Analysis Approach 1

Setting up the analysis dependencies are loaded and SNP and populations to be analysed are defined. Furthermore, paths to 1000Genomes vcf and tbi files are set, as well as to the panel file.

```
library(devtools)
library(GenomicRanges)
library(grid)
library(TxDb.Hsapiens.UCSC.hg19.knownGene)
library(Homo.sapiens)
devtools::load_all('/home/SSD-Data/Projects/haploplotR/')

lead_snps <- c("rs12569773", "rs4615961", "rs10983654", "rs1512262", "rs11119348" )
populations <- c('CEU', 'CHB', 'YRI')

vcffile <- "/home/SSD-Data/1000Genomes/ALL.%s.phase3_shapeit2_mvncall_integrated_v5a.20130502.genotypes
panelfile <- "integrated_call_samples_v3.20130502.ALL.panel"
```

Next information about SNPs is gathered from dbSNP144

Add a new chunk by clicking the *Insert Chunk* button on the toolbar or by pressing *Ctrl+Alt+I*.

When you save the notebook, an HTML file containing the code and output will be saved alongside it (click the *Preview* button or press *Ctrl+Shift+K* to preview the HTML file).

The preview shows you a rendered HTML copy of the contents of the editor. Consequently, unlike *Knit*, *Preview* does not run any R code chunks. Instead, the output of the chunk when it was last run in the editor is displayed.