

# 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
9.12    0.17    9.29
```

Compute a summary of the risks and visualize the results

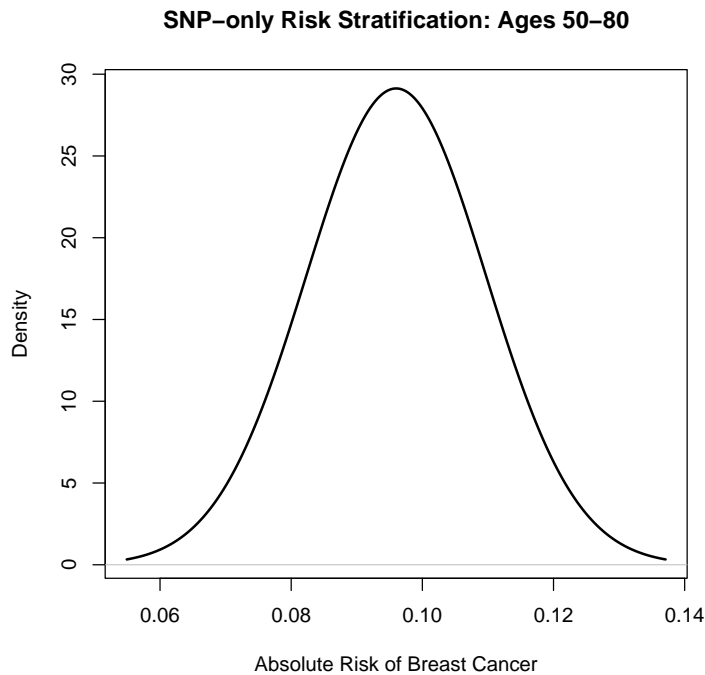
```
> summary(res_snps_miss$risk)
```

```
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.
0.05489	0.08661	0.09493	0.09601	0.10433	0.16015

```
> 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)
```

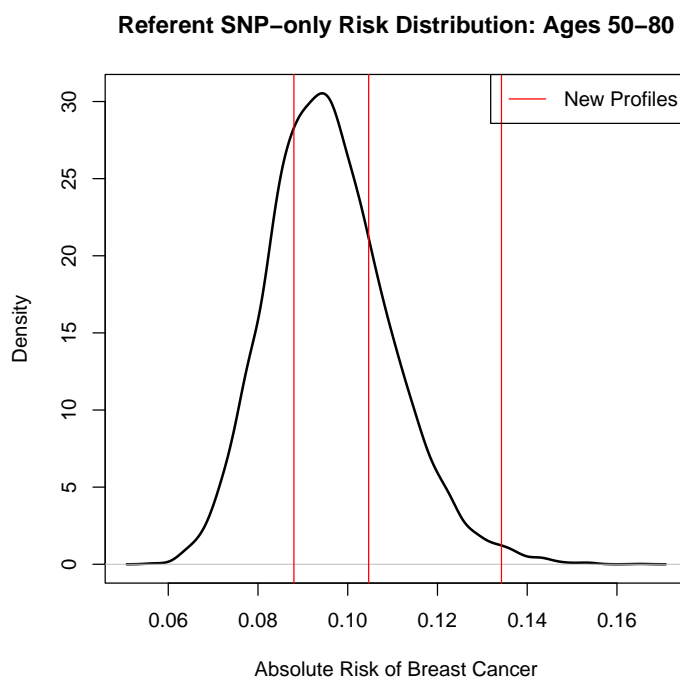
```
[1] "Note: As specified, the model does not adjust SNP imputations for family history."
      user system elapsed
      0.47    0.09    0.56
```

```
> 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,
```

```

+                                     apply.snp.profile=new_snp_prof,
+                                     return.refs.risk=TRUE)

user  system elapsed
1.01   0.14   1.15

Display details of the fit
> print(res_covs_snps$details)

Int_Start Int_End Risk_Estimate rs616488 rs11552449 rs11249433 rs12405132
1          50      80      0.1022697      NA          NA          NA          NA
2          50      80      0.0902293        2          0          NA          NA
3          50      80      0.1688550        2          0          1          1
rs12048493 rs6678914 rs4245739 rs72755295 rs12710696 rs4849887 rs2016394
1          NA        0        0        0        0        0        0
2          NA        NA        NA        NA        1        1        0
3          1         1         1        0        2        0        0
rs1550623 rs16857609 rs6762644 rs4973768 rs12493607 rs6796502 rs9790517
1          0         0         0        1        1        0        1
2          0         2         1        1        1        1        2
3          0         0         0        2        1        0        1
rs6828523 rs10069690 rs13162653 rs2012709 rs10941679 rs10472076 rs1353747
1          0         1         2        0        0        2        0
2          0         0         1        0        0        1        1
3          0         0         1        0        0        0        1
rs7707921 rs1432679 rs11242675 rs204247 rs9257408 rs4593472 rs720475
1          0         1         2        0        0        1        1
2          0         0         1        2        1        1        0
3          1         2         1        2        1        1        0
rs9693444 rs13365225 rs6472903 rs2943559 rs13267382 rs11780156 rs1011970
1          1         1         1        0        0        0        0
2          0         0         1        0        2        1        1
3          1         1         0        0        1        0        0
rs10759243 rs2380205 rs7072776 rs11814448 rs7904519 rs11199914 rs554219
1          0         2         2        0        0        1        1
2          1         0         0        0        0        0        0
3          1         1         1        0        2        0        1
rs75915166 rs11820646 rs12422552 rs17356907 rs1292011 rs11571833 rs2236007
1          0         1         1        0        1        0        1
2          0         0         0        0        0        0        0
3          0         1         1        0        2        0        0
rs2588809 rs999737 rs941764 rs11627032 rs17817449 rs11075995 rs13329835
1          0         0         1        0        1        1        1
2          1         0         0        1        1        1        0
3          0         0         1        0        0        1        1
rs146699004 rs745570 rs527616 rs1436904 rs6507583 rs4808801 rs3760982
1          0         0         0        0        0        1        0
2          1         2         0        0        0        1        1
3          1         2         1        1        0        1        1
rs2284378 rs2823093 rs17879961 rs132390 rs6001930 famhist menarche_dec parity

```

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	alcoholdec	week_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 RC (2021-05-10 r80283)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows Server x64 (build 17763)
```

```
Matrix products: default
```

```
locale:
```

```
[1] LC_COLLATE=C
[2] LC_CTYPE=English_United States.1252
[3] LC_MONETARY=English_United States.1252
[4] LC_NUMERIC=C
[5] LC_TIME=English_United States.1252
```

```
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] vctrs_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