

# Package ‘ehpoly’

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**Type** Package

**Title** What the Package Does (Title Case)

**Version** 0.1.0

**Author** Who wrote it

**Maintainer** The package maintainer <yourself@somewhere.net>

**Description** More about what it does (maybe more than one line)

Use four spaces when indenting paragraphs within the Description.

**License** What license is it under?

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 5.0.1

## R topics documented:

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ehpoly	<i>Conduct an analysis of etiologic heterogeneity using polytomous logistic regression</i>
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## Description

ehpoly takes a list of individual tumor markers and a list of risk factors and returns results related to the question of whether each risk factor differs across levels of the disease subtypes and the question of whether each risk factor differs across levels of each individual tumor marker of which the disease subtypes are comprised.

Input is a dataframe that contains the individual tumor markers and the risk factors of interest. The tumor markers must be binary and must have levels 0 or 1 for cases. The tumor markers must have a value of 999 for control subjects. For categorical tumor markers, a reference level should be selected and then indicator variables for each remaining level of the tumor marker should be created. For continuous tumor markers, categories should be formed and then indicator variables can be constructed as in the case of categorical tumor markers. Risk factors can be either binary or continuous. For categorical risk factors, a reference level should be selected and then indicator variables for each remaining level of the risk factor should be created. Categorical risk factors entered as is will be treated as ordinal.

**Usage**

```
ehpoly(tm, rf, case, df)
```

**Arguments**

<code>tm</code>	a list of the names of the binary tumor markers. Each must have levels 0 or 1 for case subjects. This value will be missing for all control subjects.
<code>rf</code>	a list of the names of the binary or continuous risk factors. For binary risk factors the lowest level will be used as the reference level.
<code>case</code>	denotes the variable that contains each subject's status as a case or control. This value should be 1 for cases and 0 for controls. Argument must be supplied in quotes.
<code>df</code>	the name of the dataframe that contains the tumor markers and risk factors.

**Value**

Returns a list.

`beta` is a matrix containing the estimated beta parameters with a column for each risk factor and a row for each disease subtype.

`beta_se` contains the associated standard errors.

`eh_pval` is a vector of p-values for testing whether each risk factor differs across levels of the disease subtype.

`gamma` is a matrix containing the estimated gamma parameters, obtained as linear combinations of the beta parameters with a column for each risk factor and a row for each tumor marker.

`gamma_se` contains the associated standard errors.

`gamma_p` is a matrix of p-values for testing whether each risk factor differs across levels of each tumor marker, with a column for each risk factor and a row for each tumor marker.

`or_ci_p` is a dataframe with a odds ratio (95 factor/subtype combination, as well as a column of etiologic heterogeneity p-values.

`beta_se_p` is a dataframe with the estimated beta parameters (SE) for each risk factor/subtype combination, as well as a column of etiologic heterogeneity p-values.

`gamma_se_p` is a dataframe with estimates of the gamma tumor marker effects (SE) and their associated p-values.

**Author(s)**

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