

## A New Regularized Least Squares Support Vector Regression for Gene Selection

### Description

This procedure provides a gene selection method proposed by Chen et al. (2008). Genes are ranked by their “importance”, and the whole original set of genes can be reduced into a candidate subset, in which genes are considered influential.

### Usage

```
var_select<-function(gamma,C,A,y,select_time=2,final_size=10,  
intermedia_size=final_size*10)
```

### Arguments

gamma	Parameter for Gaussian kernel, the value has to be larger than 0
C	Parameter used in regularized least squares support vector regression, the value is larger than 0
A	Training input data
y	Class labels of training data, coded as 1,2,3...
select_time	1 or 2, the times of reducing gene set.
final_size	The size of the final candidate subset. Default value is 10.
intermedia_size	The size of intermediate gene subset, it is only needed when select_time=2.

### Details

Standardization will be done in the program, and users do not need to do the preprocessing step.

## Value

B            The absolutely weighted sums of genes in the candidate subset  
IND         Indexes of genes in the candidate subset

## References

Pei-Chun Chen, Su-Yun Huang, Wei J. Chen, Chuhsing Kate Hsiao (2008)  
A new regularized least squares support vector regression for gene selection.  
Submitted.

## Examples

```
# the leukemia data with two classes case
A=read.table("ALL2.txt", header=F)        # read data
y=read.table("y.txt",header=F)
A=as.matrix(A)
y=as.matrix(y)
result=var_select(0.0002,300,A,y) # select with default
result$B        # absolutelweighted sums of genes in candidate subset
result$IND      # index of gene in candidate subset
```