iCARE (Individualized Coherent Absolute Risk Estimators) Package

October 24, 2023

```r
> library(iCARE)

Example 1.A

Load the breast cancer data.

```r
> data("bc_data", package="iCARE")
```

In this example, we will estimate the risk of breast cancer in ages 50-80. A SNP-only model is fit, with no specific genotypes supplied for estimation. The population disease rates are from SEER.

```r
> res_snps_miss = computeAbsoluteRisk(model.snp.info = bc_72_snps,
+ model.disease.incidence.rates = bc_inc,
+ model.competing.incidence.rates = mort_inc,
+ apply.age.start = 50,
+ apply.age.interval.length = 30,
+ return.refs.risk=TRUE)
```

Note: You did not provide apply.snp.profile. Will impute SNPs for 10000 people.

If require more, please provide apply.snp.profile input.

[1] "Note: As specified, the model does not adjust SNP imputations for family history."

```
user  system elapsed
11.338  0.145  11.483
```

Compute a summary of the risks and visualize the results

```r
> summary(res_snps_miss$risk)
```

<table>
<thead>
<tr>
<th>Risk_Estimate</th>
</tr>
</thead>
<tbody>
<tr>
<td>Min.</td>
</tr>
<tr>
<td>1st Qu.</td>
</tr>
<tr>
<td>Median</td>
</tr>
<tr>
<td>Mean</td>
</tr>
<tr>
<td>3rd Qu.</td>
</tr>
<tr>
<td>Max.</td>
</tr>
</tbody>
</table>

```r
> summary(res_snps_miss$refs.risk)
```

1
Example 1.B

In this example, we will again estimate the risk of breast cancer in ages 50-80. This time however, three specific genotypes are supplied for estimation (with some missing data). The argument return.refs.risk = TRUE, includes the referent dataset risks be included in results.

```r
> res_snps_dat = computeAbsoluteRisk(model.snp.info = bc_72_snps,
+     model.disease.incidence.rates = bc_inc,
+     model.competing.incidence.rates = mort_inc,
+     apply.age.start = 50,
+     apply.age.interval.length = 30,
+     apply.snp.profile = new_snp_prof,
+     return.refs.risk = TRUE)

Note: As specified, the model does not adjust SNP imputations for family history.
```

[1] "Note: As specified, the model does not adjust SNP imputations for family history."
Visualize the Results

```r
> plot(density(res_snps_dat$refs.risk), lwd=2,
+     main="Referent SNP-only Risk Distribution: Ages 50-80",
+     xlab="Absolute Risk of Breast Cancer")
> abline(v=res_snps_dat$risk, col="red")
> legend("topright", legend="New Profiles", col="red", lwd=1)
```

Example 2

In this example, we will estimate the risk of breast cancer in ages 50-80 by fitting a model with 13 risk factors and 72 SNPs.

```r
> res_covs_snps = computeAbsoluteRisk(model.formula=bc_model_formula,
+                                        model.cov.info=bc_model_cov_info,
+                                        model.snp.info=bc_72_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,
```
Display details of the fit

```r
> print(res_covs_snps$details)

<table>
<thead>
<tr>
<th>Int_Start</th>
<th>Int_End</th>
<th>Risk_Estimate</th>
<th>rs616488</th>
<th>rs11552449</th>
<th>rs11249433</th>
<th>rs12405132</th>
<th>rs12048493</th>
<th>rs6678914</th>
<th>rs4245739</th>
<th>rs72755295</th>
<th>rs12710696</th>
<th>rs4849887</th>
<th>rs2016394</th>
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</thead>
<tbody>
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<td>NA</td>
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<td>NA</td>
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<th>rs132390</th>
<th>rs6001930</th>
<th>famhist</th>
<th>menarche_dec</th>
<th>parity</th>
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</table>
```
```
1 1 1 0 0 0 0 8 0
2 1 0 0 0 0 0 10 0
3 0 0 0 0 0 0 1 0

birth_dec agemeno_dec height_dec bmi_dec rd_menohrt rd2_everhrt_e
1 2 2 6 10 1 0
2 2 1 6 4 1 0
3 1 7 1 10 1 0

rd2_everhrt_c rd2_currhrt alcoholdweek_dec ever_smoke
1 0 0 1 1
2 0 0 6 0
3 0 0 1 1
```

Session Information

```r
> sessionInfo()

R version 4.3.1 (2023-06-16)
Platform: x86_64-pc-linux-gnu (64-bit)
Running under: Ubuntu 22.04.3 LTS

Matrix products: default
BLAS: /home/biocbuild/bbs-3.18-bioc/R/lib/libRblas.so
LAPACK: /usr/lib/x86_64-linux-gnu/lapack/liblapack.so.3.10.0

locale:
[1] LC_CTYPE=en_US.UTF-8 LC_NUMERIC=C
[3] LC_TIME=en_GB LC_COLLATE=C
[5] LC_MONETARY=en_US.UTF-8 LC_MESSAGES=en_US.UTF-8
[7] LC_PAPER=en_US.UTF-8 LC_NAME=C
[9] LC_ADDRESS=C LC_TELEPHONE=C

time zone: America/New_York
tzcode source: system (glibc)
```

attached base packages:
- [1] stats
- [2] graphics
- [3] grDevices
- [4] utils
- [5] datasets
- [6] methods
- [7] base

other attached packages:
- [1] iCARE_1.30.0
- [2] Hmisc_5.1-1
- [3] gtools_3.9.4

loaded via a namespace (and not attached):
- [1] gtable_0.3.4
dplyr_1.1.3
- [5] compiler_4.3.1
rpart_4.1.21
- [9] cluster_2.1.4
scales_1.2.1
fastmap_1.1.1
ggplot2_3.4.4
- [13] R6_2.5.1
generics_0.1.3
Formula_1.2-5
knitr_1.44
- [17] htmlwidgets_1.6.2
backports_1.4.1
checkmate_2.2.0
tibble_3.2.1
- [21] munsell_0.5.0
net_7.3-19
pillar_1.9.0
rlang_1.1.1
- [25] utf8_1.2.4
stringi_1.7.12
xfun_0.40
cli_3.6.1
```
[29] magrittr_2.0.3  digest_0.6.33  grid_4.3.1  rstudioapi_0.15.0
[33] base64enc_0.1-3  lifecycle_1.0.3  vctrs_0.6.4  data.table_1.14.8
[37] evaluate_0.22  glue_1.6.2  fansi_1.0.5  colorspace_2.1-0
[41] rmarkdown_2.25  foreign_0.8-85  tools_4.3.1  pkgconfig_2.0.3
[46] htmltools_0.5.6.1