

iCARE(Individualized Coherent Absolute Risk Estimators) Package

November 1, 2022

```
> 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  
11.567 0.112 11.679
```

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)
```

```

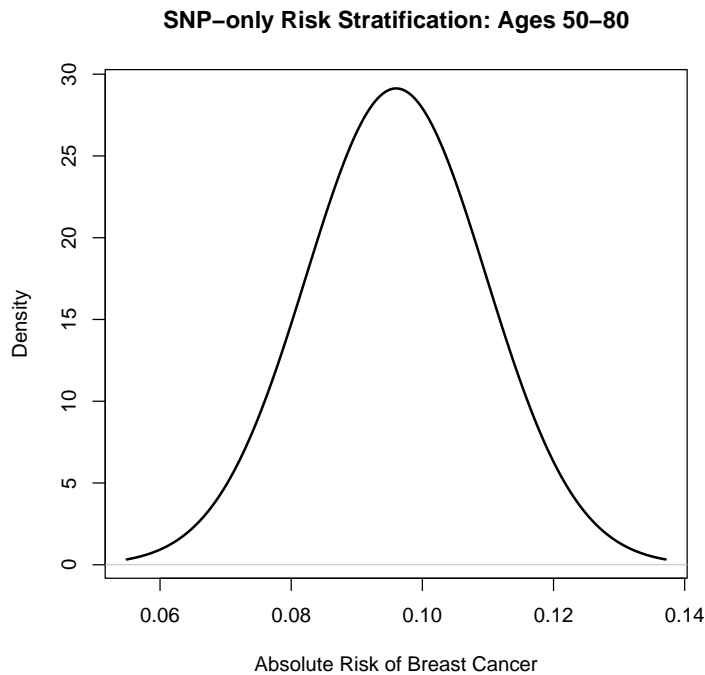
      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
0.05500 0.08647 0.09502 0.09601 0.10443 0.16457

```

```

> 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
0.440  0.016  0.456

```

```

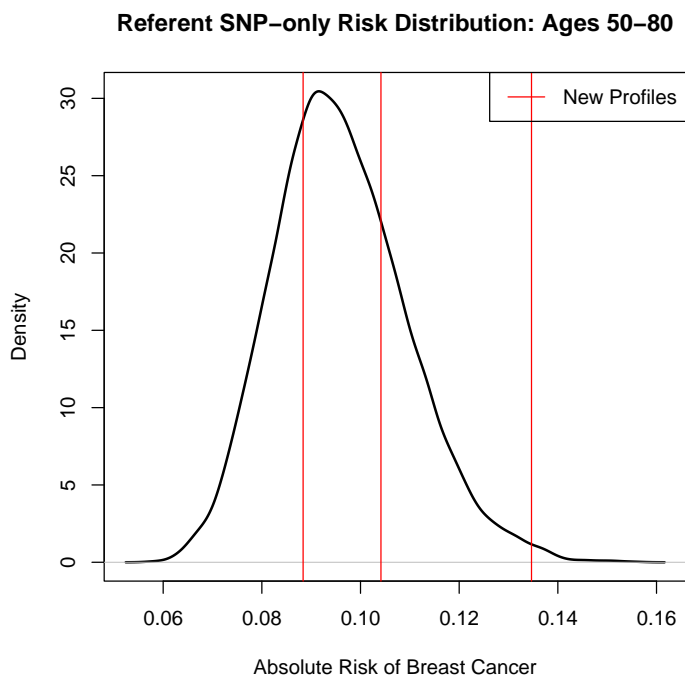
> names(res_snps_dat)

```

```
[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 4.2.1 (2022-06-23)
Platform: x86_64-pc-linux-gnu (64-bit)
Running under: Ubuntu 20.04.5 LTS
```

```
Matrix products: default
```

```
BLAS: /home/biocbuild/bbs-3.16-bioc/R/lib/libRblas.so
LAPACK: /home/biocbuild/bbs-3.16-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_1.26.0   Hmisc_4.7-1    ggplot2_3.3.6  Formula_1.2-4
[5] survival_3.4-0 lattice_0.20-45 gtools_3.9.3   plotrix_3.8-2
```

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

```
[1] tidyselect_1.2.0  xfun_0.34      splines_4.2.1
[4] colorspace_2.0-3 vctrs_0.5.0    generics_0.1.3
[7] htmltools_0.5.3  base64enc_0.1-3 utf8_1.2.2
[10] rlang_1.0.6      pillar_1.8.1   foreign_0.8-83
[13] glue_1.6.2       withr_2.5.0    DBI_1.1.3
[16] RColorBrewer_1.1-3 jpeg_0.1-9     lifecycle_1.0.3
[19] stringr_1.4.1    munsell_0.5.0  gtable_0.3.1
[22] htmlwidgets_1.5.4 latticeExtra_0.6-30 knitr_1.40
[25] fastmap_1.1.0    fansi_1.0.3    htmlTable_2.4.1
```

[28]	Rcpp_1.0.9	scales_1.2.1	backports_1.4.1
[31]	checkmate_2.1.0	deldir_1.0-6	interp_1.1-3
[34]	gridExtra_2.3	png_0.1-7	digest_0.6.30
[37]	stringi_1.7.8	dplyr_1.0.10	grid_4.2.1
[40]	cli_3.4.1	tools_4.2.1	magrittr_2.0.3
[43]	tibble_3.1.8	cluster_2.1.4	pkgconfig_2.0.3
[46]	Matrix_1.5-1	data.table_1.14.4	assertthat_0.2.1
[49]	rstudioapi_0.14	R6_2.5.1	rpart_4.1.19
[52]	nnet_7.3-18	compiler_4.2.1	