1. The power of a test (at Type I error rate of, say, 0.05) is the probability that its p-value will be less than 0.05. One way to estimate the power is by simulating the study many times and calculating the proportion of simulations where the p-value is less than 0.05.

Suppose we are to test whether there is a significant change in blood pressure (from e.g. before treatment to after treatment) in 100 individuals. An appropriate statistical test is a one-sample t-test, and it is reasonable to assume that the 100 subjects’ changes are sampled from a Normal distribution, with mean 2mmHg, and standard deviation 7mmHg.

Using rnorm(), t.test() and replicate(), compute the power of this test, by simulation. Keen people: compare your answer to that computed by the power.t.test() function.

2. In this question we investigate differences in mean systolic blood pressure by genotype, for the data on 11 SNPs you saw before. To obtain p-values for linear regression analysis of the association between blood pressure and genotype for a single variant, we can use e.g.

```r
# read in the data, and merge
justsnps <- read.table("example-snp.txt",header=TRUE)
sampleinfo <- read.csv("example-pheno.csv", header=TRUE)
merged <- merge(justsnps, sampleinfo, by="id")

# computing p-value for linear regression of SBP on snp3
lm.temp <- lm(merged$sbp~as.numeric(merged[,4]))
summary(lm.temp)
coef(summary(lm.temp))[2,4]

To do this in a loop, we could use apply(), e.g.

```r
all.p <- apply(merged[,2:12], 2, function(snpi){
    n.minor <- as.numeric(factor(snpi)) # turn CC/CT/TT into 0/1/2
    lm1 <- lm(merged$sbp~n.minor) # do regression
    coef(summary(lm1))[2,4] # extract p-value
})
```

The ‘best’ (i.e. minimum) p-value is obtained by e.g.

```r
min(all.p)
```

Use a permutation test of this minimum p-value across all 11 SNPs to assess whether there is really a statistically significant effect of any of these SNPs on systolic blood pressure.