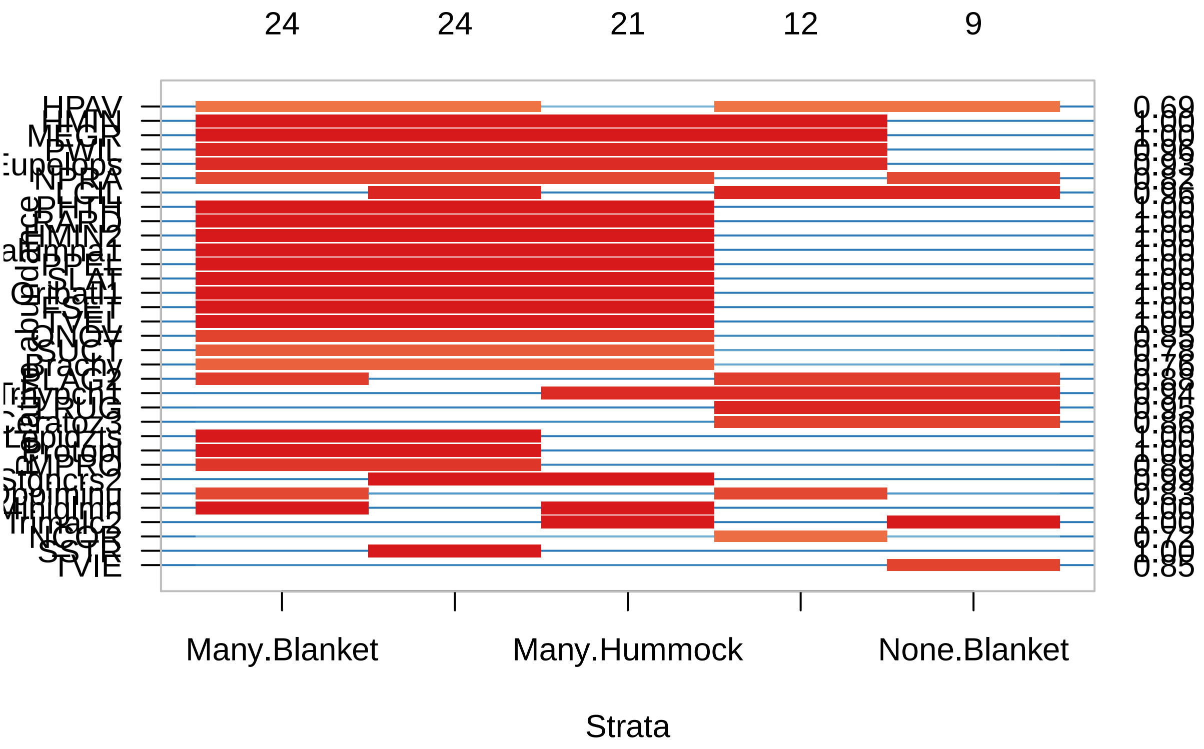
```
## Loading required package: lattice
```

```
## This is vegan 2.4-1
```

```r
data(mite)
data(mite.env)
mite.env$hab <- with(mite.env, interaction(Shrub, Topo, drop=TRUE))
summary(mod0 <- opticut(as.matrix(mite) ~ SubsDens, mite.env,
    strata=mite.env$hab, dist="poisson", comb="all"))
```

```
## Multivariate opticut results, comb = all, dist = poisson
##
## Call:
## opticut(formula = as.matrix(mite) ~ SubsDens, data = mite.env,
##     strata = mite.env$hab, dist = "poisson", comb = "all")
##
## Best supported models with logLR >= 2:
##                               split assoc      I       mu0       mu1
## HPAV                  Many.Hummock   --- 0.6920 3.500e+01 1.493e+01
## HMIN                  None.Blanket   --- 0.9990 1.880e+01 4.177e-01
## MEGR                  None.Blanket   --- 0.9969 9.729e-01 3.818e-02
## PWIL                  None.Blanket   --- 0.9574 1.637e+00 2.416e-01
## Eupelops              None.Blanket    -- 0.9345 1.564e+00 2.878e-01
## NPRA                   Few.Blanket   --- 0.8206 1.425e+00 4.474e-01
## LCIL     Many.Blanket Many.Hummock   --- 0.9577 8.923e+00 1.312e+00
## PHTH      None.Blanket Few.Blanket   --- 1.0000 1.463e+00 2.525e-09
## RARD      None.Blanket Few.Blanket   --- 1.0000 2.546e+00 1.251e-08
## HMIN2     None.Blanket Few.Blanket   --- 1.0000 1.785e+00 5.504e-09
## Galumna1  None.Blanket Few.Blanket   --- 1.0000 1.523e+00 3.486e-09
## PPEL      None.Blanket Few.Blanket    -- 1.0000 1.349e-01 6.501e-10
## SLAT      None.Blanket Few.Blanket   --- 1.0000 7.284e-01 4.062e-09
## Oribatl1  None.Blanket Few.Blanket   --- 0.9986 1.311e+00 3.441e-02
## FSET      None.Blanket Few.Blanket   --- 0.9986 2.726e+00 7.211e-02
## TVEL      None.Blanket Few.Blanket   --- 0.9983 1.297e+01 3.759e-01
## ONOV      None.Blanket Few.Blanket   --- 0.8508 4.183e+01 1.188e+01
## SUCT      None.Blanket Few.Blanket   --- 0.7799 2.901e+01 1.020e+01
## Brachy    None.Blanket Few.Blanket   --- 0.7561 1.689e+01 6.294e+00
## PLAG2     Few.Hummock Many.Hummock   --- 0.8774 1.683e+01 4.300e+00
## Trhypch1  Many.Blanket Few.Hummock   --- 0.9364 7.493e-01 1.358e-01
## LRUG      None.Blanket Few.Blanket   +++ 0.9458 8.516e+00 5.100e+01
## Ceratoz3  None.Blanket Few.Blanket   +++ 0.8555 7.098e+00 2.543e+01
## Lepidzts  Many.Blanket Few.Hummock   +++ 1.0000 2.333e-09 8.547e-01
## Protopl   Many.Blanket Few.Hummock   +++ 0.9968 7.695e-01 1.916e+01
## MPRO      Many.Blanket Few.Hummock    ++ 0.8944 2.034e-01 8.614e-01
## Stgncrs2  Few.Hummock Many.Hummock   +++ 0.9873 5.786e-03 7.230e-02
## Oppiminu  Few.Blanket Many.Blanket   +++ 0.8348 2.243e+00 7.475e+00
## Miniglmn Many.Blanket Many.Hummock   +++ 0.9975 2.716e-02 7.745e-01
## Trimalc2 None.Blanket Many.Hummock   +++ 0.9997 6.359e-02 4.929e+00
## NCOR                   Few.Blanket    ++ 0.7181 4.238e+00 1.046e+01
## SSTR                   Few.Hummock   +++ 0.9971 1.561e-03 4.080e-02
## TVIE                  None.Blanket   +++ 0.8486 2.320e+00 8.106e+00
##            logLR      w
## HPAV      26.281 0.9944
## HMIN      99.969 1.0000
## MEGR      35.465 1.0000
## PWIL      12.421 0.7564
## Eupelops   6.536 0.3863
## NPRA       8.523 0.8540
## LCIL     540.701 1.0000
## PHTH      56.766 1.0000
## RARD      54.142 1.0000
## HMIN2     87.196 1.0000
## Galumna1  42.750 1.0000
## PPEL       7.620 0.9359
## SLAT      17.854 0.9399
## Oribatl1  69.712 1.0000
## FSET      69.026 1.0000
## TVEL     331.735 1.0000
## ONOV     189.632 1.0000
## SUCT     136.668 1.0000
## Brachy    63.635 1.0000
## PLAG2      9.162 0.9210
## Trhypch1  35.539 0.9998
## LRUG     218.994 1.0000
## Ceratoz3  16.217 0.9392
## Lepidzts  13.044 0.9912
## Protopl   22.746 0.9936
## MPRO       2.539 0.2639
## Stgncrs2  29.557 0.9147
## Oppiminu  12.310 0.9245
## Miniglmn  12.918 0.9445
## Trimalc2  83.215 1.0000
## NCOR       6.241 0.4468
## SSTR      23.076 0.9724
## TVIE      11.050 0.9240
## 15 binary splits
## 2 species not shown
```

```
plot(mod0)
```



```
system.time(aa <- opticut(as.matrix(mite) ~ 1, strata=mite.env$hab, dist="poisson", comb="rank"))
```

```
##    user  system elapsed
##   0.553   0.016   0.570
```

```
system.time(bb <- opticut(as.matrix(mite) ~ 1, strata=mite.env$hab, dist="poisson", comb="all"))
```

```
##    user  system elapsed
##   1.321   0.043   1.368
```

```
## sequential
system.time(opticut(as.matrix(mite) ~ 1, strata=mite.env$hab, dist="poisson"))
```

```
##    user  system elapsed
##   0.559   0.016   0.577
```

```
## parallel -- compare system times
library(parallel)
cl <- makeCluster(3)
system.time(opticut(as.matrix(mite) ~ 1, strata=mite.env$hab, dist="poisson", cl=cl))
```

```
##    user  system elapsed
##   0.008   0.002   1.610
```

```
stopCluster(cl)
## forking -- will not work on Windows
if (!.Platform$OS.type == "windows")
system.time(opticut(as.matrix(mite) ~ 1, strata=mite.env$hab, dist="poisson", cl=3))
```

```
##    user  system elapsed
##   0.557   0.106   0.360
```

3.4 Percentages

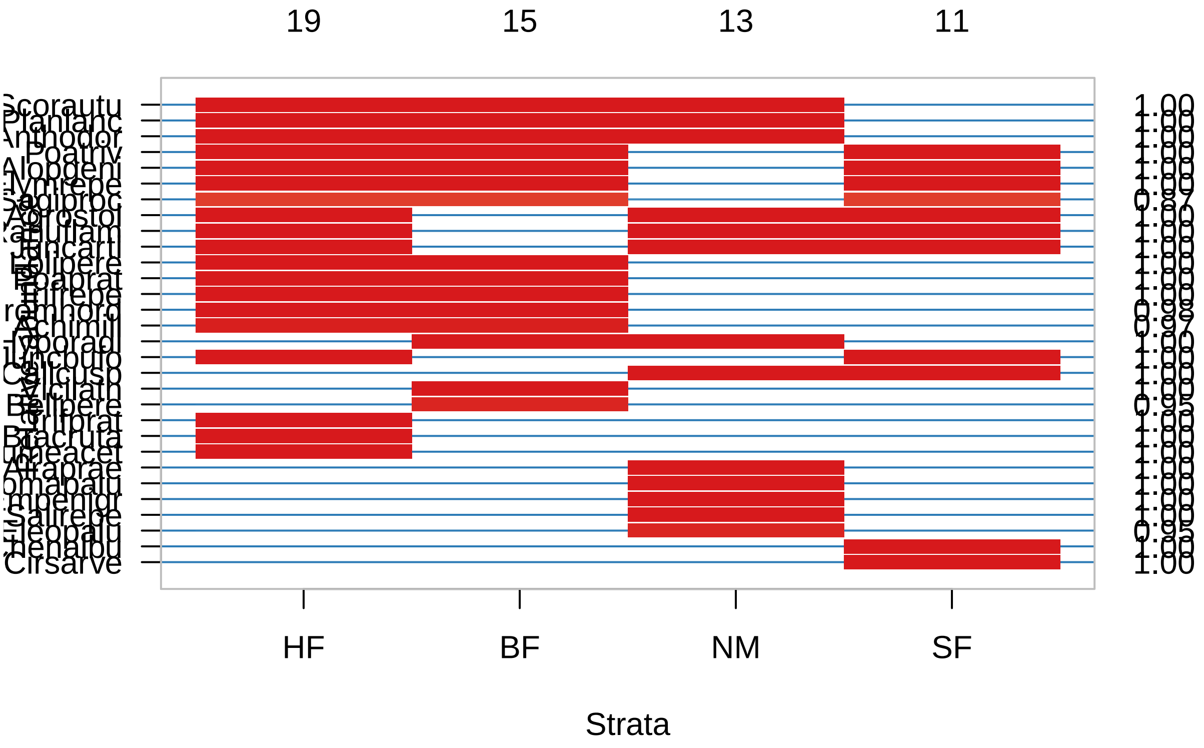
3.4.1 Dune data, cover type data as ordinal

See http://www.davidzeleny.net/anadat-r/doku.php/en:data:dune

```
library(vegan)
data(dune)
data(dune.env)
dune.env$manure <- as.integer(dune.env$Manure) - 1
dune.env$moisture <- as.integer(dune.env$Moisture) - 1

oc <- ocoptions(collapse="+", cut=-Inf)

## ordinal regr
## (when nlevels() < 3 use logistic regression instead !!!
#Dune <- as.matrix(dune)
#Dune <- Dune[,apply(Dune, 2, function(z) length(unique(z)))>2]
#x1 <- opticut(Dune ~ 1, dune.env, strata=Management, dist="ordered")
#summary(x1)

#plot(x1, mar=c(5,5,3,3))

## Binarizing data
Dune01 <- ifelse(as.matrix(dune)>0,1,0)
x2 <- opticut(Dune01 ~ 1, strata=dune.env$Management, dist="binomial")
summary(x2)
```

```
## Multivariate opticut results, comb = rank, dist = binomial
##
## Call:
## opticut(formula = Dune01 ~ 1, strata = dune.env$Management, dist = "binomial")
##
## Best supported models with logLR >= -Inf:
##             split assoc      I       mu0    mu1  logLR      w
## Scorautu BF+HF+NM    ++ 1.0000 6.667e-01 1.0000 2.6826 0.7441
## Planlanc BF+HF+NM    ++ 1.0000 8.647e-09 0.5000 3.2449 0.6890
## Anthodor BF+HF+NM    ++ 1.0000 8.647e-09 0.4286 2.6566 0.6314
## Poatriv  BF+HF+SF   +++ 1.0000 3.181e-09 0.9286 9.3465 0.7609
## Alopgeni BF+HF+SF    ++ 1.0000 8.647e-09 0.5714 3.8995 0.4732
## Elymrepe BF+HF+SF    ++ 1.0000 8.647e-09 0.4286 2.6566 0.6812
## Sagiproc BF+HF+SF     + 0.8672 1.667e-01 0.4286 0.6849 0.3726
## Agrostol HF+NM+SF    ++ 1.0000 8.647e-09 0.5882 2.3455 0.4403
## Ranuflam HF+NM+SF     + 1.0000 8.647e-09 0.3529 1.1801 0.3916
## Juncarti HF+NM+SF     + 1.0000 8.647e-09 0.2941 0.9481 0.3977
## Lolipere    BF+HF    ++ 1.0000 3.333e-01 1.0000 5.8221 0.8987
## Poaprat     BF+HF    ++ 1.0000 5.000e-01 1.0000 3.8995 0.7383
## Trifrepe    BF+HF    ++ 1.0000 6.667e-01 1.0000 2.3699 0.6700
## Bromhord    BF+HF    ++ 0.9836 8.333e-02 0.5000 2.2595 0.4345
## Achimill    BF+HF    ++ 0.9716 1.667e-01 0.6250 2.2497 0.6992
## Hyporadi    BF+NM    ++ 1.0000 1.170e-09 0.3333 2.7256 0.7635
## Juncbufo    HF+SF    ++ 1.0000 3.181e-09 0.3636 2.7977 0.7960
## Callcusp    NM+SF     + 1.0000 3.181e-09 0.2500 1.7062 0.5054
## Vicilath       BF    ++ 0.9980 5.882e-02 0.6667 2.7414 0.4650
## Bellpere       BF     + 0.9538 2.353e-01 0.6667 1.0326 0.4286
## Trifprat       HF    ++ 1.0000 1.170e-09 0.6000 5.0891 0.8579
## Bracruta       HF     + 1.0000 6.667e-01 1.0000 1.6990 0.6935
## Rumeacet       HF    ++ 0.9994 6.667e-02 0.8000 5.0707 0.7703
## Airaprae       NM    ++ 1.0000 1.170e-09 0.3333 2.6826 0.7175
## Comapalu       NM    ++ 1.0000 1.170e-09 0.3333 2.6826 0.7516
## Empenigr       NM     + 1.0000 4.305e-10 0.1667 1.2669 0.4870
## Salirepe       NM    ++ 1.0000 1.170e-09 0.5000 4.2953 0.9007
## Eleopalu       NM     + 0.9459 1.429e-01 0.5000 1.3462 0.4330
## Chenalbu       SF     + 1.0000 4.305e-10 0.1667 1.2669 0.5523
## Cirsarve       SF     + 1.0000 4.305e-10 0.1667 1.2669 0.5387
## 3 binary splits
```

```
plot(x2)
```



```
x3 <- opticut(Dune01 ~ manure + moisture, dune.env, strata=dune.env$Management, dist="binomial")
```

```
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

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## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

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## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

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## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: algorithm did not converge

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: algorithm did not converge

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: algorithm did not converge

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: algorithm did not converge

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: algorithm did not converge
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: algorithm did not converge
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: algorithm did not converge
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: algorithm did not converge
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: algorithm did not converge
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: algorithm did not converge
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: algorithm did not converge
```

```
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
```

```
## Warning: glm.fit: algorithm did not converge
```

```
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
```

```
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
```

```
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
```

```
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
```

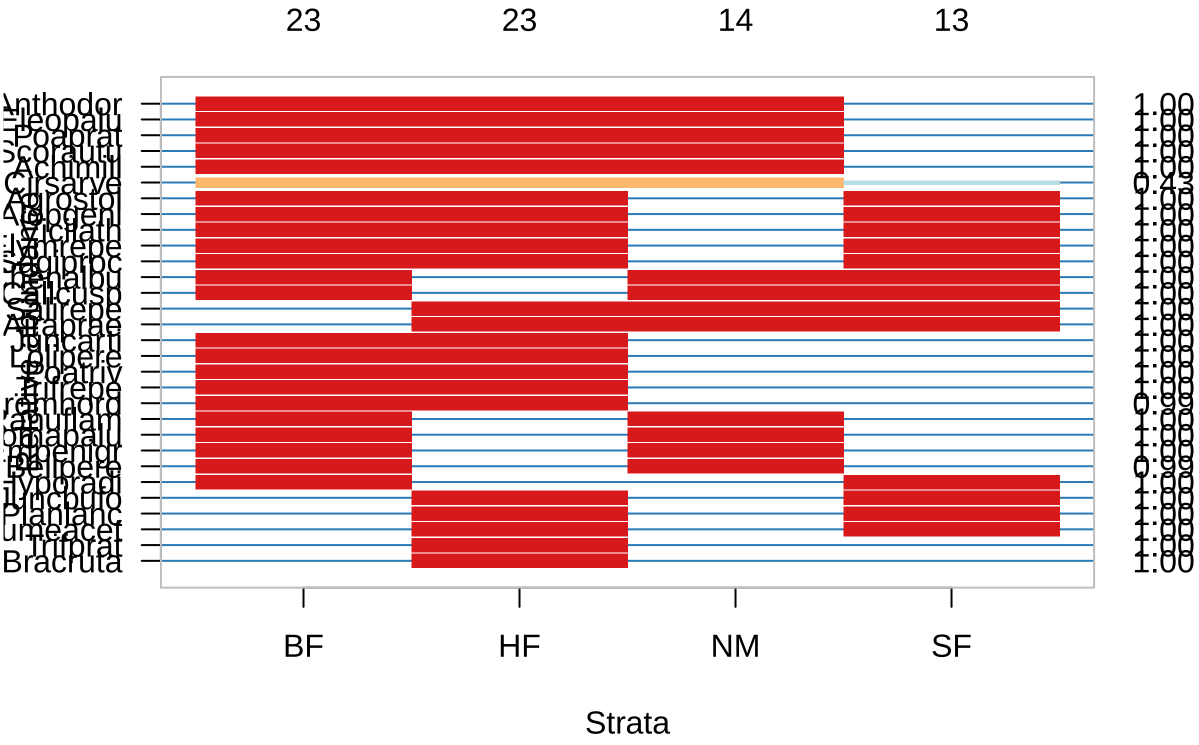
```
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
```

```
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
```

```r
summary(x3)
```

```
## Multivariate opticut results, comb = rank, dist = binomial
##
## Call:
## opticut(formula = Dune01 ~ manure + moisture, data = dune.env,
##     strata = dune.env$Management, dist = "binomial")
##
## Best supported models with logLR >= -Inf:
##             split assoc      I       mu0       mu1      logLR      w
## Anthodor BF+HF+NM     + 1.0000 3.690e-09 5.376e-01  1.629e+00 0.3705
## Eleopalu BF+HF+NM     + 1.0000 2.220e-16 2.220e-16  5.232e-01 0.4576
## Poaprat  BF+HF+NM    ++ 1.0000 2.220e-16 1.000e+00  3.253e+00 0.7463
## Scorautu BF+HF+NM     + 1.0000 9.193e-01 1.000e+00  6.534e-01 0.3693
## Achimill BF+HF+NM     + 0.9987 3.591e-02 5.923e-01  9.259e-01 0.5420
## Cirsarve BF+HF+NM     + 0.4266 2.220e-16 2.220e-16  3.386e-11 0.3333
## Agrostol BF+HF+SF     + 1.0000 2.220e-16 2.220e-16  1.341e+00 0.3333
## Alopgeni BF+HF+SF    ++ 1.0000 6.724e-13 2.381e-02  3.298e+00 0.6809
## Vicilath BF+HF+SF    ++ 1.0000 1.000e+00 1.000e+00  3.998e+00 0.4954
## Elymrepe BF+HF+SF     + 1.0000 1.186e-08 2.227e-01  3.434e-01 0.4050
## Sagiproc BF+HF+SF     + 0.9993 1.261e-02 4.009e-01  1.782e+00 0.7077
## Chenalbu BF+NM+SF     + 1.0000 2.220e-16 2.220e-16  5.232e-01 0.3857
## Callcusp BF+NM+SF     + 1.0000 2.220e-16 2.220e-16  5.232e-01 0.4576
## Salirepe HF+NM+SF     + 0.9993 3.047e-02 6.221e-01  7.491e-10 0.3333
## Airaprae HF+NM+SF     + 0.9991 1.522e-02 4.159e-01  5.392e-10 0.3333
## Juncarti    BF+HF    ++ 1.0000 2.220e-16 2.220e-16  2.660e+00 0.3857
## Lolipere    BF+HF    ++ 1.0000 1.000e+00 1.000e+00  5.209e+00 0.4966
## Poatriv     BF+HF     + 1.0000 2.220e-16 2.220e-16  1.539e-09 0.3333
## Trifrepe    BF+HF    ++ 1.0000 5.906e-01 1.000e+00  2.284e+00 0.5479
## Bromhord    BF+HF     + 0.9926 2.178e-02 2.672e-01  1.430e+00 0.4426
## Ranuflam    BF+NM     + 1.0000 2.220e-16 2.220e-16 -4.704e-09 0.3333
## Comapalu    BF+NM     + 1.0000 2.220e-16 1.837e-13  2.249e-09 0.3333
## Empenigr    BF+NM     + 1.0000 2.220e-16 2.935e-13  2.062e-09 0.3333
## Bellpere    BF+NM     + 0.9931 5.142e-02 4.786e-01  9.237e-01 0.4039
## Hyporadi    BF+SF     + 1.0000 5.289e-01 1.000e+00  7.921e-01 0.3811
## Juncbufo    HF+SF    ++ 1.0000 6.852e-10 9.064e-01  3.777e+00 0.8265
## Planlanc    HF+SF     + 1.0000 1.000e+00 1.000e+00  1.294e+00 0.3611
## Rumeacet    HF+SF   +++ 1.0000 4.887e-11 1.000e+00  1.033e+01 0.9961
## Trifprat       HF    ++ 1.0000 5.073e-12 1.000e+00  4.571e+00 0.4655
## Bracruta       HF     + 1.0000 6.414e-01 1.000e+00  1.818e+00 0.5193
## 3 binary splits
```

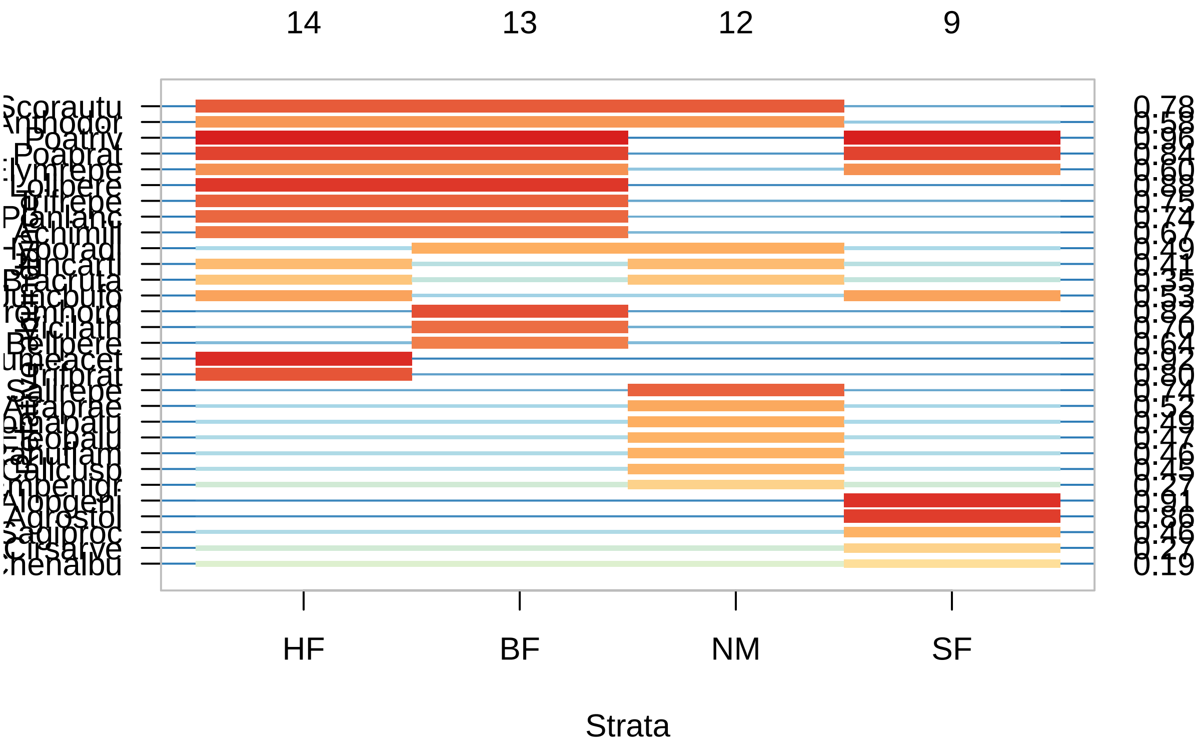
```
plot(x3)
```



```
## Beta regression
Dune2 <- as.matrix(dune+0.5) / 10
x4 <- opticut(Dune2 ~ 1, strata=dune.env$Management, dist="beta")
summary(x4)
```

```
## Multivariate opticut results, comb = rank, dist = beta
##
## Call:
## opticut(formula = Dune2 ~ 1, strata = dune.env$Management, dist = "beta")
##
## Best supported models with logLR >= -Inf:
##             split assoc      I     mu0     mu1  logLR      w
## Scorautu BF+HF+NM    ++ 0.7794 0.17817 0.38107 5.0745 0.8647
## Anthodor BF+HF+NM     + 0.5760 0.10484 0.18420 1.1481 0.4203
## Poatriv  BF+HF+SF    ++ 0.9620 0.12172 0.49912 7.3010 0.8074
## Poaprat  BF+HF+SF    ++ 0.8433 0.13521 0.34908 4.3908 0.4868
## Elymrepe BF+HF+SF     + 0.5986 0.12205 0.21717 1.1230 0.4244
## Lolipere    BF+HF    ++ 0.8840 0.21057 0.51807 4.1041 0.5739
## Trifrepe    BF+HF    ++ 0.7511 0.20483 0.40589 3.3954 0.6065
## Planlanc    BF+HF    ++ 0.7389 0.12810 0.27492 2.4674 0.5496
## Achimill    BF+HF    ++ 0.6717 0.09444 0.19051 2.5958 0.6056
## Hyporadi    BF+NM     + 0.4898 0.07977 0.12901 1.1369 0.4604
## Juncarti    HF+NM     + 0.4131 0.11643 0.16976 0.6153 0.3946
## Bracruta    HF+NM     + 0.3542 0.24927 0.32468 0.4567 0.3813
## Juncbufo    HF+SF     + 0.5259 0.08819 0.14786 1.2161 0.5040
## Bromhord       BF    ++ 0.8161 0.10488 0.26913 2.5352 0.6478
## Vicilath       BF    ++ 0.7049 0.05974 0.13249 4.3694 0.9287
## Bellpere       BF     + 0.6419 0.10238 0.19628 1.3851 0.5455
## Rumeacet       HF    ++ 0.9233 0.09043 0.33240 6.2240 0.9885
## Trifprat       HF    ++ 0.7962 0.07273 0.18889 3.8461 0.8910
## Salirepe       NM    ++ 0.7439 0.08105 0.18708 2.8623 0.8470
## Airaprae       NM     + 0.5190 0.06399 0.10832 1.7093 0.6509
## Comapalu       NM     + 0.4882 0.05980 0.09784 1.8817 0.6948
## Eleopalu       NM     + 0.4683 0.17312 0.25811 0.5215 0.3772
## Ranuflam       NM     + 0.4621 0.10558 0.16291 0.8663 0.3943
## Callcusp       NM     + 0.4476 0.09076 0.13910 0.7674 0.3972
## Empenigr       NM     + 0.2717 0.05575 0.07237 0.7740 0.4539
## Alopgeni       SF    ++ 0.9077 0.15803 0.46035 4.2254 0.8093
## Agrostol       SF    ++ 0.8612 0.20803 0.49026 3.0958 0.7098
## Sagiproc       SF     + 0.4617 0.13397 0.20313 0.7063 0.3997
## Cirsarve       SF     + 0.2717 0.05575 0.07237 0.7740 0.4539
## Chenalbu       SF     + 0.1918 0.05200 0.06245 0.9312 0.5111
## 3 binary splits
```

```r
plot(x4)
```

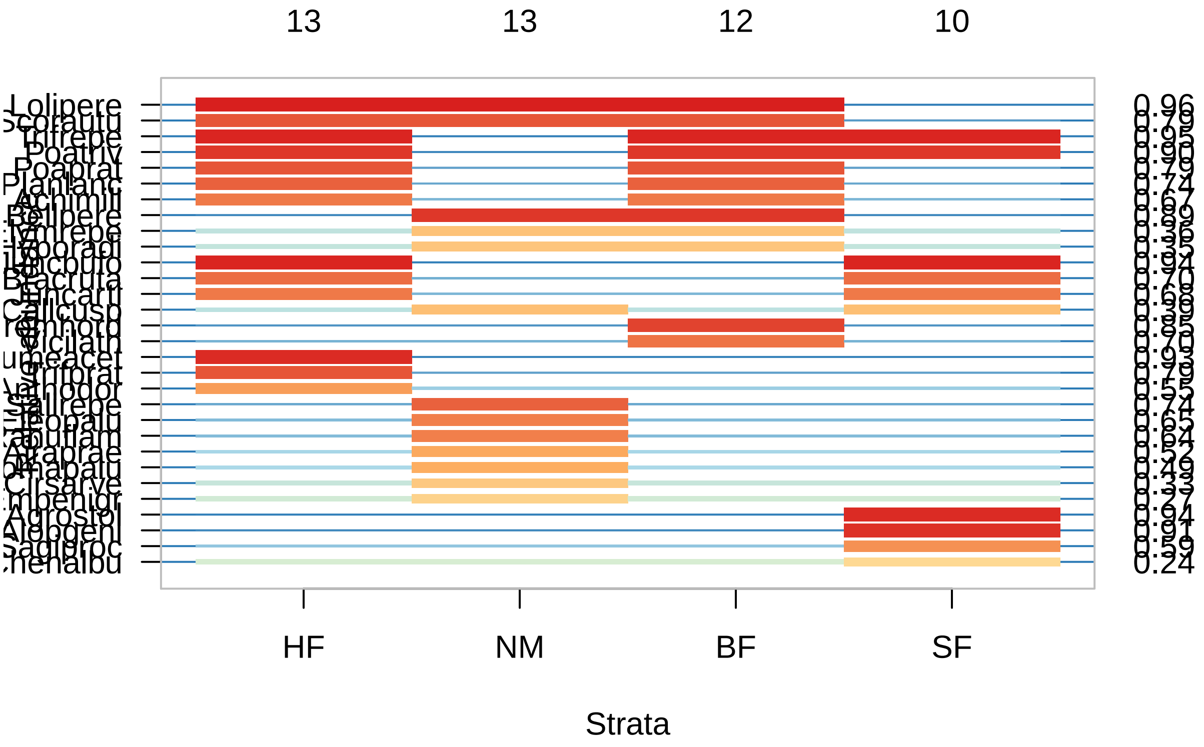


```r
x5 <- opticut(Dune2 ~ manure, dune.env, strata=dune.env$Management, dist="beta")
summary(x5)
```

```
## Multivariate opticut results, comb = rank, dist = beta
```

```
##
## Call:
## opticut(formula = Dune2 ~ manure, data = dune.env, strata = dune.env$Management,
##     dist = "beta")
##
## Best supported models with logLR >= -Inf:
##             split assoc      I     mu0     mu1   logLR      w
## Lolipere BF+HF+NM    ++ 0.9628 0.02503 0.15721 4.52994 0.6104
## Scorautu BF+HF+NM    ++ 0.7883 0.17329 0.37858 2.78625 0.6581
## Trifrepe BF+HF+SF    ++ 0.9473 0.21532 0.62509 3.90047 0.4742
## Poatriv  BF+HF+SF    ++ 0.8963 0.11822 0.36436 2.00207 0.6594
## Poaprat     BF+HF    ++ 0.7948 0.11196 0.27161 5.10107 0.6029
## Planlanc    BF+HF    ++ 0.7433 0.14503 0.30657 2.53058 0.4590
## Achimill    BF+HF    ++ 0.6711 0.09329 0.18824 2.58564 0.4552
## Bellpere    BF+NM    ++ 0.8885 0.02647 0.10061 2.12610 0.5576
## Elymrepe    BF+NM     + 0.3640 0.08561 0.12057 0.07552 0.3407
## Hyporadi    BF+NM     + 0.3544 0.09572 0.13293 0.21056 0.3572
## Juncbufo    HF+SF    ++ 0.9446 0.09242 0.37623 3.10402 0.8621
## Bracruta    HF+SF     + 0.7044 0.31627 0.52623 0.92747 0.4554
## Juncarti    HF+SF     + 0.6770 0.15362 0.29256 0.70062 0.3922
## Callcusp    NM+SF     + 0.3886 0.09554 0.13733 0.63669 0.3964
## Bromhord       BF    ++ 0.8499 0.07911 0.23168 3.00961 0.7403
## Vicilath       BF    ++ 0.6987 0.06912 0.14988 4.62302 0.8194
## Rumeacet       HF    ++ 0.9302 0.09680 0.36044 6.26423 0.7311
## Trifprat       HF    ++ 0.7931 0.07088 0.18342 3.76058 0.7219
## Anthodor       HF     + 0.5504 0.16814 0.27289 0.87929 0.3494
## Salirepe       NM     + 0.7439 0.08105 0.18708 1.19959 0.5531
## Eleopalu       NM     + 0.6457 0.13865 0.25755 0.50249 0.3632
## Ranuflam       NM     + 0.6416 0.08310 0.16247 0.83466 0.3694
## Airaprae       NM     + 0.5190 0.06399 0.10832 0.66716 0.4815
## Comapalu       NM     + 0.4882 0.05980 0.09784 0.73272 0.4966
## Cirsarve       NM     + 0.3253 0.04022 0.05547 0.38506 0.3667
## Empenigr       NM     + 0.2717 0.05575 0.07237 0.29145 0.3942
## Agrostol       SF    ++ 0.9356 0.23871 0.63227 2.70445 0.7902
## Alopgeni       SF    ++ 0.9124 0.15916 0.46926 2.10605 0.7632
## Sagiproc       SF     + 0.5929 0.14226 0.24704 0.56757 0.4104
## Chenalbu       SF     + 0.2400 0.05312 0.06686 0.71117 0.4983
## 3 binary splits
```

```
plot(x5)
```



```
xx <- data.frame(#ord0=summary(x1)$summary$split,
    bin0=summary(x2)$summary$split,
    binx=summary(x3)$summary$split,
    bet0=summary(x4)$summary$split,
    betx=summary(x5)$summary$split)
rownames(xx) <- rownames(summary(x2)$summary)
xx
```

```
##               bin0     binx     bet0     betx
## Achimill     BF+HF BF+HF+NM    BF+HF    BF+HF
## Agrostol HF+NM+SF BF+HF+SF       SF       SF
## Airaprae        NM HF+NM+SF       NM       NM
## Alopgeni BF+HF+SF BF+HF+SF       SF       SF
## Anthodor BF+HF+NM BF+HF+NM BF+HF+NM       HF
## Bellpere        BF    BF+NM       BF    BF+NM
## Bromhord     BF+HF    BF+HF       BF       BF
## Chenalbu        SF BF+NM+SF       SF       SF
## Cirsarve        SF BF+HF+NM       SF       NM
## Comapalu        NM    BF+NM       NM       NM
## Eleopalu        NM BF+HF+NM       NM       NM
## Elymrepe BF+HF+SF BF+HF+SF BF+HF+SF    BF+NM
## Empenigr        NM    BF+NM       NM       NM
## Hyporadi     BF+NM    BF+SF    BF+NM    BF+NM
## Juncarti HF+NM+SF    BF+HF    HF+NM    HF+SF
## Juncbufo     HF+SF    HF+SF    HF+SF    HF+SF
## Lolipere     BF+HF    BF+HF    BF+HF BF+HF+NM
## Planlanc BF+HF+NM    HF+SF    BF+HF    BF+HF
## Poaprat      BF+HF BF+HF+NM BF+HF+SF    BF+HF
## Poatriv  BF+HF+SF    BF+HF BF+HF+SF BF+HF+SF
## Ranuflam HF+NM+SF    BF+NM       NM       NM
## Rumeacet       HF    HF+SF       HF       HF
## Sagiproc BF+HF+SF BF+HF+SF       SF       SF
## Salirepe       NM HF+NM+SF       NM       NM
## Scorautu BF+HF+NM BF+HF+NM BF+HF+NM BF+HF+NM
## Trifprat       HF       HF       HF       HF
## Trifrepe    BF+HF    BF+HF    BF+HF BF+HF+SF
## Vicilath       BF BF+HF+SF       BF       BF
## Bracruta       HF       HF    HF+NM    HF+SF
## Callcusp    NM+SF BF+NM+SF       NM    NM+SF
```

```
ocoptions(oc)
```

3.4.2 Varespec data (% cover)

```
library(vegan)
data(varespec)
data(varechem)
y <- as.matrix(varespec / 100)
range(y[y>0])
```

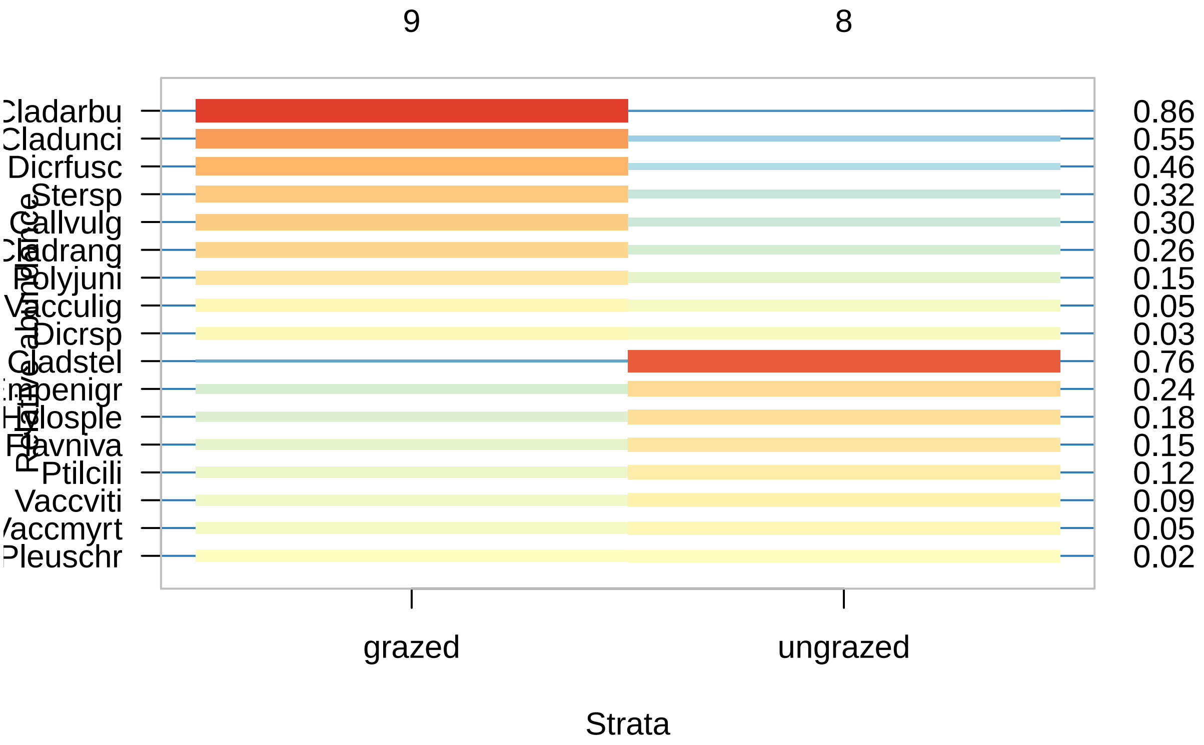
```
## [1] 0.0002 0.8430
```

```
y[y <= 0] <- 0.0001
y <- y[,apply(y, 2, max) > 0.05]
varechem$grazing <- as.factor(ifelse(rownames(varechem) %in% c(5,6,7,8,13,14,15,16,
    18,19,20,22,23,24,26), "grazed", "ungrazed"))

x <- opticut(y ~ 1, varechem, strata=grazing, dist="beta")
summary(x)
```

```
## Multivariate opticut results, comb = rank, dist = beta
##
## Call:
## opticut(formula = y ~ 1, data = varechem, strata = grazing, dist = "beta")
##
## Best supported models with logLR >= 2:
##             split assoc      I     mu0   mu1 logLR w
## Cladarbu   grazed    ++ 0.8616 0.04831 0.157 6.213 1
## Cladstel ungrazed    ++ 0.7619 0.13055 0.290 2.091 1
## 1 binary split
## 15 species not shown
```

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



Implement ZI-Beta (quite unreliable for such small data set)

```r
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)
}
y <- as.matrix(varespec / 100)
```

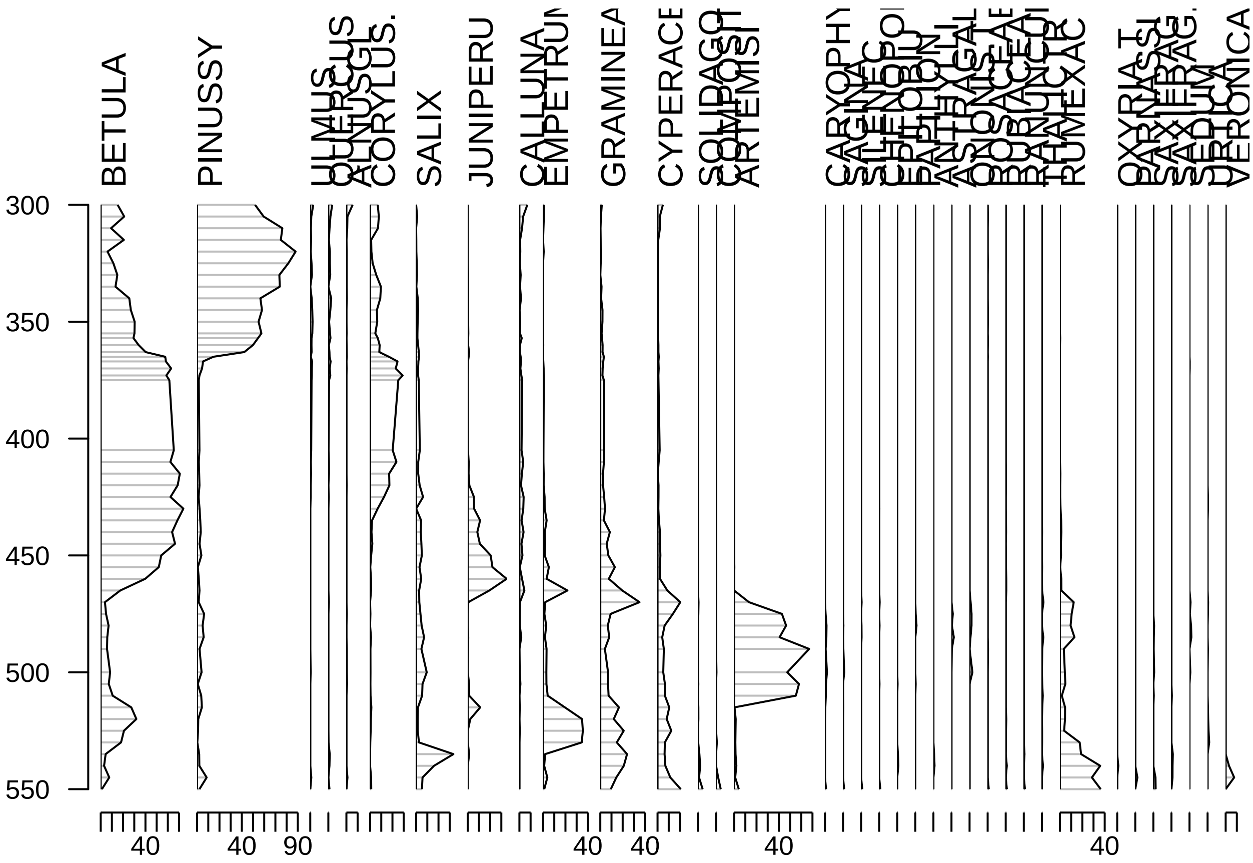
```
range(y[y>0])
y <- y[,apply(y, 2, max) > 0.05]
zi_beta_fun(y[,3], data.frame(matrix(1, nrow(y), 1)))
opticut1(y[,1], matrix(1, nrow(y), 1), varechem$grazing, dist=zi_beta_fun)
```

3.4.3 Stratigraphy example

```
library(rioja)
```

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

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

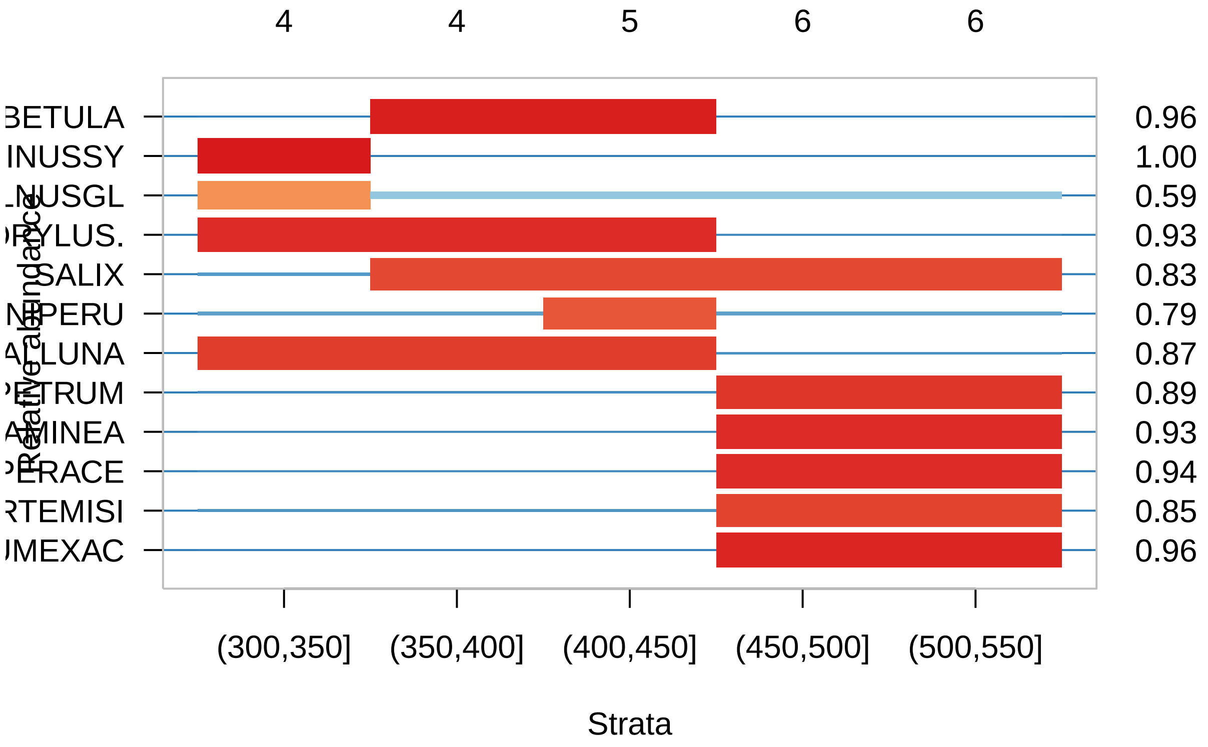


```
z <- as.factor(cut(aber$ages$Depth, 5))
ab <- as.matrix(aber$spec) / 100
ab[ab == 0] <- 0.0001
ab <- ab[,apply(ab, 2, max) > 0.05]

a <- opticut(ab ~ 1, strata=z, comb="rank", dist="beta")
summary(a)
```

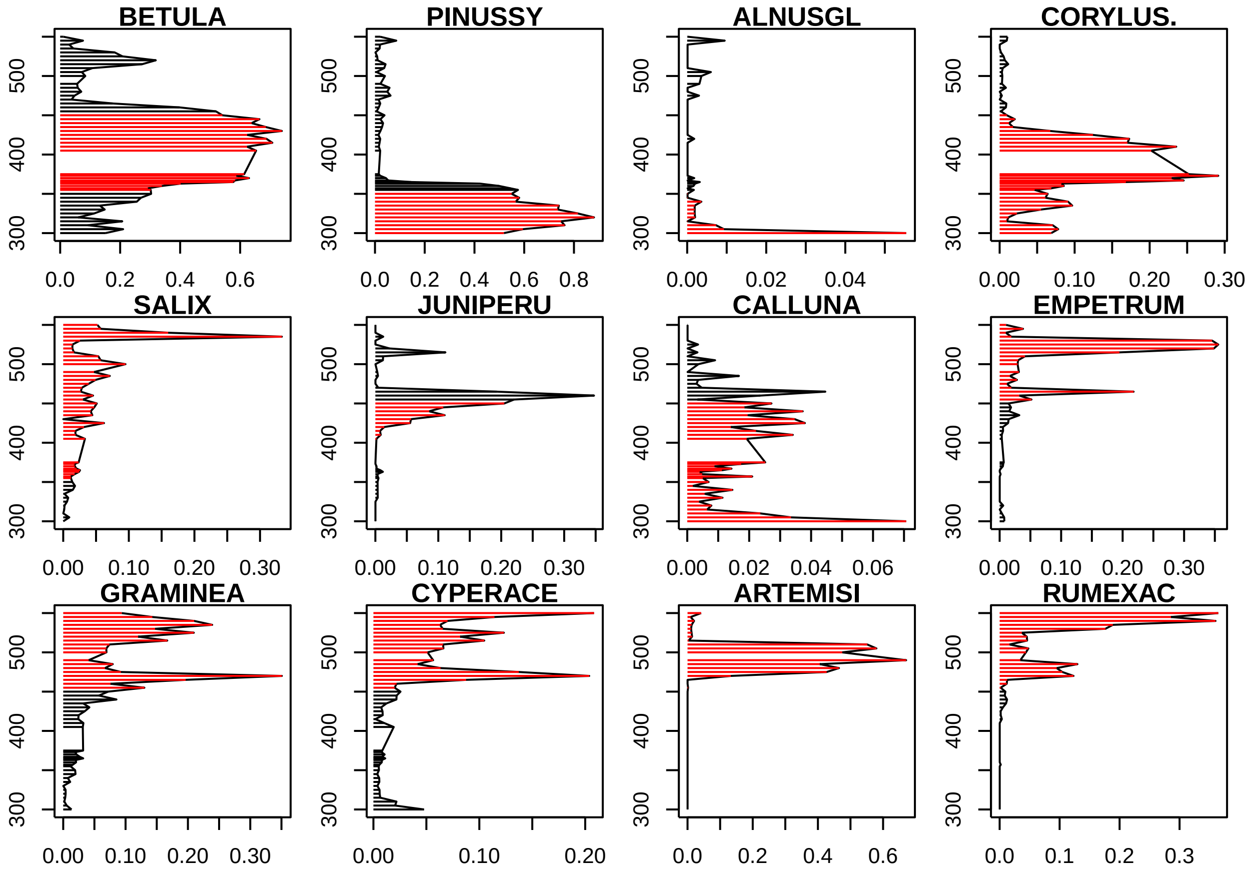
```
## Multivariate opticut results, comb = rank, dist = beta
##
## Call:
## opticut(formula = ab ~ 1, strata = z, dist = "beta", comb = "rank")
##
## Best supported models with logLR >= 2:
##                                             split assoc      I      mu0
## SALIX    (350,400] (400,450] (450,500] (500,550]   +++ 0.8306 0.014015
## CORYLUS.           (300,350] (350,400] (400,450]   +++ 0.9341 0.019366
## CALLUNA            (300,350] (350,400] (400,450]   +++ 0.8682 0.005234
## BETULA                       (350,400] (400,450]   +++ 0.9627 0.153662
## RUMEXAC                      (450,500] (500,550]   +++ 0.9554 0.015648
## CYPERACE                     (450,500] (500,550]   +++ 0.9353 0.015826
## GRAMINEA                     (450,500] (500,550]   +++ 0.9299 0.028003
## EMPETRUM                     (450,500] (500,550]   +++ 0.8857 0.020863
## ARTEMISI                     (450,500] (500,550]    ++ 0.8515 0.046111
## PINUSSY                                (300,350]   +++ 0.9960 0.083196
## ALNUSGL                                (300,350]    ++ 0.5936 0.002089
## JUNIPERU                               (400,450]    ++ 0.7935 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
```

```r
plot(a, sort=FALSE)
```



```
bp <- bestpart(a)

op <- 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(op)
```

3.5 Presence-only data

Describe RSF/RSPF differences especially related to covariates.

```
## presence-only data
## single species model only:
## because the used distr is different for
## each species by definition.

library(ResourceSelection)
```

```
## ResourceSelection 0.2-6   2016-02-15
```

```
## settings
n.used <- 1000
m <- 10
n <- n.used * m
set.seed(1234)
x <- data.frame(x0=as.factor(sample(1:3, n, replace=TRUE)),
    x1=rnorm(n), x2=runif(n))
cfs <- c(1, -0.5, 0.1, -1, 0.5)
## Logistic RSPF model
```

```r
dd <- simulateUsedAvail(x, cfs, n.used, m, link="logit")

Y <- dd$status
X <- model.matrix(~ x1 + x2, dd)
Z <- allComb(as.integer(dd$x0))

mod1 <- opticut(Y ~ x1 + x2, dd, strata=x0, dist="rsf", m=0, B=0)
mod1$species
```

```
## $Species.1
## Univariate opticut results, comb = rank, dist = rsf
## I = 0.2344; w = 0.59; H = 0.5162; logL_null = -9184
##
## Best supported models with logLR >= 2:
##     assoc      I mu0   mu1 logLR    w
## 3      ++ 0.2344   1 1.270 6.649 0.59
## 1 3    ++ 0.2397   1 1.277 6.285 0.41
## 2 binary splits
```

```r
mod2 <- opticut(Y ~ x1 + x2, dd, strata=x0, dist="rspf", m=0, B=0)
mod2$species
```

```
## $Species.1
## Univariate opticut results, comb = rank, dist = rspf
## I = 0.5854; w = 0.73; H = 0.6058; logL_null = -9169
##
## Best supported model with logLR >= 2:
##   assoc      I    mu0    mu1 logLR    w
## 3    ++ 0.5854 0.7359 0.8449 2.508 0.73
## 2 binary splits (1 model not shown)
```

4 Custom distributions

The distr argument accepts a function, so other parametric models can be supplied which are avoided due to package dependencies.

4.1 Mixed models

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

```r
library(lme4)
```

```
## Loading required package: Matrix
```

```r
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)
```

```r
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>
```

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

```
## Univariate opticut results, comb = all, dist = lmefun
## I = 0.4736; w = 0.9985; H = 0.997; logL_null = -345.2
##
## Best supported models with logLR >= 2:
##     assoc      I   mu0   mu1  logLR         w
## 1 2   +++ 0.4736 1.480 2.476 13.582 0.9984969
## 1      ++ 0.4057 1.745 2.683  6.864 0.0012072
## 4      -- 0.3473 2.168 1.509  4.739 0.0001441
## 3      -- 0.3495 2.134 1.482  4.620 0.0001279
## 2      ++ 0.2447 1.858 2.386  2.813 0.0000210
## 7 binary splits (2 models not shown)
```

4.2 Imperfect detectability: N-mixture case

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:

```r
library(detect)
```

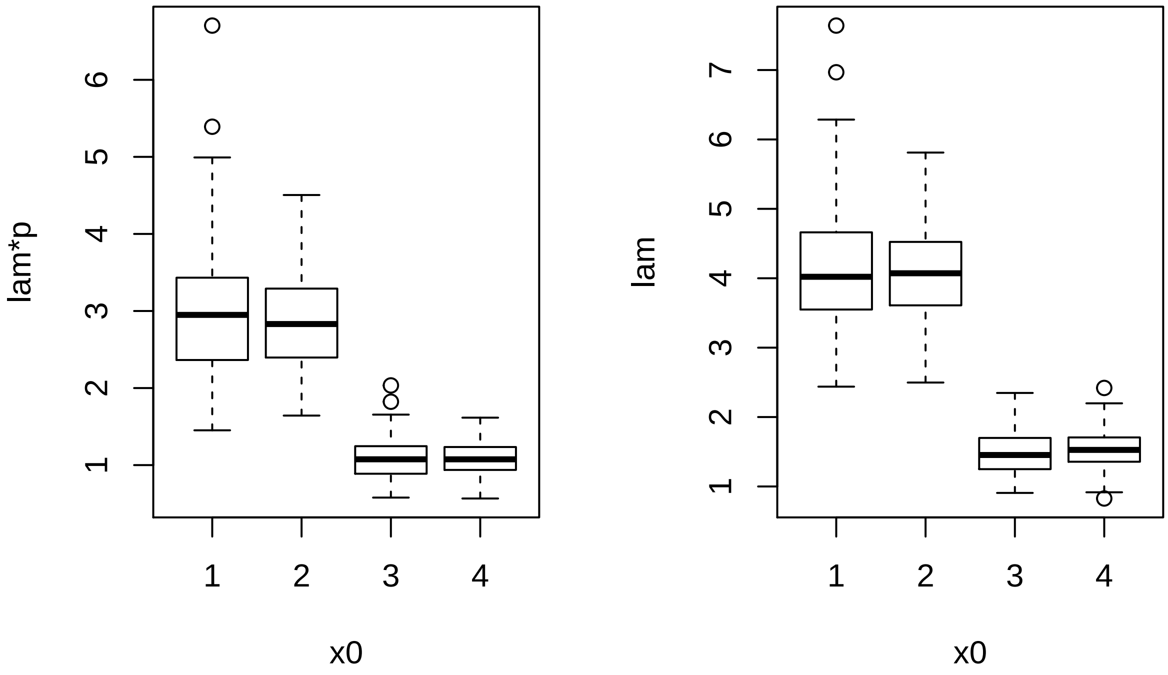
```
## Loading required package: Formula
## Loading required package: stats4

## detect 0.4-0      2016-03-02
```

```
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 = 0.7741; w = 1; H = 1; logL_null = -930
##
## Best supported models with logLR >= -Inf:
##       assoc      I   mu0   mu1  logLR         w
## 1 2     +++ 0.7741 1.139 3.193 115.16 1.000e+00
## 1 2 4   +++ 0.6998 1.078 2.566  52.38 5.383e-28
## 2       +++ 0.5260 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)
```

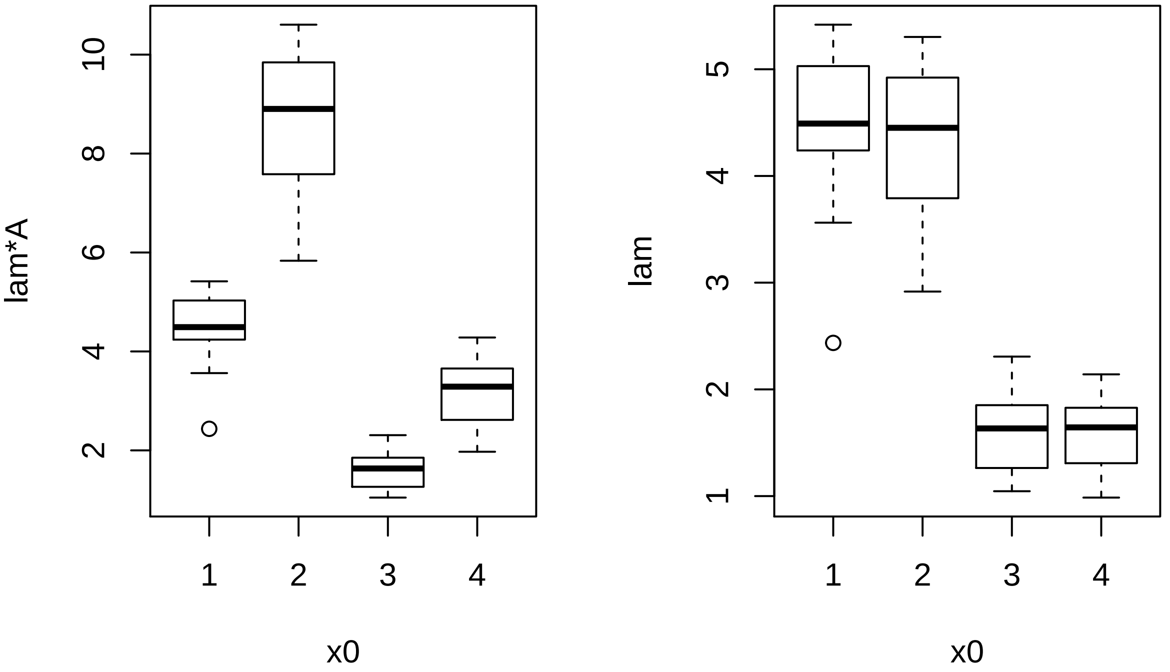
```
## Univariate opticut results, comb = rank, dist = svfun
## I = 0.7876; w = 1; H = 0.9999; logL_null = -884.6
##
## Best supported models with logLR >= -Inf:
##       assoc      I   mu0   mu1  logLR         w
## 1 2     +++ 0.7876 2.409 6.989 26.239 1.000e+00
## 1 2 3   +++ 0.7261 1.936 4.859 15.787 2.888e-05
## 2        ++ 0.4664 4.142 6.866  3.284 1.073e-10
## 3 binary splits
```

4.3 Sampling differences: using offsets

Not accounting for unequal sampling effort can be quite misleading, especially if that is related to habitat classes. This example shows how to take advantage of the other arguments passed to the `...` in the `opticut` function.

```
set.seed(1234)
n <- 50
x0 <- sample(1:4, n, TRUE)
x1 <- ifelse(x0 %in% 1:2, 1, 0)
x2 <- rnorm(n, 0.5, 1)
lam <- exp(0.5 + 1*x1 + -0.2*x2)
A <- ifelse(x0 %in% c(1,3), 1, 2)
Y <- rpois(n, lam*A)
```

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



```r
par(op)

## no offset: incorrect
opticut(Y ~ x2, strata=x0, dist="poisson", comb="rank")$species
```

```
## $Species.1
## Univariate opticut results, comb = rank, dist = poisson
## I = 0.8354; w = 0.9895; H = 0.9792; logL_null = -154.2
##
## Best supported models with logLR >= 2:
##       assoc      I   mu0    mu1 logLR         w
## 2       +++ 0.8354 3.028 10.110 42.01 9.895e-01
## 1 2     +++ 0.8412 2.192  7.464 37.46 1.049e-02
## 1 2 4   +++ 0.8483 1.766  6.164 24.77 3.243e-08
## 3 binary splits
```

```r
## with offsets: log Area
opticut(Y ~ x2, strata=x0, dist="poisson", offset=log(A), comb="rank")$species
```

```
## $Species.1
## Univariate opticut results, comb = rank, dist = poisson
## I = 0.8153; w = 1; H = 1; logL_null = -135.7
##
## Best supported models with logLR >= 2:
##       assoc      I   mu0   mu1 logLR         w
## 1 2     +++ 0.8153 1.572 4.930 32.34 1.000e+00
## 1 2 3   +++ 0.7780 1.431 4.049 17.29 2.919e-07
## 2       +++ 0.6356 2.388 5.060 16.68 1.584e-07
## 3 binary splits
```

4.4 GAM models

```
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)
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 = 0.8815; 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   +++ 0.8815 0.1847 0.7359 46.906 9.985e-01
## decid conif mix        +++ 0.8681 0.2049 0.7712 40.373 1.451e-03
## decid mix              +++ 0.8196 0.2298 0.7298 37.182 5.973e-05
## decid                   ++ 0.4631 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 = 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
## Species.1 open decid conif mix   +++ 0.8815 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 = count ~ 1, data = oven, strata = veg, dist = "poisson")
##
## Best supported model with logLR >= 2:
```

```
##                             split assoc     I    mu0   mu1 logLR      w
## Species.1 open decid conif mix   +++ 0.935 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 = 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
## Species.1 open decid conif mix   +++ 0.9388 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 = pa ~ 1, data = oven, strata = veg, dist = "binomial")
##
## Best supported model with logLR >= 2:
##                             split assoc      I    mu0    mu1 logLR      w
## Species.1 open decid conif mix   +++ 0.9629 0.1377 0.5374 82.37 0.6569
## 4 binary splits
```

5 Finding best partitions

It is useful to access the best binary partition

```
set.seed(2345)
n <- 50
x0 <- sample(1:4, n, TRUE)
x1 <- ifelse(x0 %in% 1:2, 1, 0)
x2 <- rnorm(n, 0.5, 1)
lam <- exp(0.5 + 1*x1 + -0.2*x2)
Y <- rpois(n, lam)
o <- opticut(Y ~ x2, strata=x0, dist="poisson", comb="rank")
summary(o)
```

```
## Multivariate opticut results, comb = rank, dist = poisson
##
## Call:
## opticut(formula = Y ~ x2, strata = x0, dist = "poisson", comb = "rank")
```

```
##
## Best supported model with logLR >= 2:
##           split assoc      I   mu0   mu1 logLR      w
## Species.1   1 2   +++ 0.7037 1.819 4.361 12.46 0.9918
## 3 binary splits
```

```r
bp <- bestpart(o)
head(bp)
```

```
##   Species.1
## 1         1
## 1         1
## 3         0
## 1         1
## 2         1
## 2         1
```

The model based on the best partition can be returned as:

```r
bestmodel(o, which=1)
```

```
## $Species.1
##
## Call:  stats::glm(formula = Y ~ . - 1, family = Family, data = XX)
##
## Coefficients:
## `(Intercept)`             Z1             x2
##        0.5981         0.8747        -0.1246
##
## Degrees of Freedom: 50 Total (i.e. Null);  47 Residual
## Null Deviance:       180.3
## Residual Deviance: 46.98     AIC: 184.8
```

the `which` argument can be used to subset the species.

6 Uncertainty

Uncertainty in I values might be of interest. The `type` argument for the `uncertainty` method can take the following values:

- `"asymp"`: asymptotic distribution of I, μ_0 and μ_1 based on best partition found for the input object.
- `"boot"`: non-parametric bootstrap distribution of I, μ_0 and μ_1 based on best partition found for the input object.
- `"multi"`: non-parametric bootstrap distribution of I, μ_0 and μ_1 based on best partition found for the bootstrap data (i.e. the model ranking is re-evaluated each time).

```r
uc1 <- uncertainty(o, type="asymp", B=5000)
uc2 <- uncertainty(o, type="boot", B=200)
uc3 <- uncertainty(o, type="multi", B=200)

uc1$uncertainty[[1]]
```

```
## Univariate opticut uncertainty results, type = asymp, B = 5000
##
##   best            I               mu0             mu1
##  1 2:5001   Min.   :0.2381   Min.   :1.120   Min.   :2.863
##             1st Qu.:0.5299   1st Qu.:1.640   1st Qu.:4.022
##             Median :0.5846   Median :1.814   Median :4.356
##             Mean   :0.5764   Mean   :1.835   Mean   :4.387
##             3rd Qu.:0.6319   3rd Qu.:2.001   3rd Qu.:4.727
##             Max.   :0.7970   Max.   :3.401   Max.   :6.587
```

```r
uc2$uncertainty[[1]]
```

```
## Univariate opticut uncertainty results, type = boot, B = 200
##
##   best           I               mu0             mu1
##  1 2:201   Min.   :0.3206   Min.   :1.244   Min.   :3.178
##            1st Qu.:0.5356   1st Qu.:1.651   1st Qu.:4.014
##            Median :0.5801   Median :1.801   Median :4.408
##            Mean   :0.5780   Mean   :1.819   Mean   :4.365
##            3rd Qu.:0.6270   3rd Qu.:1.986   3rd Qu.:4.685
##            Max.   :0.7412   Max.   :2.522   Max.   :5.930
```

```r
uc3$uncertainty[[1]]
```

```
## Univariate opticut uncertainty results, type = multi, B = 200
##
##     best            I               mu0              mu1
##  1    :  1   Min.   :0.4628   Min.   :0.7104   Min.   :3.137
##  1 2  :183   1st Qu.:0.6463   1st Qu.:1.6341   1st Qu.:4.046
##  1 2 4:  2   Median :0.7165   Median :1.8144   Median :4.532
##  2    : 15   Mean   :0.7132   Mean   :1.8115   Mean   :4.530
##              3rd Qu.:0.7833   3rd Qu.:1.9957   3rd Qu.:4.915
##              Max.   :0.9322   Max.   :2.6809   Max.   :6.141
```

```r
## performance comparisons for 10 species
YYY <- cbind(Y, Y, Y, Y, Y, Y, Y, Y, Y, Y)
colnames(YYY) <- LETTERS[1:10]
o <- opticut(YYY ~ x2, strata=x0, dist="poisson", comb="rank")

library(parallel)
cl <- makeCluster(2)
system.time(uncertainty(o, type="asymp", B=5000))
```

```
##    user  system elapsed
##   0.085   0.001   0.086
```

```r
system.time(uncertainty(o, type="asymp", B=5000, cl=cl))
```

```
##    user  system elapsed
##   0.009   0.002   1.015
```

```r
system.time(uncertainty(o, type="boot", B=100))
```

```
##    user  system elapsed
##   2.887   0.069   2.965
```

```r
system.time(uncertainty(o, type="boot", B=100, cl=cl))
```

```
##    user  system elapsed
##   0.008   0.001   1.468
```

```r
system.time(uncertainty(o, type="multi", B=100))
```

```
##    user  system elapsed
##  13.688   0.266  13.991
```

```r
system.time(uncertainty(o, type="multi", B=100, cl=cl))
```

```
##    user  system elapsed
##   0.008   0.001   7.028
```

```r
stopCluster(cl)
```