

# Package ‘BCRA’

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**Type** Package

**Title** Breast Cancer Risk Assessment

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**Description** Functions provide risk projections of invasive breast cancer based on Gail model according to National Cancer Institute's Breast Cancer Risk Assessment Tool algorithm for specified race/ethnic groups and age intervals.

**License** GPL (>= 2)

**NeedsCompilation** no

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## Description

This package is to project absolute risk of invasive breast cancer according to NCI's Breast Cancer Risk Assessment Tool (BCRAT) algorithm for specified race/ethnic groups and age intervals. The updated version 2.0 includes the new Hispanic model.

## Details

This package can be used to estimate the risk of developing breast cancer over a predetermined time interval with risk factors. As the same as Breast Cancer Risk Assessment SAS Macro, the users can specify the time interval as appropriate, not only limited to the 5 years risk prediction available with BCRAT.

The main function in this package is `absolute.risk`, which is defined based on a statistical model known as the "Gail model". Parameters and constants needed in this function include initial and projection age, recoded covariates using function `recode.check`, relative risks of BrCa at age "<50" and "≥50" obtained from function `relative.risk` as well as other known constants listed from function `list.constants` like BrCa composite incidences, competing hazards, 1-attributable risk using in NCI BrCa Risk Assessment Tool (NCI BCRAT). With risk factors and projection interval ages for a group of women, the function `absolute.risk` will return the corresponding absolute risk projections. If the function returns any missing values, the function `error.table` or `error.table.all` is used to find where the errors occurred. The function `check.summary` can give a quick check for errors of input file and missing values of risks.

For further analysis, a data frame is created from the function `risk.summary`, which includes age, duration of the projection time interval, covariates and the projected risk.

The version 2.0 includes absolute risk projections for Hispanic women (US born and Foreign born) based on race specific RR risk models developed on the San Francisco Bay Area Breast Cancer Study (SFBCS). Race specific attributable risks, breast cancer composite incidences and competing hazards are added to the updated package.

## Author(s)

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## References

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Gail MH, Brinton LA, Byar DP, Corle DK, Green SB, Shairer C, Mulvihill JJ. Projecting individualized probabilities of developing breast cancer for white females who are being examined annually. *JNCI* 81(24): 1879-86, 1989.

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absolute.risk

*Estimate absolute risks*

---

## Description

A function to estimate absolute risks of developing breast cancer

## Usage

```
absolute.risk(data, Raw_Ind=1, Avg_White=0)
```

## Arguments

data	A data set containing all the required input data needed to perform risk projections, such as initial age, projection age, BrCa relative risk covariates and race. See <code>exampledata</code> for details.
Raw_Ind	The raw file indicator with default value 1. <code>Raw_Ind=1</code> means RR covariates are in raw/original format. <code>Raw_Ind=0</code> means RR covariates have already been re-coded to 0, 1, 2 or 3.
Avg_White	Calculation indicator. <code>Avg_White=0</code> , calculate absolute risks; <code>Avg_White=1</code> , calculate average absolute risks based on the rates for average non-hispanic white women and average other (native american) women. The default value is 0.

## Details

For the projection of absolute risks, this function is defined based on Gail Model. Parameters and constants needed in this function include initial and projection age, recoded covariates from function `recode.check`, relative risks of BrCa at age "<50" and ">=50" from function `relative.risk` as well as other known constants like BrCa composite incidences, competing hazards, 1-attributable risk using in NCI BrCa Risk Assessment Tool (NCI BCRAT).

## Value

A vector which returns absolute risk values when `Avg_White=0` or average absolute risk values when `Avg_White=1`.

## See Also

[recode.check](#), [relative.risk](#)

**Examples**

```

data(exampledata)
# calculate absolute risk
absolute.risk(exampledata)
# calculate average absolute risk
Avg_White <- 1
absolute.risk(exampledata, Raw_Ind=1, Avg_White)

```

BrCa\_1\_AR

*Breast cancer 1-Attributable Risk***Description**

1-Attributable Risk

**Usage**

```
data("BrCa_1_AR")
```

**Format**

A data frame with 2 observations on the following 5 variables.

Wh.Gail White  
 AA.CARE African-American  
 HU.Gail Hispanic-American (US born)  
 NA.Gail Other (Native American and unknown race)  
 HF.Gail Hispanic-American (Foreign born)  
 Asian.AABCS Asian-American

BrCa\_beta

*Breast cancer beta***Description**

The logistic regression coefficients derived from the Gail model.

**Usage**

```
data("BrCa_beta")
```

**Format**

A data frame with 6 observations on the following 5 variables.

Wh.Gail White, Gail model  
 AA.CARE African-American, Care model  
 HU.Gail Hispanic-American (US born), Gail model  
 NA.Gail Other (Native American and unknown race), Gail model  
 HF.Gail Hispanic-American (Foreign born), Gail model  
 Asian.AABCS Asian-American, AABCS model

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 BrCa\_lambda1

*Breast cancer composite incidences*


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**Description**

Breast cancer composite incidences for different races and age groups from 20 to 90 by 5 years.

**Usage**

```
data("BrCa_lambda1")
```

**Format**

A data frame with 14 age groups on the following 12 variables.

Wh.1983\_87 White SEER 1983:1987

AA.1994\_98 African-American SEER 1994:1998

HU.1995\_04 Hispanic-American (US born) 1995:2004

NA.1983\_87 Native American and unknown race 1983:1987

HF.1995\_04 Hispanic-American (Foreign born) 1995:2004

Ch.1998\_02 Chinese-American SEER 18 1998:2002

Ja.1998\_02 Japanese-American SEER 18 1998:2002

Fi.1998\_02 Filipino-American SEER 18 1998:2002

Hw.1998\_02 Hawaiian SEER 18 1998:2002

oP.1998\_02 Other Pacific Islander SEER 18 1998:2002

oA.1998\_02 Other Asian SEER 1998:2002

Wh\_Avg.1992\_96 Average White SEER 1992:1996

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 BrCa\_lambda2

*Breast cancer competing mortality*


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**Description**

Breast cancer competing mortality for different races and age groups from 20 to 90 by 5 years.

**Usage**

```
data("BrCa_lambda2")
```

**Format**

A data frame with 14 age groups on the following 12 variables.

Wh.1983\_87 White SEER 1983:1987  
 AA.1994\_98 African-American SEER 1994:1998  
 HU.1995\_04 Hispanic-American (US born) 1995:2004  
 NA.1983\_87 Native American and unknown race 1983:1987  
 HF.1995\_04 Hispanic-American (Foreign born) 1995:2004  
 Ch.1998\_02 Chinese-American SEER 18 1998:2002  
 Ja.1998\_02 Japanese-American SEER 18 1998:2002  
 Fi.1998\_02 Filipino-American SEER 18 1998:2002  
 Hw.1998\_02 Hawaiian SEER 18 1998:2002  
 oP.1998\_02 Other Pacific Islander SEER 18 1998:2002  
 oA.1998\_02 Other Asian SEER 1998:2002  
 Wh\_Avg.1992\_96 Average White SEER 1992:1996

---

check.summary

*Summarize the error indicators, relative risks and absolute risks*

---

**Description**

A function to show descriptive statistics by applying function mean and sd to the quantities Error\_Ind, AbsRisk, RR\_Star1 and RR\_Star2.

**Usage**

```
check.summary(data, Raw_Ind=1, Avg_White=0)
```

**Arguments**

data	A data set containing all the required input data needed to perform risk projections, such as initial age, projection age, BrCa relative risk covariates and race. See <code>exampledata</code> for details.
Raw_Ind	The raw file indicator with default value 1. Raw_Ind=1 means RR covariates are in raw/original format. Raw_Ind=0 means RR covariates have already been re-coded to 0, 1, 2 or 3.
Avg_White	Calculation indicator. Avg_White=0, calculate absolute risks; Avg_White=1, calculate average absolute risks based on the rates for average non-hispanic white women and average other (native american) women. The default value is 0.

**Details**

When the mean and standard deviation for the variable Error\_Ind is 0, implies that no errors have not been found. Otherwise when the mean and std for Error\_Ind is not 0, implies that errors have been found. When errors are found, the number of records with errors is the count associated with AbsRisk listed under NMiss (number of missing).

**Value**

A summary table for error indicators, relative risks and absolute risks

**See Also**

[recode.check](#), [relative.risk](#), [absolute.risk](#)

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error.table	<i>List the records and errors for IDs with missing absolute risks</i>
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---

**Description**

A function to list the records and errors for IDs with missing absolute risks. For each of the records with error, the record is listed followed by a line which gives some indication as to where the error occurred. Relative risks and risk pattern numbers are also included.

**Usage**

```
error.table(data, Raw_Ind=1)
```

**Arguments**

data	A data set containing all the required input data needed to perform risk projections, such as initial age, projection age, BrCa relative risk covariates and race. See <code>exampledata</code> for details.
Raw_Ind	The raw file indicator with default value 1. <code>Raw_Ind=1</code> means RR covariates are in raw/original format. <code>Raw_Ind=0</code> means RR covariates have already been re-coded to 0, 1, 2 or 3.

**Value**

A data frame listing the raw records, errors, relative risks and pattern numbers for IDs with missing absolute risks. If there is nothing wrong with the input data, the function will return "NO ERROR!".

**See Also**

[recode.check](#), [error.table.all](#)

`error.table.all`      *List all records and errors*

---

### Description

A function to list all records with both raw values and recoded values (or indications for errors). For each of the records, the record is listed followed by a line which gives some indication as to where the error occurred.

### Usage

```
error.table.all(data, Raw_Ind=1)
```

### Arguments

<code>data</code>	A data set containing all the required input data needed to perform risk projections, such as initial age, projection age, BrCa relative risk covariates and race. See <code>exampledata</code> for details.
<code>Raw_Ind</code>	The raw file indicator with default value 1. <code>Raw_Ind=1</code> means RR covariates are in raw/original format. <code>Raw_Ind=0</code> means RR covariates have already been re-coded to 0, 1, 2 or 3.

### Value

A data frame listing all records and errors. If there is nothing wrong with the input data, the function will return "NO ERROR!".

### See Also

[recode.check](#), [error.table](#)

---

`exampledata`      *Example data set*

---

### Description

A data set containing all the required input data needed to perform risk projections, such as initial age, projection age, BrCa relative risk covariates and race.

### Usage

```
data("exampledata")
```



**Format**

A data frame with 26 observations on the following 9 variables.

ID Woman's ID, positive integer 1, 2, 3,...

T1 Initial age, all real numbers T1 in [20, 90).

T2 BrCa projection age, all real numbers T2 in (20,90] such that T1<T2.

N\_Biop The number of biopsies, 0, 1, 2, ..., 99=unk (99 recoded to 0).

HypPlas Did biopsy display atypical hyperplasia? 0=no, 1=yes, 99=unk or not applicable.

AgeMen Age at menarchy, less than or equal to initial age, 99=unk.

Age1st Age at first live birth, greater or equal to age at menarchy and less than or equal to initial age, 98=nulliparous, 99=unk.

N\_Rels The number of 1st degree relatives with BrCa, 0, 1, 2, ... 99=unk.

Race Race, positive integer 1, 2, 3, ..., 11. See details.

**Details**

1=Wh	White 1983-87 SEER rates (rates used in NCI BCRAT)
2=AA	African-American
3=HU	Hispanic-American (US born) 1995-04
4=NA	Other (Native American and unknown race)
5=HF	Hispanic-American (Foreign born) 1995-04
6=Ch	Chinese-American
7=Ja	Japanese-American
8=Fi	Filipino-American
9=Hw	Hawaiian-American
10=oP	Other Pacific Islander
11=oA	Other Asian

---

list.constants

*List all constants required for BrCa absolute risk projections*

---

**Description**

A function to create a text file under user's working directory which contains all constants required for BrCa absolute risk projections.

**Usage**

```
list.constants(BrCa_lambda1, BrCa_lambda2, BrCa_beta, BrCa_1_AR)
```

**Arguments**

BrCa_lambda1	Breast Cancer Composite Incidences
BrCa_lambda2	Breast Cancer Competing Mortality
BrCa_beta	The logistic regression coefficients (beta) derived from the Gail model
BrCa_1_AR	1-Attributable Risk

**Details**

See "BrCa\_lambda1.rda", "BrCa\_lambda2.rda", "BrCa\_beta.rda", "BrCa\_1\_AR.rda" in package data folder.

**Value**

A text file "list\_all\_constants.txt" exported under user's working directory for reading convenience.

---

recode.check

*Recode and check the relative risk covariate values*

---

**Description**

A function to recode the relative risk covariates and check errors.

**Usage**

```
recode.check(data, Raw_Ind=1)
```

**Arguments**

data	A data set containing all the required input data needed to perform risk projections, such as initial age, projection age, BrCa relative risk covariates and race. See <code>exampledata</code> for details.
Raw_Ind	The raw file indicator with default value 1. Raw_Ind=1 means RR covariates are in raw/original format. Raw_Ind=0 means RR covariates have already been re-coded to 0, 1, 2 or 3.

**Details**

This function is to recode the following relative risk covariates. Recoded RR covariates are named as NB\_Cat, AM\_Cat, AF\_Cat and NR\_Cat for N\_Biop, AgeMen, Age1st and N\_Rels, respectively.

N_Biop:	The number of biopsies.
AgeMen:	Age at menarchy.
Age1st:	Age at first live birth.
N_Rels:	The number of first degree relatives with BrCa.

See the following table for recoding details.

Covariate	Raw Value	Recoded to
N_Biop	0 or 99 (unk or not applicable)	0
	1	1
	2,3,4 ... and not 99	2
AgeMen	14,15,16 ... or 99 (unk)	0
	12,13	1
	11 and younger	2
Age1st	19 and younger or 99 (unk)	0

	20,21,22,23,24	1
	25,26,27,28,29 or 98 (nulliparous)	2
	30,31,32 ... and not 98 and not 99	3
N_Rels	0 or 99 (unk)	0
	1	1
	2,3,4 ... and not 99	2

This function is also used to check consistency and errors of input data. Let set\_T1\_missing and set\_T2\_missing be the checking variables for T1 and T2. The constraint on T1 and T2 is  $20 \leq T1 < T2 \leq 90$ . If it is violated, set\_T1\_missing and set\_T2\_missing and the absolute risk will be set to the missing value NA.

Let RacCat be the checking variable for Race. If the Race value is not included in the 11 races defined, the absolute risk will be set to the missing value NA and RacCat will be set to "U" (undefined). The corresponding character of Race CharRace will be set to "??".

Let set\_HyperP\_missing and set\_R\_Hyp\_missing be the checking variables for HypPlas and R\_Hyp. Consistency patterns for the number of Biopsies and Hyperplasia are:

- Requirement (A) N\_Biops=0 or 99, then HypPlas MUST = 99 (not applicable).
- Requirement (B) N\_Biops>0 and <99, then HypPlas = 0, 1 or 99.

If ANY of the above 2 REQUIREMENTS is violated, NB\_Cat, set\_HyperP\_missing and set\_R\_Hyp\_missing will be set to the corresponding character "A" or "B" and the absolute risk will be set to the missing value NA. The consequences to the relative risk (RR) for the above two requirements are:

- (A) N\_Biops=0 or 99, HypPlas=99 (not applicable) inflates RR by 1.00.
- (B) N\_Biops>0 and <99, HypPlas=0 (no) inflates RR by 0.93;
- N\_Biops>0 and <99, HypPlas=1 (yes) inflates RR by 1.82;
- N\_Biops>0 and <99, HypPlas=99 (unk) inflates RR by 1.00.

For remaining relative risk covariates, AgeMen, Age1st and N\_Rels:

- AgeMen Age at menarchy must be postive integer less than or equal to initial age T1.  
NOTE: (1) For African-American women AgeMen<=11 are grouped with AgeMen=12 or 13. (2) For US Born Hispanic women AgeMen is not included in the RR model and all values for this variable are recoded to 0.
- Age1st Age at 1st live birth must be postive integer greater than equal to AgeMen and less than or equal to initial age T1.  
NOTE: (1) For African-American women, Age1st is not included in the RR model and all values for this variable are recoded to 0. (2) For US Born and Foreign Born Hispanic women, the recoding for this variable follows:

Age1st	19 and younger or 99 (unk)	0
	20 - 29	1
	30+ or 98 (nulliparous) and not 99	2

N\_Rels The number of 1st degree relatives with BrCa must be 0,1,2....

NOTE: For Asian-Americans Race=6-11 and Hispanic-Americans (US and foreign born), the number of 1st degree relative coded value of 2 gets grouped with 1.

### Value

A data frame containing the error indicators, recoded covariates as well as other checking variables defined for checking the consistency of the input data.

### See Also

[error.table.all](#), [error.table](#)

### Examples

```
data(exampledata)
recode.check(exampledata)
```

---

relative.risk	<i>Estimate relative risks</i>
---------------	--------------------------------

---

### Description

A function to estimate relative risks for risk factor combinations

### Usage

```
relative.risk(data, Raw_Ind=1)
```

### Arguments

data	A data set containing all the required input data needed to perform risk projections, such as initial age, projection age, BrCa relative risk covariates and race. See <code>exampledata</code> for details.
Raw_Ind	The raw file indicator with default value 1. Raw_Ind=1 means RR covariates are in raw/original format. Raw_Ind=0 means RR covariates have already been re-coded to 0, 1, 2 or 3.

### Details

The age is dichotomized as "age less than 50 years" and "age 50 years or more". The relative risks can be obtained from Gail Model, an unconditional logistic regression that included main effects NB\_Cat, AM\_Cat, AF\_Cat, NR\_Cat as well as interactions between AF\_Cat and NR\_Cat and between the age category and NR\_Cat.

### Value

RR_Star1	Relative risk for woman of interest at ages < 50.
RR_Star2	Relative risk for woman of interest at ages >= 50.
PatternNumber	The sequence number of risk patterns. There are 3 levels for NB_Cat, 3 for AM_Cat, 4 for AF_Cat, 3 for NR_Cat, $3*3*4*3 = 108$ patterns in total. Pattern Number=NB_Cat*3*3*4+AM_Cat*3*4+AF_Cat*3+NR_Cat*1+1.

**See Also**[recode.check](#)**Examples**

```
data(exampdata)
relative.risk(exampdata)
```

---

`risk.summary`*List the records with relative risks and absolute risks*

---

**Description**

A function to list all the records with relative risks and absolute risks.

**Usage**

```
risk.summary(data, Raw_Ind=1)
```

**Arguments**

<code>data</code>	A data set containing all the required input data needed to perform risk projections, such as initial age, projection age, BrCa relative risk covariates and race. See <code>exampdata</code> for details.
<code>Raw_Ind</code>	The raw file indicator with default value 1. <code>Raw_Ind=1</code> means RR covariates are in raw/original format. <code>Raw_Ind=0</code> means RR covariates have already been re-coded to 0, 1, 2 or 3.

**Value**

A data frame that includes age, duration of the projection time interval, covariates and the projected risk. A CSV file is created to save the data frame under user's working directory for reading convenience.

**See Also**[relative.risk](#), [absolute.risk](#)**Examples**

```
data(exampdata)
risk.summary(exampdata)
```

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