

Current Default Penetrance of BRCAPRO

Description

Data frame of penetrance functions for breast and ovarian cancer by gender, BRCA mutation status, and age.

Usage

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data(BRCApenet.metaDSL.2006)
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Format

A data frame of penetrance information by gender, mutation status on BRCA1/2, and age. Entries are the net probability of developing cancer in a one-year interval, in the absence of death or censoring. The female penetrances are obtained by combining the best available published estimates with a large set of tested families assembled through the NCI's Cancer Genetics Network. For details, please see the reference.

The female penetrance estimates are based on a nine study meta-analysis using the DerSimonian and Laird random effect modeling approach (Chen et al. 2006). The male penetrance estimates are based on one of the largest US-based cohort collected both prospectively and retrospectively through the Cancer Genetics Network (Tai et al. 2006).

The data frame has 16 columns, each with 110 entries corresponding to ages 1 to 110; the column names are coded as follows

f generic for density, or probability in one-year intervals, as opposed to cumulative probability

M/F gender

X/Y cancer site, X–Breast, Y–Ovarian

1/2/0/12 Mutation status of gene1 (BRCA1) and gene2 (BRCA2)

1 mutation(s) of gene 1 only

2 mutation(s) of gene 2 only

0 no mutation on gene1 or gene2

12 mutation(s) of both gene 1 and gene 2

This results in the following 16 labels

fFX0 breast cancer, females, noncarriers

fFY0 ovarian cancer, females, noncarriers

fFX1 breast cancer, females, deleterious mutation(s) of BRCA1

fFY1 ovarian cancer, females, deleterious mutation(s) of BRCA1

fFX2 breast cancer, females, deleterious mutation(s) of BRCA2

fFY2 ovarian cancer, females, deleterious mutation(s) of BRCA2

fFX12 breast cancer, females, deleterious mutation(s) of both BRCA1 and BRCA2

fFY12 ovarian cancer, females, deleterious mutation(s) of both BRCA1 and BRCA2

fMX0 breast cancer, males, noncarriers

fMY0 ovarian cancer, males, noncarriers

fMX1 breast cancer, males, deleterious mutation(s) of BRCA1
fMY1 ovarian cancer, males, deleterious mutation(s) of BRCA1
fMX2 breast cancer, males, deleterious mutation(s) of BRCA2
fFY2 ovarian cancer, males, deleterious mutation(s) of BRCA2
fMX12 breast cancer, males, deleterious mutation(s) of both BRCA1 and BRCA2
fMY12 ovarian cancer, males, deleterious mutation(s) of both BRCA1 and BRCA2

Male cancer incidence at cancer site Y (ovaries) are set to 0.

References

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[Package *BayesMendel* version 1.4-1] [_____](#)