

iCARE(Individualized Coherent Absolute Risk Estimators) Package

April 30, 2024

```
> 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
9.771    0.344   10.141
```

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)
```

```

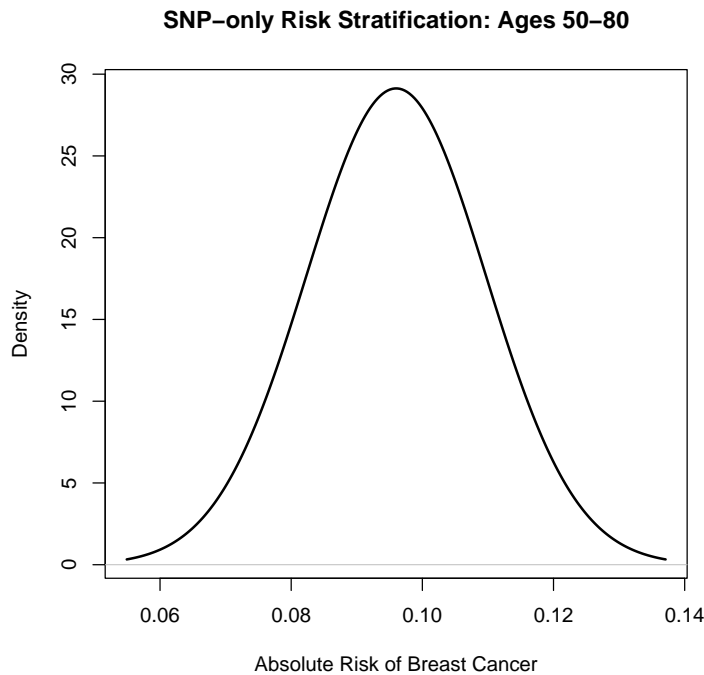
      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
0.05312 0.08671 0.09514 0.09601 0.10437 0.15828

```

```

> 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
0.390  0.098  0.492

```

```

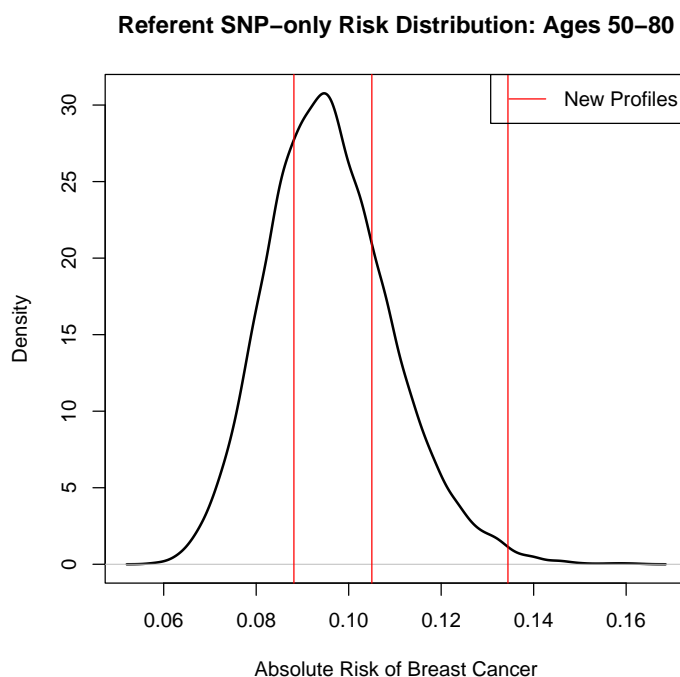
> names(res_snps_dat)

```

```
[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
1.542   0.270   1.821

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

Int_Start Int_End Risk_Estimate rs616488 rs11552449 rs11249433 rs12405132
1         50      80    0.10267534      NA      NA      NA      NA
2         50      80    0.09004078       2       0      NA      NA
3         50      80    0.16884293       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	alcoholweek_dec	ever_smoke				
1	0	0		1	1			
2	0	0		6	0			
3	0	0		1	1			

Session Information

```
> sessionInfo()
```

R version 4.4.0 beta (2024-04-14 r86421)

Platform: x86_64-apple-darwin20

Running under: macOS Monterey 12.7.1

Matrix products: default

BLAS: /Library/Frameworks/R.framework/Versions/4.4-x86_64/Resources/lib/libRblas.0.dylib

LAPACK: /Library/Frameworks/R.framework/Versions/4.4-x86_64/Resources/lib/libRlapack.dylib

locale:

[1] en_US.UTF-8/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_1.32.0 Hmisc_5.1-2 gtools_3.9.5 plotrix_3.8-4

loaded via a namespace (and not attached):

[1] gtable_0.3.5	dplyr_1.1.4	compiler_4.4.0	rpart_4.1.23
[5] tidyselect_1.2.1	htmlTable_2.4.2	stringr_1.5.1	gridExtra_2.3
[9] cluster_2.1.6	scales_1.3.0	fastmap_1.1.1	ggplot2_3.5.1
[13] R6_2.5.1	generics_0.1.3	Formula_1.2-5	knitr_1.46
[17] htmlwidgets_1.6.4	backports_1.4.1	checkmate_2.3.1	tibble_3.2.1
[21] munsell_0.5.1	nnet_7.3-19	pillar_1.9.0	rlang_1.1.3
[25] utf8_1.2.4	stringi_1.8.3	xfun_0.43	cli_3.6.2
[29] magrittr_2.0.3	digest_0.6.35	grid_4.4.0	rstudioapi_0.16.0
[33] base64enc_0.1-3	lifecycle_1.0.4	vctrs_0.6.5	data.table_1.15.4
[37] evaluate_0.23	glue_1.7.0	fansi_1.0.6	colorspace_2.1-0
[41] rmarkdown_2.26	foreign_0.8-86	tools_4.4.0	pkgconfig_2.0.3
[45] htmltools_0.5.8.1			