

iCARE(Individualized Coherent Absolute Risk Estimators) Package

October 27, 2020

```
> 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
12.334   0.241  12.582
```

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)
```

```

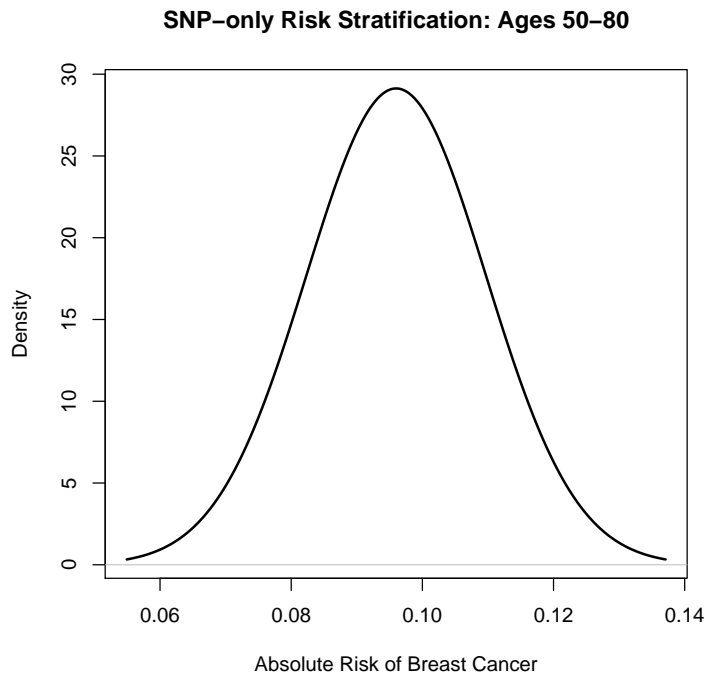
      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
0.05380 0.08658 0.09515 0.09600 0.10435 0.15861

```

```

> 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
0.547   0.112   0.663

```

```

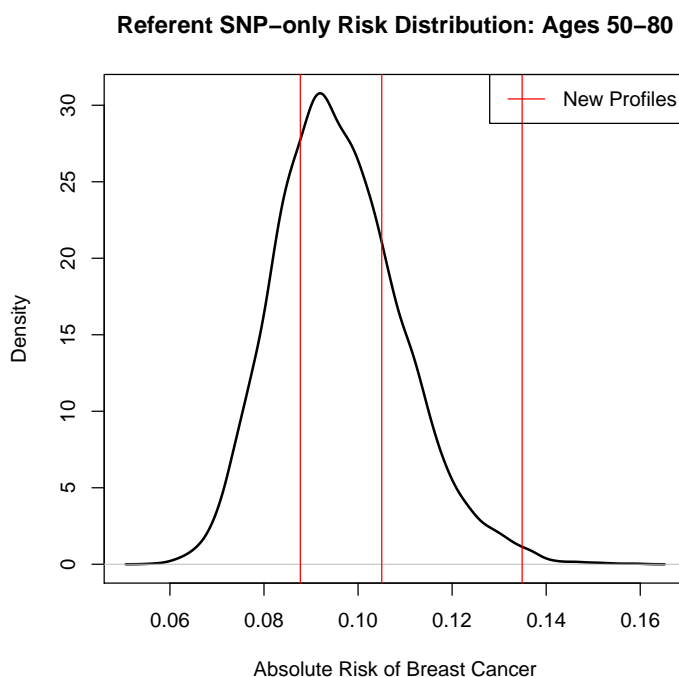
> names(res_snps_dat)

```

```
[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 4.0.3 (2020-10-10)
Platform: x86_64-apple-darwin17.0 (64-bit)
Running under: macOS Mojave 10.14.6
```

```
Matrix products: default
```

```
BLAS: /Library/Frameworks/R.framework/Versions/4.0/Resources/lib/libRblas.dylib
LAPACK: /Library/Frameworks/R.framework/Versions/4.0/Resources/lib/libRlapack.dylib
```

```
locale:
```

```
[1] C/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
```

```
attached base packages:
```

```
[1] stats      graphics  grDevices  utils      datasets  methods    base
```

```
other attached packages:
```

```
[1] iCARE_1.18.0   Hmisc_4.4-1    ggplot2_3.3.2   Formula_1.2-4
[5] survival_3.2-7 lattice_0.20-41 gtools_3.8.2    plotrix_3.7-8
```

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

```
[1] pillar_1.4.6      compiler_4.0.3    RColorBrewer_1.1-2
[4] base64enc_0.1-3    tools_4.0.3       digest_0.6.27
[7] rpart_4.1-15       checkmate_2.0.0   lifecycle_0.2.0
[10] tibble_3.0.4       gtable_0.3.0      htmlTable_2.1.0
[13] pkgconfig_2.0.3    png_0.1-7         rlang_0.4.8
[16] Matrix_1.2-18      rstudioapi_0.11   xfun_0.18
[19] gridExtra_2.3      stringr_1.4.0     knitr_1.30
[22] withr_2.3.0        dplyr_1.0.2       cluster_2.1.0
[25] htmlwidgets_1.5.2  generics_0.0.2    vctrs_0.3.4
[28] grid_4.0.3         nnet_7.3-14       tidyselect_1.1.0
[31] data.table_1.13.2  glue_1.4.2        R6_2.4.1
[34] jpeg_0.1-8.1       foreign_0.8-80    latticeExtra_0.6-29
[37] purrr_0.3.4        magrittr_1.5      htmltools_0.5.0
[40] backports_1.1.10   scales_1.1.1      ellipsis_0.3.1
```

[43]	splines_4.0.3	colorspace_1.4-1	stringi_1.5.3
[46]	munsell_0.5.0	crayon_1.3.4	