

iCARE(Individualized Coherent Absolute Risk Estimators) Package

July 20, 2026

```
> library(iCARE)
```

Example 1.A

Load the breast cancer data.

```
> 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.

```
> 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
8.260    0.001    7.423
```

Compute a summary of the risks and visualize the results

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

```
Risk_Estimate
Min.      :0.09601
1st Qu.:0.09601
Median :0.09601
Mean     :0.09601
3rd Qu.:0.09601
Max.     :0.09601
```

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

```

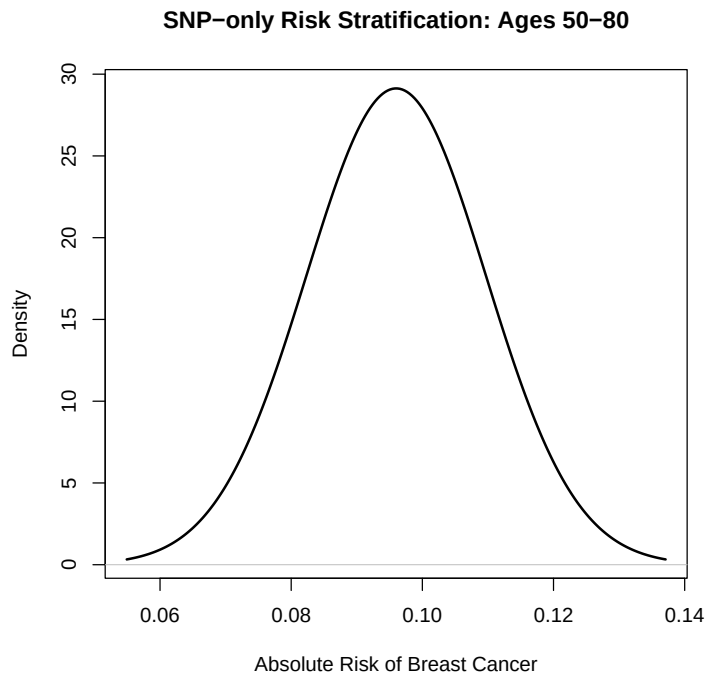
      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
0.05312 0.08671 0.09514 0.09601 0.10437 0.15828

```

```

> plot(density(res_snps_miss$risk), lwd=2,
+      main="SNP-only Risk Stratification: Ages 50-80",
+      xlab="Absolute Risk of Breast Cancer")

```



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.

```

> 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)

```

```

[1] "Note: As specified, the model does not adjust SNP imputations for family history."
      user system elapsed
0.690   0.000   0.225

```

```

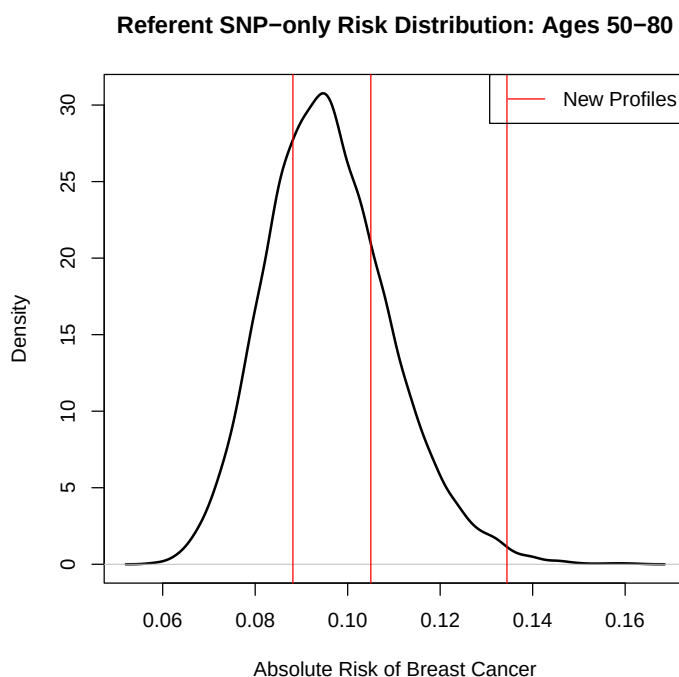
> names(res_snps_dat)

```

```
[1] "risk"      "details"   "beta.used" "refs.risk"
```

Visualize the Results

```
> 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.

```
> 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,
```

```

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

user system elapsed
1.126  0.033  0.575

Display details of the fit
> print(res_covs_snps$details)

Int_Start Int_End Risk_Estimate rs616488 rs11552449 rs11249433 rs12405132
1          50      80    0.10267534      NA      NA      NA      NA
2          50      80    0.09004078       2       0      NA      NA
3          50      80    0.16884293       2       0       1       1
rs12048493 rs6678914 rs4245739 rs72755295 rs12710696 rs4849887 rs2016394
1          NA       0       0       0       0       0       0
2          NA      NA      NA      NA      1       1       0
3           1       1       1       0       2       0       0
rs1550623 rs16857609 rs6762644 rs4973768 rs12493607 rs6796502 rs9790517
1           0       0       0       1       1       0       1
2           0       2       1       1       1       1       2
3           0       0       0       2       1       0       1
rs6828523 rs10069690 rs13162653 rs2012709 rs10941679 rs10472076 rs1353747
1           0       1       2       0       0       2       0
2           0       0       1       0       0       1       1
3           0       0       1       0       0       0       1
rs7707921 rs1432679 rs11242675 rs204247 rs9257408 rs4593472 rs720475
1           0       1       2       0       0       1       1
2           0       0       1       2       1       1       0
3           1       2       1       2       1       1       0
rs9693444 rs13365225 rs6472903 rs2943559 rs13267382 rs11780156 rs1011970
1           1       1       1       0       0       0       0
2           0       0       1       0       2       1       1
3           1       1       0       0       1       0       0
rs10759243 rs2380205 rs7072776 rs11814448 rs7904519 rs11199914 rs554219
1           0       2       2       0       0       1       1
2           1       0       0       0       0       0       0
3           1       1       1       0       2       0       1
rs75915166 rs11820646 rs12422552 rs17356907 rs1292011 rs11571833 rs2236007
1           0       1       1       0       1       0       1
2           0       0       0       0       0       0       0
3           0       1       1       0       2       0       0
rs2588809 rs999737 rs941764 rs11627032 rs17817449 rs11075995 rs13329835
1           0       0       1       0       1       1       1
2           1       0       0       1       1       1       0
3           0       0       1       0       0       1       1
rs146699004 rs745570 rs527616 rs1436904 rs6507583 rs4808801 rs3760982
1           0       0       0       0       0       1       0
2           1       2       0       0       0       1       1
3           1       2       1       1       0       1       1
rs2284378 rs2823093 rs17879961 rs132390 rs6001930 famhist menarche_dec parity

```

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	alcoholweek_dec	ever_smoke
1	0	0	1	1
2	0	0	6	0
3	0	0	1	1

Session Information

```
> sessionInfo()
```

R version 4.6.1 (2026-06-24)

Platform: x86_64-pc-linux-gnu

Running under: Ubuntu 26.04 LTS

Matrix products: default

BLAS: /usr/lib/x86_64-linux-gnu/openblas-pthread/libblas.so.3

LAPACK: /usr/lib/x86_64-linux-gnu/openblas-pthread/libopenblas-r0.3.32.so; LAPACK version 3.12.0

locale:

```
[1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
[3] LC_TIME=en_US.UTF-8      LC_COLLATE=en_US.UTF-8
[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
[11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
```

time zone: Etc/UTC

tzcode source: system (glibc)

attached base packages:

```
[1] stats      graphics  grDevices  utils      datasets  methods    base
```

other attached packages:

```
[1] iCARE_1.40.0  Hmisc_5.2-6  gtools_3.9.5  plotrix_3.8-14
```

loaded via a namespace (and not attached):

```
[1] gtable_0.3.6      compiler_4.6.1    rpart_4.1.27      htmlTable_2.5.0
[5] stringr_1.6.0     gridExtra_2.3.1   cluster_2.1.8.2   scales_1.4.0
[9] fastmap_1.2.0     ggplot2_4.0.3     R6_2.6.1          Formula_1.2-5
[13] knitr_1.51        htmlwidgets_1.6.4 backports_1.5.1    checkmate_2.3.4
[17] maketools_1.3.2   nnet_7.3-20       RColorBrewer_1.1-3 rlang_1.3.0
[21] stringi_1.8.7     xfun_0.60         sys_3.4.3         S7_0.2.2
[25] cli_3.6.6         magrittr_2.0.5    digest_0.6.39     grid_4.6.1
```

[29]	rstudioapi_0.19.0	base64enc_0.1-6	lifecycle_1.0.5	vctr_0.7.3
[33]	data.table_1.18.4	evaluate_1.0.5	glue_1.8.1	farver_2.1.2
[37]	buildtools_1.0.0	colorspace_2.1-3	rmarkdown_2.31	foreign_0.8-91
[41]	tools_4.6.1	htmltools_0.5.9		