

# 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  
17.648 0.026 21.383
```

Compute a summary of the risks and visualize the results

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

```
Risk_Estimate  
Min. :0.09601  
1st Qu.:0.09601  
Median :0.09601  
Mean :0.09601  
3rd Qu.:0.09601  
Max. :0.09601
```

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

```

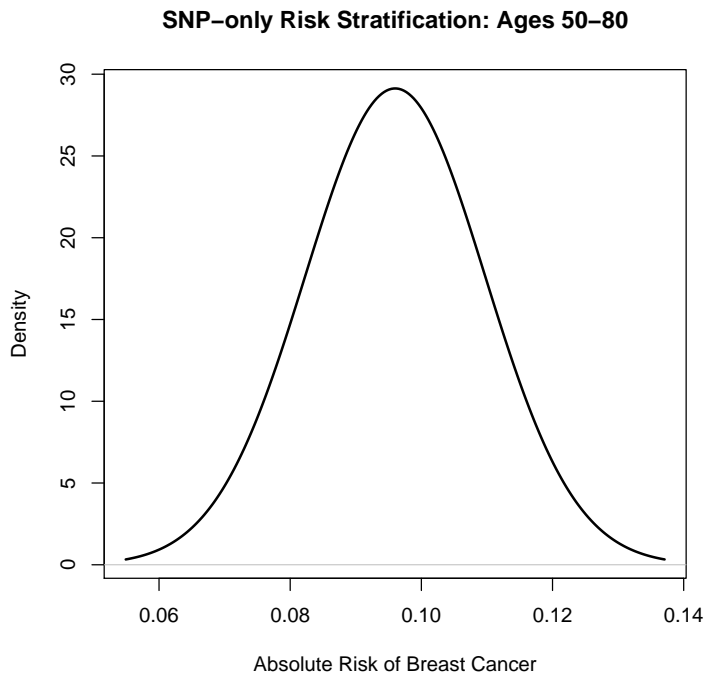
      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
0.05618 0.08654 0.09486 0.09601 0.10458 0.16548

```

```

> 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
0.501  0.036  0.537

```

```

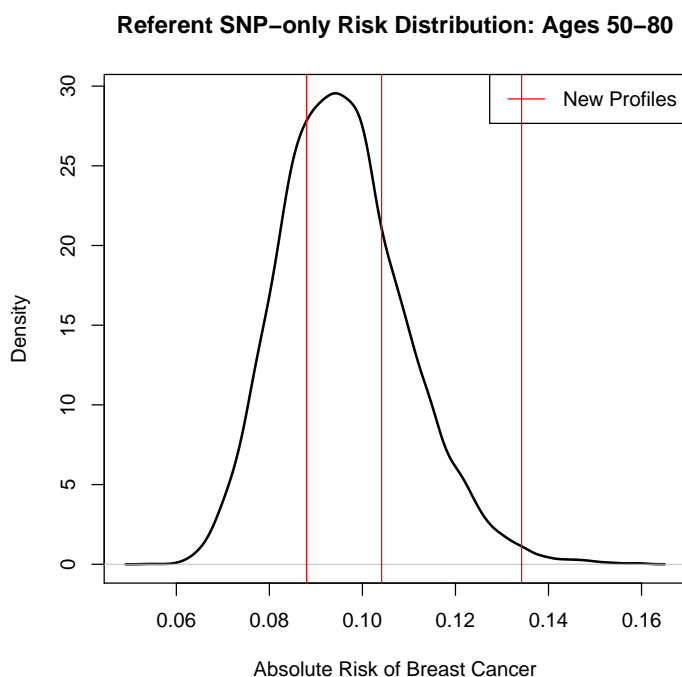
> names(res_snps_dat)

```

```
[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,
```

```
+ apply.snp.profile=new_snp_prof,  
+ return.refs.risk=TRUE)
```

```
user system elapsed  
1.696 0.168 1.864
```

```
Display details of the fit
```

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

	Int_Start	Int_End	Risk_Estimate	rs616488	rs11552449	rs11249433	rs12405132
1	50	80	0.10230489	NA	NA	NA	NA
2	50	80	0.08996985	2	0	NA	NA
3	50	80	0.16855872	2	0	1	1
	rs12048493	rs6678914	rs4245739	rs72755295	rs12710696	rs4849887	rs2016394
1	NA	0	0	0	0	0	0
2	NA	NA	NA	NA	1	1	0
3	1	1	1	0	2	0	0
	rs1550623	rs16857609	rs6762644	rs4973768	rs12493607	rs6796502	rs9790517
1	0	0	0	1	1	0	1
2	0	2	1	1	1	1	2
3	0	0	0	2	1	0	1
	rs6828523	rs10069690	rs13162653	rs2012709	rs10941679	rs10472076	rs1353747
1	0	1	2	0	0	2	0
2	0	0	1	0	0	1	1
3	0	0	1	0	0	0	1
	rs7707921	rs1432679	rs11242675	rs204247	rs9257408	rs4593472	rs720475
1	0	1	2	0	0	1	1
2	0	0	1	2	1	1	0
3	1	2	1	2	1	1	0
	rs9693444	rs13365225	rs6472903	rs2943559	rs13267382	rs11780156	rs1011970
1	1	1	1	0	0	0	0
2	0	0	1	0	2	1	1
3	1	1	0	0	1	0	0
	rs10759243	rs2380205	rs7072776	rs11814448	rs7904519	rs11199914	rs554219
1	0	2	2	0	0	1	1
2	1	0	0	0	0	0	0
3	1	1	1	0	2	0	1
	rs75915166	rs11820646	rs12422552	rs17356907	rs1292011	rs11571833	rs2236007
1	0	1	1	0	1	0	1
2	0	0	0	0	0	0	0
3	0	1	1	0	2	0	0
	rs2588809	rs999737	rs941764	rs11627032	rs17817449	rs11075995	rs13329835
1	0	0	1	0	1	1	1
2	1	0	0	1	1	1	0
3	0	0	1	0	0	1	1
	rs146699004	rs745570	rs527616	rs1436904	rs6507583	rs4808801	rs3760982
1	0	0	0	0	0	1	0
2	1	2	0	0	0	1	1
3	1	2	1	1	0	1	1
	rs2284378	rs2823093	rs17879961	rs132390	rs6001930	famhist	menarche_dec parity

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 3.6.0 (2019-04-26)
Platform: x86_64-pc-linux-gnu (64-bit)
Running under: Ubuntu 18.04.2 LTS
```

```
Matrix products: default
```

```
BLAS: /home/biocbuild/bbs-3.9-bioc/R/lib/libRblas.so
```

```
LAPACK: /home/biocbuild/bbs-3.9-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_1.12.0      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] tidyselect_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
```