

# iCARE(Individualized Coherent Absolute Risk Estimators) Package

May 19, 2021

```
> 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  
11.477    0.116    11.594
```

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)
```

```

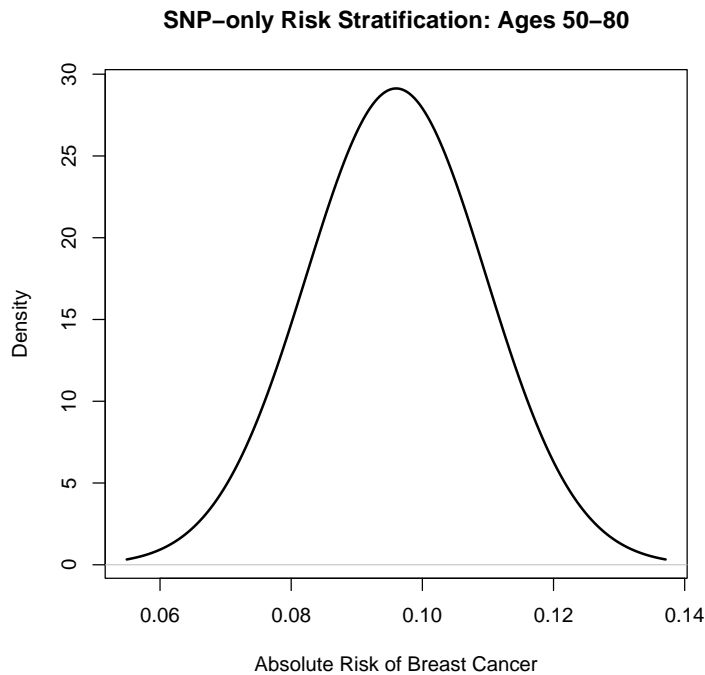
      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
0.05599 0.08662 0.09489 0.09601 0.10427 0.15622

```

```

> 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
0.479   0.064   0.542

```

```

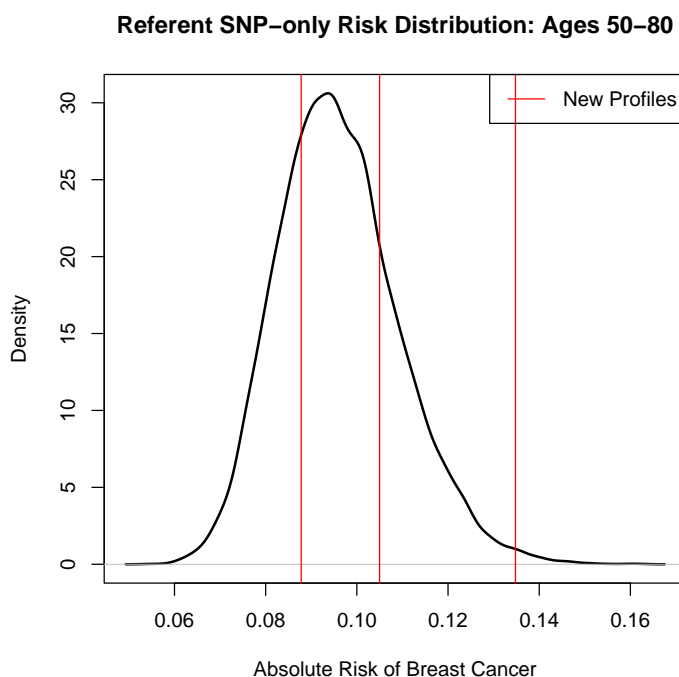
> names(res_snps_dat)

```

```
[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 4.1.0 beta (2021-05-03 r80259)

Platform: x86\_64-pc-linux-gnu (64-bit)

Running under: Ubuntu 20.04.2 LTS

Matrix products: default

BLAS: /home/biocbuild/bbs-3.14-bioc/R/lib/libRblas.so

LAPACK: /home/biocbuild/bbs-3.14-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_1.21.0    Hmisc_4.5-0      ggplot2_3.3.3    Formula_1.2-4
[5] survival_3.2-11 lattice_0.20-44  gtools_3.8.2     plotrix_3.8-1
```

loaded via a namespace (and not attached):

```
[1] pillar_1.6.1      compiler_4.1.0    RColorBrewer_1.1-2
[4] base64enc_0.1-3    tools_4.1.0       digest_0.6.27
[7] rpart_4.1-15       checkmate_2.0.0    htmlTable_2.2.1
[10] lifecycle_1.0.0    tibble_3.1.2      gtable_0.3.0
[13] pkgconfig_2.0.3    png_0.1-7         rlang_0.4.11
[16] Matrix_1.3-3       rstudioapi_0.13   DBI_1.1.1
[19] xfun_0.23          gridExtra_2.3     stringr_1.4.0
[22] knitr_1.33         withr_2.4.2       dplyr_1.0.6
[25] cluster_2.1.2      htmlwidgets_1.5.3 generics_0.1.0
```

|      |                  |                     |                 |
|------|------------------|---------------------|-----------------|
| [28] | vctrs_0.3.8      | nnet_7.3-16         | grid_4.1.0      |
| [31] | tidyselect_1.1.1 | data.table_1.14.0   | glue_1.4.2      |
| [34] | R6_2.5.0         | jpeg_0.1-8.1        | fansi_0.4.2     |
| [37] | foreign_0.8-81   | latticeExtra_0.6-29 | purrr_0.3.4     |
| [40] | magrittr_2.0.1   | htmltools_0.5.1.1   | backports_1.2.1 |
| [43] | scales_1.1.1     | ellipsis_0.3.2      | splines_4.1.0   |
| [46] | assertthat_0.2.1 | colorspace_2.0-1    | utf8_1.2.1      |
| [49] | stringi_1.6.2    | munsell_0.5.0       | crayon_1.4.1    |