

iCARE(Individualized Coherent Absolute Risk Estimators) Package

April 15, 2025

```
> 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
10.04    0.44    10.49
```

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)
```

```

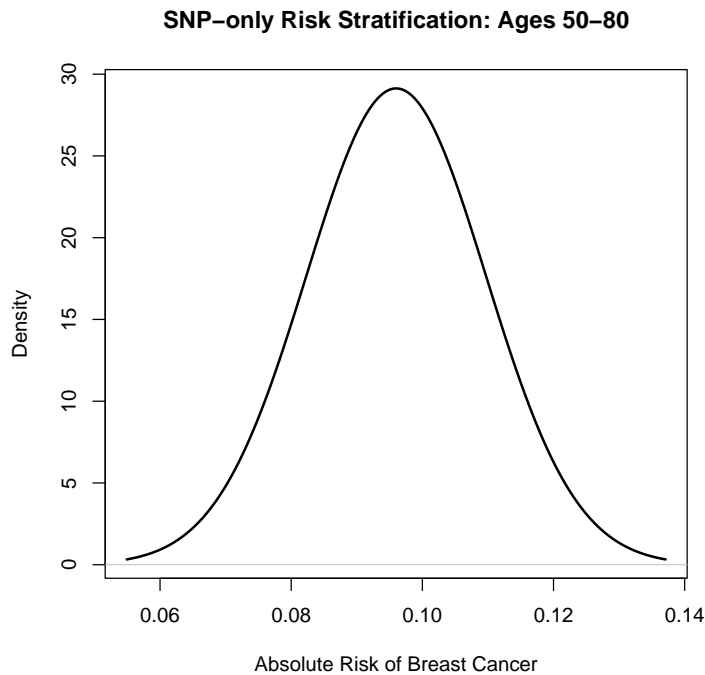
      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
0.05702 0.08653 0.09496 0.09601 0.10445 0.16754

```

```

> 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
0.58    0.19    0.77

```

```

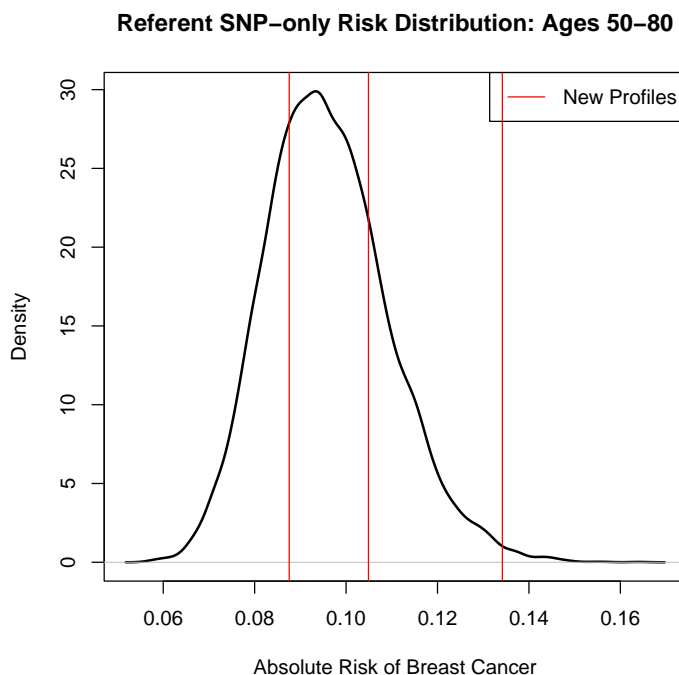
> names(res_snps_dat)

```

```
[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 4.5.0 RC (2025-04-03 r88103 ucrt)
Platform: x86_64-w64-mingw32/x64
Running under: Windows Server 2022 x64 (build 20348)
```

```
Matrix products: default
LAPACK version 3.12.1
```

```
locale:
[1] LC_COLLATE=C
[2] LC_CTYPE=English_United States.utf8
[3] LC_MONETARY=English_United States.utf8
[4] LC_NUMERIC=C
[5] LC_TIME=English_United States.utf8
```

```
time zone: America/New_York
tzcode source: internal
```

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

```
other attached packages:
[1] iCARE_1.37.0 Hmisc_5.2-3 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_4.5.0   rpart_4.1.24
[5] tidyselect_1.2.1  htmlTable_2.4.3  stringr_1.5.1    gridExtra_2.3
[9] cluster_2.1.8.1   scales_1.3.0     fastmap_1.2.0    ggplot2_3.5.2
[13] R6_2.6.1          generics_0.1.3   Formula_1.2-5    knitr_1.50
[17] htmlwidgets_1.6.4 backports_1.5.0  checkmate_2.3.2  tibble_3.2.1
[21] munsell_0.5.1     nnet_7.3-20      pillar_1.10.2    rlang_1.1.6
[25] stringi_1.8.7     xfun_0.52        cli_3.6.4        magrittr_2.0.3
[29] digest_0.6.37     grid_4.5.0       rstudioapi_0.17.1 base64enc_0.1-3
[33] lifecycle_1.0.4   vctrs_0.6.5     data.table_1.17.0 evaluate_1.0.3
```

```
[37] glue_1.8.0      colorspace_2.1-1  rmarkdown_2.29    foreign_0.8-90
[41] tools_4.5.0     pkgconfig_2.0.3   htmltools_0.5.8.1
```