

# iCARE(Individualized Coherent Absolute Risk Estimators) Package

May 19, 2021

```
> 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  
11.823 0.172 11.995
```

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)
```

```

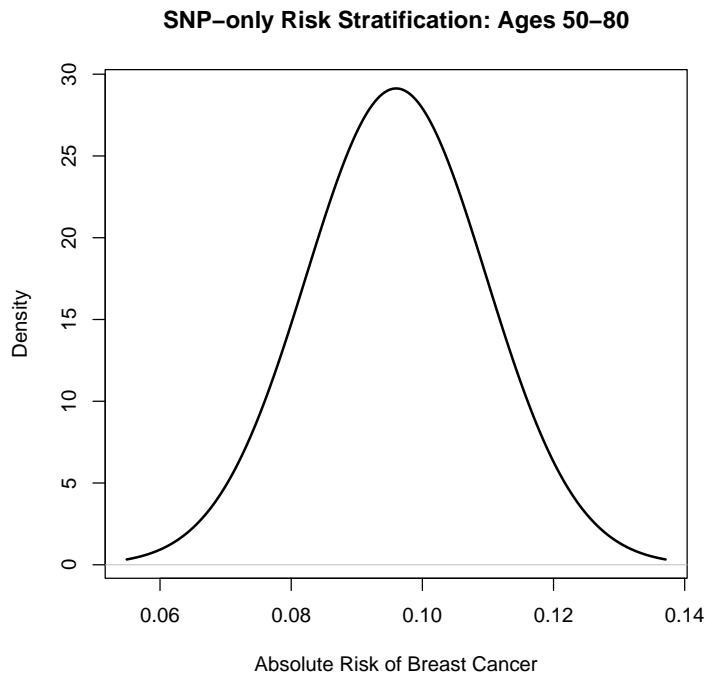
      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
0.05832 0.08666 0.09484 0.09601 0.10431 0.19027

```

```

> 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
0.422  0.068  0.489

```

```

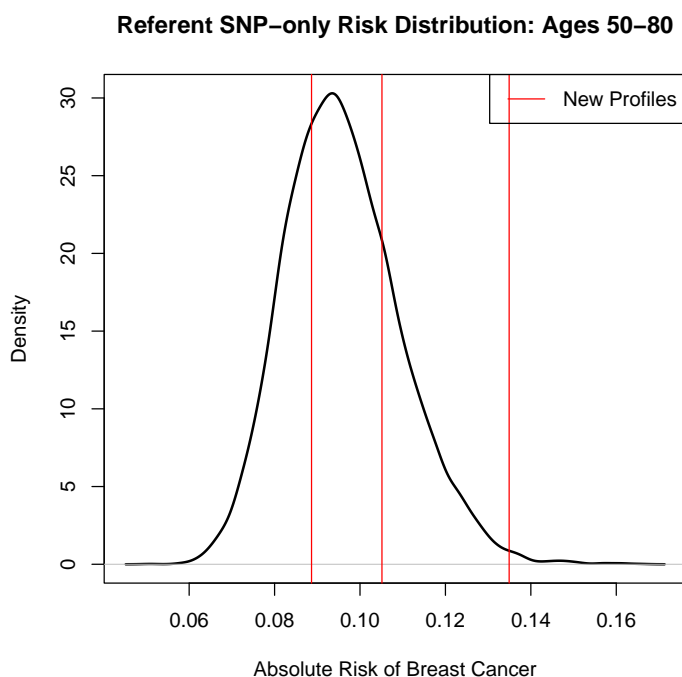
> names(res_snps_dat)

```

```
[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 4.1.0 (2021-05-18)
Platform: x86_64-pc-linux-gnu (64-bit)
Running under: Ubuntu 20.04.2 LTS
```

```
Matrix products: default
```

```
BLAS: /home/biocbuild/bbs-3.13-bioc/R/lib/libRblas.so
LAPACK: /home/biocbuild/bbs-3.13-bioc/R/lib/libRlapack.so
```

```
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
```

```
attached base packages:
```

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

```
other attached packages:
```

```
[1] iCARE_1.20.0  Hmisc_4.5-0    ggplot2_3.3.3  Formula_1.2-4
[5] survival_3.2-11 lattice_0.20-44 gtools_3.8.2   plotrix_3.8-1
```

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

```
[1] pillar_1.6.1      compiler_4.1.0    RColorBrewer_1.1-2
[4] base64enc_0.1-3   tools_4.1.0       digest_0.6.27
[7] rpart_4.1-15      checkmate_2.0.0   htmlTable_2.2.1
[10] lifecycle_1.0.0   tibble_3.1.2      gtable_0.3.0
[13] pkgconfig_2.0.3   png_0.1-7         rlang_0.4.11
[16] Matrix_1.3-3      rstudioapi_0.13   DBI_1.1.1
[19] xfun_0.23         gridExtra_2.3     stringr_1.4.0
[22] knitr_1.33        withr_2.4.2       dplyr_1.0.6
[25] cluster_2.1.2     htmlwidgets_1.5.3 generics_0.1.0
```

[28]	vctr_0.3.8	nnet_7.3-16	grid_4.1.0
[31]	tidyselect_1.1.1	data.table_1.14.0	glue_1.4.2
[34]	R6_2.5.0	jpeg_0.1-8.1	fansi_0.4.2
[37]	foreign_0.8-81	latticeExtra_0.6-29	purrr_0.3.4
[40]	magrittr_2.0.1	htmltools_0.5.1.1	backports_1.2.1
[43]	scales_1.1.1	ellipsis_0.3.2	splines_4.1.0
[46]	assertthat_0.2.1	colorspace_2.0-1	utf8_1.2.1
[49]	stringi_1.6.2	munsell_0.5.0	crayon_1.4.1