

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  
12.712 0.064 12.788
```

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)
```

```

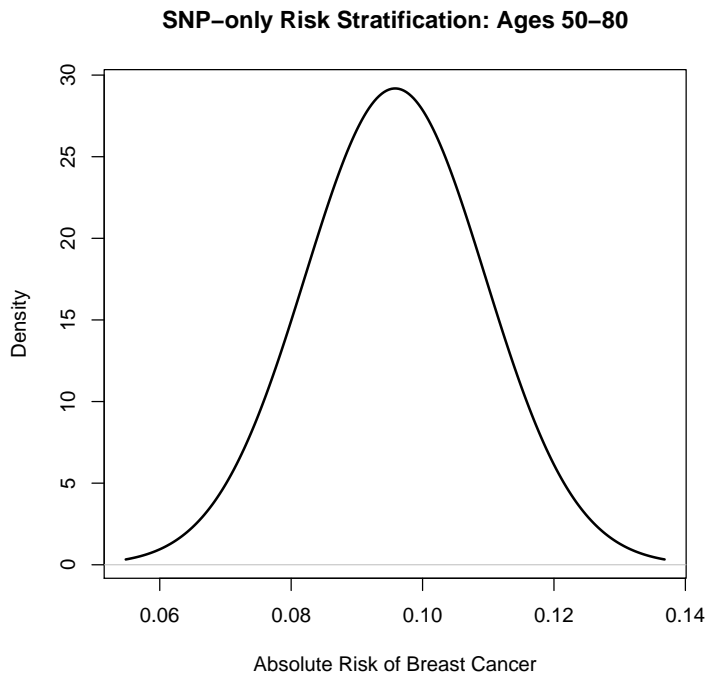
      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
0.07783 0.09184 0.09569 0.09583 0.09955 0.11757

```

```

> 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
0.244  0.024  0.265

```

```

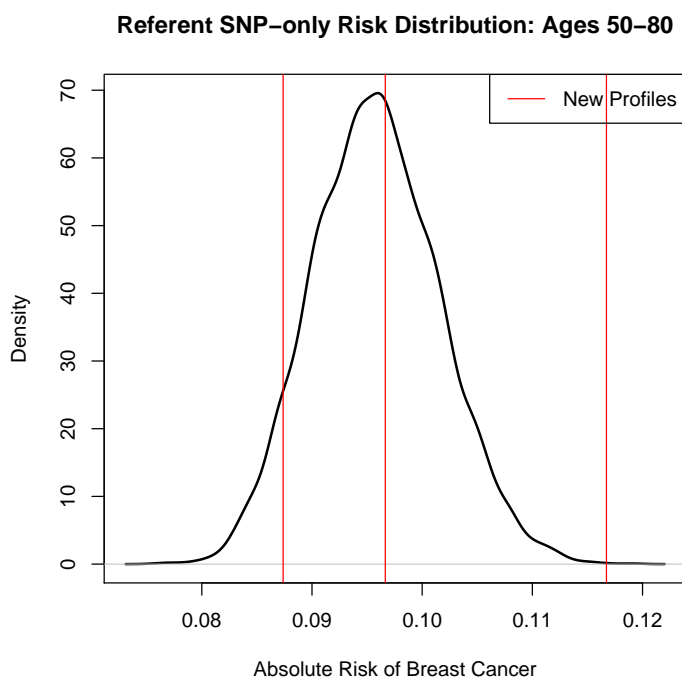
> names(res_snps_dat)

```

```
[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
0.044  0.032  0.076

```

Display details of the fit

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

	Int_Start	Int_End	Risk_Estimate	rs12405132	rs12048493	rs72755295		
193502	50	80	0.08180111	NA	NA	0		
126252	50	80	0.07724808	0	0	0		
15756	50	80	0.12979595	0	1	0		
	rs6796502	rs13162653	rs2012709	rs7707921	rs9257408	rs4593472	rs13365225	
193502	0	1	1	0	1	1	1	1
126252	0	2	1	0	1	1	1	0
15756	1	0	1	0	1	1	1	0
	rs13267382	rs11627032	rs146699004	rs745570	rs6507583	famhist	parity	
193502	0	0	1	2	0	0	0	2
126252	1	1	0	1	0	0	0	4
15756	1	0	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_1.10.3 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