

iCARE(Individualized Coherent Absolute Risk Estimators) Package

May 29, 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  
    8.700  0.740  8.613
```

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)
```

```

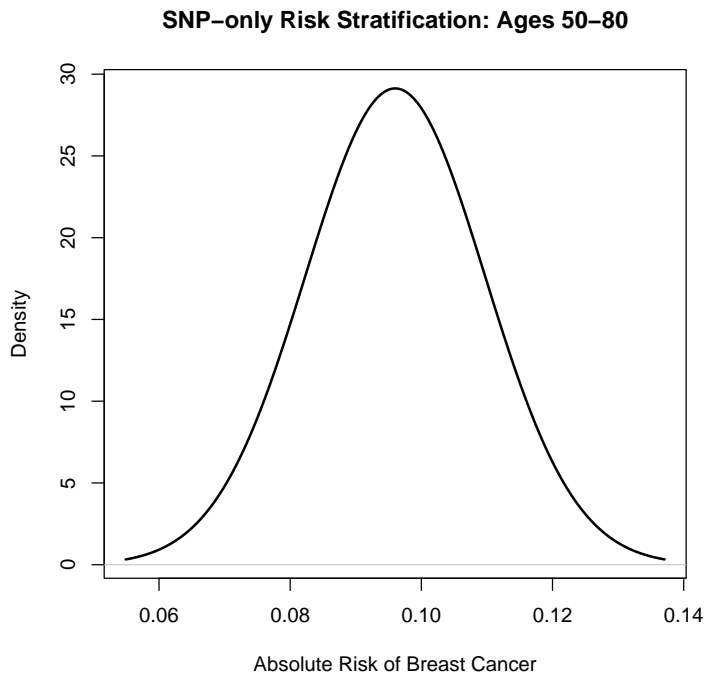
      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
0.05312 0.08671 0.09514 0.09601 0.10437 0.15828

```

```

> 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
0.317  0.412  0.265

```

```

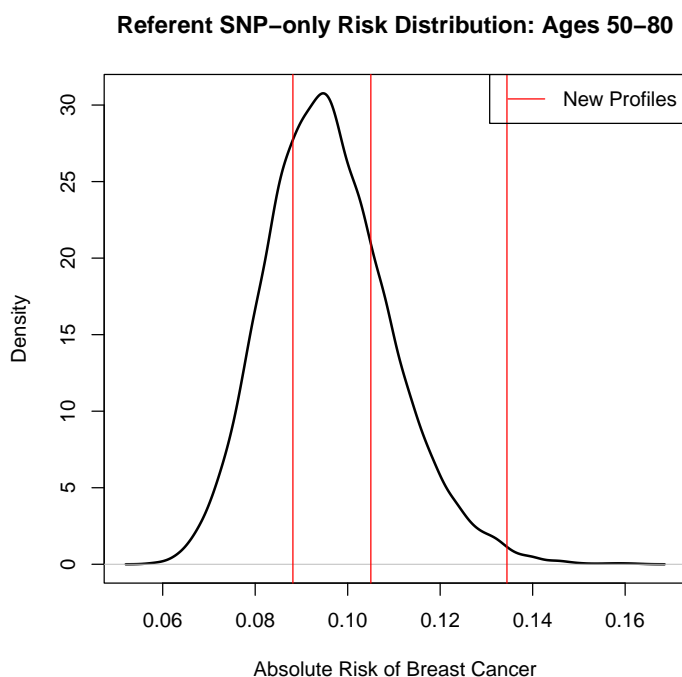
> names(res_snps_dat)

```

```
[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 4.6.0 (2026-04-24)
Platform: x86_64-pc-linux-gnu
Running under: Ubuntu 24.04.4 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=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_5.2-5  gtools_3.9.5  plotrix_3.8-14
```

```
loaded via a namespace (and not attached):
```

```
[1] gtable_0.3.6      compiler_4.6.0  rpart_4.1.27    htmlTable_2.5.0
[5] stringr_1.6.0     gridExtra_2.3   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_1.2.0
[21] stringi_1.8.7     xfun_0.57       sys_3.4.3       S7_0.2.2
[25] cli_3.6.6         magrittr_2.0.5  digest_0.6.39   grid_4.6.0
```

[29]	rstudioapi_0.18.0	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_2.1-2	rmarkdown_2.31	foreign_0.8-91
[41]	tools_4.6.0	htmltools_0.5.9		