Read in BMI GIANT GWAS meta-analysis data

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Load the relevant libraries first:

```
library(readr)
library(dplyr)
library(reshape2)
library(curl)
library(Hmisc)
```

Now load the data (first need to download the file from https://www.broadinstitute.org/collaboration/giant/
index.php/GIANT_consortium_data_files#GWAS_Anthropometric_2015_BMI):

```
##change the directory name
tot = read_tsv("../../../../Dropbox/Research/FDR projects/Prior prob regression/code/All_ancestries_SNP_
dim(tot)
```

```
## [1] 2555510        8
```

Do some basic data filtering (to remove missing values) and data cleaning (switch to minor allele from effect
allele, add variable with frequency intervals):

```
tot = filter(tot,!is.na(Freq1.Hapmap))
dim(tot)
```

```
## [1] 2500573        8
```

```
##change the frequency to the minor allele frequency
changeWhich <- tot$Freq1.Hapmap > 0.5
tot$Freq1.Hapmap[changeWhich] <- 1-tot$Freq1.Hapmap[changeWhich]
colnames(tot)[colnames(tot)=="Freq1.Hapmap"] <- "Freq_MAF_Hapmap"
##also need to change the coefficient sign for these alleles
tot$b[changeWhich] <- -tot$b[changeWhich]
tot = mutate(tot,Freq_MAF_Int_Hapmap=cut2(Freq_MAF_Hapmap,g=3)) ##added a new variable with frequency i
table(tot$Freq_MAF_Int_Hapmap)
```

```
##
## [0.000,0.127) [0.127,0.302) [0.302,0.500]
##        838070        850600        811903
```

Save in a data frame in a .RData file:

```
BMI_GIANT_GWAS <- tot
```

```
save(x=BMI_GIANT_GWAS, file="BMI_GIANT_GWAS.RData")
```

Session Information

```
devtools::session_info()
```

```
## Session info ------------------------------------------------------------

##   setting  value
##   version  R version 3.3.1 (2016-06-21)
##   system   x86_64, mingw32
##   ui       RTerm
##   language (EN)
##   collate  English_United States.1252
##   tz       America/New_York
##   date     2016-10-28

## Packages ----------------------------------------------------------------

##   package      * version date       source
##   acepack        1.3-3.3 2014-11-24 CRAN (R 3.3.0)
##   assertthat     0.1     2013-12-06 CRAN (R 3.3.1)
##   BiocStyle    * 2.0.2   2016-05-16 Bioconductor
##   chron          2.3-47  2015-06-24 CRAN (R 3.3.1)
##   cluster        2.0.4   2016-04-18 CRAN (R 3.3.1)
##   codetools      0.2-14  2015-07-15 CRAN (R 3.3.1)
##   colorspace     1.2-6   2015-03-11 CRAN (R 3.3.1)
##   curl         * 1.0     2016-07-24 CRAN (R 3.3.1)
##   data.table     1.9.6   2015-09-19 CRAN (R 3.3.1)
##   DBI            0.4-1   2016-05-08 CRAN (R 3.3.1)
##   devtools       1.12.0  2016-06-24 CRAN (R 3.3.1)
##   digest         0.6.9   2016-01-08 CRAN (R 3.3.1)
##   dplyr        * 0.5.0   2016-06-24 CRAN (R 3.3.1)
##   evaluate       0.9     2016-04-29 CRAN (R 3.3.1)
##   foreign        0.8-66  2015-08-19 CRAN (R 3.3.1)
##   formatR        1.4     2016-05-09 CRAN (R 3.3.1)
##   Formula      * 1.2-1   2015-04-07 CRAN (R 3.3.0)
##   ggplot2      * 2.1.0   2016-03-01 CRAN (R 3.3.1)
##   gridExtra      2.2.1   2016-02-29 CRAN (R 3.3.1)
##   gtable         0.2.0   2016-02-26 CRAN (R 3.3.1)
##   Hmisc        * 3.17-4  2016-05-02 CRAN (R 3.3.1)
##   htmltools      0.3.5   2016-03-21 CRAN (R 3.3.1)
##   knitr          1.13    2016-05-09 CRAN (R 3.3.1)
##   lattice      * 0.20-33 2015-07-14 CRAN (R 3.3.1)
##   latticeExtra   0.6-28  2016-02-09 CRAN (R 3.3.1)
##   lazyeval       0.2.0   2016-06-12 CRAN (R 3.3.1)
##   magrittr       1.5     2014-11-22 CRAN (R 3.3.1)
##   Matrix         1.2-6   2016-05-02 CRAN (R 3.3.1)
##   memoise        1.0.0   2016-01-29 CRAN (R 3.3.1)
##   munsell        0.4.3   2016-02-13 CRAN (R 3.3.1)
##   nnet           7.3-12  2016-02-02 CRAN (R 3.3.1)
##   plyr           1.8.4   2016-06-08 CRAN (R 3.3.1)
##   R6             2.1.2   2016-01-26 CRAN (R 3.3.1)
##   RColorBrewer   1.1-2   2014-12-07 CRAN (R 3.3.0)
```

```
##  Rcpp          0.12.6  2016-07-19 CRAN (R 3.3.1)
##  readr       * 0.2.2   2015-10-22 CRAN (R 3.3.1)
##  reshape2    * 1.4.1   2014-12-06 CRAN (R 3.3.1)
##  rmarkdown     1.0     2016-07-08 CRAN (R 3.3.1)
##  rpart         4.1-10  2015-06-29 CRAN (R 3.3.1)
##  scales        0.4.0   2016-02-26 CRAN (R 3.3.1)
##  stringi       1.1.1   2016-05-27 CRAN (R 3.3.0)
##  stringr       1.0.0   2015-04-30 CRAN (R 3.3.1)
##  survival    * 2.39-4  2016-05-11 CRAN (R 3.3.1)
##  tibble        1.1     2016-07-04 CRAN (R 3.3.1)
##  withr         1.0.2   2016-06-20 CRAN (R 3.3.1)
##  yaml          2.1.13  2014-06-12 CRAN (R 3.3.1)
```