

iCARE(Individualized Coherent Absolute Risk Estimators) Package

December 10, 2018

```
> 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_15_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
18.420   0.413  18.988
```

Compute a summary of the risks and visualize the results

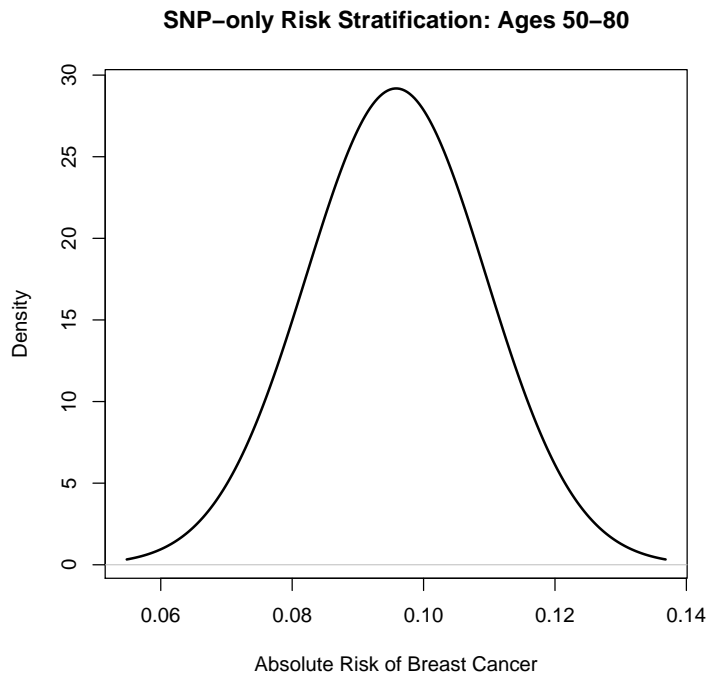
```
> summary(res_snps_miss$risk)
```

```
Risk_Estimate
Min.      :0.09583
1st Qu.:0.09583
Median :0.09583
Mean     :0.09583
3rd Qu.:0.09583
Max.     :0.09583
```

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

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. |
|---------|---------|---------|---------|---------|---------|
| 0.07740 | 0.09196 | 0.09574 | 0.09583 | 0.09954 | 0.12163 |

```
> 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_15_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)
```

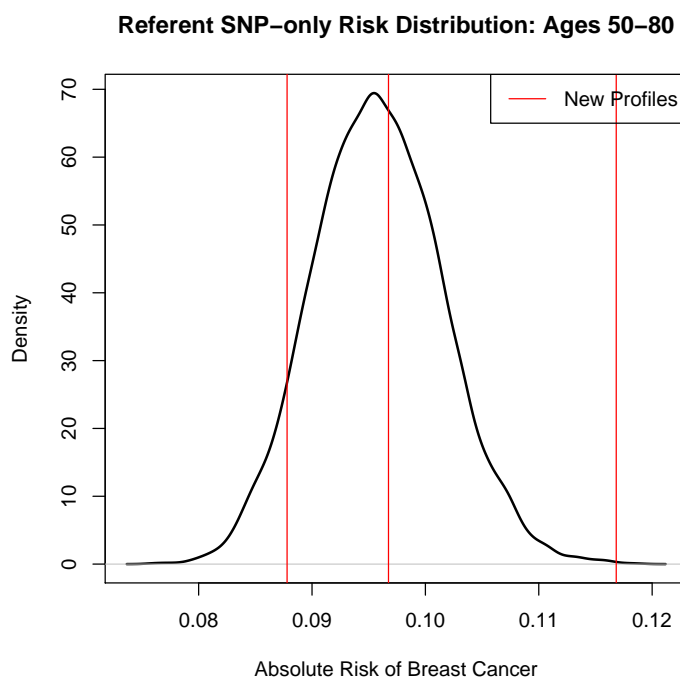
```
[1] "Note: As specified, the model does not adjust SNP imputations for family history."
      user system elapsed
0.402   0.220   0.651
```

```
> 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 two risk factors and 15 SNPs, with three specific covariate profiles supplied for estimation (with some missing data). First, the `model.cov.info` argument is created.

```
> v1 <- list(name="famhist", type="continuous")
> v2 <- list(name="parity", type="factor", levels=0:4, ref=0)
> bc_model_cov_info <- list(v1, v2)
```

Now fit the model

```
> res_covs_snps = computeAbsoluteRisk(model.formula=caco~famhist+as.factor(parity),
+                                     model.cov.info=bc_model_cov_info,
+                                     model.snp.info=bc_15_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,
+                                     apply.snp.profile=new_snp_prof,
+                                     return.refs.risk=TRUE)

```

```

user system elapsed
0.109  0.055  0.165

```

Display details of the fit

```
> print(res_covs_snps$details)
```

| | Int_Start | Int_End | Risk_Estimate | rs12405132 | rs12048493 | rs72755295 | |
|--------|------------|------------|---------------|------------|------------|------------|------------|
| 193502 | 50 | 80 | 0.08223771 | NA | NA | 0 | |
| 126252 | 50 | 80 | 0.07730933 | 0 | 0 | 0 | |
| 15756 | 50 | 80 | 0.12989575 | 0 | 1 | 0 | |
| | rs6796502 | rs13162653 | rs2012709 | rs7707921 | rs9257408 | rs4593472 | rs13365225 |
| 193502 | 0 | 1 | 1 | 0 | 1 | 1 | 1 |
| 126252 | 0 | 2 | 1 | 0 | 1 | 1 | 0 |
| 15756 | 1 | 0 | 1 | 0 | 1 | 1 | 0 |
| | rs13267382 | rs11627032 | rs146699004 | rs745570 | rs6507583 | famhist | parity |
| 193502 | 0 | 0 | 1 | 2 | 0 | 0 | 2 |
| 126252 | 1 | 1 | 0 | 1 | 0 | 0 | 4 |
| 15756 | 1 | 0 | 0 | 0 | 0 | 1 | 4 |

Session Information

```
> sessionInfo()
```

```

R version 3.5.1 Patched (2018-07-12 r74967)
Platform: x86_64-apple-darwin15.6.0 (64-bit)
Running under: OS X El Capitan 10.11.6

```

Matrix products: default

```

BLAS: /Library/Frameworks/R.framework/Versions/3.5/Resources/lib/libRblas.0.dylib
LAPACK: /Library/Frameworks/R.framework/Versions/3.5/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_1.10.3  Hmisc_4.1-1  ggplot2_3.1.0  Formula_1.2-3
```

```
[5] survival_2.43-3 lattice_0.20-38 gtools_3.8.1    plotrix_3.7-4
```

loaded via a namespace (and not attached):

```
[1] Rcpp_1.0.0          pillar_1.3.0        compiler_3.5.1
[4] RColorBrewer_1.1-2  plyr_1.8.4          bindr_0.1.1
[7] base64enc_0.1-3     tools_3.5.1         digest_0.6.18
[10] rpart_4.1-13        checkmate_1.8.5     htmlTable_1.12
[13] tibble_1.4.2        gtable_0.2.0        pkgconfig_2.0.2
[16] rlang_0.3.0.1       Matrix_1.2-15       rstudioapi_0.8
[19] bindrcpp_0.2.2      gridExtra_2.3       stringr_1.3.1
[22] knitr_1.20          withr_2.1.2         dplyr_0.7.8
[25] cluster_2.0.7-1     htmlwidgets_1.3     grid_3.5.1
[28] nnet_7.3-12         tidyselect_0.2.5    data.table_1.11.8
[31] glue_1.3.0          R6_2.3.0            foreign_0.8-71
[34] latticeExtra_0.6-28 purrr_0.2.5         magrittr_1.5
[37] htmltools_0.3.6     backports_1.1.2     scales_1.0.0
[40] splines_3.5.1       assertthat_0.2.0    colorspace_1.3-2
[43] stringi_1.2.4       acepack_1.4.1       lazyeval_0.2.1
[46] munsell_0.5.0       crayon_1.3.4
```