

# Package: saws (via r-universe)

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**Type** Package

**Title** Small-Sample Adjustments for Wald Tests Using Sandwich Estimators

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**Description** Tests coefficients with sandwich estimator of variance and with small samples. Regression types supported are gee, linear regression, and conditional logistic regression.

**Depends** R (>= 2.6.0), gee, stats

**Suggests** MASS

**License** GPL (>= 2)

**NeedsCompilation** no

**Repository** <https://michaelfay-niaid.r-universe.dev>

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saws-package

*Small-Sample Adjustments for Wald tests Using Sandwich Estimators*

---

## Description

Tests coefficients with sandwich estimator of variance and with small samples. Regression types supported are gee, linear regression, and conditional logistic regression.

## Details

Package: saws  
Type: Package  
Version: 0.9-7.0  
Date: 2022-06-23  
License: GPL-2 or greater

The main function of this package is [saws](#), which takes output from some regression models (gee, linear regression, conditional logistic regression) and gives inferences (confidence intervals, p-values) using small sample adjusted sandwich estimators of variance. Using methods described in Fay and Graubard (2001).

The output from the regression model must be a list including the following three elements: The 'coefficients' is a vector with p parameter estimates, and is a standard output from the regression. The matrix 'u' is K by p with u[i,] the ith estimating equation, where there are K approximately independent estimating equations. The array 'omega' is K by p by p where omega[i,,] is a p by p matrix estimating - du/dbeta (here beta=coefficients). See Fay and Graubard (2001) for details.

Since the 'u' matrix and 'omega' array are not normally part of standard output, there are three specialized functions for creating regression output for use in the [saws](#) function: [mgee](#) (for gee), [lmfitSaws](#) (for linear models) and [clogistCalc](#) (for conditional logistic regression). For example, the function [mgee](#) does a gee analysis using the gee function of the gee package, takes the output and runs it through the [geeUOmega](#) function to create the 'u' matrix and the 'omega' array, and adds those onto the output from the gee (in the process other output from the gee may be corrected, see [geeUOmega](#)).

The cox regression function is not included in this version of the package. Unless there is demand (and I have time) it will not be included in a future version. There is a demo recreating the example in Fay and Graubard (2001).

## Author(s)

M.P. Fay

Maintainer: Michael Fay <mfay@niaid.nih.gov>

## References

Fay and Graubard (2001). Small-Sample Adjustments for Wald-Type Tests Using Sandwich Estimators. *Biometrics* 57: 1198-1206. (for copy see /inst/doc/ directory)

## Examples

```
library(gee)
data(warpbreaks)
g<-gee(breaks~tension,id=wool, data=warpbreaks, corstr="exchangeable")
guo<-geeUOmega(g)
saws(guo)
```

---

clogistCalc

*Conditional Logistic Regression fit*

---

## Description

Perform conditional logistic regression with output formatted for input into [saws](#) which will give confidence intervals and p-values.

## Usage

```
clogistCalc(n, m, x, set, initb = NA, h = 1e-04, maxitr = 15,
  epsilon = 1e-08, conf.level = 0.95)
clogistLoglike(n, m, x, beta)
clogistInfo(n, m, x, beta, h)
```

## Arguments

n	vector of number at risk
m	vector of number of events
x	matrix of covariates
set	vector of denoting clusters
initb	vector of initial parameter estimates, initb=NA uses unconditional logistic regression for initial estimate
h	small value for numeric integration
maxitr	maximum number of iterations
epsilon	convergence criteria (see details)
conf.level	confidence level for confidence intervals
beta	vector of current parameter estimate

## Details

The main program is `clogistCalc`. It calls `clogistLoglike` and `clogistInfo` which are not to be called explicitly. The function `clogistLoglike` finds the loglikelihood using recursive methods, and `clogistInfo` calculates score vector and information matrix using numerical methods. Both methods are described in Gail, Lubin and Rubinstein (1981), and the  $h$  value is the same as is defined in that paper.

The algorithm stops when the largest absolute relative change in either the loglikelihood or in any parameter is less than `epsilon`. For parameters close to zero (i.e., less than 0.01 in absolute value) the relative change is defined as `change/0.01`.

## Value

A list for input into the `saws` function, containing the following elements ( $K$ =number of clusters,  $p$ =number of parameters):

<code>coefficients</code>	$p$ by 1 vector of parameter estimates
<code>u</code>	$K$ by $p$ matrix of scores or estimating equations
<code>omega</code>	$K$ by $p$ by $p$ array of $-1$ *information

## Author(s)

Michael Fay, modeled after a Fortran program by Doug Midthune

## References

Gail, Lubin and Rubinstein (1981) *Biometrika*, 703-707

## See Also

See also [saws](#)

## Examples

```
data(micefat)
cout<-clogistCalc(micefat$N,micefat$NTUM,micefat[,c("fatCal","totalCal")],micefat$cluster)
## usual model based variance
saws(cout,method="dm")
## sandwich based variance with small sample correction
s3<-saws(cout,method="d3")
s3
print.default(s3)
```

---

dietfat

*Mammary Tumors and Different Types of Dietary Fat in Rodents*

---

### **Description**

This is a data set from a meta analysis described in Fay, Freedman, Clifford, and Midthune (1997).

### **Usage**

```
data(dietfat)
```

### **Format**

A data frame with 442 observations on the following 9 variables.

ARTICLE a numeric vector

SET a numeric vector

N a numeric vector

RESTRICT a numeric vector

PN3 a numeric vector

PN6 a numeric vector

PZERO a numeric vector

PMONO a numeric vector

NTUM a numeric vector

### **Details**

For relationship of article numbers to references see Article.numbers.txt in the /doc/ directory.

### **References**

Fay, MP, Freedman, LS, Clifford, CK, Midthune, DN. *Cancer Research* 57: 3979-3988.

Fay, MP, Graubard, BI. *Biometrics* 57: 1198-1206.

### **Examples**

```
data(dietfat)
## maybe str(dietfat) ; plot(dietfat) ...
```

---

`geeUOmega`*Modified gee function to output extra objects for saws*

---

**Description**

This function is normally not to be called directly, but one should usually use `mgee` (see warning below).

This function takes output from the `gee` function from the `gee` package and creates a score matrix (i.e., estimating equation) and information array (i.e., minus the derivative of the estimating equation). Note the function creates the X matrix assuming the data set is the same as it was for the original call to `gee`, see Warning section.

**Usage**

```
geeUOmega(geeOutput)
```

**Arguments**

`geeOutput`      object of class `gee`, output from `gee` function

**Value**

A `gee` object with two extra elements to the list, `u` and `omega` (see `saws`).

**Warning**

It is safer to use the `mgee` function, which internally calls `gee` then `geeUOmega`. If you do not use `mgee`, and instead call `geeUOmega` directly, there could be a problem if the data set has been changed after the initial `gee` call. This is because the model matrix (i.e., the X matrix) is not saved as part of the `gee` object, we must recreate it from the `gee` call. So it is created assuming that the data argument in `gee` means the same thing that it did when `gee` was called. So if you change the data set between the original `gee` call and using the `geeUOmega` function, there may be problems.

**Note**

The function recalculates the `fitted.values` and the residuals to the `gee` object, since in `gee` (version 4.13-18 at least) the `fitted.values` and residuals can be wrong if there is an offset or if `y` is a matrix (as in the binomial model).

**Author(s)**

M.P. Fay, with some lines copied from `gee` function

**See Also**

[gee](#), [mgee](#)

**Examples**

```
## example from gee help
data(warpbreaks)
geeout<-gee(breaks~tension,id=wool,data=warpbreaks,corstr="exchangeable")
guo<-geeU0mega(geeout)
saws(guo)
```

lmfitSaws

*Linear model function to output extra objects for saws***Description**

This is a very basic linear model function. It outputs only the objects needed for input into [saws](#).

**Usage**

```
lmfitSaws(x,y)
```

**Arguments**

x	design matrix
y	response vector

**Details**

The [saws](#) function requires three inputs, the parameter estimates (coefficients), u, and omega. The value u is the K by p matrix of estimating equations evaluated at the coefficient, where each row is an independent estimating equation. For the linear model  $u[i,] = x[i,] * \text{residual}[i]$ . The value omega is a K by p by p array, where  $\text{omega}[i,,]$  is the derivative of the ith estimating equation with respect to the parameter vector. For the linear model  $\text{omega}[i,,] = t(Xi)$

**Value**

A list with the following elements

coefficients	p by 1 coefficient vector
u	K by p matrix of estimating equations
omega	K by p by p array, see details

**Author(s)**

M.P. Fay

**References**

Fay and Graubard (2001). Small-Sample Adjustments for Wald-Type Tests Using Sandwich Estimators. *Biometrics* 57: 1198-1206. (for copy see /inst/doc/ directory)

**See Also**

link{lm}

**Examples**

```
set.seed(1)
n<-20
x1<-rnorm(n)
x2<-factor(c(rep("a",n/2),rep("b",n/2)))
y<-rnorm(n,x1)
out<-lmfitSaws(model.matrix(~x1*x2),y)
saws(out)
```

---

mgee

*Modified gee function to output extra objects for saws*

---

**Description**

This function calls the [gee](#) function from the [gee](#) package, then applies the [geeUOmega](#) function to it to create a score matrix (i.e., estimating equation) and information array (i.e., minus the derivative of the estimating equation). Since the [mgee](#) function just calls the [gee](#) function all help for [gee](#) applies to [mgee](#).

**Usage**

```
mgee(formula = formula(data), id = id, data = parent.frame(),
      subset, na.action, R = NULL, b = NULL, tol = 0.001,
      maxiter = 25, family = gaussian, corstr = "independence",
      Mv = 1, silent = TRUE, contrasts = NULL, scale.fix = FALSE,
      scale.value = 1, v4.4compat = FALSE)
```

**Arguments**

formula	see <a href="#">gee</a> help
id	see <a href="#">gee</a> help
data	see <a href="#">gee</a> help
subset	see <a href="#">gee</a> help
na.action	see <a href="#">gee</a> help
R	see <a href="#">gee</a> help
b	see <a href="#">gee</a> help
tol	see <a href="#">gee</a> help
maxiter	see <a href="#">gee</a> help
family	see <a href="#">gee</a> help
corstr	see <a href="#">gee</a> help

Mv	see gee help
silent	see gee help
contrasts	see gee help
scale.fix	see gee help
scale.value	see gee help
v4.4compat	see gee help

**Value**

A gee object with two extra elements to the list, u and omega (see [saws](#)).

**Note**

You can alternatively take the output from gee and apply the [geeUOmega](#) function. But see the warning for that function.

**Author(s)**

last few lines by M.P. Fay, for the rest see [gee](#) package DESCRIPTION

**See Also**

[gee](#), [geeUOmega](#)

**Examples**

```
## example from gee help
data(warpbreaks)
mout<-mgee(breaks~tension,id=wool,data=warpbreaks,corstr="exchangeable")
saws(mout)
```

---

micefat

*Dietary fat and Mammary tumors in Mice*

---

**Description**

Data from meta analysis of mice bred for spontaneous tumors and their response to different diets. The sources for the data are from the literature and listed in Freedman et al (1990).

**Usage**

```
data(micefat)
```

**Format**

A data frame with 57 observations on the following 5 variables.

NTUM number of mice in group with any mammary tumor

N number of mice in group

fatCal fat calories per day (kcal)

totalCal total calories per day (kcal)

cluster different experiments

**Source**

Freedman, LS, Clifford, C, and Messina, M (1990). *Cancer Research* 50: 5710-5719.

**Examples**

```
data(micefat)
head(micefat)
```

---

```
print.saws          Print saws object
```

---

**Description**

Prints confidence intervals and p-values from saws object.

**Usage**

```
## S3 method for class 'saws'
print(x, digits = NULL, ...)
```

**Arguments**

<code>x</code>	object of class 'saws'
<code>digits</code>	number of digits
<code>...</code>	other objects passed to print default

**Details**

The default is to test that each parameter (i.e., each Estimate) is 0. Then the output printed is those estimates with confidence intervals and p-values. Under the default the test matrix is a  $p \times p$  diagonal matrix, and `beta0` is a  $p \times 1$  matrix of 0. If the default is not true then the  $j$ th Estimate column represents the  $j$ th row of `test * coef - beta0`, where '\*' is matrix multiplication and 'coef' are the parameter estimates. Also when the default is not true, then the test matrix and `beta0` vector are printed.

---

saws	<i>Small sample Adjustments for Wald-type tests using Sandwich estimator of variance</i>
------	--

---

## Description

This function takes an object from a regression function and gives confidence intervals and p-values using the sandwich estimator of variance corrected for small samples.

## Usage

```
saws(x, test = diag(p), beta0 = matrix(0, p, 1),
     conf.level = 0.95, method = c("d3", "d5", "d1", "d2", "d4", "dm"), bound=.75)
```

## Arguments

<code>x</code>	a list containing three elements: coefficients, u, omega (see details)
<code>test</code>	either a numeric vector giving elements of coefficient to test, or an r by p matrix of constants for testing (see details)
<code>beta0</code>	null parameters for testing (see details)
<code>conf.level</code>	level for confidence intervals
<code>method</code>	one of "d3", "d5", "d1", "d2", "d4", or "dm" (see details)
<code>bound</code>	bound for bias correction, denoted b in Fay and Graubard, 2001

## Details

Typically, the x object is created in a specialized function. Currently there are three such functions, `link{lmfitSaws}`, `geeU0mega` and `clogistCalc`. The function `lmfitSaws` is a simple linear model function that creates all the output needed. The function `geeU0mega` takes output from the `gee` function of the `gee` package and creates the 'u' matrix and the 'omega' array. The 'coefficients' is a vector with p parameter estimates, and is a standard output from the regression. The matrix 'u' is K by p with `u[i,]` the ith estimating equation, where there are K approximately independent estimating equations. The array 'omega' is K by p by p where `omega[i,,]` is a p by p matrix estimating  $-du/dbeta$  (here `beta=coefficients`). See Fay and Graubard (2001) for details.

Suppose that the coefficient vector from the regression is `beta`. Then we test r hypotheses, based on the the matrix product,  $TEST (beta - beta_0) = 0$ , where TEST is an r by p matrix. If the argument 'test' is an r by p matrix (where r is arbitrary), then  $TEST = test$ . If 'test' is a vector, then each element of test corresponds to testing that row of beta is 0, i.e.,  $TEST <- diag(p)[test,]$ , where p is the length of the coefficient vector. For example, `test <- c(2,5)`, tests that  $beta[2] - beta_0[2] = 0$  and that  $beta[5] - beta_0[5] = 0$ . The alternatives are always two-sided.

There are several methods available. They are all discussed in Fay and Graubard (2001). The naming of the methods follows that paper (see for example Table 1, where `deltam` corresponds to `dm`, etc.):

**dm** the usual model based method which does not use the sandwich, uses a chi squared distribution

- d1** the standard sandwich method which makes no corrections for small samples
- d2** sandwich method, no bias correction, uses F distribution with  $df=dhat$  (see paper)
- d3** (default method:sandwich method, no bias correction, uses F distribution with  $df=dtilde$  (see paper)
- d4** sandwich method, with bias correction, uses F distribution with  $df=dhatH$  (see paper)
- d5** sandwich method, with bias correction, uses F distribution with  $df=dtildeH$  (see paper)

### Value

An object of class 'saws'. A list with elements:

<code>originalCall</code>	call from the original object
<code>method</code>	method used (see details)
<code>test</code>	test matrix (see details)
<code>beta0</code>	beta0 vector (see details)
<code>coefficients</code>	estimated coefficients
<code>df</code>	a vector of estimated degrees of freedom. This will have as many elements as there are coefficients
<code>V</code>	variance-covariance matrix
<code>se</code>	vector of standard errors of the coefficients
<code>t.value</code>	a vector of t-values: $test (coef - beta0)/se$
<code>p.value</code>	a vector of two-sided p-values
<code>conf.int</code>	p by 2 matrix of confidence intervals

### Note

For versions prior to 0.9-7.0, when there was an offset in the formula, the results where incorrect. See the NEWS file.

### Author(s)

M.P. Fay

### References

Fay and Graubard (2001). Small-Sample Adjustments for Wald-Type Tests Using Sandwich Estimators. *Biometrics* 57: 1198-1206. (for copy see `/inst/doc/` directory)

### See Also

For examples, see [geeUOmega](#) and [clogistCalc](#). See also [print.saws](#)

---

SDcorn

*Mammary tumors in Sprague-Dawley rats fed Corn Oil*

---

### Description

These data are part of a meta analysis to determine how fat calories and total calories effect the changes of getting a mammary tumor.

### Usage

```
data(SDcorn)
```

### Format

A data frame with 104 observations on the following 10 variables.

ARTICLE a numeric vector

NTUM a numeric vector

N a numeric vector

TFA2 a numeric vector

KCA2 a numeric vector

PFC a numeric vector

LOGIT a numeric vector

KCAL a numeric vector

SET a numeric vector

TEMPSET a numeric vector

### Details

Note the adjustment in Fay, Graubard, Freedman, and Midthune (1998) is slightly different from the one in Fay and Graubard (2001) so the [saws](#) does not match exactly with the 1998 paper.

For relationship of article numbers to references see Article.numbers.txt in the /doc/ directory.

### References

Fay, MP, Freedman, LS, Clifford, CK, Midthune, DN. Cancer Research 57: 3979-3988.

Fay, MP, Graubard, BI, Freedman, LS, Midthune, DN. Biometrics 54: 195-208.

Fay, MP, Graubard, BI. Biometrics 57: 1198-1206.

### Examples

```
data(SDcorn)
## maybe str(SDcorn) ; plot(SDcorn) ...
```

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