Package ‘sanon’

October 1, 2015

Type Package
Title Stratified Analysis with Nonparametric Covariable Adjustment
Version 1.5
Date 2015-10-01
Author Atsushi Kawaguchi
Maintainer Atsushi Kawaguchi <kawa_a24@yahoo.co.jp>
Description There are several functions to implement the method for analysis in a randomized clinical trial with strata with following key features. A stratified Mann-Whitney estimator addresses the comparison between two randomized groups for a strictly ordinal response variable. The multivariate vector of such stratified Mann-Whitney estimators for multivariate response variables can be considered for one or more response variables such as in repeated measurements and these can have missing completely at random (MCAR) data. Non-parametric covariance adjustment is also considered with the minimal assumption of randomization. The p-value for hypothesis test and confidence interval are provided.
License GPL (>= 2)
NeedsCompilation no
Repository CRAN
Date/Publication 2015-10-01 13:46:37

R topics documented:

sanon-package ................................................................. 2
catecovar ................................................................. 2
disp.sanon ................................................................. 3
drain.sanon ................................................................. 4
disp.sanon ................................................................. 5
disp.sanon ................................................................. 6
crate ................................................................. 7
covar ................................................................. 7
heartburn ................................................................. 8
resp ................................................................. 9
sanon ................................................................. 10
The Stratified Analysis with Nonparametric covariable adjustment Package

Description

A Package for Implementation of the method in Kawaguchi, Koch, and Wang (2011)

Author(s)

Atsushi Kawaguchi. <kawa_a24@yahoo.co.jp>

References


See Also

sanon

catecovar

Identify Categorical Covariables

Description

This is a special function used in the context of sanon. It identifies categorical covariables when they appear on the right hand side of a formula.

Usage

catecovar(x, ref = NULL)
Arguments

- `x` variable name
- `ref` character for the reference group for the categorical covariable.

Details

In the `sanon`, the categorical covariable is converted into a dummy variable. The reference group is specified in the `ref` argument.

---

**Extract Model Coefficients**

Description

`coef` is a generic function which extracts model coefficients from objects returned by modeling functions. `coefficients` is an alias for it.

Usage

```r
## S3 method for class 'sanon'
coef(object, ...)
```

Arguments

- `object` an object of class "sanon", usually, a result of a call to `sanon`
- `...` further arguments passed to or from other methods.

Details

All object classes which are returned by model fitting functions should provide a `coef` method or use the default one.

Value

Coefficients extracted from the model object `object`.

Examples

```
## Example 3.1 Randomized Clinical Trial of Chronic Pain
data(cpain)
out1 = sanon(response ~ grp(treat, ref="placebo") + strat(center) + strat(diagnosis), data=cpain)
coef(out1)
coefficients(out1)

## Example 3.2 Randomized Clinical Trial of Respiratory Disorder
data(resp)
P = rbind(rep(0, 4), diag(4), rep(0, 4))
out23 = sanon(cbind(baseline, visit1, visit2, visit3, visit4) ~ grp(treatment, ref="P")
```
Description

Computes confidence intervals for one or more parameters in a fitted model.

Usage

```r
## S3 method for class 'sanon'
confint(object, parm = NULL, level = 0.95, ...)

## S3 method for class 'confint.sanon'
print(x, ...)
```

Arguments

- `object`: an object of class "sanon", usually, a result of a call to `sanon`
- `parm`: a specification of which parameters are to be given confidence intervals, either a vector of numbers or a vector of names. If missing, all parameters are considered.
- `level`: the confidence level required.
- `...`: further arguments passed to or from other methods.

Details

Confidence intervals for adjusted parameters in the weighted least squares are computed based on an asymptotic normal.

Value

- `ci`: A matrix (or vector) with columns giving Mann-Whitney estimates and their lower and upper confidence limits for each parameter with estimates. The interval will be labelled as Lower for (1 - level)/2 limit and Upper for 1 - (1 - level)/2 limit (by default 0.025 and 0.975).
- `level`: Confidence level
- `advarnames`: Adjust variable names in the weighted least squares method
Examples

```
#### Example 3.1 Randomized Clinical Trial of Chronic Pain ####
data(cpain)
out1 = sanon(response ~ grp(treat, ref="placebo") + strt(center) + strt(diagnosis), data=cpain)
confint(out1)
```

```
#### Example 3.2 Randomized Clinical Trial of Respiratory Disorder ####
data(resp)
P = rbind(rep(0, 4), diag(4), rep(0, 4))
out23 = sanon(cbind(baseline, visit1, visit2, visit3, visit4) ~ grp(treatment, ref="P")
   + strt(center) + strt(sex) + covar(age), data=resp, P=P)
# each four visits
confint(out23)
```

---

**contrast**  
*Contrast for Model Parameters*

**Description**
Inference by contrast of parameters in a fitted model.

**Usage**

```r
contrast(object, C = diag(length(object$b)), confint = FALSE,
level = 0.95, ...)
```

```r
## S3 method for class 'contrast'
print(x, ...)
```

**Arguments**

- `object,x` an object of class "sanon", usually, a result of a call to `sanon`.
- `C` contrast matrix. The number of column should be same as the length of b in outputs of `sanon`.
- `confint` logical value for whether the confidence interval is computed (only if C has one row).
- `level` the confidence level required (only if C has one row).
- `...` further arguments passed to or from other methods.

**Details**
This function provide the inference based on contrast after applying the function `sanon`. The contrast matrix C should be defined by the user. If the the number of row of C = 1, the confidence interval for the estimator is produced.
Value

- **C**: contrast matrix
- **Cb**: contrast estimates
- **VCb**: variance and covariance matrix of Cb
- **se**: standard error of Cb
- **level**: confidence level
- **UL**: upper confidence limit (only if the number of row of C = 1, otherwise NULL)
- **LL**: lower confidence limit (only if the number of row of C = 1, otherwise NULL)
- **Q**: test statistic
- **df**: degree of freedom
- **p**: p-value

Examples

#### Example 3.2 Randomized Clinical Trial of Respiratory Disorder

```r
data(resp)
P = rbind(rep(0, 4), diag(4), rep(0, 4))
out23 = sanon(cbind(baseline, visit1, visit2, visit3, visit4) ~ grp(treatment, ref="P")
+ strt(center) + strt(sex) + covar(age), data=resp, P=P)

# Homogeneity of the xi_k across the four visits
calcontrast(out23, C=cbind(diag(3), rep(-1, 3)))

# Comparison between treatments for the average of the xi_k across the 4 visits
contrast(out23, C=matrix(rep(1, 4)/4, ncol=4))
```

---

**covar**: Identify Covariates

Description

This is a special function used in the context of `sanon`. It identifies covariates when they appear on the right hand side of a formula.

Usage

`covar(x)`

Arguments

- **x**: variable name
Cpain

**Chronic Pain Data**

**Description**

The data are from a multicenter randomized clinical trial to compare test and control treatments for the management of chronic pain, and they have had previous consideration in Stokes et al. (2000, chap. 13).

**Usage**

data(cpain)

**Format**

A data frame with 193 observations and 4 variables

**Details**

treat a factor with levels active and placebo for treatment
response a factor with five levels poor, fair, moderate, good and excel for pain status after treatment for 4 weeks
center a factor with two levels I and II for two centers
diagnosis a factor with four levels A, B, C, and D for diagnoses

**References**


**grp**

**Identify Group Variables**

**Description**

This is a special function used in the context of sanon. It identifies group variables when they appear on the right hand side of a formula.

**Usage**

grp(x, ref = NULL)

**Arguments**

- **x** variable name
- **ref** character for the reference group for treatment group.
Description

The data are from two period cross-over design clinical trial for relief of heartburn, and listings of
the data appear in Koch, Gitomer, Skalland, and Stokes (1983). The variables are as follows:

Usage

data(heartburn)

Format

A data frame with 60 observations and 9 variables.

Details

center  a factor vector for two centers
sequence  a factor with levels AP and PA for sequence groups
age  a numeric vector for age
sex  a factor for sex with levels female and male
freq  a numeric vector for weekly frequency of condition from previous medical history
MD1  a numeric vector for time to relief from first dose during period 1
MD2  a numeric vector for time to relief from first dose during period 2
res1  a factor vector for relief status for period 1 (R = relief from first dose within 15 min, NF = no
       relief from first dose within 15 min)
ref2  a factor vector for relief status for period 2 with same categories as res1

References

analyses for a change-over design study and discussion of apparent carry-over effects." Statistics in
Medicine, 2(3), 397–412.
Description

The data are from a randomized clinical trial to compare a test treatment to placebo for a respiratory disorder, and listings of the data appear in Stokes et al. (2000, chap. 15, pp. 495-496) and Koch et al. (1990). The variables are as follows:

Usage

data(resp)

Format

A data frame with 111 observations and 9 variables.

Details

center  a factor vector for two centers
treatment a factor with levels A and P for active and placebo treatments, respectively
sex  a factor with levels F and M for female and male, respectively
age  a numeric vector for age
baseline  a numeric vector for patient global ratings of symptom control according to 5 categories (4 = excellent, 3 = good, 2 = fair, 1 = poor, 0 = terrible) at baseline measurement
visit1  a numeric vector for patient global ratings of symptom control at visit 1 with same categories as baseline
visit2  a numeric vector for patient global ratings of symptom control at visit 2 with same categories as baseline
visit3  a numeric vector for patient global ratings of symptom control at visit 3 with same categories as baseline
visit4  a numeric vector for patient global ratings of symptom control at visit 4 with same categories as baseline

References


Non-Parametric Covariable Adjustment for Stratified Rank Measures of Association

Description

This is a function for computing a stratified multivariate Mann-Whitney estimator that addresses the comparison between two randomized groups for a strictly ordinal response variable. Response variables may have some missing completely at random (MCAR) values for some patients. Non-parametric covariable adjustment is considered through the difference estimates between mean covariable and the weighted least squares method. Although such estimators can be computed directly as weighted linear combinations of within-stratum Mann-Whitney estimators, consistent estimation of their covariance matrix is done using methods for multivariate U-statistics.

Usage

sanon(outcome, ...)

## S3 method for class 'formula'

sanon(formula, data = list(), ...)

## Default S3 method:

sanon(outcome, group, strt = NULL, covar = NULL,
       catecovar = NULL, ref = NULL, covref = NULL, P = NULL,
       res.na.action = "default", ...)

## S3 method for class 'sanon'

print(x, ...)

Arguments

outcome vector of observations of length n, or a matrix with n rows for the response (or outcome) variables

... further arguments passed to or from other methods.

formula a formula object, with the response on the left of a ~ operator, and the terms on the right.

data a data.frame in which to interpret the variables named in the formula.

group numeric vector of observations of length n for treatment group. The reference group can be specified in ref.

strt numeric or factor vector of observations of length n, or a matrix with n rows for strata.

covar numeric or factor vector of observations of length n, or a matrix with n rows for covariable.

catecovar numeric or factor vector of observations of length n, or a matrix with n rows for categorical covariable.
sanon

**ref** character for the reference group for treatment group in group.
**covref** character vector for the reference group for categorical covariables in catecovar.
**P** a matrix for weighted least squares estimation.
**res.na.action** character for setting NA actions. "default", "LOCF1", "LOCF2", "replace", and "remove" are available. default is "default". see the details.
**x** an object of class "sanon", usually, a result of a call to sanon.

**Details**
sanon has two specifications for the input, variable and formula based. In the variable based input, one can specify R objects to outcome, group, and strata variables, and covariable. In the formula based input, the formula consists of variable names in a data.frame. The strata and group variables, and covariable are recognized by functions strt, grp, covar, and catecovar. outcome can be contained missing values, which should be coded by NA. Five options for the management of missing values can be specified in the argument res.na.action: "default" = the method in Kawaguchi et al. (2011), "LOCF1" and "LOCF2" = last observation carried forward with respect to kernels of U-statistics and observed velues, respecively, "replace" = missing values are managed as tied with all other values in the same stratum, and "remove" = the complete cases analaysis. For res.na.action = "LOCF1" or "LOCF2", the order in the outcome is considered as the time order in imputing. if the baseline measurement is missing, then the corresponding subject is removed. outcome can be also multiple (repeatly measured). If more than two strata are specified, these are taking a cross-classification. The group variable can be specifies its reference group in the argument ref in the sanon or in the function grp.

**Value**

- **N** Sample size
- **Nna** the number of subjects with missing values
- **nhik** Sample size in each strata, group, and response
- **nik** Sample size in each group and response
- **xi** (multivariate) Mann-Whitney estimate(s) that addresses the comparison between two randomized groups
- **g** the difference estimates between mean covariable
- **f** a vector consisting of xi and g
- **vf** estimated covariance matrix of f
- **b** fully adjustedmented estimators for all covariables and the strata
- **vb** covariance matrix of b
- **se** standard error of b
- **Q** test statistics for b
- **p** p-value for b
- **outnames** outcome or response names
- **covarnames** covariable names
- **advarnames** variable names adjusting in the weighted least squares
bnames  variable names of adjusted in the weighted least squares
reslevels levels for response variables
grouplevels levels for the group variable
strtout resulting (cross-classification) strata
strtlevels resulting (cross-classification) strata levels
strtnames resulting (cross-classification) strata names
matP design matrix used in the weighted least squares

References

Examples

```
### Example 3.1 Randomized Clinical Trial of Chronic Pain ###
data(cpain)
out11 = sanon(response ~ grp(treat, ref="placebo") + strt(center) + strt(diagnosis), data=cpain)
out11
summary(out11)

# R objects are also available
attach(cpain)
out12 = sanon(outcome=response, group=treat, strt=cbind(center, diagnosis, ref="placebo")
out12
summary(out12)

### Example 3.2 Randomized Clinical Trial of Respiratory Disorder ###
data(resp)
out21 = sanon(cbind(baseline, visit1, visit2, visit3, visit4) ~ grp(treatment, ref="P") + strt(center) + strt(sex) + covar(age), data=resp)
out21
summary(out21)

# the matrix P can be specified
P = rbind(rep(0, 4), diag(4), rep(0, 4))
out22 = sanon(cbind(baseline, visit1, visit2, visit3, visit4) ~ grp(treatment, ref="P") + strt(center) + strt(sex) + covar(age), data=resp, P=P)
out22
summary(out22)
```
Seborrheic Dermatitis Data

Description

The data are from a randomized clinical trial to compare a test treatment to placebo for a seborrheic dermatitis, and listings of the data appear in Ramaswamy, Koch, and Amara (1997). The variables are as follows:

Usage
data(sebor)

Format

A data frame with 167 observations and 8 variables.

Details

center  a factor vector for eight centers
treat   a factor with levels placebo and test for placebo and test treatments, respectively
scoreQ  a numeric vector for patient global scores for the face according to 6 categories (0 = cleared, 1 = excellent improvement, 2 = moderate improvement, 3 = slight improvement, 4 = no change, 5 = exacerbation)
scoreR  a numeric vector for patient global scores for the scalp with same categories as scoreQ
scoreS  a numeric vector for patient global scores for the chest with same categories as scoreQ
severityQ a numeric vector for the baseline disease severity for the face according to 3 categories (1 = mild, 2 = moderate, 3 = severe)
severityR a numeric vector for the baseline disease severity for the scalp with same categories as severityQ
severityS a numeric vector for the baseline disease severity for the chest with same categories as severityQ

References

Skin Condition Data

Description

The data are from a randomized clinical trial to compare a test treatment to placebo for skin conditions, and listings of the data appear in Stanish, Gillings, Koch (1978a, b). The variables are as follows:

Usage

data(skin)

Format

A data frame with 172 observations and 6 variables.

Details

center  a factor vector for two centers
treat   a factor with levels A and P for active and placebo treatments, skinectively
stage   a numeric vector for initial severity of the skin condition according to 3 categories (3 = fair, 4 = poor, 5 = exacerbation) at baseline measurement
resQ    a numeric vector for extent of improvement at visit 1 according to 5 categories (1 = rapidly improving, 2 = slowly improving, 3 = stable, 4 = slowly worsening, 5 = rapidly worsening)
resR    a numeric vector for extent of improvement at visit 2 with same categories as resQ
resS    a numeric vector for extent of improvement at visit 3 with same categories as resQ

References

**strt**  
*Identify Stratification Variables*

**Description**  
This is a special function used in the context of **sanon**. It identifies stratification variables when they appear on the right hand side of a formula.

**Usage**  
$strt(x)$

**Arguments**  
x variable name

--

**summary.sanon**  
*Summarizing Weighted Least Squares Fits*

**Description**  
summary method for class "sanon".

**Usage**  

```r
## S3 method for class 'sanon'
summary(object, ...)
```

```r
## S3 method for class 'summary.sanon'
print(x, ...)
```

**Arguments**  
object, x an object of class "sanon", usually, a result of a call to **sanon**  
... further arguments passed to or from other methods.

**Details**  
This function provide the p value for the hypothesis test of coefficient in the model of weighted least squares method. Note that the estimates in the output are for the $(x_i - 0.5)$.

**Value**  
coefficients a p x 4 matrix with columns for the estimated coefficient, its standard error, chi-squared statistic and corresponding (two-sided) p-value.  
advarnames adjust variable names in weighted least squares method
Examples

 modelosname Example 3.1 Randomized Clinical Trial of Chronic Pain modelosname

data(cpain)
sum1 = summary(sanon(response ~ grp(treat, ref="placebo") + strt(center) + strt(diagnosis)
, data=cpain))
sum1

 modelosname Example 3.2 Randomized Clinical Trial of Respiratory Disorder modelosname

data(resp)
sum22 = summary(sanon(cbind(baseline, visit1, visit2, visit3, visit4)
~ grp(treatment, ref="P") + strt(center) + strt(sex) + covar(age), data=resp))
sum22

vcov.sanon Calculate Variance-Covariance Matrix for a Fitted Model Object

Description

Returns the variance-covariance matrix of the main parameters of a fitted model object.

Usage

## S3 method for class 'sanon'
vcov(object, ...)

Arguments

object an object of class "sanon", usually, a result of a call to sanon
...

Details

This is a generic function.

Value

Coefficients extracted from the model object object.

Examples

 modelosname Example 3.1 Randomized Clinical Trial of Chronic Pain modelosname

data(cpain)
out1 = sanon(response ~ grp(treat, ref="placebo") + strt(center) + strt(diagnosis), data=cpain)
vcov(out1)

 modelosname Example 3.2 Randomized Clinical Trial of Respiratory Disorder modelosname

data(resp)
P = rbind(rep(0, 4), diag(4), rep(0, 4))
out23 = sanon(cbind(baseline, visit1, visit2, visit3, visit4) ~ grp(treatment, ref="P")
+ strt(center) + strt(sex) + covar(age), data=resp, P=P)
# each four visits
vcov(out23)
Index

*Topic datasets
  cpain, 7
  heartburn, 8
  resp, 9
  sebor, 13
  skin, 14
*Topic documentation
  sanon-package, 2

catecovar, 2, 11
coef.sanon, 3
confint.sanon, 4
contrast, 5
covar, 6, 11
cpain, 7
grp, 7, 11

heartburn, 8

print.confint.sanon (confint.sanon), 4
print.contrast (contrast), 5
print.sanon (sanon), 10
print.summary.sanon (summary.sanon), 15

resp, 9

sanon, 2–7, 10, 11, 15, 16
sanon-package, 2
sebor, 13
skin, 14
strt, 11, 15
summary.sanon, 15

vcov.sanon, 16