

iCARE(Individualized Coherent Absolute Risk Estimators) Package

November 14, 2025

```
> 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  
8.138   0.792   8.052
```

Compute a summary of the risks and visualize the results

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

```
Risk_Estimate  
Min.      :0.096  
1st Qu.   :0.096  
Median    :0.096  
Mean      :0.096  
3rd Qu.   :0.096  
Max.      :0.096
```

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

```

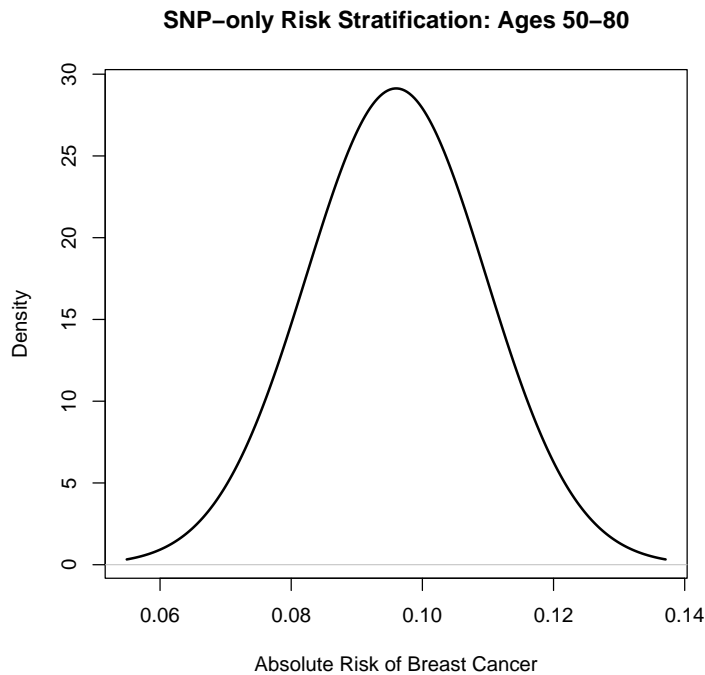
      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
0.05773 0.08677 0.09492 0.09600 0.10435 0.16282

```

```

> 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
0.282   0.353   0.224

```

```

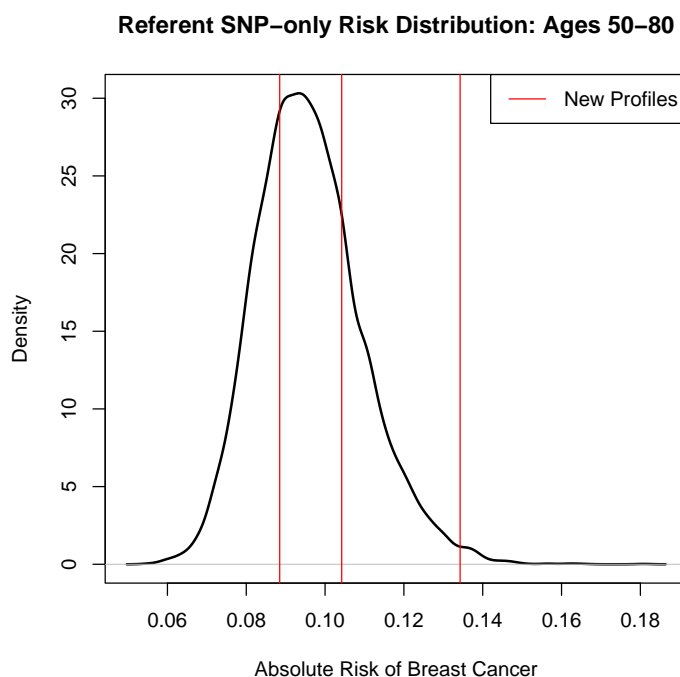
> names(res_snps_dat)

```

```
[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,
```


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 4.5.2 (2025-10-31)

Platform: x86_64-pc-linux-gnu

Running under: Ubuntu 24.04.3 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-r0.3.26.so; LAPACK version 3.11.0

locale:

```
[1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
[3] LC_TIME=en_US.UTF-8      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
[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_1.38.0 Hmisc_5.2-4 gtools_3.9.5 plotrix_3.8-4
```

loaded via a namespace (and not attached):

```
[1] gtable_0.3.6      compiler_4.5.2    rpart_4.1.24      htmlTable_2.4.3
[5] stringr_1.6.0     gridExtra_2.3     cluster_2.1.8.1   scales_1.4.0
[9] fastmap_1.2.0     ggplot2_4.0.0     R6_2.6.1          Formula_1.2-5
[13] knitr_1.50        htmlwidgets_1.6.4 backports_1.5.0   checkmate_2.3.3
[17] maketools_1.3.2   nnet_7.3-20       RColorBrewer_1.1-3 rlang_1.1.6
[21] stringi_1.8.7     xfun_0.54         sys_3.4.3         S7_0.2.0
[25] cli_3.6.5         magrittr_2.0.4    digest_0.6.38     grid_4.5.2
```

[29]	rstudioapi_0.17.1	base64enc_0.1-3	lifecycle_1.0.4	vctr_0.6.5
[33]	data.table_1.17.8	evaluate_1.0.5	glue_1.8.0	farver_2.1.2
[37]	buildtools_1.0.0	colorspace_2.1-2	rmarkdown_2.30	foreign_0.8-90
[41]	tools_4.5.2	htmltools_0.5.8.1		