

# iCARE(Individualized Coherent Absolute Risk Estimators) Package

April 25, 2023

```
> 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  
11.369 0.121 11.489
```

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)
```

```

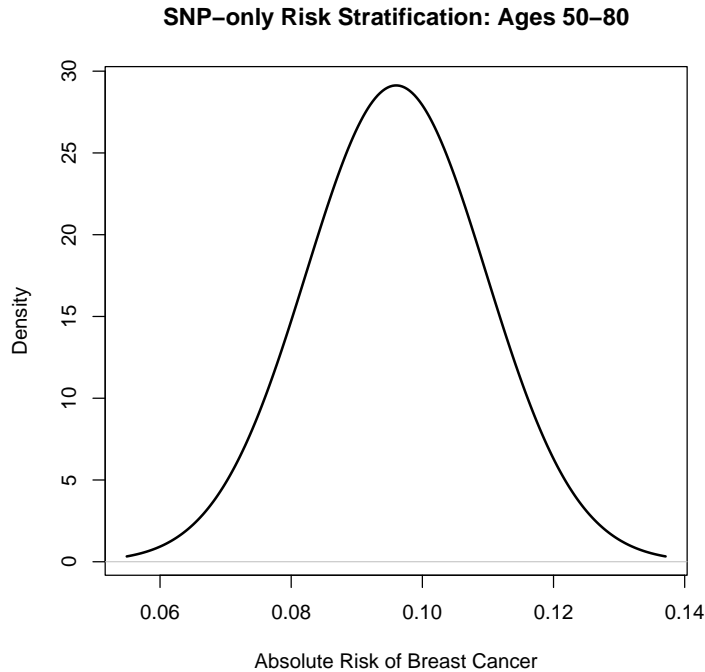
      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
0.05194 0.08650 0.09504 0.09601 0.10448 0.15495

```

```

> 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
0.446  0.008  0.454

```

```

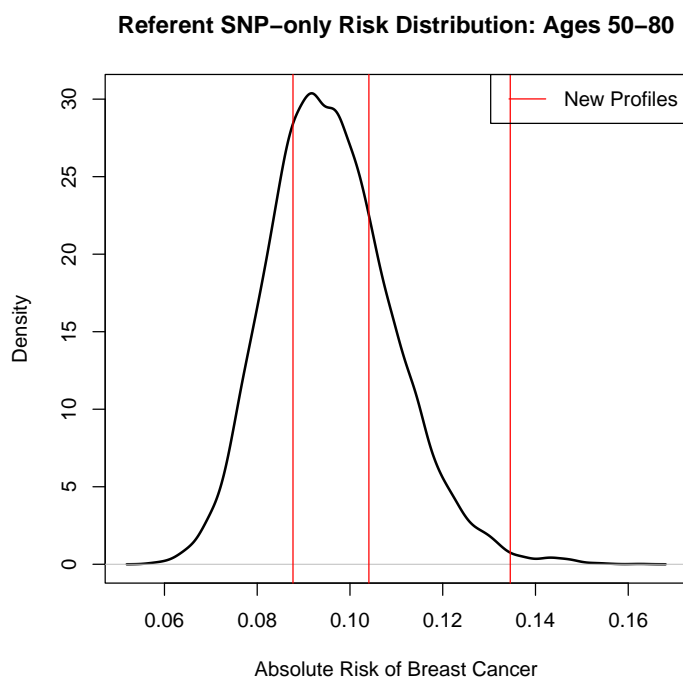
> names(res_snps_dat)

```

```
[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 4.3.0 RC (2023-04-18 r84287)

Platform: x86\_64-pc-linux-gnu (64-bit)

Running under: Ubuntu 22.04.2 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
[11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
```

time zone: America/New\_York

tzcode source: system (glibc)

attached base packages:

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

other attached packages:

```
[1] iCARE_1.29.0 Hmisc_5.0-1 gtools_3.9.4 plotrix_3.8-2
```

loaded via a namespace (and not attached):

```
[1] gtable_0.3.3      dplyr_1.1.2      compiler_4.3.0   rpart_4.1.19
[5] tidymodels_1.2.0 htmlTable_2.4.1  stringr_1.5.0    gridExtra_2.3
[9] cluster_2.1.4     scales_1.2.1     fastmap_1.1.1    ggplot2_3.4.2
[13] R6_2.5.1          generics_0.1.3   Formula_1.2-5    knitr_1.42
[17] htmlwidgets_1.6.2 backports_1.4.1  checkmate_2.1.0  tibble_3.2.1
[21] munsell_0.5.0     nnet_7.3-18      pillar_1.9.0     rlang_1.1.0
[25] utf8_1.2.3        stringi_1.7.12   xfun_0.39        cli_3.6.1
```

[29]	magrittr_2.0.3	digest_0.6.31	grid_4.3.0	rstudioapi_0.14
[33]	base64enc_0.1-3	lifecycle_1.0.3	vctrs_0.6.2	data.table_1.14.8
[37]	evaluate_0.20	glue_1.6.2	fansi_1.0.4	colorspace_2.1-0
[41]	rmarkdown_2.21	foreign_0.8-84	tools_4.3.0	pkgconfig_2.0.3
[45]	htmltools_0.5.5			