Example 1.A

Load the breast cancer data.

```r
> 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.

```r
> 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
11.648 0.036 11.691
```

Compute a summary of the risks and visualize the results.

```r
> 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
```

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

1
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.

```r
> 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
0.280    0.000    0.281
```

```r
> names(res_snps_dat)
```
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,
Display details of the fit

> print(res_covs_snps$details)

<table>
<thead>
<tr>
<th>Int_Start</th>
<th>Int_End</th>
<th>Risk_Estimate</th>
<th>rs12405132</th>
<th>rs12048493</th>
<th>rs72755295</th>
</tr>
</thead>
<tbody>
<tr>
<td>193502</td>
<td>50 80</td>
<td>0.08079822 NA</td>
<td>NA</td>
<td></td>
<td>0</td>
</tr>
<tr>
<td>126252</td>
<td>50 80</td>
<td>0.07724603 0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>15756</td>
<td>50 80</td>
<td>0.12979261 0</td>
<td>1</td>
<td>1</td>
<td>0</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>rs6796502</th>
<th>rs13162653</th>
<th>rs2012709</th>
<th>rs7707921</th>
<th>rs9257408</th>
<th>rs4593472</th>
<th>rs13365225</th>
</tr>
</thead>
<tbody>
<tr>
<td>193502</td>
<td>0 1 1 0</td>
<td>1 1 1 1</td>
<td>1 1 1 1</td>
<td>1 1 1 1</td>
<td>1 1 1 1</td>
<td>1 1 1 1</td>
</tr>
<tr>
<td>126252</td>
<td>0 2 1 0</td>
<td>0 1 1 0</td>
<td>0 1 1 0</td>
<td>0 1 1 0</td>
<td>0 1 1 0</td>
<td>0 1 1 0</td>
</tr>
<tr>
<td>15756</td>
<td>1 0 1 0</td>
<td>0 1 1 0</td>
<td>0 1 1 0</td>
<td>0 1 1 0</td>
<td>0 1 1 0</td>
<td>0 1 1 0</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>rs13267382</th>
<th>rs11627032</th>
<th>chr17:29230520:D</th>
<th>rs745570</th>
<th>rs6507583</th>
<th>famhist</th>
<th>parity</th>
</tr>
</thead>
<tbody>
<tr>
<td>193502</td>
<td>0 0 1 2</td>
<td>0 1 0 0 0 0 0</td>
<td>2 0 0 0 0 0 0</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>126252</td>
<td>1 1 0 0</td>
<td>0 1 0 0 0 0 0</td>
<td>4 0 0 0 0 0 0</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>15756</td>
<td>1 0 0 0</td>
<td>0 0 0 1 1 1 1</td>
<td>4 0 0 0 0 0 0</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Session Information

> sessionInfo()

R version 3.4.0 (2017-04-21)
Platform: x86_64-pc-linux-gnu (64-bit)
Running under: Ubuntu 16.04.2 LTS

Matrix products: default
BLAS: /home/biocbuild/bbs-3.5-bioc/R/lib/libRblas.so
LAPACK: /home/biocbuild/bbs-3.5-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
attached base packages:
[1] stats  graphics  grDevices  utils  datasets  methods  base

other attached packages:
[1] iCARE_1.4.0

loaded via a namespace (and not attached):
[1] compiler_3.4.0  tools_3.4.0