

# iCARE(Individualized Coherent Absolute Risk Estimators) Package

November 16, 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
9.632   0.323   9.975
```

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)
```

```

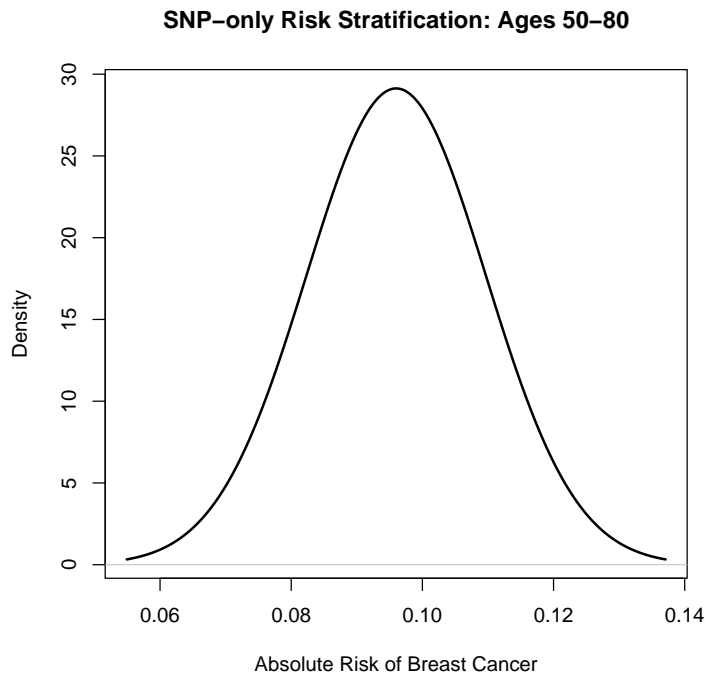
      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
0.05518 0.08659 0.09507 0.09600 0.10449 0.16344

```

```

> 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
0.395   0.131   0.528

```

```

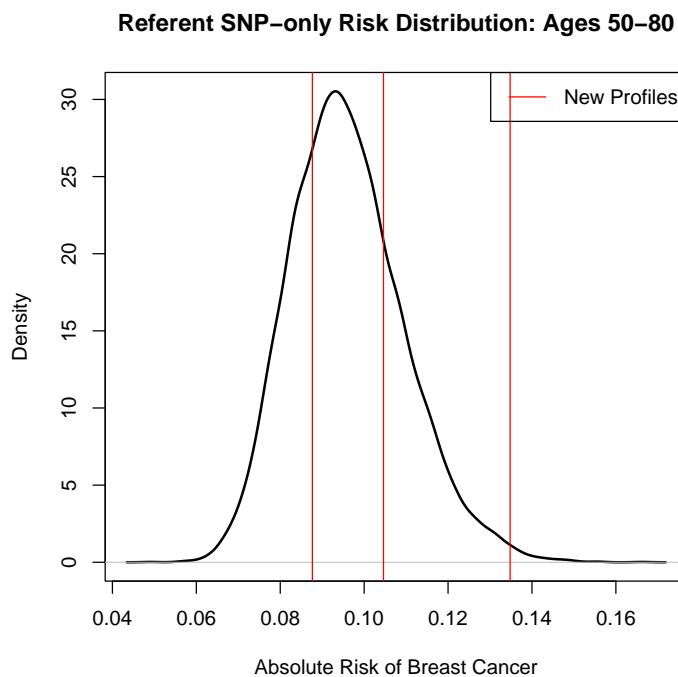
> names(res_snps_dat)

```

```
[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 Under development (unstable) (2025-10-21 r88958)

Platform: x86\_64-apple-darwin20

Running under: macOS Ventura 13.7.8

Matrix products: default

BLAS: /Library/Frameworks/R.framework/Versions/4.6-x86\_64/Resources/lib/libRblas.0.dylib

LAPACK: /Library/Frameworks/R.framework/Versions/4.6-x86\_64/Resources/lib/libRlapack.dylib

locale:

[1] C/en\_US.UTF-8/en\_US.UTF-8/C/en\_US.UTF-8/en\_US.UTF-8

time zone: America/New\_York

tzcode source: internal

attached base packages:

[1] stats graphics grDevices utils datasets methods base

other attached packages:

[1] iCARE\_1.39.0 Hmisc\_5.2-4 gtools\_3.9.5 plotrix\_3.8-13

loaded via a namespace (and not attached):

[1] gtable_0.3.6	dplyr_1.1.4	compiler_4.6.0	rpart_4.1.24
[5] tidyselect_1.2.1	htmlTable_2.4.3	stringr_1.6.0	dichromat_2.0-0.1
[9] gridExtra_2.3	cluster_2.1.8.1	scales_1.4.0	fastmap_1.2.0
[13] ggplot2_4.0.1	R6_2.6.1	generics_0.1.4	Formula_1.2-5
[17] knitr_1.50	htmlwidgets_1.6.4	backports_1.5.0	checkmate_2.3.3
[21] tibble_3.3.0	nnet_7.3-20	pillar_1.11.1	RColorBrewer_1.1-3
[25] rlang_1.1.6	stringi_1.8.7	xfun_0.54	S7_0.2.1
[29] cli_3.6.5	magrittr_2.0.4	digest_0.6.38	grid_4.6.0
[33] rstudioapi_0.17.1	base64enc_0.1-3	lifecycle_1.0.4	vctrs_0.6.5
[37] data.table_1.17.8	evaluate_1.0.5	glue_1.8.0	farver_2.1.2
[41] colorspace_2.1-2	rmarkdown_2.30	foreign_0.8-90	tools_4.6.0
[45] pkgconfig_2.0.3	htmltools_0.5.8.1		