

iCARE(Individualized Coherent Absolute Risk Estimators) Package

October 29, 2019

```
> 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
```

```
14.246 0.434 14.794
```

Compute a summary of the risks and visualize the results

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

```
Risk_Estimate
```

```
Min. :0.096
```

```
1st Qu.:0.096
```

```
Median :0.096
```

```
Mean :0.096
```

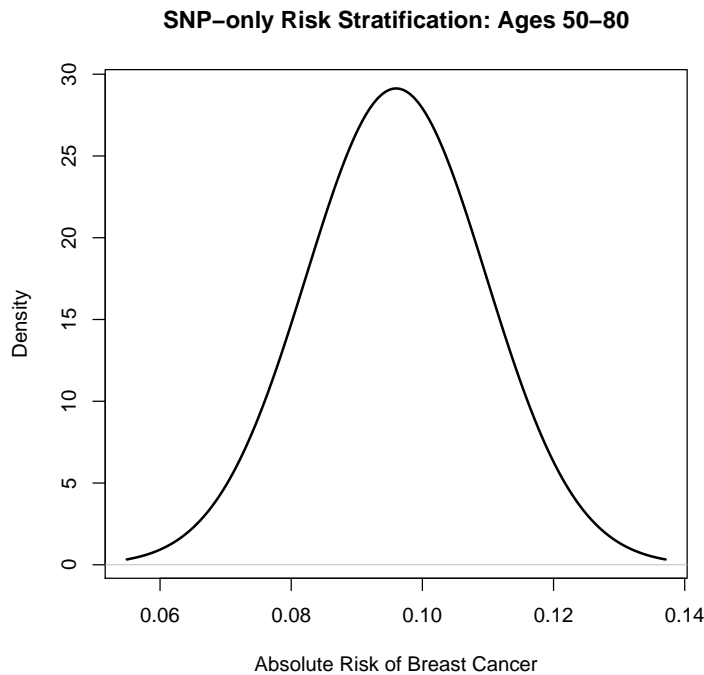
```
3rd Qu.:0.096
```

```
Max. :0.096
```

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

	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
	0.05797	0.08640	0.09497	0.09600	0.10437	0.16879

```
> 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)
```

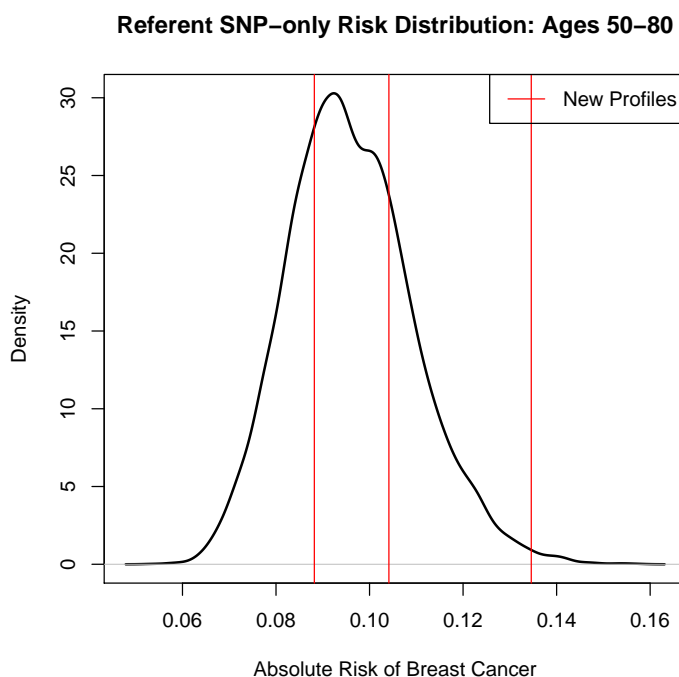
```
[1] "Note: As specified, the model does not adjust SNP imputations for family history."
      user system elapsed
0.654   0.322   0.984
```

```
> 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
1.964  0.654   2.657

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

Int_Start Int_End Risk_Estimate rs616488 rs11552449 rs11249433 rs12405132
1          50      80      0.1027986      NA      NA      NA      NA
2          50      80      0.0904343      2      0      NA      NA
3          50      80      0.1685318      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 3.6.1 (2019-07-05)

Platform: x86_64-apple-darwin15.6.0 (64-bit)

Running under: OS X El Capitan 10.11.6

Matrix products: default

BLAS: /Library/Frameworks/R.framework/Versions/3.6/Resources/lib/libRblas.0.dylib

LAPACK: /Library/Frameworks/R.framework/Versions/3.6/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_1.14.0 Hmisc_4.2-0 ggplot2_3.2.1 Formula_1.2-3

[5] survival_2.44-1.1 lattice_0.20-38 gtools_3.8.1 plotrix_3.7-6

loaded via a namespace (and not attached):

[1] Rcpp_1.0.2	pillar_1.4.2	compiler_3.6.1
[4] RColorBrewer_1.1-2	base64enc_0.1-3	tools_3.6.1
[7] digest_0.6.22	rpart_4.1-15	checkmate_1.9.4
[10] htmlTable_1.13.2	tibble_2.1.3	gtable_0.3.0
[13] pkgconfig_2.0.3	rlang_0.4.1	Matrix_1.2-17
[16] rstudioapi_0.10	xfun_0.10	gridExtra_2.3
[19] stringr_1.4.0	knitr_1.25	withr_2.1.2
[22] dplyr_0.8.3	cluster_2.1.0	htmlwidgets_1.5.1
[25] grid_3.6.1	nnet_7.3-12	tidyselect_0.2.5
[28] data.table_1.12.6	glue_1.3.1	R6_2.4.0
[31] foreign_0.8-72	latticeExtra_0.6-28	purrr_0.3.3
[34] magrittr_1.5	htmltools_0.4.0	backports_1.1.5
[37] scales_1.0.0	splines_3.6.1	assertthat_0.2.1
[40] colorspace_1.4-1	stringi_1.4.3	acepack_1.4.1
[43] lazyeval_0.2.2	munsell_0.5.0	crayon_1.3.4