

# Package ‘SOIL’

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**Type** Package

**Title** Sparsity Oriented Importance Learning

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**Author**

Chenglong Ye <yexxx323@umn.edu>, Yi Yang <yi.yang6@mcgill.ca>, Yuhong Yang <yyang@stat.umn.edu>

**Maintainer** Yi Yang <yi.yang6@mcgill.ca>

**Imports** stats, glmnet, ncvreg, MASS, parallel, brglm2

**Description** Sparsity Oriented Importance Learning (SOIL) provides a new variable importance measure for high dimensional linear regression and logistic regression from a sparse penalization perspective, by taking into account the variable selection uncertainty via the use of a sensible model weighting. The package is an implementation of Ye, C., Yang, Y., and Yang, Y. (2017+).

**License** GPL-2

**URL** <https://github.com/emeryyi/SOIL>

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**NeedsCompilation** no

**Repository** CRAN

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SOIL

*Sparsity Oriented Importance Learning (SOIL)***Description**

Sparsity Oriented Importance Learning (SOIL) provides a new variable importance measure for high dimensional linear regression and logistic regression from a sparse penalization perspective, by taking into account the variable selection uncertainty via the use of a sensible model weighting. The package is an implementation of Ye, C., Yang, Y., and Yang, Y. (2017+) DOI: <doi:10.1080/01621459.2017.1377080>.

**Usage**

```
SOIL(x, y, n_train = ceiling(n/2), no_rep = 100,
     n_train_bound = n_train - 2, n_bound = n - 2,
     psi = 1, family = c("gaussian",
                        "binomial"), method = c("lasso", "union", "customize"),
     candidate_models, weight_type = c("BIC", "AIC",
                                       "ARM"), prior = TRUE, reduce_bias = FALSE)
```

**Arguments**

x	Matrix of predictors.
y	Response variable.
n_train	Size of training set when the weight function is ARM or ARM with prior=TRUE. The default value is n_train=ceiling(n/2).
no_rep	Number of replications when the weight function is ARM and ARM with prior=TRUE. The default value is no_rep=100.
n_train_bound	When computing the weights using ARM, the candidate models with the size larger than n_train_bound will be dropped. The default value is n_train-2.
n_bound	When computing the weights using AIC or BIC, the candidate models with the size larger than n_train_bound will be dropped. The default value is n-2.
psi	A positive number to control the improvement of the prior weight. The default value is 1.
family	Choose the family for GLM models. So far gaussian and binomial are implemented. The default is gaussian.
method	Users can choose lasso, union or customize. If method=="lasso", then the program automatically provides the candidate models as a union of solution paths of Lasso, Adaptive Lasso; If method=="union", then the program automatically provides the candidate models as a union of solution paths of Lasso, Adaptive Lasso, SCAD, and MCP; If method=="customize", users must provide their own set of candidate models in the input argument candidate_models as a matrix, each row of which is a 0/1 index vector representing whether each variable is included/excluded in the model. For details see Example section. The default option is method=="lasso".

candidate_models	Only available when method="customize". It is a matrix of candidate models, each row of which is a 0/1 index vector representing whether each variable is included/excluded in the model. For details see Example section.
weight_type	Options for computing weights for SOIL measure. Users can choose among ARM, AIC and BIC. The default is BIC.
prior	Whether to use prior in the weighting function. The default is TRUE.
reduce_bias	If the binomial model is used, occasionally the algorithm might has convergence issue when the problem of so-called complete separation or quasi-complete separation happens. Users can set reduce_bias=TRUE to solve the issue. The algorithm will use an adjusted-score approach when fitting the binomial model for computing the weights. This method is developed in Firth, D. (1993). Bias reduction of maximum likelihood estimates. <i>Biometrika</i> 80, 27-38.

### Details

See the paper provided in Reference section.

### Value

A "SOIL" object is returned. The components are:

importance	SOIL importance values for each variable.
weight	The weight for each candidate model.
candidate_models_cleaned	Cleaned candidate models: the duplicated candidate models are cleaned; When computing SOIL weights using AIC and BIC, the models with more than $n-2$ variables are removed ( $n$ is the number of observations); When computing SOIL weights using ARM, the models with more than $n_{\text{train}}-2$ variables are removed ( $n_{\text{train}}$ is the number of training observations).

### References

Ye, C., Yang, Y., and Yang, Y. (2017+). "Sparsity Oriented Importance Learning for High-dimensional Linear Regression". *Journal of the American Statistical Association*. (Accepted) DOI: 10.1080/01621459.2017.1377080

BugReport: <https://github.com/emeryyi/SOIL>

### Examples

```
# REGRESSION CASE

# generate simulation data
n <- 50
p <- 8
beta <- c(3,1.5,0,0,2,0,0,0)
b0 <- 1
x <- matrix(rnorm(n*p,0,1),nrow=n,ncol=p)
```

```

e <- rnorm(n)
y <- x %*% beta + b0 + e

# compute SOIL using ARM with prior
v_ARM <- SOIL(x, y, family = "gaussian",
weight_type = "ARM", prior = TRUE)

# compute SOIL using BIC
v_BIC <- SOIL(x, y, family = "gaussian", weight_type = "BIC")

# compute SOIL using AIC
v_AIC <- SOIL(x, y, family = "gaussian",
weight_type = "AIC", prior = TRUE)

# user supplied candidate models
candidate_models = rbind(c(0,0,0,0,0,0,0,0,1),
c(0,1,0,0,0,0,0,0,1), c(0,1,1,1,0,0,0,0,1),
c(0,1,1,0,0,0,0,0,1), c(1,1,0,1,1,0,0,0,0),
c(1,1,0,0,1,0,0,0,0))

v1_BIC <- SOIL(x, y,
psi=1,
family = "gaussian",
method = "customize",
candidate_models = candidate_models,
weight_type = "BIC", prior = TRUE)

# CLASSIFICATION CASE

# generate simulation data
n = 300
p = 8
b <- c(1,1,1,-3*sqrt(2)/2)
x=matrix(rnorm(n*p, mean=0, sd=1), n, p)
feta=x[, 1:4]%*%b
fprob=exp(feta)/(1+exp(feta))
y=rbinom(n, 1, fprob)

# compute SOIL for model_check using BIC with prior
b_BIC <- SOIL(x, y, family = "binomial", weight_type = "BIC")

candidate_models =
rbind(c(0,0,0,0,0,0,0,0,1),
c(0,1,0,0,0,0,0,0,1),
c(1,1,1,1,0,0,0,0,0),
c(0,1,1,0,0,0,0,0,1),
c(1,1,0,1,1,0,0,0,0),
c(1,1,0,0,1,0,0,0,0),
c(0,0,0,0,0,0,0,0,0),
c(1,1,1,1,1,0,0,0,0))

```

```
# compute SOIL for model_check using AIC
# user supplied candidate models
b_AIC <- SOIL(x, y, family = "binomial",
method = "customize", candidate_models = candidate_models,
weight_type = "AIC")
```

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