

iCARE(Individualized Coherent Absolute Risk Estimators) Package

May 2, 2019

```
> 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
```

```
14.77    0.42    15.19
```

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
```

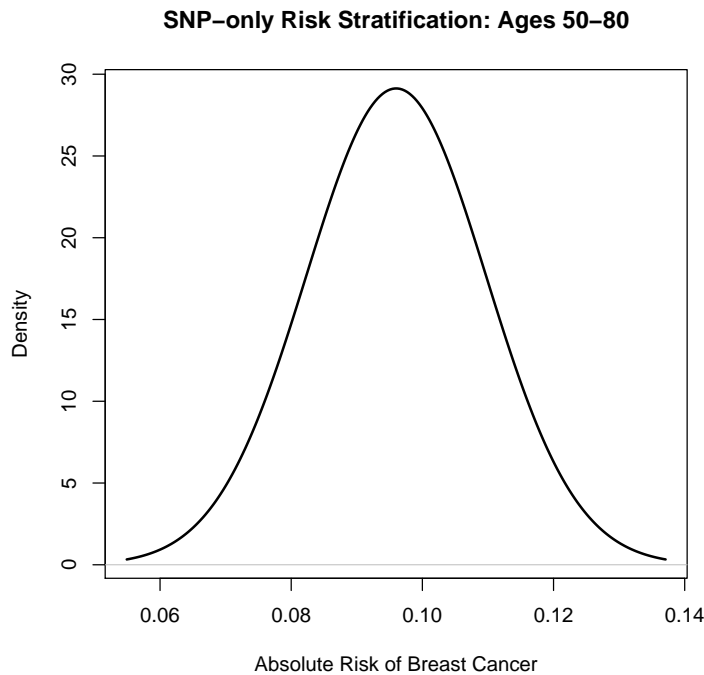
```
3rd Qu.:0.096
```

```
Max.      :0.096
```

```
> summary(res_snps_miss$refs.risk)
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
0.05678	0.08669	0.09494	0.09600	0.10445	0.16022

```
> 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)
```

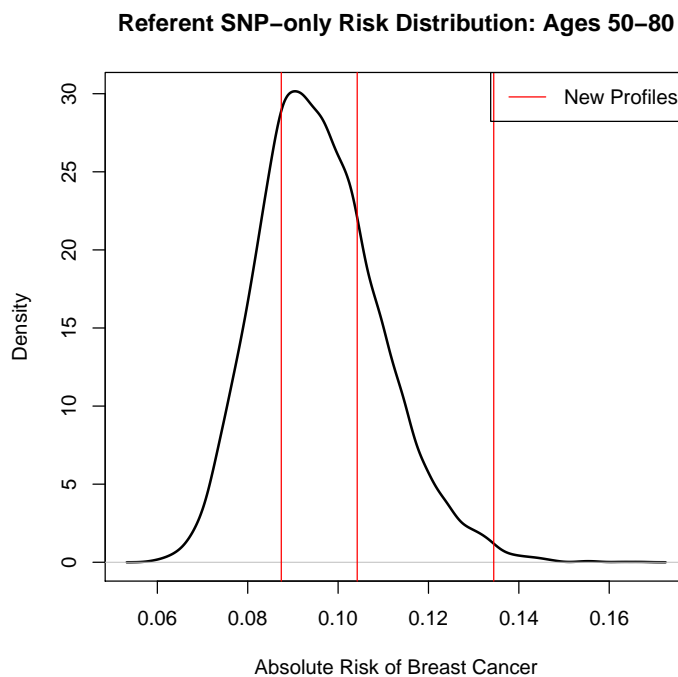
```
[1] "Note: As specified, the model does not adjust SNP imputations for family history."
      user system elapsed
      0.64    0.18    0.81
```

```
> 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	alcoholdecweek_dec	ever_smoke
1	0	0	1	1
2	0	0	6	0
3	0	0	1	1

Session Information

```
> sessionInfo()
```

```
R version 3.6.0 (2019-04-26)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows Server 2012 R2 x64 (build 9600)
```

```
Matrix products: default
```

```
locale:
```

```
[1] LC_COLLATE=C
[2] LC_CTYPE=English_United States.1252
[3] LC_MONETARY=English_United States.1252
[4] LC_NUMERIC=C
[5] LC_TIME=English_United States.1252
```

```
attached base packages:
```

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

```
other attached packages:
```

```
[1] iCARE_1.12.0      Hmisc_4.2-0      ggplot2_3.1.1     Formula_1.2-3
[5] survival_2.44-1.1 lattice_0.20-38   gtools_3.8.1      plotrix_3.7-5
```

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

```
[1] Rcpp_1.0.1        pillar_1.3.1      compiler_3.6.0
[4] RColorBrewer_1.1-2 plyr_1.8.4        base64enc_0.1-3
[7] tools_3.6.0       digest_0.6.18     rpart_4.1-15
[10] checkmate_1.9.1   htmlTable_1.13.1  tibble_2.1.1
[13] gtable_0.3.0      pkgconfig_2.0.2   rlang_0.3.4
[16] Matrix_1.2-17     rstudioapi_0.10   xfun_0.6
[19] gridExtra_2.3     stringr_1.4.0     knitr_1.22
[22] withr_2.1.2       dplyr_0.8.0.1     cluster_2.0.9
[25] htmlwidgets_1.3   grid_3.6.0        nnet_7.3-12
[28] tidyselct_0.2.5   data.table_1.12.2 glue_1.3.1
[31] R6_2.4.0          foreign_0.8-71    latticeExtra_0.6-28
[34] purrr_0.3.2       magrittr_1.5      htmltools_0.3.6
```

[37]	backports_1.1.4	scales_1.0.0	splines_3.6.0
[40]	assertthat_0.2.1	colorspace_1.4-1	stringi_1.4.3
[43]	acepack_1.4.1	lazyeval_0.2.2	munsell_0.5.0
[46]	crayon_1.3.4		