

iCARE(Individualized Coherent Absolute Risk Estimators) Package

October 29, 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  
12.895  0.120  13.016
```

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)
```

```

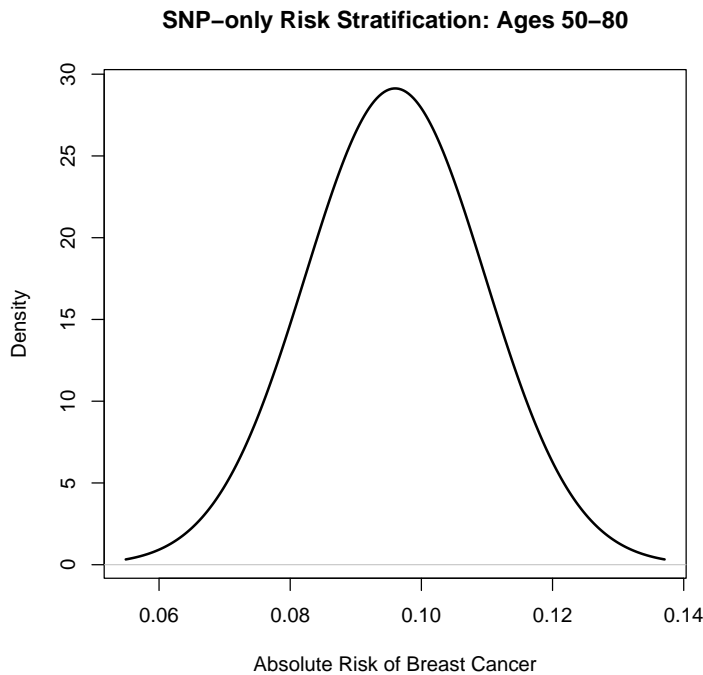
      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
0.05085 0.08642 0.09517 0.09600 0.10422 0.16201

```

```

> 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
0.382  0.011  0.394

```

```

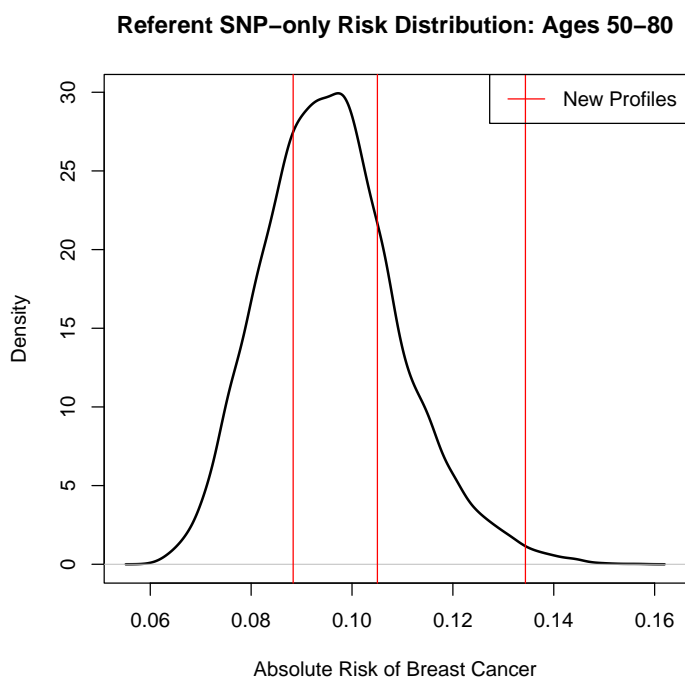
> names(res_snps_dat)

```

```
[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 4.4.1 (2024-06-14)
Platform: x86_64-pc-linux-gnu
Running under: Ubuntu 24.04.1 LTS
```

```
Matrix products: default
BLAS: /home/biocbuild/bbs-3.20-bioc/R/lib/libRblas.so
LAPACK: /usr/lib/x86_64-linux-gnu/lapack/liblapack.so.3.12.0
```

```
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
```

```
time zone: America/New_York
tzcode source: system (glibc)
```

```
attached base packages:
[1] stats      graphics  grDevices  utils      datasets  methods   base
```

```
other attached packages:
[1] iCARE_1.34.0 Hmisc_5.2-0 gtools_3.9.5 plotrix_3.8-4
```

```
loaded via a namespace (and not attached):
 [1] gtable_0.3.6      dplyr_1.1.4      compiler_4.4.1   rpart_4.1.23
 [5] tidyselect_1.2.1 htmlTable_2.4.3  stringr_1.5.1   gridExtra_2.3
 [9] cluster_2.1.6    scales_1.3.0    fastmap_1.2.0   ggplot2_3.5.1
[13] R6_2.5.1         generics_0.1.3   Formula_1.2-5   knitr_1.48
[17] htmlwidgets_1.6.4 backports_1.5.0  checkmate_2.3.2 tibble_3.2.1
[21] munsell_0.5.1    nnet_7.3-19     pillar_1.9.0    rlang_1.1.4
[25] utf8_1.2.4       stringi_1.8.4    xfun_0.48       cli_3.6.3
```

```
[29] magrittr_2.0.3    digest_0.6.37    grid_4.4.1      rstudioapi_0.17.1
[33] base64enc_0.1-3   lifecycle_1.0.4  vctrs_0.6.5     data.table_1.16.2
[37] evaluate_1.0.1    glue_1.8.0       fansi_1.0.6     colorspace_2.1-1
[41] rmarkdown_2.28    foreign_0.8-87   tools_4.4.1     pkgconfig_2.0.3
[45] htmltools_0.5.8.1
```