

# iCARE(Individualized Coherent Absolute Risk Estimators) Package

May 9, 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  
14.751   0.229   22.429
```

Compute a summary of the risks and visualize the results

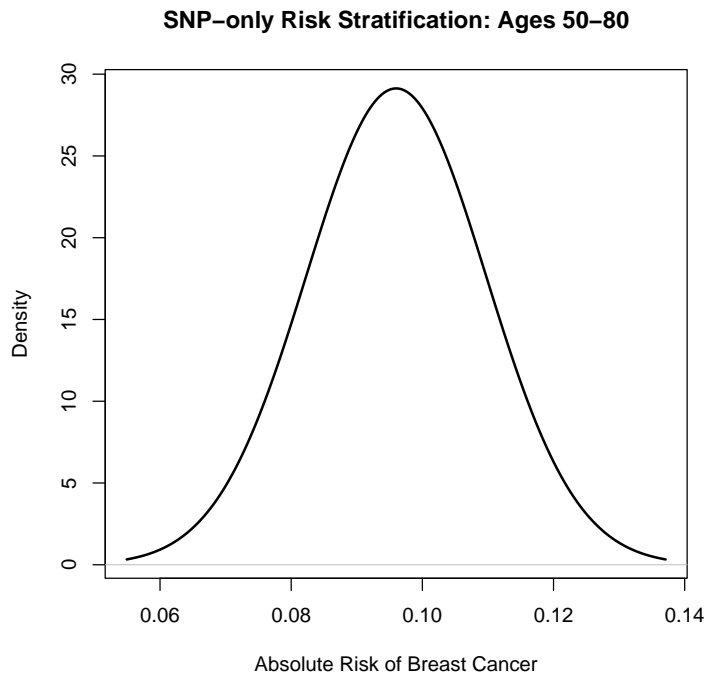
```
> summary(res_snps_miss$risk)
```

```
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.
	0.05794	0.08655	0.09491	0.09601	0.10441	0.15039

```
> 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)
```

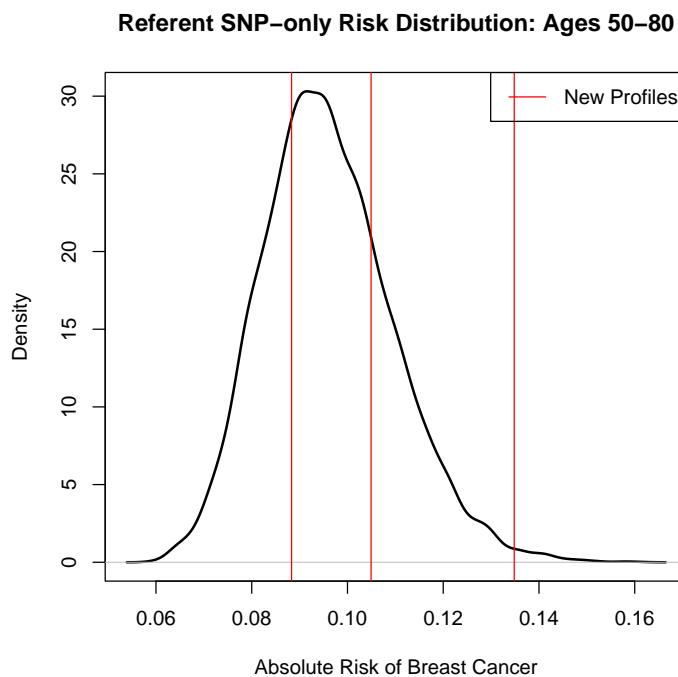
```
[1] "Note: As specified, the model does not adjust SNP imputations for family history."
      user system elapsed
0.637   0.081   1.094
```

```
> 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 (2023-04-13 r84266)
Platform: aarch64-apple-darwin20 (64-bit)
Running under: macOS Monterey 12.6.1
```

```
Matrix products: default
```

```
BLAS: /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/lib/libRblas.0.dylib
```

```
LAPACK: /Library/Frameworks/R.framework/Versions/4.3-arm64/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_1.28.0 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_1.1.1      compiler_4.3.0   rpart_4.1.19
[5] tidyselect_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_0.38        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_0.6.1      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
```