Package ‘iCARE’

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Title A Tool for Individualized Coherent Absolute Risk Estimation (iCARE)

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Description An R package to compute Individualized Coherent Absolute Risk Estimators.

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Suggests RUnit, BiocGenerics

License GPL-3 + file LICENSE

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biocViews Software, StatisticalMethod, GenomeWideAssociation

NeedsCompilation yes

R topics documented:

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bc_data Data for examples

Description

Data for `computeAbsoluteRisk` and `computeAbsoluteRiskSplitInterval`

Details

"mort_inc" contains age-specific incidence rates of all-cause mortality from reference (1) below
"bc_15_snps" contains published SNP information from reference (2)
"bc_inc" contains age-specific incidence rates of breast cancer from reference (3)
"ref_cov_dat" contains a subsample of data imputed using reference (4) and (5)
computeAbsoluteRisk

References


Examples
```r
temp <- data(bc_data, package="iCARE")
# Display the object names
temp
```

computeAbsoluteRisk  Building and Applying an Absolute Risk Model

Description
This function is used to build absolute risk models and apply them to estimate absolute risks.

Usage
```r
computeAbsoluteRisk(model.formula = NULL, model.cov.info = NULL, model.snp.info = NULL, model.log.RR = NULL, model.ref.dataset = NULL, model.ref.dataset.weights = NULL, model.disease.incidence.rates, model.competing.incidence.rates = NULL, model.bin.fh.name = NA, n.imp = 5, apply.age.start, apply.age.interval.length, apply.cov.profile = NULL, apply.snp.profile = NULL, use.c.code = 1, return.lp = FALSE, return.refs.risk = FALSE)
```
computeAbsoluteRisk

Arguments

- **model.formula**: an object of class `formula`: a symbolic description of the model to be fitted, e.g. `Y~Parity+FamilyHistory`.
- **model.cov.info**: contains information about the risk factors in the model; a main list containing a list for each covariate, which must have the fields:
  - **"name"**: a string with the covariate name, matching name in `model.formula`
  - **"type"**: a string that is either "continuous" or "factor". If factor variable, then:
    - **"levels"**: vector with strings of level names
    - **"ref"**: optional field, string with name of referent level
- **model.snp.info**
  - dataframe with three columns, named: ["snp.name", "snp.odds.ratio", "snp.freq" ]
- **model.log.RR**: vector with log odds ratios corresponding to the model params; no intercept; names must match design matrix arising from `model.formula` and `model.cov.info`; check names using function `check_design_matrix()`.
- **model.ref.dataset**: dataframe of risk factors for a sample of subjects representative of underlying population, no missing values. Variables must be in same order with same names as in `model.formula`.
- **model.ref.dataset.weights**: optional vector of sampling weights for `model.ref.dataset`.
- **model.disease.incidence.rates**: two column matrix [ integer ages, incidence rates] or three column matrix [start age, end age, rate] with incidence rate of disease. Must fully cover age interval for estimation.
- **model.competing.incidence.rates**: two column matrix [ integer ages, incidence rates] or three column matrix [start age, end age, rate] with incidence rate of competing events. Must fully cover age interval for estimation.
- **model.bin.fh.name**: string name of family history variable, if in model. This must refer to a variable that only takes values 0,1, NA.
- **n.imp**: integer value for number of imputations for handling missing SNPs.
- **apply.age.start**: single integer or vector of integer ages for the start of the interval over which to compute absolute risk.
- **apply.age.interval.length**: single integer or vector of integer years over which absolute risk should be computed.
- **apply.cov.profile**: dataframe containing the covariate profiles for which absolute risk will be computed. Covariates must be in same order with same names as in `model.formula`.
- **apply.snp.profile**: data frame with observed SNP data (coded 0,1, 2, or NA). May have missing values.
computeAbsoluteRisk

use.c.code  
binary indicator of whether to run the c program for fast computation.

return.lp  
binary indicator of whether to return the linear predictor for each subject in apply.cov.profile.

return.refs.risk  
binary indicator of whether to return the absolute risk prediction for each subject in model.ref.dataset.

Details

Individualized Coherent Absolute Risk Estimators (iCARE) is a tool that allows researchers to quickly build models for absolute risk and apply them to estimate individuals’ risk based on a set of user defined input parameters. The software gives users the flexibility to change or update models rapidly based on new risk factors or tailor models to different populations based on the specification of simply three input arguments:

• (1) a model for relative risk assumed to be externally derived
• (2) an age-specific disease incidence rate and
• (3) the distribution of risk factors for the population of interest.

The tool can handle missing information on risk factors for risk estimation using an approach where all estimates are derived from a single model through appropriate model averaging.

Value

This function returns a list of results objects, including:

• risk: absolute risk estimates over the specified interval for subjects given by apply.cov.profile
• details: dataframe with the start of the interval, the end of the interval, the covariate profile, and the risk estimates for each individual
• beta.used: the log odds ratios used in the model
• lps: linear predictors for subjects in model.cov.profile, if requested by return.lp
• refs.risk: absolute risk estimates for subjects in model.ref.dataset, if requested by return.refs.risk; computes for first age interval provided

Examples

data(bc_data, package="iCARE")
results = computeAbsoluteRisk(model.formula = caco ~ famhist + as.factor(parity),
model.cov.info = bc_model_cov_info,
model.snp.info = bc_15_snps,
model.log.RR = bc_model_log_or,
model.ref.dataset = ref_cov_dat,
model.disease.incidence.rates = bc_inc,
model.competing.incidence.rates = mort_inc,
model.bin.fh.name = "famhist",
apply.age.start = 50,
apply.age.interval.length = 30,
apply.cov.profile = new_cov_prof,
computeAbsoluteRiskSplitInterval

apply.snp.profile = new_snp_prof,
return.refs.risk = TRUE)

summary(results$risk)
plot(density(results$risk, na.rm=TRUE))
boxplot(results$risk ~ new_cov_prof$famhist, na.rm=TRUE)

computeAbsoluteRiskSplitInterval

Building and Applying an Absolute Risk Model: Compute Risk over Interval Split in Two Parts

Description
This function is used to build an absolute risk model that incorporates different input parameters before and after a given time point. The model is then applied to estimate absolute risks.

Usage
computeAbsoluteRiskSplitInterval(apply.age.start, apply.age.interval.length,
apply.cov.profile, model.formula, model.disease.incidence.rates, model.log.RR,
model.ref.dataset, model.ref.dataset.weights=NULL, model.cov.info, use.c.code=1,
model.competing.incidence.rates=NULL, return.lp=FALSE, apply.snp.profile=NULL,
model.snp.info=NULL, model.bin.fh.name=NULL, cut.time=NULL,
apply.cov.profile.2=NULL, model.formula.2=NULL, model.log.RR.2=NULL,
model.ref.dataset.2=NULL, model.ref.dataset.weights.2=NULL, model.cov.info.2=NULL,
model.bin.fh.name.2=NULL, n.imp=5, return.refs.risk=FALSE)

Arguments
apply.age.start
single integer or vector of integer ages for the start of the interval over which to compute absolute risk.

apply.age.interval.length
single integer or vector of integer years over which absolute risk should be computed.

apply.cov.profile
dataframe containing the covariate profiles for which absolute risk will be computed. Covariates must be in same order with same names as in model.formula.

model.formula
an object of class formula: a symbolic description of the model to be fitted, e.g. Y~Parity+FamilyHistory.

model.disease.incidence.rates	
two column matrix [integer ages, incidence rates] or three column matrix [start age, end age, rate] with incidence rate of disease. Must fully cover age interval for estimation.

model.log.RR
vector with log odds ratios corresponding to the model params; no intercept; names must match design matrix arising from model.formula and model.cov.info; check names using function check_design_matrix().

model.ref.dataset
dataframe of risk factors for a sample of subjects representative of underlying population, no missing values. Variables must be in same order with same names as in model.formula.
model.ref.dataset.weights
optional vector of sampling weights for model.ref.dataset.

model.cov.info
contains information about the risk factors in the model; a main list containing
a list for each covariate, which must have the fields:

• "name": a string with the covariate name, matching name in model.formula

• "type": a string that is either "continuous" or "factor".

If factor variable, then:

• "levels": vector with strings of level names

• "ref": optional field, string with name of referent level

use.c.code
binary indicator of whether to run the c program for fast computation.

model.competing.incidence.rates
two column matrix [integer ages, incidence rates] or three column matrix [start age, end age, rate] with incidence rate of competing events. Must fully cover age interval for estimation.

return.lp
binary indicator of whether to return the linear predictor for each subject in apply.cov.profile.

apply.snp.profile
data frame with observed SNP data (coded 0, 1, 2, or NA). May have missing values.

model.snp.info
dataframe with three columns [rs number, odds ratio, allele frequency]

model.bin.fh.name
string name of family history variable, if in model. This must refer to a variable that only takes values 0, 1, NA.

cut.time
integer age for which to split computation into before and after

apply.cov.profile.2
see apply.cov.profile, to be used for estimation in ages after the cutpoint

model.formula.2
see model.formula, to be used for estimation in ages after the cutpoint

model.log.RR.2
see model.log.RR, to be used for estimation in ages after the cutpoint

model.ref.dataset.2
see model.ref.dataset, to be used for estimation in ages after the cutpoint

model.ref.dataset.weights.2
see model.ref.dataset.weights, to be used for estimation in ages after the cutpoint

model.cov.info.2
see model.cov.info, to be used for estimation in ages after the cutpoint

model.bin.fh.name.2
see model.bin.fh.name, to be used for estimation in ages after the cutpoint

n.imp
integer value for number of imputations for handling missing SNPs.

return.refs.risk
binary indicator of whether to return the absolute risk prediction for each subject in model.ref.dataset.
Details

Individualized Coherent Absolute Risk Estimators (iCARE) is a tool that allows researchers to quickly build models for absolute risk and apply them to estimate individuals' risk based on a set of user defined input parameters. The software gives users the flexibility to change or update models rapidly based on new risk factors or tailor models to different populations based on the specification of simply three input arguments:

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The tool can handle missing information on risk factors for risk estimation using an approach where all estimates are derived from a single model through appropriate model averaging.

Value

This function returns a list of results objects, including:

- risk: absolute risk estimates over the specified interval for subjects given by apply.cov.profile
- details: dataframe with the start of the interval, the end of the interval, the covariate profile, and the risk estimates for each individual
- beta.used: the log odds ratios used in the model
- lps.1: linear predictors based on first set of parameters for subjects in model.cov.profile, if requested by return.lp
- lps.2: linear predictors based on second set of parameters for subjects in model.cov.profile, if requested by return.lp
- refs.risk: absolute risk estimates for subjects in model.ref.dataset, if requested by return.refs.risk; computes for first age interval provided

Examples

data(bc_data, package="iCARE")

form <- caco ~ famhist + as.factor(parity)
results <- computeAbsoluteRiskSplitInterval(model.formula=form,
cut.time = 50,
model.cov.info = bc_model_cov_info,
model.snp.info = bc_15_snps,
model.log.RR = bc_model_log_or,
model.log.RR.2 = bc_model_log_or_post_50,
model.ref.dataset = ref_cov_dat,
model.ref.dataset.2 = ref_cov_dat_post_50,
model.disease.incidence.rates = bc_inc,
model.competing.incidence.rates = mort_inc,
model.bin.fh.name = "famhist",
apply.age.start = 30,
apply.age.interval.length = 40,
iCARE

A Tool for Individualized Coherent Absolute Risk Estimation (iCARE)

Description

Individualized Coherent Absolute Risk Estimators (iCARE) is a tool that allows researchers to quickly build models for absolute risk and apply them to estimate individuals’ risk based on a set of user defined input parameters. The software gives users the flexibility to change or update models rapidly based on new risk factors or tailor models to different populations based on the specification of simply three input arguments: (1) a model for relative risk assumed to be externally derived (2) an age-specific disease incidence rate and (3) the distribution of risk factors for the population of interest. The tool can handle missing information on risk factors for risk estimation using an approach where all estimates are derived from a single model through appropriate model averaging.

Details

The main functions for building and applying an absolute risk model are computeAbsoluteRisk and computeAbsoluteRiskSplitInterval. The first of these computes absolute risks over the specified time interval using a single set of parameters. The second provides more advanced functionality and computes absolute risk over the interval in two parts. computeAbsoluteRiskSplitInterval allows the user to compute absolute risk over the interval in two parts, incorporating two different sets of parameters before and after a specified cutpoint. This function allows a different cutpoint for each covariate profile if desired.

Author(s)

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