

Inputs

- df** : The data frame
- treatment** : The name of the treatment variable as a character string, or the number of the treatment variable column
- t1** : The name of the value to be used as group 1, so that delta has the desired sign.
- response** : The name of the response variable as a character string, or the number of the response variable column
- X** : A character vector with the names of explanatory variables to use, or a numeric vector with the column numbers of the explanatory variables
- support** : Observations with estimated propensity scores not between $(1 - \text{support})/2$ and $(1 + \text{support})/2$ will be removed. Default is 0.99.
- alpha** : Numeric. Used to create a $(1 - \text{alpha})$ confidence interval. Default is 0.05
- r1** : Optional. If response is binary, **r1** specifies the name of the outcome to be considered 1 in $P(Y = 1)$.

Example:

```
DR.est(df, treatment = 'Major', t1 = '31FYC', response = 'semesterGPA',  
      X = c('SATVerb', 'SATMath', 'HighSchoolGPA', 'Gender'), support = 0.98)
```

Outputs

The function returns a list with the following elements

- estimates** : A vector containing $\hat{\mu}_1, \hat{\mu}_0, \hat{\Delta}$, The lower and upper bounds of a $(1 - \text{alpha})$ confidence interval, \hat{SE} , p-value, and **alpha**
Note: \hat{SE} calculated using the delta method
- removed** : A matrix showing the number and percent of observations removed for missing values and extreme propensity scores
- model0** : The **glm** object from the regression of the response on **X** for the untreated
- model1** : The **glm** object from the regression of the response on **X** for the treated
- modelZ** : The **glm** object from the regression of the treatment on **X**
- e0** : Vector of estimated propensity scores for the treated
- e1** : Vector of estimated propensity scores for the untreated