opticut: likelihood based optimal partitioning for indicator species analysis

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November 17, 2015

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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, no model,

- data types not always compatible with randomization (i.e. decimals),
- confounding effects to classification accuracy can impact power.

Goals:

- describe a general and extensible approach,
- 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 describe 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 cadidate 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.

The indicator value (I) for each candidate partition can be calculated 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}.

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")
library(opticut)
```

```
## opticut 0.1-0     2015-11-23
```

```
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] "_"
```

```
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)
```

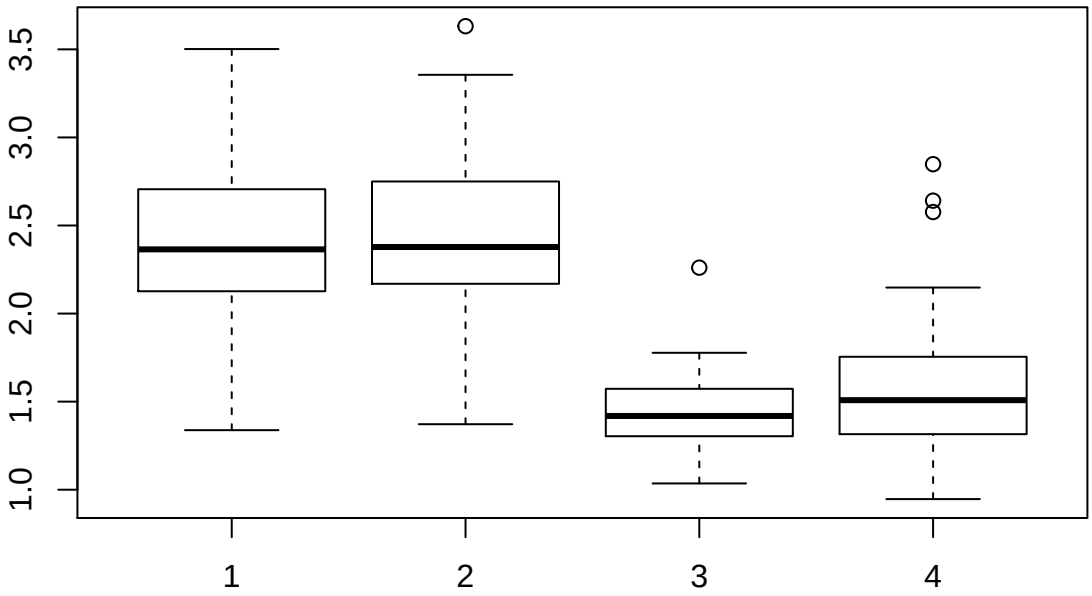
```
## [1] FALSE
## attr(,"comp")
##      i j
## [1,] 1 2
## [2,] 1 9
## attr(,"same")
##      i j
## [1,] 9 2
```

2.3 Poisson count model example

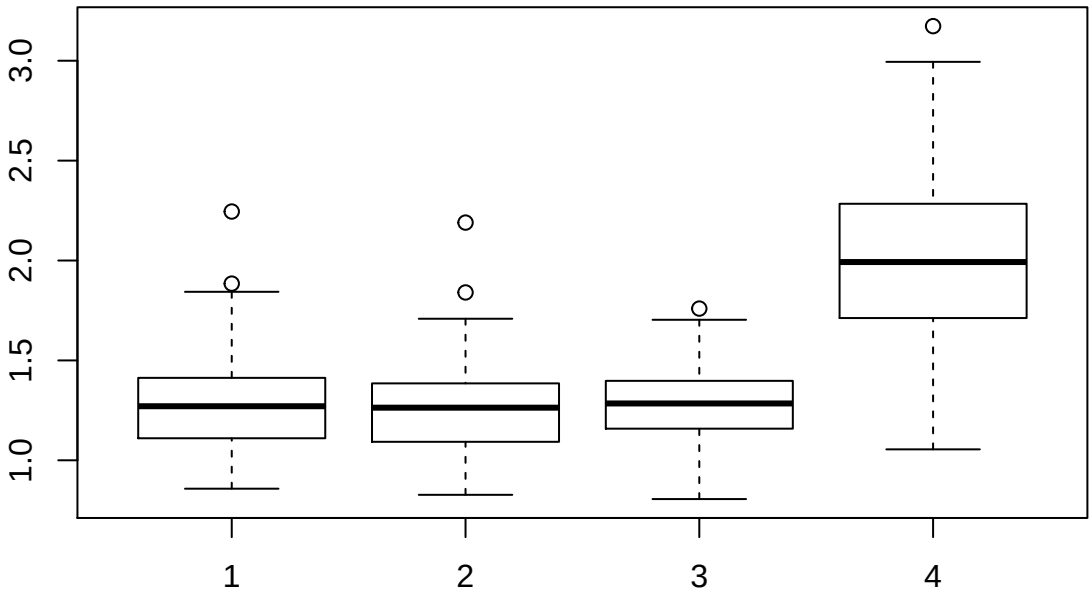
```
set.seed(1234)
n <- 200
x0 <- sample(1:4, n, TRUE)
x1 <- ifelse(x0 %in% 1:2, 1, 0)
x2 <- rnorm(n, 0.5, 1)
table(x0,x1)
```

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

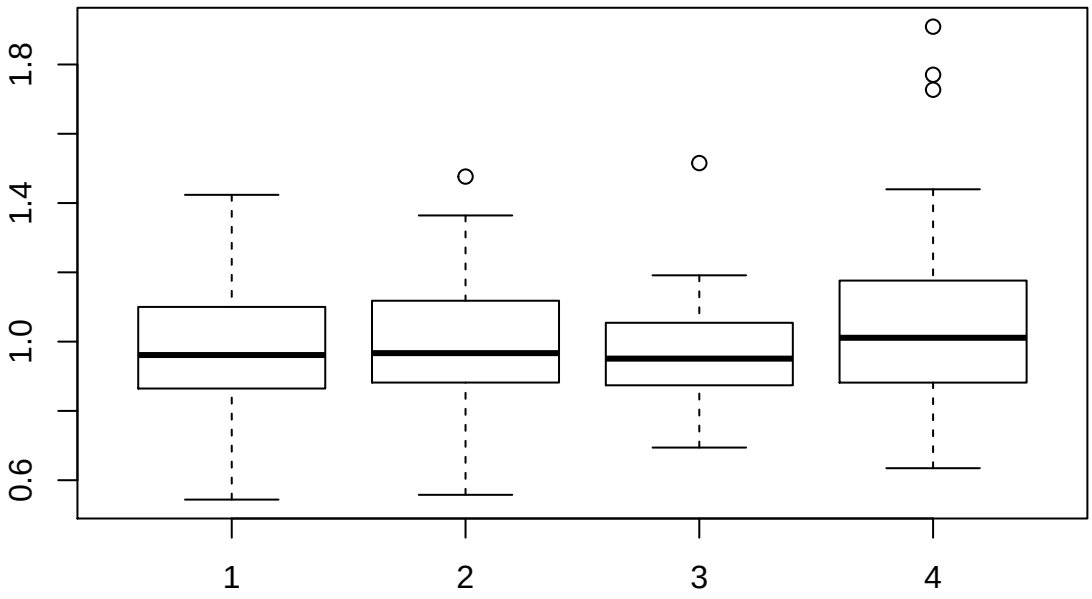
```
lam1 <- exp(0.5 + 0.5*x1 + -0.2*x2)
boxplot(lam1~x0)
```




```
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 = 0.3431; w = 0.9842; H = 0.9687; logL_null = -343.8
##
## Best supported models with logLR >= 2:
##     assoc      I   mu0   mu1 logLR        w
## 1 2   +++ 0.3431 1.739 2.647 8.396 0.984200
## 3      -- 0.2667 2.337 1.714 3.051 0.004694
## 4      -- 0.2666 2.371 1.739 3.027 0.004583
## 2      ++ 0.2258 2.048 2.645 2.633 0.003092
## 1      ++ 0.2240 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 = 0.3706; w = 0.9254; H = 0.8584; logL_null = -315.6
##
## Best supported models with logLR >= 2:
##     assoc      I   mu0   mu1 logLR       w
## 4      ++ 0.3706 1.134 1.803 6.245 0.92545
## 1 3    -- 0.2552 1.486 1.107 3.119 0.04063
## 1 2    -- 0.2123 1.458 1.149 2.064 0.01415
## 7 binary splits (4 models not shown)
```

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

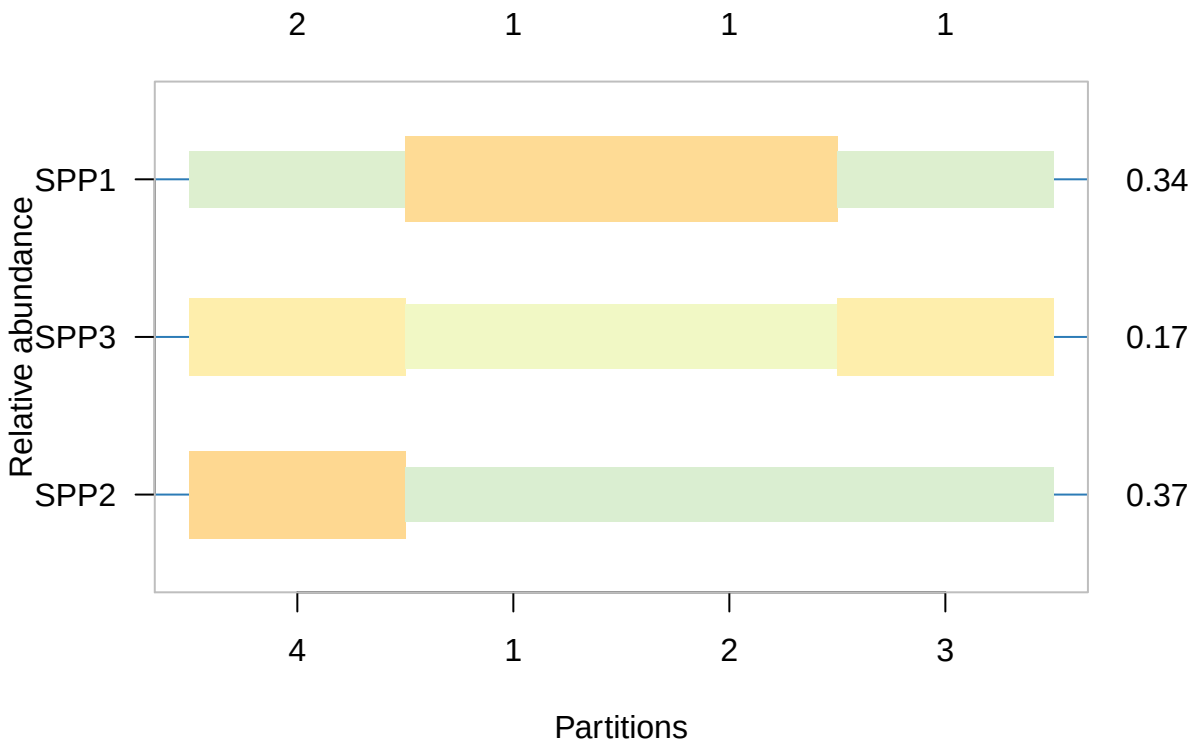
```
## Univariate opticut results, comb = all, dist = poisson
```

```
## I = 0.1749; w = 0.2205; H = 0.1562; logL_null = -244.4
##
## Best supported model:
##     assoc      I   mu0    mu1 logLR      w
## 1 2     - 0.1749 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")
##
##      split assoc      I   mu0   mu1 logLR      w
## SPP1  X1.2   +++ 0.3431 1.739 2.647 8.396 0.9842
## SPP2    X4    ++ 0.3706 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")
##
##      split assoc      I   mu0   mu1 logLR      w
## SPP1 X1 X2   +++ 0.3431 1.739 2.647 8.396 0.9922
## SPP2    X4    ++ 0.3706 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"`: zero-inflated Poisson counts,
- `"zinb"`: zero-inflated Negative Binomial counts,
- `"ordered"`: response measured on ordinal scale, e.g. ordinal vegetation cover,
- `"rspf"`: presence-only data using 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(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
spp
```

```
##   Species1 Species2 Species3
## 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")
##
##          split assoc      I mu0  mu1 logLR      w
## Species2  X1.3   +++ 0.7143 2.0  7.0 14.82 0.4995
## Species1  X2.3   +++ 0.4545 3.0  5.5 17.33 0.4999
## Species3    X1   +++ 0.9722 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")
##
##          split assoc      I mu0  mu1 logLR      w
## Species2 X1 X3   +++ 0.7143 2.0  7.0 14.82 0.4996
## Species1 X2 X3   +++ 0.4545 3.0  5.5 17.33 0.4999
## Species3    X1   +++ 0.9722 0.5 18.0 55.19 1.0000
## 4 binary splits
```

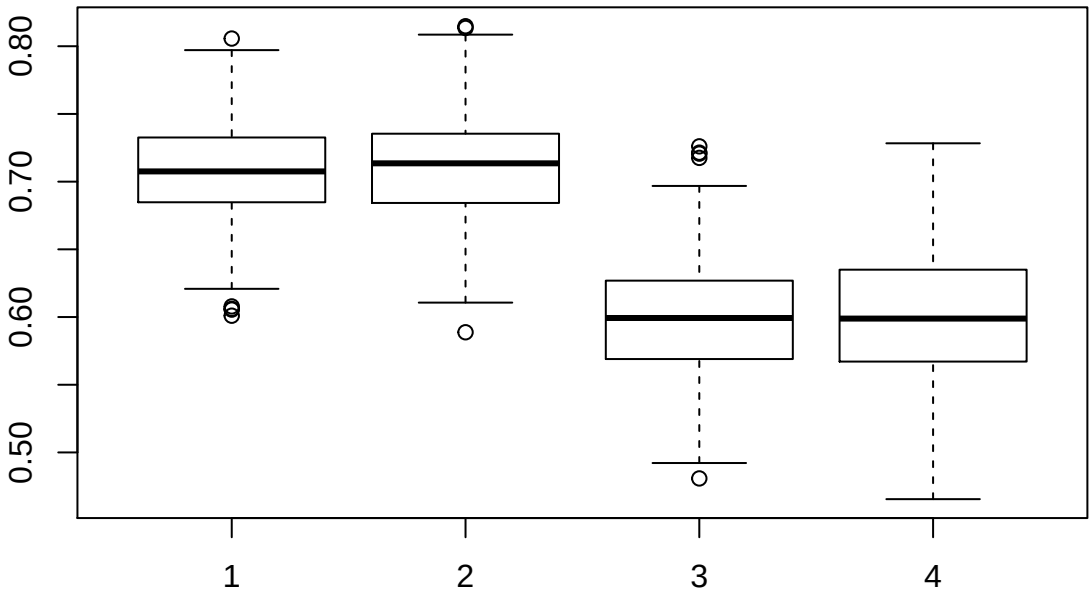
3.2 Binomial

```
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)
```

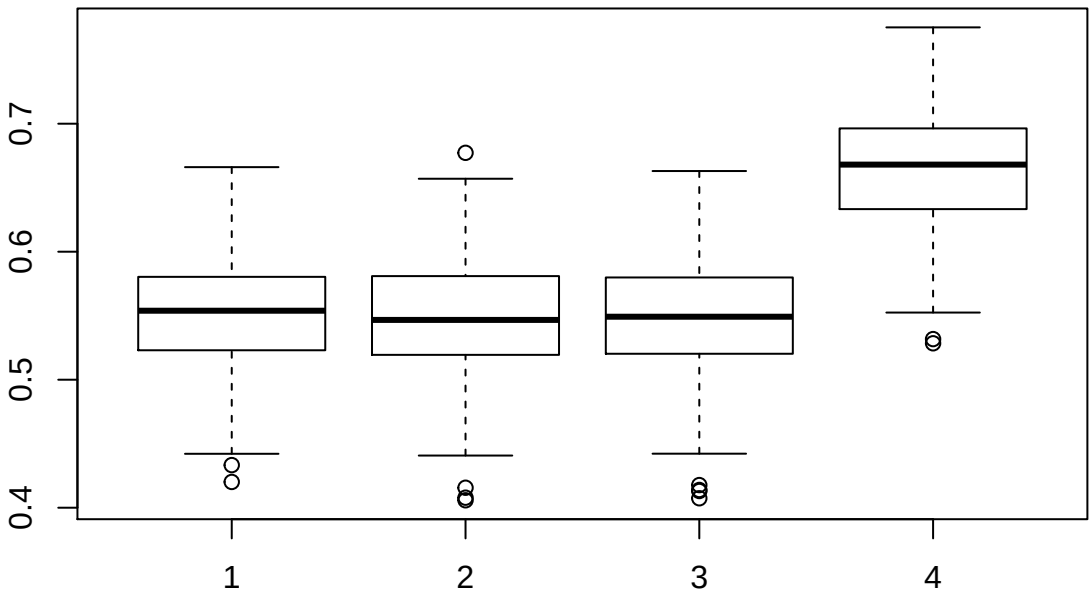
```
##    x1
## x0    0   1
```

```
##   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")
##
##      split assoc      I    mu0    mu1 logLR      w
## SPP1 X1 X2    ++ 0.1465 0.6301 0.7383 6.954 0.9222
## SPP2    X4    ++ 0.1731 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.

```
library(vegan)
```

```
## Loading required package: permute
## Loading required package: lattice
## This is vegan 2.3-1
```

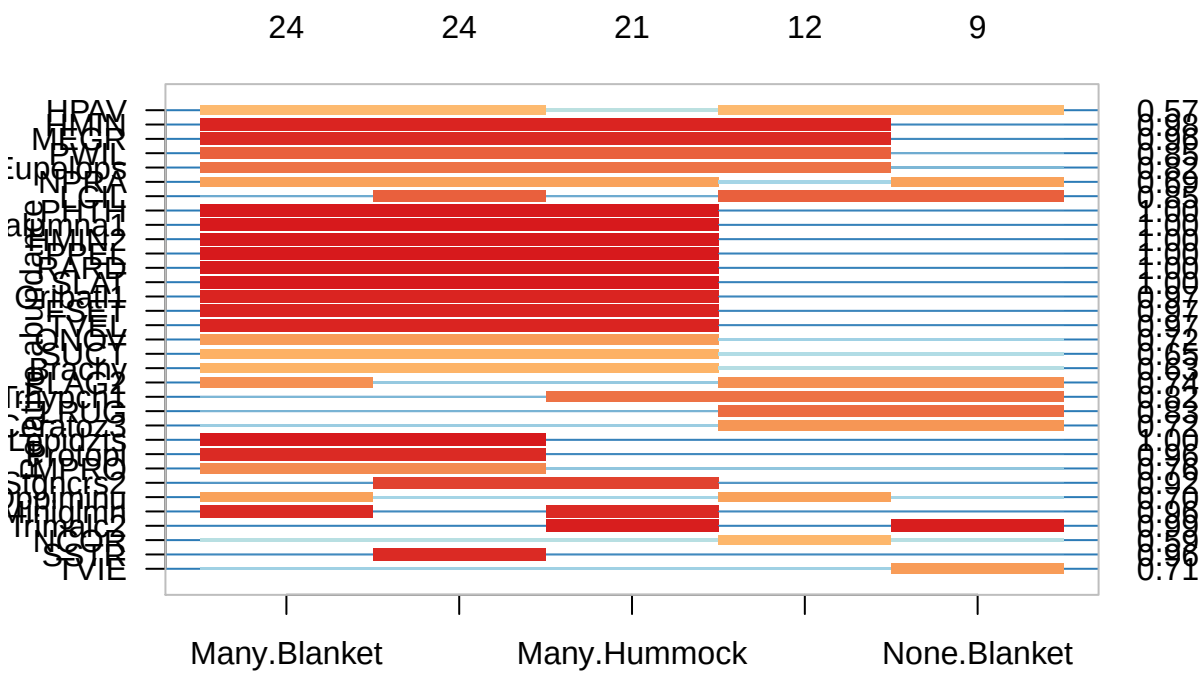
```
data(mite)
data(mite.env)
mite.env$hab <- with(mite.env, interaction(Shrub, Topo, drop=TRUE))
summary(mod0 <- opticut(as.matrix(mite) ~ SubsDens, mite.env,
    strata=mite.env$hab, dist="poisson", comb="all"))
```

```
## 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")
##
##                              split assoc      I       mu0       mu1
## HPAV                  Many.Hummock   --- 0.5733 3.500e+01 1.493e+01
## HMIN                  None.Blanket   --- 0.9778 1.880e+01 4.177e-01
## MEGR                  None.Blanket   --- 0.9608 9.729e-01 3.818e-02
## PWIL                  None.Blanket   --- 0.8524 1.637e+00 2.416e-01
## Eupelops              None.Blanket    -- 0.8159 1.564e+00 2.878e-01
## NPRA                   Few.Blanket   --- 0.6860 1.425e+00 4.474e-01
## LCIL     Many.Blanket.Many.Hummock   --- 0.8529 8.923e+00 1.312e+00
## PHTH      None.Blanket.Few.Blanket   --- 1.0000 1.463e+00 2.525e-09
## Galumna1  None.Blanket.Few.Blanket   --- 1.0000 1.523e+00 3.486e-09
## HMIN2     None.Blanket.Few.Blanket   --- 1.0000 1.785e+00 5.504e-09
## PPEL      None.Blanket.Few.Blanket    -- 1.0000 1.349e-01 6.501e-10
## RARD      None.Blanket.Few.Blanket   --- 1.0000 2.546e+00 1.251e-08
## SLAT      None.Blanket.Few.Blanket   --- 1.0000 7.284e-01 4.062e-09
```

```
## Oribatl1  None.Blanket.Few.Blanket   --- 0.9738 1.311e+00 3.441e-02
## FSET      None.Blanket.Few.Blanket   --- 0.9735 2.726e+00 7.211e-02
## TVEL      None.Blanket.Few.Blanket   --- 0.9710 1.297e+01 3.759e-01
## ONOV      None.Blanket.Few.Blanket   --- 0.7161 4.183e+01 1.188e+01
## SUCT      None.Blanket.Few.Blanket   --- 0.6484 2.901e+01 1.020e+01
## Brachy    None.Blanket.Few.Blanket   --- 0.6273 1.689e+01 6.294e+00
## PLAG2     Few.Hummock.Many.Hummock   --- 0.7445 1.683e+01 4.300e+00
## Trhypch1  Many.Blanket.Few.Hummock   --- 0.8187 7.493e-01 1.358e-01
## LRUG      None.Blanket.Few.Blanket   +++ 0.8330 8.516e+00 5.100e+01
## Ceratoz3  None.Blanket.Few.Blanket   +++ 0.7209 7.098e+00 2.543e+01
## Lepidzts  Many.Blanket.Few.Hummock   +++ 1.0000 2.333e-09 8.547e-01
## Protopl   Many.Blanket.Few.Hummock   +++ 0.9598 7.695e-01 1.916e+01
## MPRO      Many.Blanket.Few.Hummock    ++ 0.7639 2.034e-01 8.614e-01
## Stgncrs2  Few.Hummock.Many.Hummock   +++ 0.9200 5.786e-03 7.230e-02
## Oppiminu  Few.Blanket.Many.Blanket   +++ 0.7000 2.243e+00 7.475e+00
## Miniglmn Many.Blanket.Many.Hummock   +++ 0.9649 2.716e-02 7.745e-01
## Trimalc2 None.Blanket.Many.Hummock   +++ 0.9871 6.359e-02 4.929e+00
## NCOR                  Few.Blanket    ++ 0.5949 4.238e+00 1.046e+01
## SSTR                  Few.Hummock   +++ 0.9617 1.561e-03 4.080e-02
## TVIE                 None.Blanket   +++ 0.7138 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
## Galumna1   42.750 1.0000
## HMIN2      87.196 1.0000
## PPEL        7.620 0.9359
## RARD       54.142 1.0000
## 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
##   0.580   0.023   0.607
```

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

```
##    user  system elapsed
##   1.430   0.062   1.500
```

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

```
##    user  system elapsed
##   0.577   0.026   0.607
```

```
## 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
##   0.009   0.001   2.198
```

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

```
##    user  system elapsed
##   0.583   0.172   0.421
```

3.4 Percentages

3.4.1 Dune data, cover type data

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

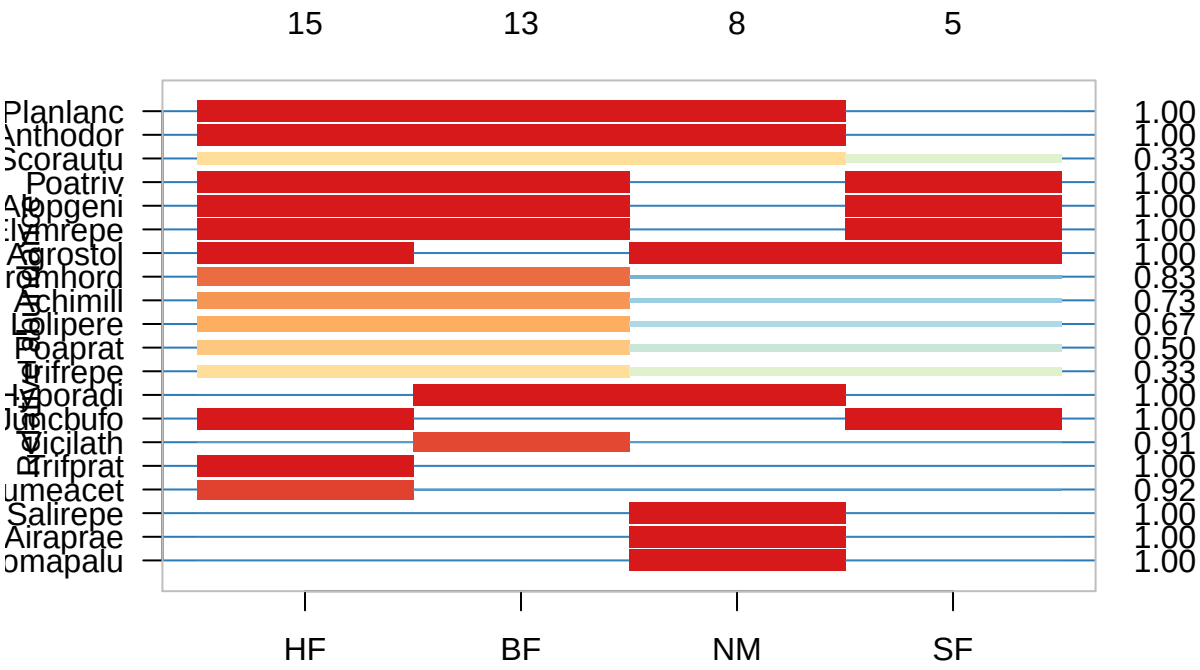
```
library(vegan)
data(dune)
data(dune.env)

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

```
## Multivariate opticut results, comb = rank, dist = ordered
##
## Call:
## opticut(formula = Dune ~ 1, strata = dune.env$Management, dist = "ordered")
##
##             split assoc      I      mu0    mu1 logLR      w
## Planlanc BF HF NM    ++ 0.5000 5.00e-01 1.0000 3.245 0.4406
## Anthodor BF HF NM    ++ 0.5000 5.00e-01 1.0000 2.657 0.7082
## Scorautu BF HF NM    ++ 0.5000 5.00e-01 1.0000 6.034 0.9175
## Poatriv  BF HF SF   +++ 0.5000 5.00e-01 1.0000 9.346 0.9827
## Elymrepe BF HF SF    ++ 0.5000 5.00e-01 1.0000 2.657 0.6848
## Lolipere BF HF SF    ++ 0.4786 5.00e-01 0.9590 4.351 0.6845
## Poaprat  BF HF SF    ++ 0.4724 5.00e-01 0.9476 4.309 0.7658
## Achimill    BF HF    ++ 0.4567 5.00e-01 0.9204 3.009 0.6036
## Trifrepe    BF HF    ++ 0.4549 5.00e-01 0.9173 3.457 0.5762
## Hyporadi    BF NM    ++ 0.5000 5.00e-01 1.0000 2.726 0.7053
## Juncbufo    HF SF    ++ 0.5000 5.00e-01 1.0000 2.798 0.7000
## Vicilath       BF    ++ 0.4873 5.00e-01 0.9752 3.024 0.5264
## Bromhord       BF    ++ 0.4844 5.00e-01 0.9697 2.741 0.4712
## Trifprat       HF    ++ 0.5000 5.00e-01 1.0000 5.089 0.8579
## Rumeacet       HF    ++ 0.4936 5.00e-01 0.9873 5.801 0.8744
## Comapalu       NM    ++ 1.0000 1.17e-09 0.3333 2.683 0.7516
## Salirepe       NM    ++ 0.5000 5.00e-01 1.0000 4.295 0.7984
## Airaprae       NM    ++ 0.5000 5.00e-01 1.0000 2.683 0.6520
## Alopgeni       SF    ++ 0.4724 5.00e-01 0.9476 4.135 0.4060
## Agrostol       SF    ++ 0.4627 5.00e-01 0.9306 3.382 0.5417
## 3 binary splits
## 10 species not shown
```

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

```
## Multivariate opticut results, comb = rank, dist = binomial
##
## Call:
## opticut(formula = Dune ~ 1, strata = dune.env$Management, dist = "binomial")
##
##             split assoc      I       mu0    mu1 logLR      w
## Planlanc BF HF NM    ++ 1.0000 8.647e-09 0.5000 3.245 0.6890
## Anthodor BF HF NM    ++ 1.0000 8.647e-09 0.4286 2.657 0.6314
## Scorautu BF HF NM    ++ 0.3333 6.667e-01 1.0000 2.683 0.7441
## Poatriv  BF HF SF   +++ 1.0000 3.181e-09 0.9286 9.346 0.7609
## Alopgeni BF HF SF    ++ 1.0000 8.647e-09 0.5714 3.900 0.4732
## Elymrepe BF HF SF    ++ 1.0000 8.647e-09 0.4286 2.657 0.6812
## Agrostol HF NM SF    ++ 1.0000 8.647e-09 0.5882 2.346 0.4403
## Bromhord    BF HF    ++ 0.8333 8.333e-02 0.5000 2.259 0.4345
## Achimill    BF HF    ++ 0.7333 1.667e-01 0.6250 2.250 0.6992
## Lolipere    BF HF    ++ 0.6667 3.333e-01 1.0000 5.822 0.8987
## Poaprat     BF HF    ++ 0.5000 5.000e-01 1.0000 3.900 0.7383
## Trifrepe    BF HF    ++ 0.3333 6.667e-01 1.0000 2.370 0.6700
## Hyporadi    BF NM    ++ 1.0000 1.170e-09 0.3333 2.726 0.7635
## Juncbufo    HF SF    ++ 1.0000 3.181e-09 0.3636 2.798 0.7960
## Vicilath       BF    ++ 0.9118 5.882e-02 0.6667 2.741 0.4650
## Trifprat       HF    ++ 1.0000 1.170e-09 0.6000 5.089 0.8579
## Rumeacet       HF    ++ 0.9167 6.667e-02 0.8000 5.071 0.7703
## Salirepe       NM    ++ 1.0000 1.170e-09 0.5000 4.295 0.9007
## Airaprae       NM    ++ 1.0000 1.170e-09 0.3333 2.683 0.7175
## Comapalu       NM    ++ 1.0000 1.170e-09 0.3333 2.683 0.7516
## 3 binary splits
## 10 species not shown
```

```r
plot(x)
```




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

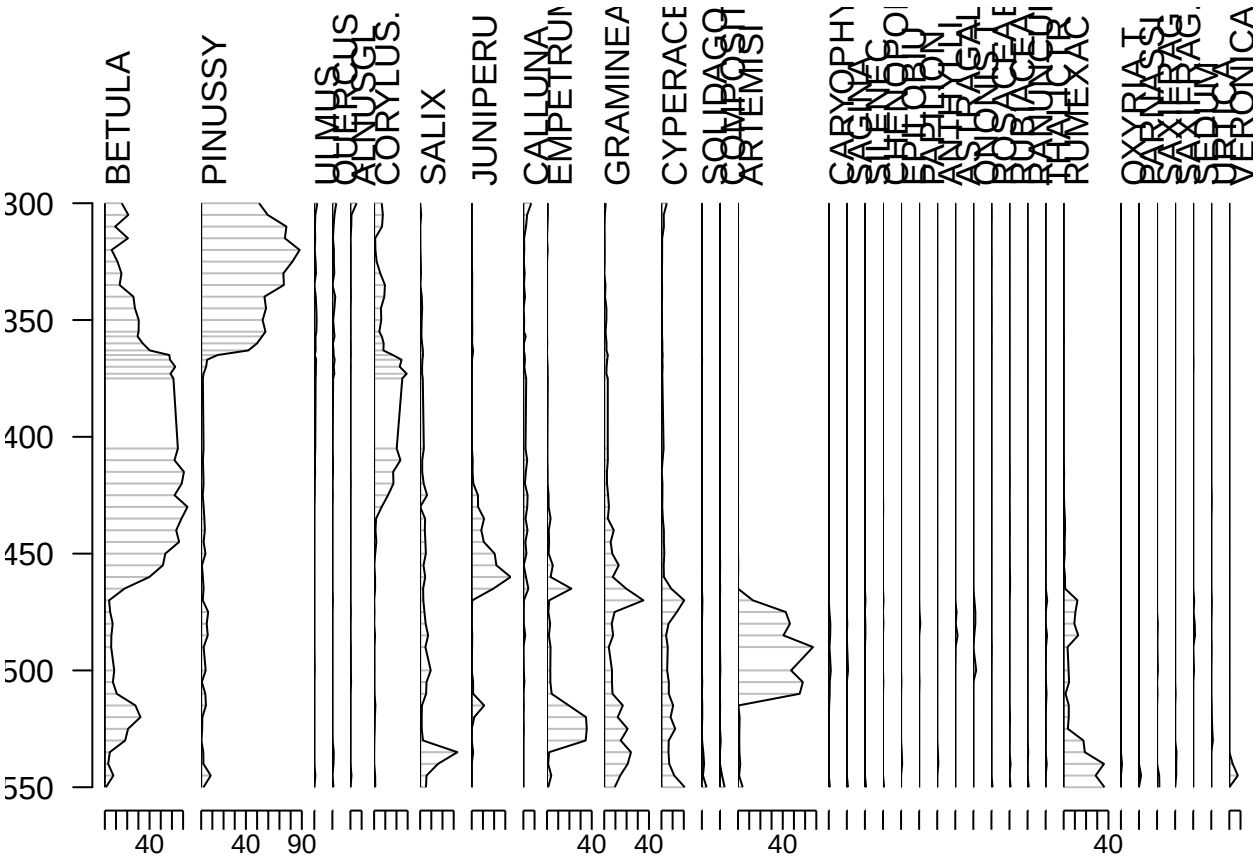
```
## Multivariate opticut results, comb = rank, dist = beta
##
## Call:
## opticut(formula = Dune ~ 1, strata = dune.env$Management, dist = "beta")
##
##             split assoc      I     mu0    mu1 logLR      w
## Scorautu BF HF NM    ++ 0.5325 0.17817 0.3811 5.074 0.8647
## Poatriv  BF HF SF    ++ 0.7561 0.12172 0.4991 7.301 0.8074
## Poaprat  BF HF SF    ++ 0.6127 0.13521 0.3491 4.391 0.4868
## Lolipere    BF HF    ++ 0.5935 0.21057 0.5181 4.104 0.5739
## Planlanc    BF HF    ++ 0.5340 0.12810 0.2749 2.467 0.5496
## Achimill    BF HF    ++ 0.5043 0.09444 0.1905 2.596 0.6056
## Trifrepe    BF HF    ++ 0.4954 0.20483 0.4059 3.395 0.6065
## Bromhord       BF    ++ 0.6103 0.10488 0.2691 2.535 0.6478
## Vicilath       BF    ++ 0.5491 0.05974 0.1325 4.369 0.9287
## Rumeacet       HF    ++ 0.7280 0.09043 0.3324 6.224 0.9885
## Trifprat       HF    ++ 0.6150 0.07273 0.1889 3.846 0.8910
## Salirepe       NM    ++ 0.5668 0.08105 0.1871 2.862 0.8470
## Alopgeni       SF    ++ 0.6567 0.15803 0.4603 4.225 0.8093
## Agrostol       SF    ++ 0.5757 0.20803 0.4903 3.096 0.7098
## 3 binary splits
## 16 species not shown
```

3.4.2 Stratigraphy example

```
library(rioja)
```

```
## This is rioja 0.9-5
```

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

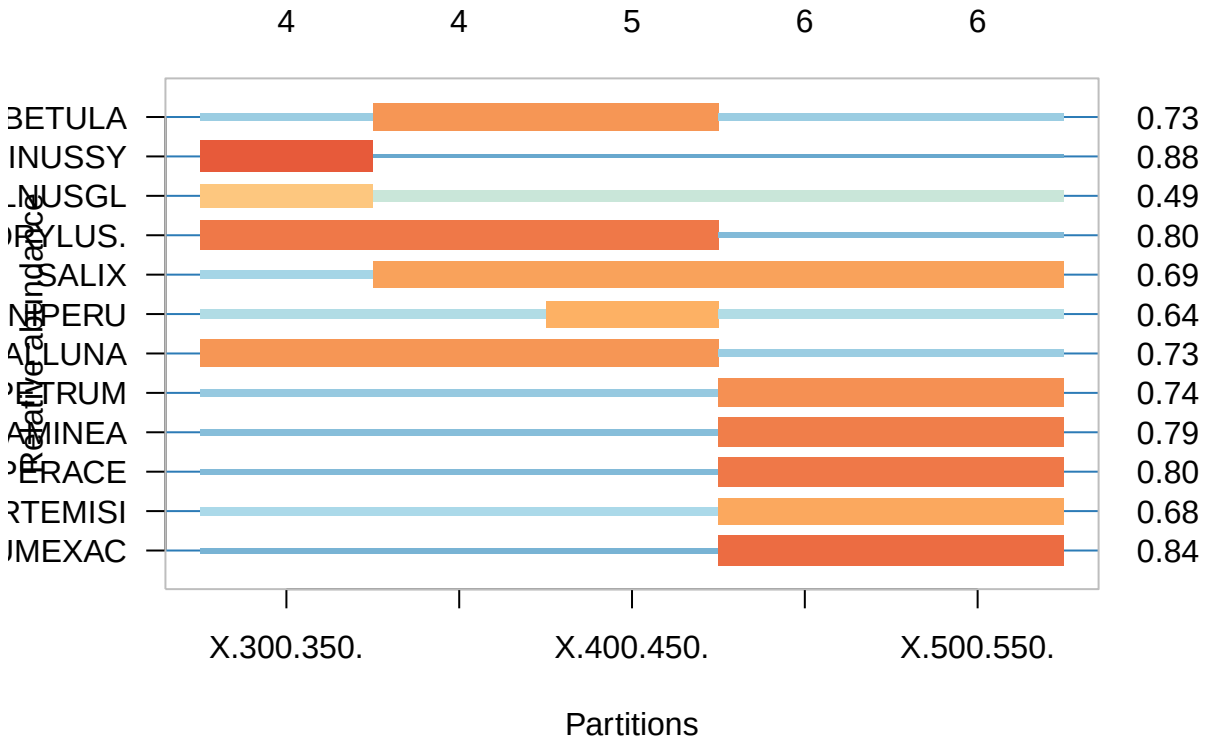



```
z <- as.factor(cut(aber$ages$Depth, 5))
ab <- as.matrix(aber$spec) / 100
ab[ab == 0] <- 0.0001
ab <- ab[,apply(ab, 2, max) > 0.05]

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

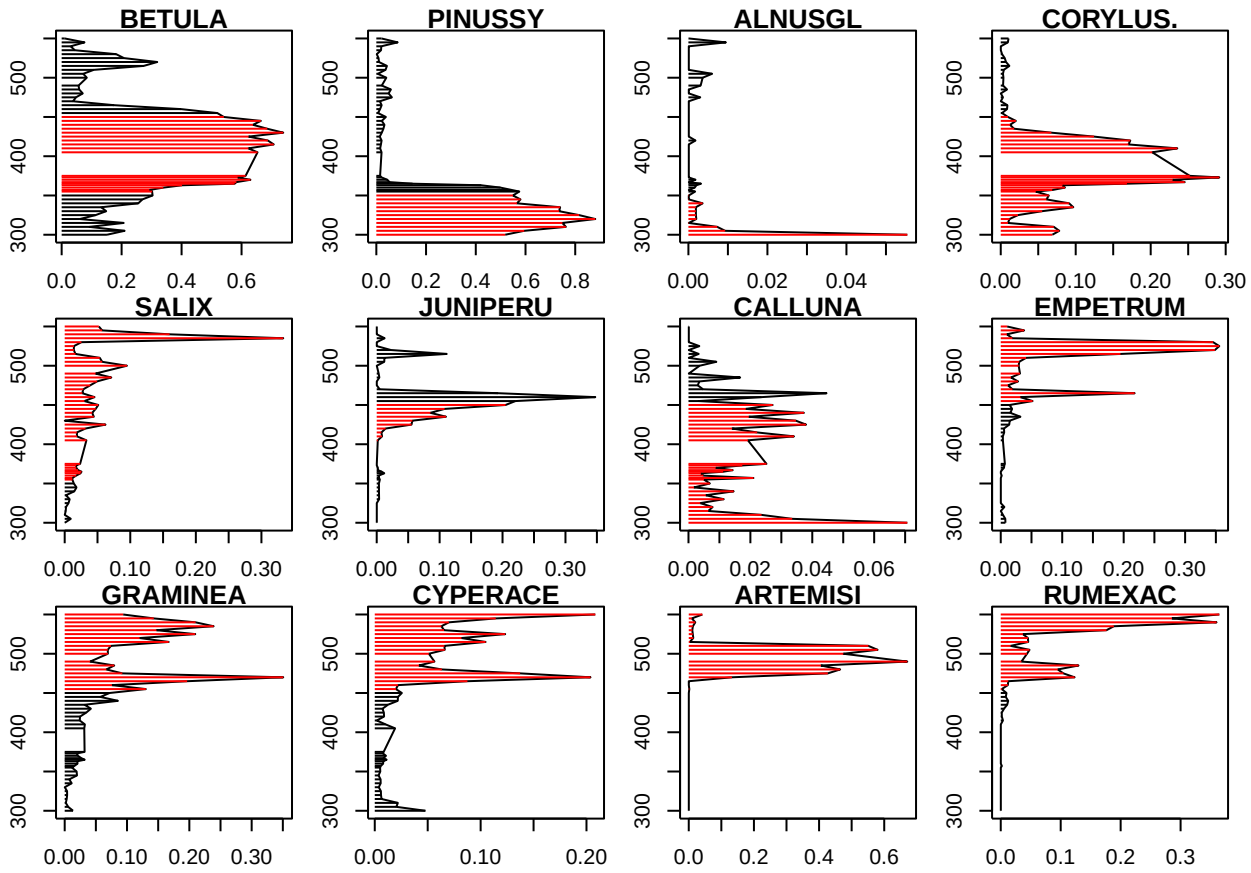
```
## Multivariate opticut results, comb = rank, dist = beta
##
## Call:
## opticut(formula = ab ~ 1, strata = z, dist = "beta", comb = "rank")
##
##                                              split assoc      I      mu0
```

```
## SALIX    X.350.400. X.400.450. X.450.500. X.500.550.   +++ 0.6860 0.014015
## CORYLUS.            X.300.350. X.350.400. X.400.450.   +++ 0.7996 0.019366
## CALLUNA             X.300.350. X.350.400. X.400.450.   +++ 0.7305 0.005234
## BETULA                         X.350.400. X.400.450.   +++ 0.7296 0.153662
## RUMEXAC                        X.450.500. X.500.550.   +++ 0.8357 0.015648
## CYPERACE                       X.450.500. X.500.550.   +++ 0.8043 0.015826
## GRAMINEA                       X.450.500. X.500.550.   +++ 0.7867 0.028003
## EMPETRUM                       X.450.500. X.500.550.   +++ 0.7380 0.020863
## ARTEMISI                       X.450.500. X.500.550.    ++ 0.6837 0.046111
## PINUSSY                                   X.300.350.   +++ 0.8757 0.083196
## ALNUSGL                                   X.300.350.    ++ 0.4940 0.002089
## JUNIPERU                                  X.400.450.    ++ 0.6440 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 aspecially related to covariates.

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

library(ResourceSelection)
```

```
## ResourceSelection 0.2-5   2015-11-06
```

```
## 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
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 = 0.2125; w = 0.59; H = 0.5162; logL_null = -9184
##
## Best supported models with logLR >= 2:
##       assoc      I mu0   mu1 logLR    w
## X3       ++ 0.2125   1 1.270 6.649 0.59
## X1 X3    ++ 0.2169   1 1.277 6.285 0.41
## 2 binary splits
```

```
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 = 0.129; w = 0.73; H = 0.6058; logL_null = -9169
##
## Best supported model with logLR >= 2:
##    assoc     I    mu0    mu1 logLR    w
## X3    ++ 0.129 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)
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 = 0.4023; w = 0.9985; H = 0.997; logL_null = -345.2
##
## Best supported models with logLR >= 2:
##     assoc      I   mu0   mu1  logLR         w
## 1 2   +++ 0.4023 1.480 2.476 13.582 0.9984969
## 1      ++ 0.3498 1.745 2.683  6.864 0.0012072
## 4      -- 0.3039 2.168 1.509  4.739 0.0001441
## 3      -- 0.3057 2.134 1.482  4.620 0.0001279
## 2      ++ 0.2210 1.858 2.386  2.813 0.0000210
## 7 binary splits (2 models not shown)
```

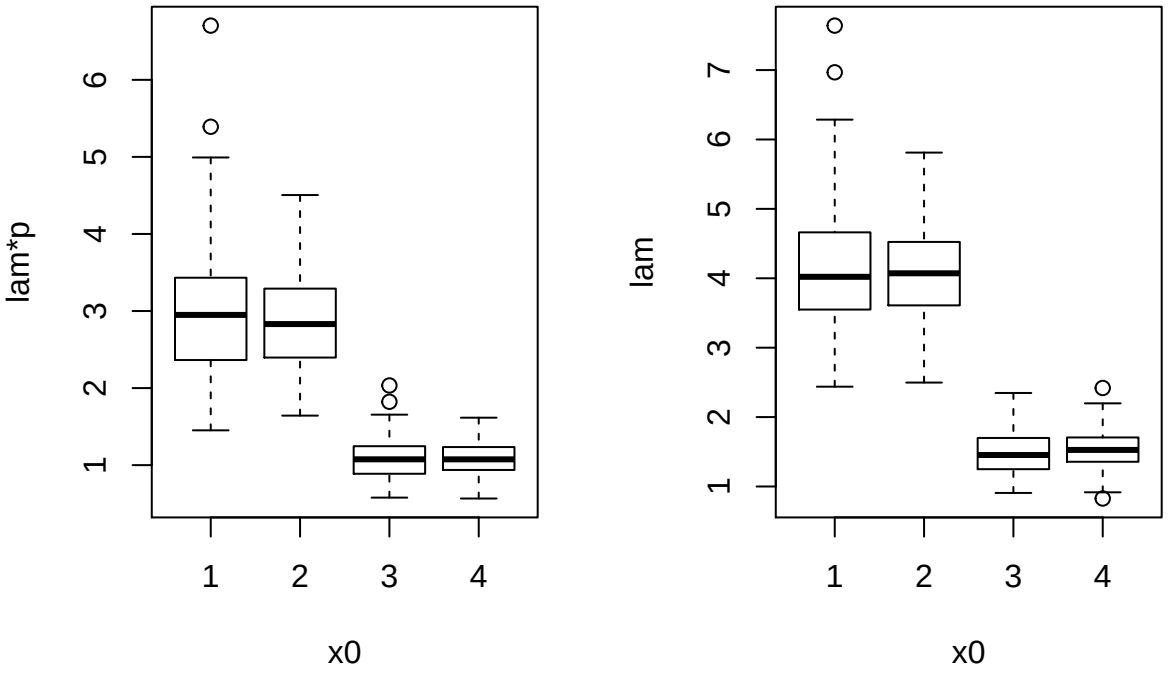
4.2 Imperfect detectability: N-mixture case

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:

```
library(detect)
```

```
## Loading required package: Formula
## Loading required package: stats4
## detect 0.3-2      2014-05-15
```

```
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 = 0.6432; w = 1; H = 1; logL_null = -930
##
## Best supported models with logLR >= -Inf:
##       assoc      I   mu0   mu1  logLR         w
## 1 2     +++ 0.6432 1.139 3.193 115.16 1.000e+00
## 1 2 4   +++ 0.5797 1.078 2.566  52.38 5.383e-28
## 2       +++ 0.4426 1.808 3.243  38.04 3.211e-34
## 3 binary splits
```

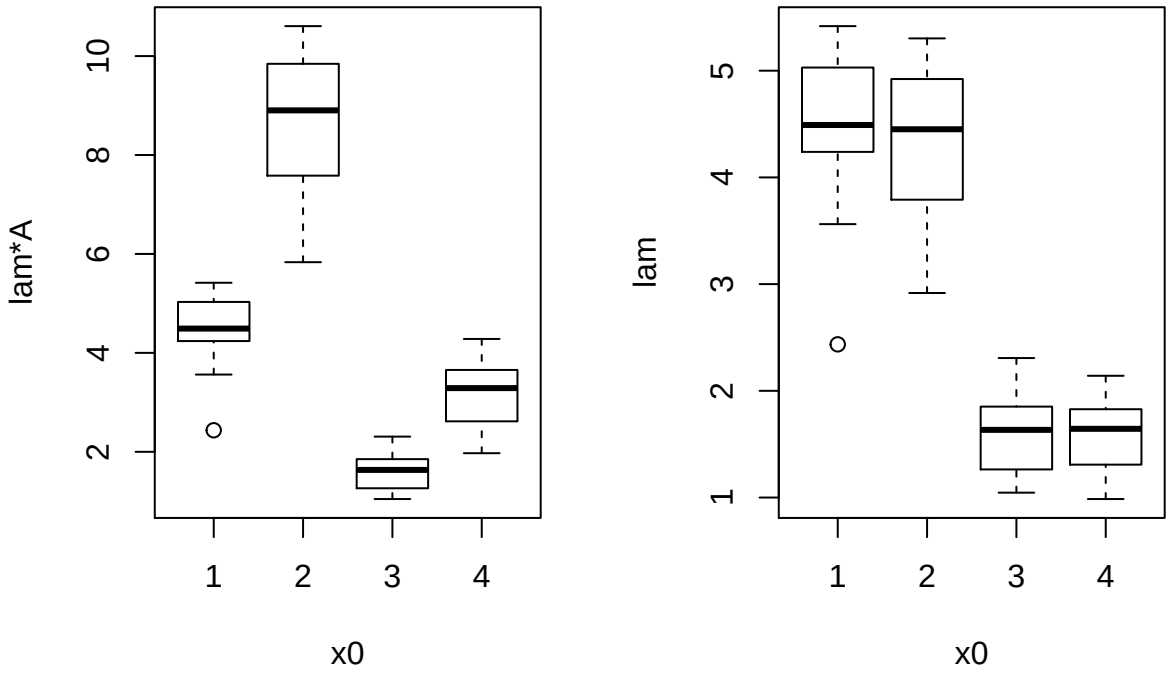
```
## N-mixture
print(opticut1(Y, X, as.factor(x0), dist=svfun), cut=-Inf)
```

```
## Univariate opticut results, comb = rank, dist = svfun
## I = 0.6553; w = 1; H = 0.9999; logL_null = -884.6
##
## Best supported models with logLR >= -Inf:
##       assoc      I   mu0   mu1  logLR         w
## 1 2     +++ 0.6553 2.409 6.989 26.239 1.000e+00
## 1 2 3   +++ 0.6017 1.936 4.859 15.787 2.888e-05
## 2        ++ 0.3968 4.142 6.866  3.284 1.073e-10
## 3 binary splits
```

4.3 Sampling error 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.

```r
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)

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 = 0.7005; w = 0.9895; H = 0.9792; logL_null = -154.2
##
## Best supported models with logLR >= 2:
##          assoc      I   mu0    mu1 logLR         w
## X2         +++ 0.7005 3.028 10.110 42.01 9.895e-01
## X1 X2      +++ 0.7064 2.192  7.464 37.46 1.049e-02
## X1 X2 X4   +++ 0.7135 1.766  6.164 24.77 3.243e-08
## 3 binary splits
```

```
## 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 = 0.6811; w = 1; H = 1; logL_null = -135.7
##
## Best supported models with logLR >= 2:
##          assoc      I   mu0   mu1 logLR         w
## X1 X2      +++ 0.6811 1.572 4.930 32.34 1.000e+00
## X1 X2 X3   +++ 0.6466 1.431 4.049 17.29 2.919e-07
## X2         +++ 0.5280 2.388 5.060 16.68 1.584e-07
## 3 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")
##
##           split assoc     I   mu0   mu1 logLR      w
## Species.1 X1 X2   +++ 0.583 1.819 4.361 12.46 0.9918
## 3 binary splits
```

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

```
##    Species.1
## X1         1
## X1         1
## X3         0
## X1         1
## X2         1
## X2         1
```

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

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

```
## $Species.1
##
## Call:  stats::glm(formula = Y ~ . - 1, family = poisson(link), 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).

```
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
##  X1 X2:5001   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
```

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

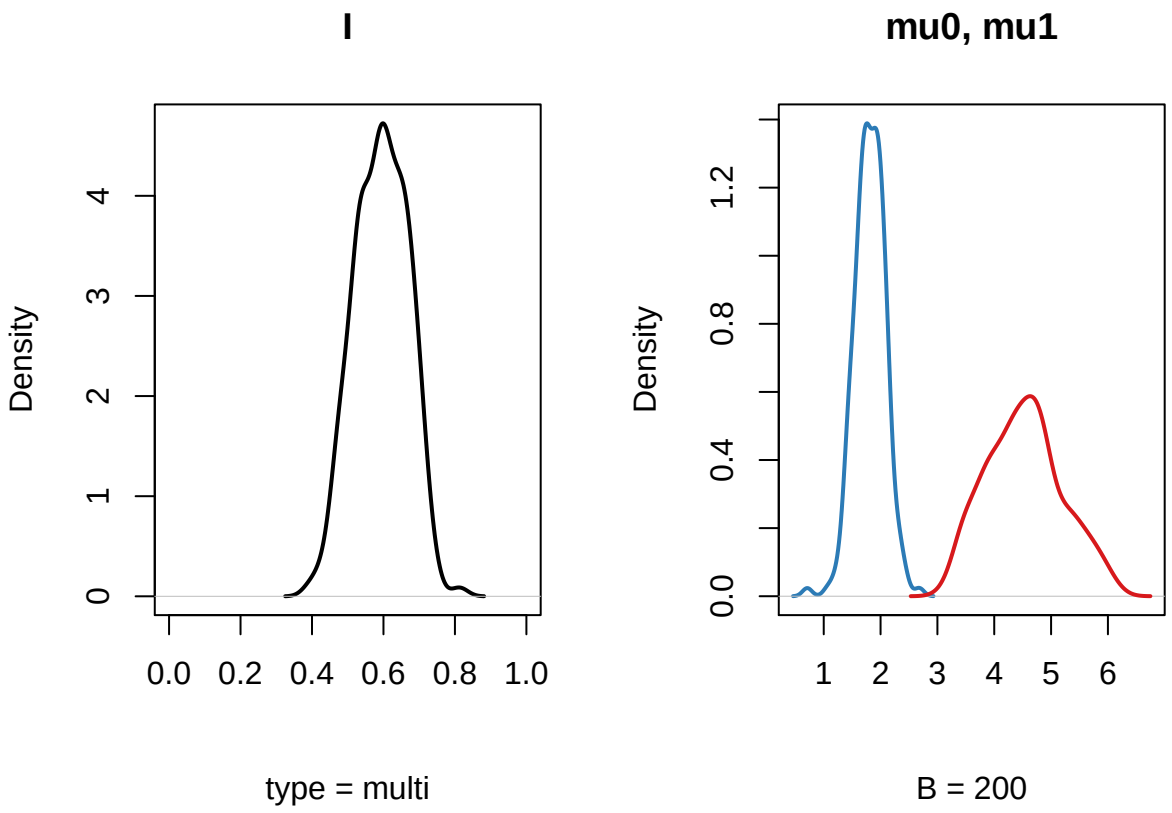
```
## Univariate opticut uncertainty results, type = boot, B = 200
##
##     best           I               mu0             mu1
##  X1 X2:201   Min.   :0.3206   Min.   :1.244   Min.   :3.178
```

```
##              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
```

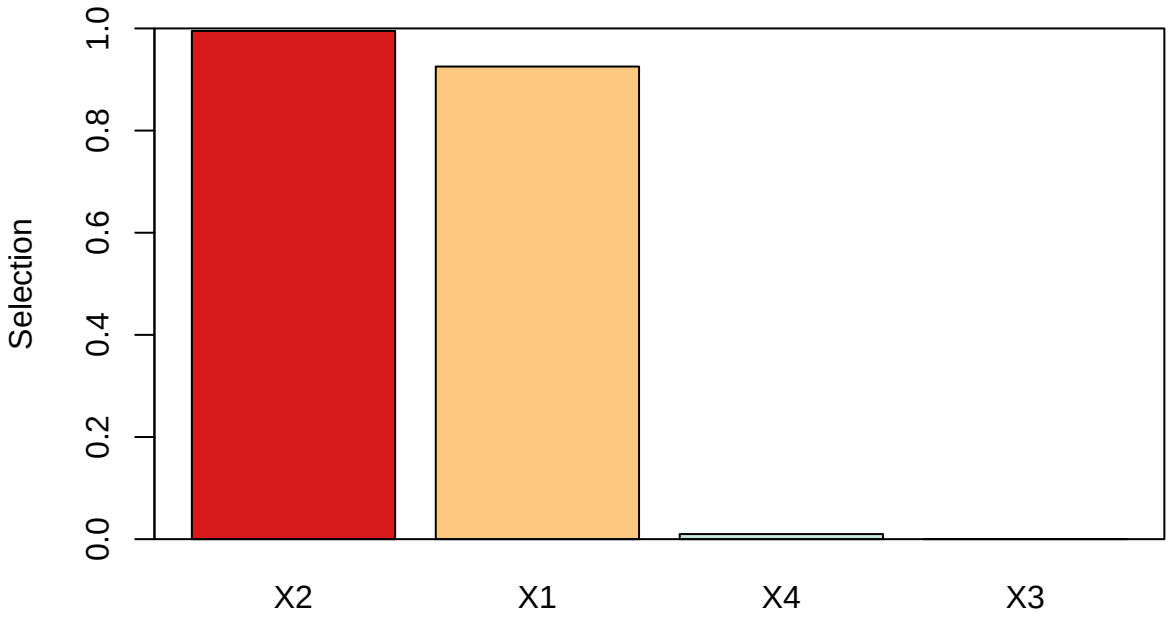
```
uc3$uncertainty[[1]]
```

```
## Univariate opticut uncertainty results, type = multi, B = 200
##
##        best           I               mu0              mu1
##  X1      :  1   Min.   :0.3940   Min.   :0.7104   Min.   :3.137
##  X1 X2   :183   1st Qu.:0.5365   1st Qu.:1.6341   1st Qu.:4.046
##  X1 X2 X4:  2   Median :0.5936   Median :1.8144   Median :4.532
##  X2      : 15   Mean   :0.5937   Mean   :1.8115   Mean   :4.530
##                 3rd Qu.:0.6514   3rd Qu.:1.9957   3rd Qu.:4.915
##                 Max.   :0.8127   Max.   :2.6809   Max.   :6.141
```

```
plot(uc3$uncertainty[[1]])
```




```
wplot(uc3$uncertainty[[1]])
```




```
## 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
##   0.099   0.001   0.101
```

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

```
##    user  system elapsed
##   0.009   0.002   1.270
```

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

```
##    user  system elapsed
##   3.340   0.098   3.653
```

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

```
##    user  system elapsed
##   0.010   0.001   2.232
```

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

```
##    user  system elapsed
##  16.853   0.472  18.224
```

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

```
##    user  system elapsed
##   0.014   0.001   8.129
```

```
stopCluster(cl)
```