

# iCARE(Individualized Coherent Absolute Risk Estimators) Package

April 7, 2020

```
> 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  
16.588   0.357   16.954
```

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)
```

```

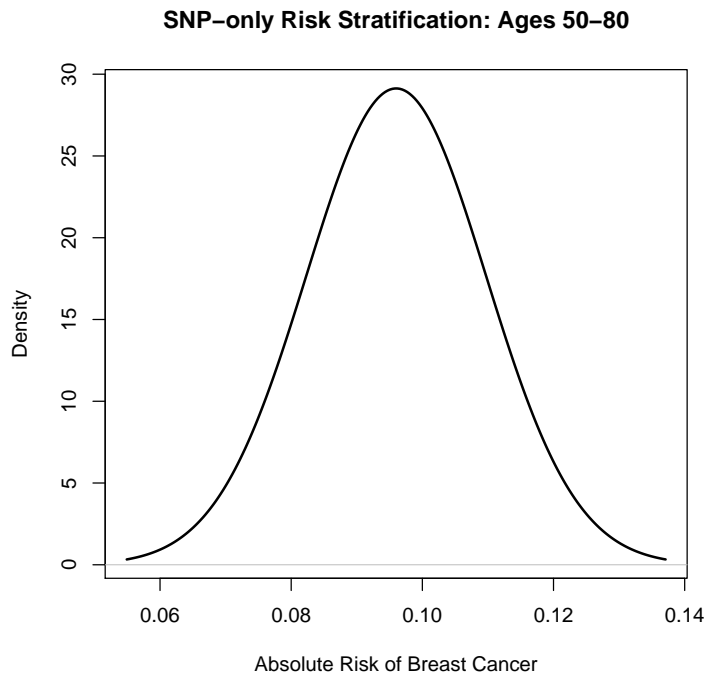
      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
0.05704 0.08646 0.09510 0.09601 0.10435 0.15584

```

```

> 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
0.751   0.166   0.916

```

```

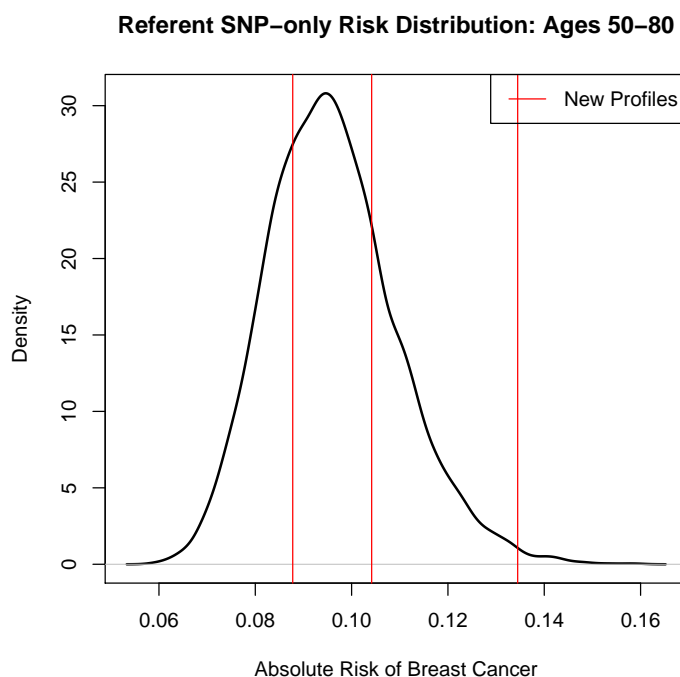
> names(res_snps_dat)

```

```
[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 4.0.0 alpha (2020-04-05 r78150)
Platform: x86_64-apple-darwin17.0 (64-bit)
Running under: macOS Mojave 10.14.6
```

```
Matrix products: default
```

```
BLAS: /Library/Frameworks/R.framework/Versions/4.0/Resources/lib/libRblas.dylib
```

```
LAPACK: /Library/Frameworks/R.framework/Versions/4.0/Resources/lib/libRlapack.dylib
```

```
locale:
```

```
[1] C/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
```

```
attached base packages:
```

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

```
other attached packages:
```

```
[1] iCARE_1.15.0   Hmisc_4.4-0    ggplot2_3.3.0   Formula_1.2-3
[5] survival_3.1-11 lattice_0.20-41 gtools_3.8.2    plotrix_3.7-7
```

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

```
[1] tidyselect_1.0.0    xfun_0.12      purrr_0.3.3
[4] splines_4.0.0       colorspace_1.4-1 vctrs_0.2.4
[7] htmltools_0.4.0     base64enc_0.1-3 rlang_0.4.5
[10] pillar_1.4.3        foreign_0.8-77 glue_1.4.0
[13] withr_2.1.2         RColorBrewer_1.1-2 jpeg_0.1-8.1
[16] lifecycle_0.2.0     stringr_1.4.0  munsell_0.5.0
[19] gtable_0.3.0        htmlwidgets_1.5.1 latticeExtra_0.6-29
[22] knitr_1.28          fansi_0.4.1    htmlTable_1.13.3
[25] Rcpp_1.0.4.6        acepack_1.4.1  scales_1.1.0
[28] backports_1.1.6     checkmate_2.0.0 gridExtra_2.3
[31] png_0.1-7           digest_0.6.25  stringi_1.4.6
[34] dplyr_0.8.5         grid_4.0.0     cli_2.0.2
[37] tools_4.0.0         magrittr_1.5   tibble_3.0.0
[40] cluster_2.1.0       crayon_1.3.4   pkgconfig_2.0.3
```

[43]	ellipsis_0.3.0	Matrix_1.2-18	data.table_1.12.8
[46]	assertthat_0.2.1	rstudioapi_0.11	R6_2.4.1
[49]	rpart_4.1-15	nnet_7.3-13	compiler_4.0.0