

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
9.90    0.31    10.21
```

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)
```

```

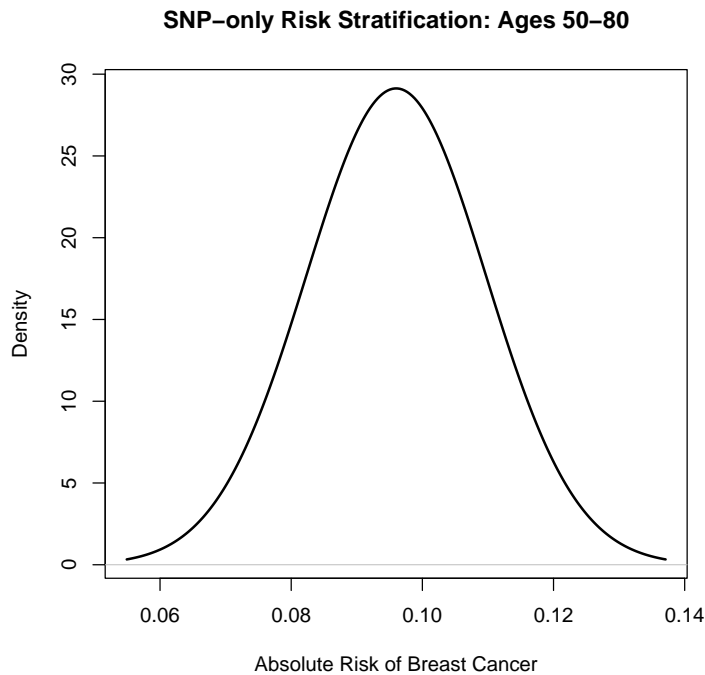
      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
0.05299 0.08645 0.09504 0.09601 0.10437 0.17343

```

```

> 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
0.72    0.16    0.88

```

```

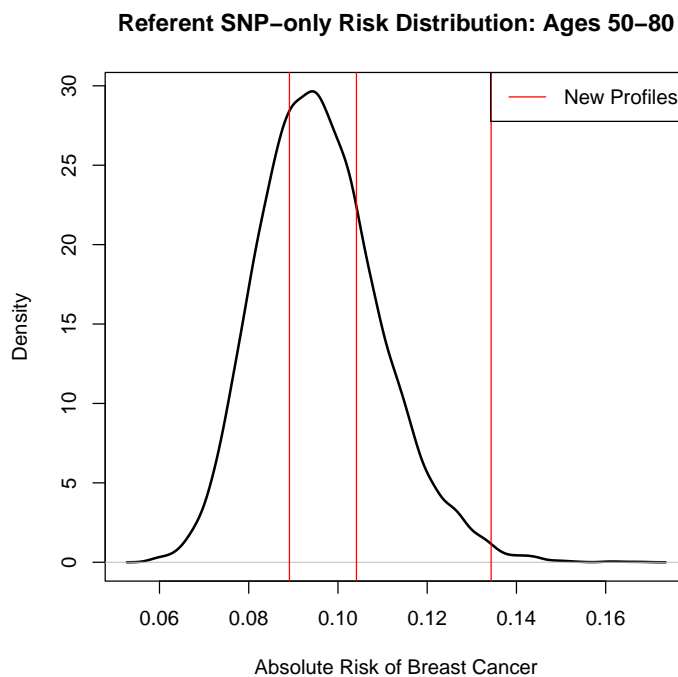
> names(res_snps_dat)

```

```
[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 | alcoholdec | week_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 ucrt)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows Server x64 (build 20348)
```

```
Matrix products: default
```

```
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
```

```
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 | |