Package ‘clinUtiDNA’

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Type Package

Title Clinical Utility of DNA Testing

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Description This package provides the estimation of an index measuring the clinical utility of DNA testing in the context of gene-environment interactions on a disease. The corresponding gene-environment interaction effect on the additive scale can also be obtained. The estimation is based on case-control or cohort data. The method was developed by Nguyen et al. 2013.

License GPL-3

LazyLoad yes

NeedsCompilation no

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R topics documented:

`gxe.cc` *Estimation of gene-environment interaction on the additive scale for case-control data*

Description

Estimation of gene-environment interaction on the additive scale for case-control data

Usage

```
gxe.cc(cases, contr, pD)
```

Arguments

`cases`	a vector containing numbers of cases observed in the gene environment groups <G=0,E=0>, <G=1,E=0>, <G=0,E=1> and <G=1,E=1>
`contr`	a vector containing numbers of controls observed in the gene environment groups <G=0,E=0>, <G=1,E=0>, <G=0,E=1> and <G=1,E=1>
`pD`	disease prevalence should be either less than 1 (for a known value) or a vector of observed numbers of affected and unaffected individuals from an external data set

Details

see Nguyen et al. 2013

Value

`GxE.cc`	a list containing the interaction estimate, the corresponding variance and the boundaries of the 95% of the confidence interval

Author(s)

Thuy Trang Nguyen

References

Making Medical Decisions in Dependence of Genetic Background: Estimation of the Utility of DNA Testing in Clinical, Pharmaco-Epidemiological or Genetic Studies. Nguyen TT, Schaefer H, Timmesfeld N. Genet Epidemiol. 2013 Apr 4. doi: 10.1002/gepi.21701

See Also

`gxe.coh`, `utility.coh`, `utility.cc`

Examples

```
## Parameter initialisation
cases <- c(36,10,84,25)
contr <- c(100,4,63,2)
pD <- c(22,9420)
## Calculation of the interaction effect
gxe.cc(cases,contr,pD)  # with pD estimated from external data
gxe.cc(cases,contr,pD=0.002) # with known pD
```

`gxe.coh` *Estimation of gene-environment interaction on the additive scale for cohort data*

Description

Estimation of gene-environment interaction on the additive scale for cohort data

Usage

```
gxe.coh(aff, unaff)
```

Arguments

`aff`	a vector containing numbers affected individuals observed in the gene environment groups <G=0,E=0>, <G=1,E=0>, <G=0,E=1> and <G=1,E=1>
`unaff`	a vector containing numbers of unaffected individuals observed in the gene environment groups <G=0,E=0>, <G=1,E=0>, <G=0,E=1> and <G=1,E=1>

Details

see Nguyen et al. 2013

Value

`GxE.coh`	a list containing the interaction estimate, the corresponding variance and the boundaries of the 95% of the confidence interval

Author(s)

Thuy Trang Nguyen

References

Making Medical Decisions in Dependence of Genetic Background: Estimation of the Utility of DNA Testing in Clinical, Pharmaco-Epidemiological or Genetic Studies. Nguyen TT, Schaefer H, Timmesfeld N. Genet Epidemiol. 2013 Apr 4. doi: 10.1002/gepi.21701

See Also

`gxe.cc`, `utility.coh`, `utility.cc`

Examples

```
## Parameter initialisation
aff <-  c(150,24,135,39)
unaff <- c(544,111,393,63)
## Calculation of the interaction effect
gxe.coh(aff,unaff)
```

`utility.cc` *Calculation of the utility index for case-control data*

Description

Calculation of the utility index for case-control data

Usage

```
utility.cc(cases, contr, pD,pG)
```

Arguments

`cases`	a vector containing numbers of cases observed in the gene environment groups <G=0,E=0>, <G=1,E=0>, <G=0,E=1> and <G=1,E=1>
`contr`	a vector containing numbers of controls observed in the gene environment groups <G=0,E=0>, <G=1,E=0>, <G=0,E=1> and <G=1,E=1>
`pD`	disease prevalence should be either less than 1 (for a known value) or a vector of observed numbers of affected and unaffected individuals from an external data set
`pG`	frequency of the genetic risk variant should be either less than 1 (for a known value) or a vector of observed numbers of carriers and non-carriers observed from an external data set

Details

see Nguyen et al. 2013

Value

`Utility.cc`	a list containing the utility estimate, the corresponding variance and the boundaries of the 95% of the confidence interval

Author(s)

Thuy Trang Nguyen

References

Making Medical Decisions in Dependence of Genetic Background: Estimation of the Utility of DNA Testing in Clinical, Pharmaco-Epidemiological or Genetic Studies. Nguyen TT, Schaefer H, Timmesfeld N. Genet Epidemiol. 2013 Apr 4. doi: 10.1002/gepi.21701

See Also

`gxe.coh`, `utility.coh`, `gxe.cc`

Examples

```
## Parameter initialisation
cases <- c(36,10,84,25)
contr <- c(100,4,63,2)
pD <- c(22,9420)
pG <- c(52,618)
## Calculation of the utility index
utility.cc(cases,contr,pD,pG)  # with pD and pG estimated from external data
utility.cc(cases,contr,pD,pG=0.078) # with known pG
utility.cc(cases,contr,pD=0.002,pG) #  with known pD
utility.cc(cases,contr,pD=0.002,pG=0.078) # with known pD and pG
```

`utility.coh` *Calculation of the utility index for cohort data*

Description

Calculation of the the utility index for cohort data

Usage

```
utility.coh(aff, unaff)
```

Arguments

`aff`	a vector containing numbers affected individuals observed in the gene environment groups <G=0,E=0>, <G=1,E=0>, <G=0,E=1> and <G=1,E=1>
`unaff`	a vector containing numbers unaffected individuals observed in the gene environment groups <G=0,E=0>, <G=1,E=0>, <G=0,E=1> and <G=1,E=1>

Details

see Nguyen et al. 2013

Value

`Utility.coh`	a list containing the utility estimate, the corresponding variance and the boundaries of the 95% of the confidence interval

Author(s)

Thuy Trang Nguyen

References

Making Medical Decisions in Dependence of Genetic Background: Estimation of the Utility of DNA Testing in Clinical, Pharmaco-Epidemiological or Genetic Studies. Nguyen TT, Schaefer H, Timmesfeld N. Genet Epidemiol. 2013 Apr 4. doi: 10.1002/gepi.21701

See Also

`gxe.cc`, `gxe.coh`, `utility.cc`

Examples

```
## Parameter initialisation
aff <-  c(150,24,135,39)
unaff <- c(544,111,393,63)
## Calculation of the utility index
utility.coh(aff,unaff)
```

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