

iCARE(Individualized Coherent Absolute Risk Estimators) Package

December 5, 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
15.320   0.032  17.756
```

Compute a summary of the risks and visualize the results

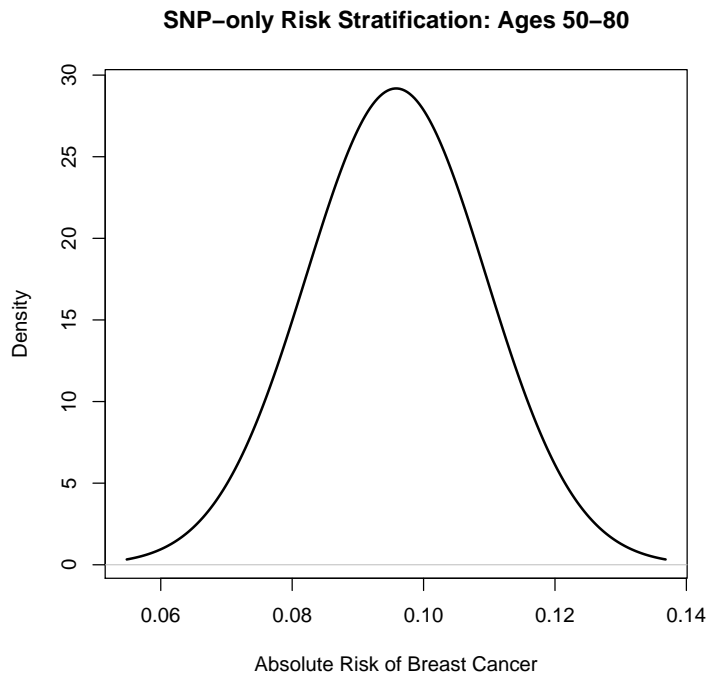
```
> summary(res_snps_miss$risk)
```

```
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.
	0.07485	0.09188	0.09566	0.09583	0.09970	0.11756

```
> 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)
```

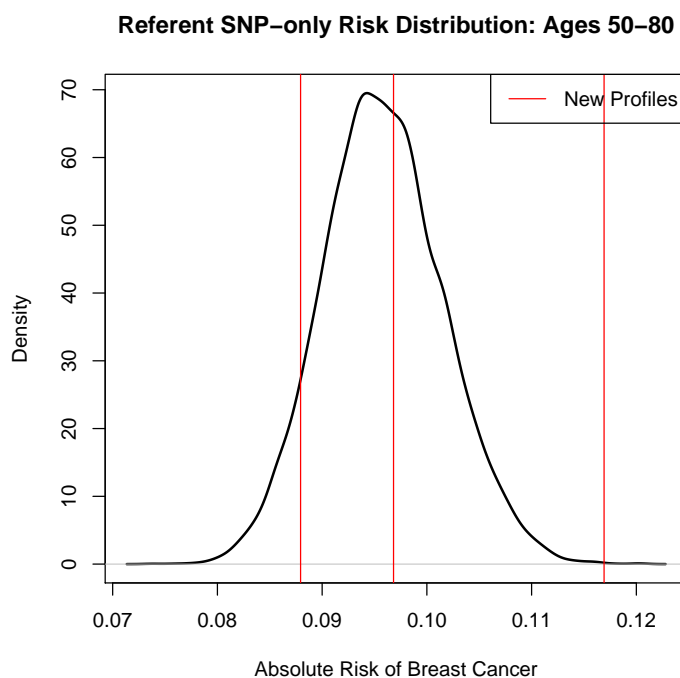
```
[1] "Note: As specified, the model does not adjust SNP imputations for family history."
      user system elapsed
0.208  0.012  0.223
```

```
> 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
0.052   0.024   0.079

```

Display details of the fit

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

	Int_Start	Int_End	Risk_Estimate	rs12405132	rs12048493	rs72755295	
193502	50	80	0.08126291	NA	NA	0	
126252	50	80	0.07719616	0	0	0	
15756	50	80	0.12971135	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-pc-linux-gnu (64-bit)
Running under: Ubuntu 16.04.5 LTS

```

Matrix products: default

BLAS: /home/biocbuild/bbs-3.8-bioc/R/lib/libRblas.so

LAPACK: /home/biocbuild/bbs-3.8-bioc/R/lib/libRlapack.so

locale:

```

[1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
[3] LC_TIME=en_US.UTF-8       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_1.10.2   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
```