Package ‘VLMC’

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alpha2int

'Single Character' <--> Integer Conversion for Discrete Data

Description

Simple conversion functions for discrete data (e.g., time series), between 0:k integers and single letter characters.

Usage

alpha2int(x, alpha)
int2alpha(i, alpha)

Arguments

x character vector of single letters.
alpha the alphabet, as one character string.
i integer vector of numbers in 0:k.

Value

alpha2int(x,*) returns an integer vector of the same length as x, consisting of values from 0:k where k + 1 is the length of the alphabet, nchar(alpha).
int2alpha(i,*) returns a vector of single letter character of the same length as i.

See Also

vlmc, and int2char() and its inverse, char2int(), both working with multi-character strings instead of vectors of single characters; further, alphabet.

Examples

alphabet <- "abcdefghijk"
(ch <- sample(letters[1:10], 30, replace = TRUE))
(ic <- alpha2int(ch, alphabet))
stopifnot(int2alpha(ic, alphabet) == ch)
Description

Return the alphabet in use, as a vector of “characters”.

Usage

alphabet(x, ...)
## S3 method for class 'vlmc'
alphabet(x, ...)

Arguments

x any R object, currently only available for vlmc ones.
...
potential further arguments passed to and from methods.

Value

a character vector, say r, with length equal to the alphabet size. Currently, typically all r[i] are strings of just one character.

See Also

alpha2int for conversion to and from integer codings.

Examples

data(bnrf1)
vb <- vlmc(bnrf1EB, cutoff = 5)
alphabet(vb) # i --> "a" "c" "g" "t"

as.dendrogram.vlmc Dendrogram Construction from VLMCs

Description

This is a method for the as.dendrogram generic function

Usage

## S3 method for class 'vlmc'
as.dendrogram(object, ...)

Arguments

object a vlmc object.

... further arguments passed to and from methods.

Value

An object of class dendrogram, i.e. a nested list described on that page.

See Also

as.dendrogram, plot.dendrogram.

Examples

data(presidents)
dpr <- factor(cut(presidents, c(0,45,70,100)), exclude=FALSE, NA = 4th level)
(vlmc.pres <- vlmc(dpr))
draw(vlmc.pres)
dv <- as.dendrogram(vlmc.pres)
str(dv)
str(unclass(dv))

plot(dv, type = "tr", nodePar = list(pch=c(1,16), cex = 1.5))

## Artificial example
f1 <- c(1,0,0,0) ; f2 <- rep(1:0, 2)
dt1 <- c(f1,f1,f2,f1,f2,f1)
(vlmc.dt1c01 <- vlmc(dts = dt1, cutoff.prune = 0.1))
(dvlmc <- as.dendrogram(vlmc.dt1c01))
str(dvlmc)

## not so useful:
plot(dvlmc, nodePar= list(pch=c(1,16)))

## complete disaster:
plot(dvlmc, type ="tr", nodePar= list(pch=c(1,16)))

## but this is not (yet) so much better (want the same angles to left
## and right!!
plot(dvlmc, type ="tr", nodePar = list(pch=c(1,16)), center=TRUE,
    main = format(vlmc.dt1c01$call))
mtext(paste("dt1 =", gsub(" ",","deparse(dt1,width=100))))
bnrf1

Description

Two gene DNA data “discrete time series”,

bnrf1EB the BNRF1 gene from the Epstein-Barr virus,
bnrf1HV the BNRF1 gene from the herpes virus.

Usage

data(bnrf1)

Format

The EB sequence is of length 3954, whereas the HV has 3741 nucleotides. Both are R factors with the four levels c("a", "c", "g", "t").

Author(s)

Martin Maechler (packaging for R).

Source

See the references, data are online at http://anson.ucdavis.edu/~shumway/hsa.html

References


Examples

data(bnrf1)
bnrf1EB[1:500]
table(bnrf1EB)
table(bnrf1HV)
n <- length(bnrf1HV)
table(t = bnrf1HV[-1], "t-1" = bnrf1HV[-n])

plot(as.integer(bnrf1EB[1:500]), type = "b")

## Simplistic gene matching:
percent.eq <- sapply(0:200,
    function(i) 100 * sum(bnrf1EB[1+i:(n+i)] == bnrf1HV))/n
plot.ts(percent.eq)
deviance.vlmc  

*Compute the Deviance of a Fitted VLMC Object*

**Description**

Compute the Deviance, i.e., \(-2 \log \text{[likelihood(*)]}\) of a fitted VLMC object. The log-likelihood is also known as “entropy”.

**Usage**

```r
## S3 method for class 'vlmc'
deviance(object, ...) 
```

**Arguments**

- `object` typically the result of `vlmc(..)`.
- `...` possibly further arguments (none at the moment).

**Value**

A number, the deviance, i.e., \(-2 \log \text{likelihood(*)}\). where the log.likelihood is really what we currently have as `entropy()`.

**Author(s)**

Martin Maechler

**See Also**

`entropy`, `vlmc`, `residuals.vlmc`

**Examples**

```r
e
devianceR <- function(object)
{
  dn <- dimnames(pr <- predict(object))
  -2 * sum(log(pr[cbind(2:nrow(pr), match(dn[[1]][[1]], dn[[2]])])))
}
all.equal(deviance(vlmc.pres), devianceR(vlmc.pres), tol = 1e-14)
```
Description

Draws a vlmc object, typically the result of vlmc(.), to the R console, using one line per node.

Usage

draw(x, ...)  # S3 method for class 'vlmc'
draw(x, kind = 3, flag = TRUE, show.hidden = 0,
    cumulative = TRUE, delta = cumulative, debug = FALSE, ...)

Arguments

x  typically the result of vlmc(.).
kind  integer code for the “kind of drawing”, in {0,1,2,3}.
flag  logical; ..
show.hidden  integer code; if not 0, give some indications about hidden (final) nodes ..... 
cumulative  logical indicating if the cumulative counts should be shown for nonterminal nodes; the ‘delta’s can only be computed from the cumulative counts, i.e., cumulative = FALSE should be used only by the knowing one.
delta  logical indicating if delta, i.e. \( \delta(n, p(n)) \) should be computed and printed for each (non-root) node \( n \) with parent \( p(n) \). Note that this does not really make sense when cumulative = FALSE.
debug  logical; if TRUE, some extraneous progress information is printed to the R console.
...  (potentially more arguments)

Details

Note that the counts internally are stored “non-cumulatively”, i.e., as difference counts which is useful for likelihood (ratio) computations. In the internal C code, the difference counts are originally computed by the comp_difference() function after tree generation. draw(*, cumulative = TRUE) internally calls the C function cumulate() for the cumulative sums.

Value

nothing is returned.
Author(s)
Martin Maechler

See Also
vlmc.

Examples

```r
example(vlmc)
draw(vlmc.dt1c01)
draw(vlmc.dt1c01, flag = FALSE)
draw(vlmc.dt1c01, kind = 1)
draw(vlmc.dt1)
draw(vlmc.dt1, show = 3)
draw(vlmc.dt1, cumulative = FALSE)
```

d2ctxt <- VLMC Context ID Conversion

Description
Utility for converting a vlmc state ID to the corresponding context. Of rare interest to the average user.

Usage

```r
d2ctxt(id, m=nchar(alpha), alpha=NULL)
```

Arguments

- `id` integer, a context ID such as optionally returned by `predict.vlmc`.
- `m` integer, the alphabet length. Defaults to `nchar(alpha)`, the alphabet size if that is given.
- `alpha` alphabet string

Value

A list (if `alpha` is not specified) or character vector of the same length as `id`, giving the context (as integer vector or single string) of the corresponding `id`

See Also

`predict.vlmc(*, type = "ID")`.

Examples

```r
id2ctxt(c(2,3,5,9), alpha = "Ab")
str(id2ctxt(c(2,3,5,9), 2))
```
**int2char**

*Character - Integer Conversion*

**Description**

Simple conversion utilities for character to integer conversion and vice versa.

**Usage**

```
int2char(i, alpha)
char2int(x, alpha)
```

**Arguments**

- `i` : integer vectors, typically in 0:m when `alpha` has `m + 1` letters.
- `alpha` : character string with several letters, representing the alphabet.
- `x` : character string, typically with letters from `alpha`.

**Value**

- `int2char()` gives a string (length 1 character) with as many characters as `length(i)`, by 0-indexing into the alphabet `alpha`.
- `char2int()` gives an integer vector of length `nchar(x)` of integer codes according to `alpha` (starting at 0!).

**See Also**

`int2alpha()` (which is used by `int2char`) and its inverse, `int2alpha()`, both working with vectors of *single* characters instead of multi-character strings.

**Examples**

```
char2int("vlmc", paste(letters, collapse=""))
int2char(c(0:3, 3:1), "abcd")
int2char(c(1:0,3,3), "abc")  # to eat ;-)"
Description

Compute the log-likelihood or “entropy” of a fitted \texttt{vlmc} object. This is a method for the generic \texttt{logLik}.

Usage

\begin{verbatim}
entropy(object)
## S3 method for class 'vlmc'
logLik(object, ...)
entropy2(ivlmc1, ivlmc2, alpha.len = ivlmc1[1])
\end{verbatim}

Arguments

- \texttt{object} typically the result of \texttt{vlmc} (..).
- \texttt{ivlmc1, ivlmc2} two \texttt{vlmc} (sub) trees, see \texttt{vlmc}.
- \texttt{alpha.len} positive integer specifying the alphabet length.
- ... (potentially more arguments; required by generic)

Details

The \texttt{logLik.vlmc()} method computes the log likelihood for a fitted \texttt{vlmc} object. \texttt{entropy} is an alias for \texttt{logLik} for reasons of back compatibility.

\texttt{entropy2} is less clear ... ... \[\text{[[ FIXME ]]}\] ...

Value

a negative number, in some contexts typically further divided by $\log(x$\$alpha.len)$.

Note that the \texttt{logLik} method is used by the default method of the \texttt{AIC} generic function (from R version 1.4.x), and hence provides \texttt{AIC(object)} for \texttt{vlmc} objects. Also, since \texttt{vlmc} version 1.3-13, \texttt{BIC()} works as well.

Author(s)

Martin Maechler

See Also

\texttt{deviance.vlmc, vlmc, draw.vlmc}. 
Examples

```r
dd <- cumsum(rpois(999, 1.5)) %% 10
(vd <- vlmc(dd))
entropy(vd)# the bare number
logLik(vd)
logLik(vdL <- vlmc(dd, cutoff = 3))
entropy2(vdL$vlmc.vec,
  vdl$vlmc.vec)
```

```r
## AIC model selection:
f1 <- c(1,0,0,0) # as in example(vlmc)
f2 <- rep(1:0,2)
(dt1 <- c(f1,f1,f1,f1,f2,f2,f1))
AIC(print(vlmc(dt1)))
AIC(print(vlmc(dt1, cutoff = 2.6)))
AIC(print(vlmc(dt1, cutoff = 0.4)))## these two differ `not really'
AIC(print(vlmc(dt1, cutoff = 0.1)))
```

```r
## Show how to compute it from the fitted conditional probabilities :
logLikR <- function(x) {
  dn <- dimnames(pr <- predict(x))
  sum(log(pr[cbind(2:nrow(pr), match(dn[[1]][-1], dn[[2]]))]))
}
all.equal( logLikR(vd),
  c(logLik(vd), tol=1e-10) # TRUE, they do the same
```

```r
## Compare different ones: [cheap example]:
example(draw)
for(n in ls()) {
  if(is.vlmc(get(n))) {
    vv <- get(n)
    cat(n,":",formatC(logLik(vv) / log(vv$alpha.len),
                        format= "f", wid=10),"\n")
  }
}
```

---

**OZrain**

*Daily Rainfall in Melbourne, Australia, 1981-1990*

---

**Description**

Amount of daily rainfall in Melbourne, Australia, 1981-1990, measured in millimeters. The amounts are integers with many zeros and three days of more than 500mm rain.

**Usage**

data(OZrain)
predict.vlmc

Format
A time-series of length 3653 with the amount of daily rainfall in mm. Because of the two leap years 1984 and '88, we have constructed it with `ts(*, start=1981, frequency=365.25, end = 1981+ (3653 - 1)/365.25)`.

Note
There must be one extra observation since for the ten years with two leap years, there are only 3652 days. In 61 out of 100 days, there’s no rain.

Source

Examples
```r
data(OZrain)
(n <- length(OZrain)) ## should be 1 more than
ISOdate(1990,12,31) - ISOdate(1981,1,1)## but it's 2 ..

has.rain <- OZrain > 0

summary(OZrain[has.rain])# Median = 18, Q3 = 50
table(rain01 <- as.integer(has.rain))
table(rain4c <- cut(OZrain, c(-.1, 0.5, 18.5, 50.1, 1000)))

AIC(v1 <- vlmc(rain01))## cutoff = 1.92
AIC(v00 <- vlmc(rain01, cut = 1.4))
AIC(v0 <- vlmc(rain01, cut = 1.5))

hist(OZrain)
hist(OZrain, breaks = c(0,1,5,10,50,1000), xlim = c(0,100))

plot(OZrain, main = "Rainfall 1981-1990 in Melbourne")
plot(OZrain, log="y", main = "Non-0 Rainfall [LOG scale]")

lOZ <- lowess(log10(OZrain[has.rain]), f=.05)
lines(time(OZrain)[has.rain], 10^lOZ$y, col = 2, lwd = 2)
```

---

*predict.vlmc Prediction of VLMC for (new) Series*
Description

Compute predictions on a fitted VLMC object for each (but the first) element of another discrete time series. Computes by default a matrix of prediction probabilities. The argument type allows other predictions such as the most probable "class" or "response", the context length (tree "depth"), or an "ID" of the corresponding context.

Usage

```r
## S3 method for class 'vlmc'
predict(object, newdata,
        type = c("probs", "class", "response", "id.node", "depth", "ALL"),
        se.fit = FALSE,
        allow.subset = TRUE, check.alphabet = TRUE,
        ...)  
## S3 method for class 'vlmc'
fitted(object, ...)  
```

Arguments

- `object`: typically the result of `vlmc(.)`.
- `newdata`: a discrete “time series”, a numeric, character or factor, as the dts argument of `vlmc(.)`.
- `type`: character indicating the type of prediction required, options given in the Usage section above, see also the Value section below. The default "probs" returns a matrix of prediction probabilities, whereas "class" or "response" give the corresponding most probable class. The value of this argument can be abbreviated.
- `se.fit`: a switch indicating if standard errors are required. — NOT YET supported —.
- `allow.subset`: logical; if TRUE, newdata may not have all different “alphabet letters” used in x.
- `check.alphabet`: logical; if TRUE, consistency of newdata’s alphabet with those of x is checked.
- `...`: (potentially further arguments) required by generic.

Value

Depending on the type argument,

- "probs": an \( n \times m \) matrix \( \mathbf{p}_\text{m} \) of (prediction) probabilities, i.e., all the rows of \( \mathbf{p}_\text{m} \) sum to 1. \( \mathbf{p}_\text{m}[i,k] \) is \( \hat{P}[Y_i = k|Y_{i-1},...] \) (and is therefore \( \text{NA} \) for \( i=1 \)). The \text{dimnames} of \( \mathbf{p}_\text{m} \) are the values of newdata[] and the alphabet letters k.

- "class", "response": the corresponding most probable value of \( Y[\] \); as factor for "class" and as integer in \( \Theta: (m-1) \) for type = "response". If there is more than one most probable value, the first one is chosen.

- "id.node": an (integer) “ID” of the current context (= node of the tree represented VLMC).
The context length, i.e., the depth of the Markov chain, at the current observation (of newdata).

An object of class "predict.vlmc", a list with the following components,

- **ID** integer vector as for type = "id.node",
- **probs** prediction probability matrix, as above,
- **flags** integer vector, non-zero for particular states only, rather for debugging.
- **ctxt** character, ctxt[i] a string giving the context (backwards) for newdata[i], using alphabet letters.
- **fitted** character with fitted values, i.e., the alphabet letter with the highest probability, using max.col where ties are broken at random.
- **alpha, alpha.len** the alphabet (single string) and its length.

Note

The predict method and its possible arguments may still be developed, and we are considering to return the marginal probabilities instead of NA for the first value(s).

The print method print.predict.vlmc uses fractions from package MASS to display the probabilities \( P(X = j) \), for \( j \in \{0, 1, \ldots\} \), as these are rational numbers, shown as fractions of integers.

See Also

vlmc and residuals.vlmc. For simulation, simulate.vlmc.

Examples

```r
f1 <- c(1,0,0,0)
f2 <- rep(1:0,2)
(dt2 <- rep(c(f1,f1,f1,f1,f2,f2,f2,f1),2))

(vlmc.dt2c15 <- vlmc(dt2, cutoff = 1.5))
draw(vlmc.dt2c15)

## Fitted Values:
all.equal(predict(vlmc.dt2c15, dt2), predict(vlmc.dt2c15))
(pa2c15 <- predict(vlmc.dt2c15, type = "ALL"))

## Depth = context length ([1] : NA):
stopifnot(nchar(pa2c15 $ ctxt)[-1] ==
    predict(vlmc.dt2c15, type = "depth")[-1])
same <- (ff1 <- pa2c15 $ fitted) ==
    (ff2 <- int2alpha(predict(vlmc.dt2c15, type = "response"), alpha="01"))
which(!same) #-> some are different, since max.col() breaks ties at random!

ndt2 <- c(rep(0,6),f1,f1,f2)
predict(vlmc.dt2c15, ndt2, "ALL")
```
(newdt2 <- sample(dt2, 17))
pm <- predict(vlmc.dt2c15, newdt2, allow.subset = TRUE)
summary(apply(pm, 1, sum))# all 1
predict(vlmc.dt2c15, newdt2, type = "ALL")
data(bnrf1)
(vbnrf <- vlmc(bnrf1EB))
(pA <- predict(vbnrf, bnrf1EB[1:24], type = "ALL"))
pc <- predict(vbnrf, bnrf1EB[1:24], type = "class")
pr <- predict(vbnrf, bnrf1EB[1:24], type = "resp")
stopifnot(as.integer (pc[-1]) == 1 + pr[-1],
          as.character(pc[-1]) == strsplit(vbnrf$alpha,NUL$)[1][1 + pr[-1]])

##-- Example of a "perfect" fit -- just for illustration:
##   the default, thresh = 2 doesn't fit perfectly(i=38)
(vlmc.dt2c0th1 <- vlmc(dt2, cutoff = 0, thresh = 1))

## "Fitted" = "Data" (but the first which can't be predicted):
stopifnot(dt2[-1] == predict(vlmc.dt2c0th1,type = "response")[-1])

prt.vvec

Recursively Print the VLMC Result Vector

Description

This is an auxiliary function which recursively displays (prints) the integer result vector of a vlmc fit.

Usage

prt.vvec(v, nalph, pad=" ")

Arguments

v typically x $ vlmc.vec[-1] where x is the result of vlmc(*).
nalph alphabet size; typically x $ vlmc.vec[1].
pad character, to be used for padding paste(*, collapse=pad).

See Also

summary.vlmc which uses prt.vvec.

Examples

eexample(vlmc)
str(vv <- vlmc.dt1$vlmc)
prt.vvec(vv[-1], n = 2)
prt.vvec(vv[-1], n = 2, pad = " | ")
RCplot

Residuals vs Context plot

Description

Plots the residuals of a fitted VLMC model against the contexts, i.e., produces a boxplot of residuals for all contexts used in the model fit.

This has proven to be useful function, and the many optional arguments allow quite a bit of customization. However, the current implementation is somewhat experimental and the defaults have been chosen from only a few examples.

Usage

RCplot(x, r2 = residuals(x, "deviance")^2,
       alphabet = x$alpha, lab.horiz = k <= 20,
       do.call = TRUE,
       cex.axis = if (k <= 20) 1 else if (k <= 40) 0.8 else 0.6,
       y.fact = if (.Device == "postscript") 1.2 else 0.75,
       col = "gray70", xlab = "Context", main = NULL,
       med.pars = list(col = "red", pch = 12, cex = 1.25 * cex.axis),
       ylim = range(0, r2, finite = TRUE),
       ...
)

Arguments

x an R object of class v1mc.

r2 numeric vector, by default of squared deviance residuals of x, but conceptually any (typically non-negative) vector of the appropriate length.

alphabet the alphabet to use for labeling the contexts, via id2ctx.

lab.horiz logical indicating if the context labels should be written horizontally or vertically.

do.call logical indicating if the v1mc call should be put as subtitle.

cex.axis the character expansion for axis labeling, see also par. The default is only approximately good.

y.fact numeric factor for expanding the space to use for the context labels (when lab.horiz is false).

col color used for filling the boxes.

xlab x axis label (with default).

main main title to be used, NULL entailing a sensible default.

med.pars graphical parameters to be used for coding of medians that are almost 0.

ylim y range limits for plotting.

... further arguments to be passed to plot().
Value

*Invisibly*, a list with components

- **k** the number of contexts (and hence box plots) used.
- **fID** a factor (as used in the internal call to `plot.factor`).
- **rp** a list as resulting from the above call to `plot.factor()`.

Author(s)

Martin Maechler

References


See Also

`summary.vlmc` for other properties of a VLMC model.

Examples

```r
eexample(vlmc)
RCplot(vlmc.pres)
RCplot(vlmc.dt1e01)## << almost perfect fit (0 resid)
```

---

```r
residuals.vlmc  # Compute Residuals of a Fitted VLMC Object

Description

Compute residuals of a fitted `vlmc` object.

This is yet a matter of research and may change in the future.

Usage

```r
## S3 method for class 'vlmc'
residuals(object, 
    type = c("classwise", 
             "deviance", "pearson", "working", "response", "partial"),
    y = object$y, ...)
```
Arguments

object

typically the result of \texttt{vlmc}(..).

type

The type of residuals to compute, defaults to "classwise" which returns an \( n \times m \) matrix, see below. The other types only make sense when the discrete values of \( y \) are ordered which always includes the binary case (\( m = 2 \)). The "deviance" residuals \( r \) are defined similarly as for logistic regression, see below.

"pearson", "working" and "response" are currently identical and give the difference of the underlying integer code (of the discrete data).

\textbf{Note} that "partial" residuals are not yet defined!

\( y \)

\( y \) discrete time series with respect to which the residuals are to be computed.

\ldots

possibly further arguments (none at the moment).

Value

If \( \text{type} = "\text{classwise}" \) (the default), a numeric matrix of dimension \( n \times m \) of values \( I_{i,j} - p_{i,j} \) where the indicator \( I_{i,j} \) is 1 iff \( y[i] = a[j] \) and \( a \) is the alphabet (or levels) of \( y \), and \( p_{i,j} \) are the elements of the estimated (1-step ahead) predicted probabilities, \( p \leftarrow \text{predict}(\text{object}) \). Hence, for each \( i \), the only positive residual stands for the observed class.

For all other types, the result is a numeric vector of the length of the original time-series (with first element NA).

For \( \text{type} = "\text{deviance}" \), \( r_i = \pm \sqrt{-2 \log(P_i)} \) where \( P_i \) is the predicted probability for the \( i \)-th observation which is the same as \( p_i, y_i \) above (now assuming \( y_i \in \{1, 2, \ldots, m\} \)). The sum of the squared deviance residuals is the deviance of the fitted model.

Author(s)

Martin Maechler

See Also

\texttt{vlmc}, \texttt{deviance.vlmc}, and \texttt{RCplot} for a novel residual plot.

Examples

def example(vlmc)
    rp <- residuals(vlmc.pres)
    stopifnot(all(abs(apply(rp[-1,],1,sum)) < 1e-15))
    matplot(seq(presidents), rp, ylab = "residuals", type="l")
    ## ``Tukey-Anscombe'' (the following is first stab at plot method):
    matplot(fitted(vlmc.pres), rp, ylab = "residuals", xaxt = "n",
            type="b", pch=vlmc.pres$alpha)
    axis(1, at = 0:(vlmc.pres$alpha.len-1),
         labels = strsplit(vlmc.pres$alpha,"\"\")[[1]])

    summary(rd <- residuals(vlmc.pres, type = "dev"))
    rd[1:7]
    ## sum of squared dev.residuals == deviance :
**Description**

Simulate from fitted VLMC model – basis of the VLMC bootstrap

**Usage**

```r
## S3 method for class 'vlmc'
simulate(object, nsim = 1, seed = NULL, n,
    n.start = 64 * object$size[["context"]],
    integer.return = FALSE, keep.RSeed = TRUE, ...)
```

**Arguments**

- `object` Typically the result of `vlmc(.)`.
- `nsim, n` non-negative integer, giving the length of the result. Note that `n` is deprecated and just there for back compatibility.
- `seed` random seed initializer; see `simulate`.
- `n.start` the number of initial values to be discarded (because of initial effects).
- `integer.return` logical: if TRUE, the result will be an `integer` vector with values in `0:(k-1)`; otherwise the resulting vector consists of letters from the alphabet `x$alpha`.
- `keep.RSeed` logical indicating if the seed should be stored with the result (as ‘required’ by the generic `simulate`). Only set this FALSE with good reasons (back compatibility).
- `...` (potentially further arguments for other `simulate` methods.

**Details**

The `.Random.seed` is used and updated as with other random number generation routines such as `rbinom`.

Note that if you want to simulate from a given start sequence `x0`, you’d use `predict.vlmc(x, x0, type= "response")` — actually not quite yet.

**Value**

A "simulate.vlmc" object, basically a vector of length `nsim`. Either `integer` or `character`, depending on the `integer.return` argument, see above. Further, if `keep.RSeed` was true (as by default), a "seed" attribute with the random seed at the start of the simulation, for reproducibility.
Author(s)

Martin Maechler

See Also

vlmc and predict.vlm.

Examples

e(x) <- example(vlm)

simulate(vlm.dtl, 100)
simulate(vlm.dtlc01, 100, int = TRUE)
# n.start = 0: 1st few observations will resemble the data
simulate(vlm.dtlc01, 20, n.start=0, int = TRUE)

summary.vlm

Description

Compute (and print) a summary of a vlm object which is typically the result of vlm(...).

Usage

## S3 method for class 'vlmc'
summary(object, ...)
## S3 method for class 'summary.vlm'
print(x, digits = getOption("digits"),
     vvec.printing = FALSE, ...)

Arguments

object

an R object of class vlm.

x

an R object of class summary.vlm.

digits

integer giving the number of significant digits for printing numbers.

vvec.printing

logical indicating if the vvec component should be printed recursively via prt.vvec().

... 

potentially further arguments [Generic].
Value
summary.vlmc() returns an object of class "summary.vlmc" for which there’s a print method. It is basically a list containing all of object, plus additionally

confusion.table
the symmetric contingency table of data vs fitted.

depth.stats
statistics of Markov chain depth along the data; currently just summary(predict(object, type="depth"))

R2
the $R^2$ statistic, i.e. the percentage (in [0,1]) of correctly predicted data.

See Also
vlmc, draw.vlmc.

Examples

data(bnrf1)
vb <- vlmc(bnrf1EB)
svb <- summary(vb)
svb

vlmc

Fit a Variable Length Markov Chain (VLMC)

Description
Fit a Variable Length Markov Chain (VLMC) to a discrete time series, in basically two steps:
First a large Markov Chain is generated containing (all if threshold.gen = 1) the context states of the time series. In the second step, many states of the MC are collapsed by pruning the corresponding context tree.
Currently, the “alphabet” may contain can at most 26 different “character”s.

Usage
vlmc(dts,
cutoff.prune = qchisq(alpha.c, df=max(.1, alpha.len-1), lower.tail=FALSE)/2,
alpha.c = 0.05,
threshold.gen = 2,
codelchar = TRUE, y = TRUE, debug = FALSE, quiet = FALSE,
dump = 0, ctl.dump = c(width.ct = 1+log10(n), nmax.set = -1) )

is.vlmc(x)
### S3 method for class 'vlmc'
print(x, digits = max(3, getOption("digits") - 3), ...)
Arguments

dts  a discrete “time series”; can be a numeric, character or factor.
cutoff.prune  non-negative number; the cutoff used for pruning; defaults to half the \( \alpha \)-quantile of a chi-sq distribution, where \( \alpha = \alpha_{\text{c}} \), the following argument:
alpha.c  number in (0,1) used to specify cutoff.prune in the more intuitive \( \chi^2 \) quantile scale; defaulting to 5%.
threshold.gen  integer \( \geq 1 \) (usually left at 2). When generating the initial large tree, only generate nodes with count \( \geq \) threshold.gen.
code1char  logical; if true (default), the data dts will be ..........FIXME............
y  logical; if true (default), the data dts will be returned. This allows to ensure that residuals (residuals.vlmc) and “k-step ahead” predictions can be computed from the result.
debug  logical; should debugging info be printed to stderr.
quiet  logical; if true, don’t print some warnings.
dump  integer in \( \emptyset : 2 \). If positive, the pruned tree is dumped to stderr; if 2, the initial unpruned tree is dumped as well.
ctl.dump  integer of length 2, say ctl[1:2] controlling the above dump when dump > 0. ctl[1] is the width (number of characters) for the “counts”, ctl[2] the maximal number of set elements that are printed per node; when the latter is not positive (by default), currently \( \max(6, 15 - \log_{10}(n)) \) is used.
x  a fitted "vlmc" object.
digits  integer giving the number of significant digits for printing numbers.
...  potentially further arguments [Generic].

Value

A "vlmc" object, basically a list with components

- nobs  length of data series when fit. (was named "n" in earlier versions.)
- threshold.gen,  cutoff.prune  the arguments (or their defaults).
- alpha.len  the alphabet size.
- alpha  the alphabet used, as one string.
- size  a named integer vector of length (>= 4), giving characteristic sizes of the fitted VLMC. Its named components are "ord.MC" the (maximal) order of the Markov chain,
- "context"  the “context tree size”, i.e., the number of leaves plus number of “hidden nodes”,
- "nr.leaves"  is the number of leaves, and
- "total"  the number of integers needed to encode the VLMC tree, i.e., \( \text{length(vlmc.vec)} \) (see below).
- vlmc.vec  integer vector, containing (an encoding of) the fitted VLMC tree.
- y  if \( y = \text{TRUE} \), the data dts, as character, using the letters from alpha.
- call  the call vlmc(...) used.
Note

Set cutoff = 0, thresh = 1 for getting a “perfect fit”, i.e. a VLMC which perfectly re-predicts
the data (apart from the first observation). Note that even with cutoff = 0 some pruning may
happen, for all (terminal) nodes with δ=0.

Author(s)

Martin Maechler

References

513.


See Also

draw.vlmc, entropy, simulate.vlmc for “VLMC bootstrapping”.

Examples

```r
f1 <- c(1,0,0,0)
f2 <- rep(1:0,2)
(dt1 <- c(f1,f1,f2,f1,f2,f2,f1))

(vlmc.dt1 <- vlmc(dt1))
vlmc(dt1, dump = 1,
  ctl.dump = c(wid = 3, nmax = 20), debug = TRUE)
(vlmc.dt1c01 <- vlmc(dts = dt1, cutoff.prune = .1, dump=1))

data(presidents)
dpres <- cut(presidents, c(0,45,70, 100)) # three values + NA
table(dpres <- factor(dpres, exclude = NULL)) # NA as 4th level
levels(dpres)#-> make the alphabet -> warning
vlmc.pres <- vlmc(dpres, debug = TRUE)
vlmc.pres

## alphabet & and its length:
vlmc.pres$alpha
stopifnot(
  length(print(strsplit(vlmc.pres$alpha,NULL)[[1]])) == vlmc.pres$ alpha.len
)

## You now can use larger alphabets (up to 95) letters:
set.seed(7); it <- sample(40, 20000, replace=TRUE)
v40 <- vlmc(it)
v40```

## vlmctree

**Compute the tree structure of a "vlmc" object**

### Description

Compute the tree representation of a "vlmc" object as `R list`.

### Usage

```r
vlmctree(x)
```

### Arguments

- `x, object` typically the result of `vlmc(.)`.
- `vv` integer vector encoding the fitted vlmc, typically `x$vlmc.vec[-1]`.
- `k` integer, the alphabet size.
- `chk.lev` integer internally used for consistency checking.
- `...` further arguments passed to or from methods.
vlmctree

Details

*.vvec2tree* is the internal (recursive) function building up the tree.

str.vtree is a method for the generic str function and typically for the output of vlmctree(). For each node, it gives the “parenting level” in braces and the counts.

Value

A list of class "vtree" representing the tree structure recursively.

Each “node” of the tree is itself a list with components

level length-2 integer giving the level in \( \{0, 1, \ldots\} \), counted from the root (which is 0) and the parenting level, i.e. the longest branch.

count integer vector of length \( k \) where \( k \) is the number of “letters” in the alphabet.

total equals to \( \sum \) of count.

child a list (of length \( k \)) of child nodes or NULL (i.e. not there).

Author(s)

Martin Maechler

See Also

vlmc.

Examples

data(presidents)
dpres <- cut(presidents, c(0, 45, 70, 100)) # three values + NA
table(dpres <- factor(dpres, exclude = NULL)) # NA as 4th level

(vlmc.prc1 <- vlmc(dpres, cut = 1, debug = TRUE))
str(vv.prc1 <- vlmctree(vlmc.prc1))
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