

Package ‘sprsmdl’

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sprsmdl-package	<i>Sparse modeling toolkit</i>
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Description

R functions to mine sparse models from data.

Details

Providing functions to find few but significant variables that can explain data well.

Author(s)

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SlrArd

*Sparse Logistic Regression***Description**

Sparse logistic regression (SLR) with automatic relevance determination (ARD).

Usage

```
SlrArd(T, X, bias = TRUE, method = c("VB", "VBMacKay", "PX-VB"), control = list(), check.lb=TRUE, a0 =
```

Arguments

T	A vector of binary categorical dependent variable.
X	A matrix, each row of which is a vector of independent variables.
bias	A logical value specifying whether to include intercept or not.
method	The method to be used. See ‘Details’.
control	A list of control parameters. See ‘Details’.
check.lb	A logical value whether to check the validity of parameter updates. Defaults to TRUE.
	Hyper parameters:
a0	Shape of Gamma distribution.
b0	Rate of Gamma distribution.
	Initial values:
mu0	Coefficients.
xi0	Variational parameter.

Details

Some independent variables can be pruned in each VB-EM iteration and never be used for successive iterations when irrelevance of the variables exceed a threshold determined by `control$pruning`. Explicitly set `control$pruning = Inf` to prevent the pruning.

Method “VB” is a variational Bayesian method that is robust. See Bishop (2006).

Method “VBMacKay” is basically same as “VB” but some parameters are updated based on method of MacKay (1992). Global convergence has not been proven but this algorithm will be faster.

Method “PX-VB” based on the Parameter eXpanded VB method proposed in Qi and Jaakkola (2007). Global convergence is proven and could be faster than “VB”.

The control argument is a list that can supply any of the following components:

- `pruning`: threshold of independent variables pruning. No variables are pruned if 'Inf'. Defaults to '1e+8'.

See `?optim` for meanings of the following control parameters.

- `maxit`: Defaults to '10^5'.
- `reltol`: Defaults to 'sqrt(.Machine\$double.eps)'.
- `trace`: Defaults to 'TRUE'.
- `REPORT`: Defaults to 'floor(control\$maxit / 20)'.

Value

<code>coefficients</code>	A named vector of coefficients.
<code>irrelevance</code>	A named vector of irrelevance.
<code>iterations</code>	A number of iterations.
<code>converged</code>	A logical value giving whether the iterations converged or not.
<code>lower.bound</code>	The lower bound of the marginal log-likelihood minus a constant term.
<code>method</code>	The method used.
<code>lb.diff</code>	The difference of the lower bounds in each update. This exists when <code>check.lb = TRUE</code> .
<code>fitted.values</code>	The fitted values.
<code>residuals</code>	The residuals, that is T minus fitted values.

Author(s)

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References

- Bishop, C. M. (2006) Pattern recognition and machine learning. Springer.
- MacKay, D. J. C. (1992) Bayesian interpolation. *Neural Computation*, 4(3), 415-447.
- Qi, Y. and Jaakkola, T. S. (2007) Parameter expanded variational Bayesian methods. *Advances in Neural Information Processing Systems*, 19, 1097.

Examples

```
data(iris)

tmp <- iris[iris$Species != 'versicolor',]
T <- tmp$Species == 'setosa'
X <- as.matrix(tmp[,1:4])

res <- SlrArd(T, X, bias=TRUE, method="VB", control = list(maxit=500))
print(coefficients(res))

res <- SlrArd(T, X, bias=TRUE, method="VBMacKay") ## faster
print(coefficients(res))

res <- SlrArd(T, X, bias=FALSE, method="VBMacKay") ## without bias
print(coefficients(res))
```

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