

# Demonstration of LyX with Knitr

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## Simulate Data

```
n = 500 # number of observations
k = 1000 # number of markers
Z = matrix(sample(c(0, 1, 2), n * k, replace = T), n, k)
alpha = rnorm(ncol(Z), 0, 1)
a = Z %*% alpha
y = a + rnorm(nrow(Z), 0, sqrt(var(a)))
h2 = var(a)/var(y)
cat("Heritability of simulated trait = ", h2, "\n")

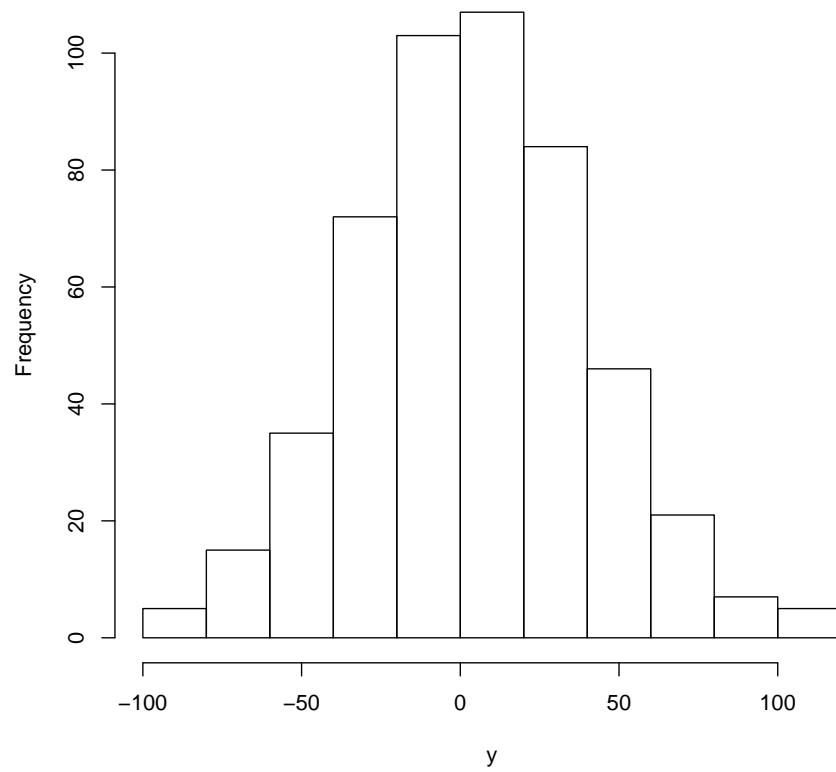
## Heritability of simulated trait = 0.5053
```

The mean for the simulated trait is 3.9877 and the variance is 1339.251; the heritability of the trait is 0.5053.

### Distribution of phenotypic values:

```
hist(y, main = "Distribution of Phenotypic Values")
```

### Distribution of Phenotypic Values



### Mixed Model Analysis

```
p = colMeans(Z)/2
vare = var(y) - var(a)
(varAlpha = var(a)/(2 * sum(p * (1 - p))))

##      [,1]
## [1,] 1.355

(lambda = vare/varAlpha)

##      [,1]
## [1,] 488.8

Z = t(t(Z) - colMeans(Z))
```

```

tstRows = sample(1:nrow(Z), 100)
Ztrn = Z[-tstRows, ]
ytrn = y[-tstRows, ]
Ztst = Z[tstRows, ]
atst = a[tstRows]
n = nrow(Ztrn)
X = cbind(matrix(1, n, 1)) # intercept
W = cbind(X, Ztrn)
MME1 = t(W) %*% W
MME2 = MME1
rhs = t(W) %*% ytrn
diag(MME1) = diag(MME1) + c(0, rep(lambda, ncol(Ztrn)))
diag(MME2) = diag(MME2) + c(0, rep(1e-08, ncol(Ztrn)))
sol1 = solve(MME1, rhs)
sol2 = solve(MME2, rhs)

```

## Accuracy:

```

ahat1 = sol1[1] + Ztst %*% sol1[-1]
(cor(atst, ahat1))

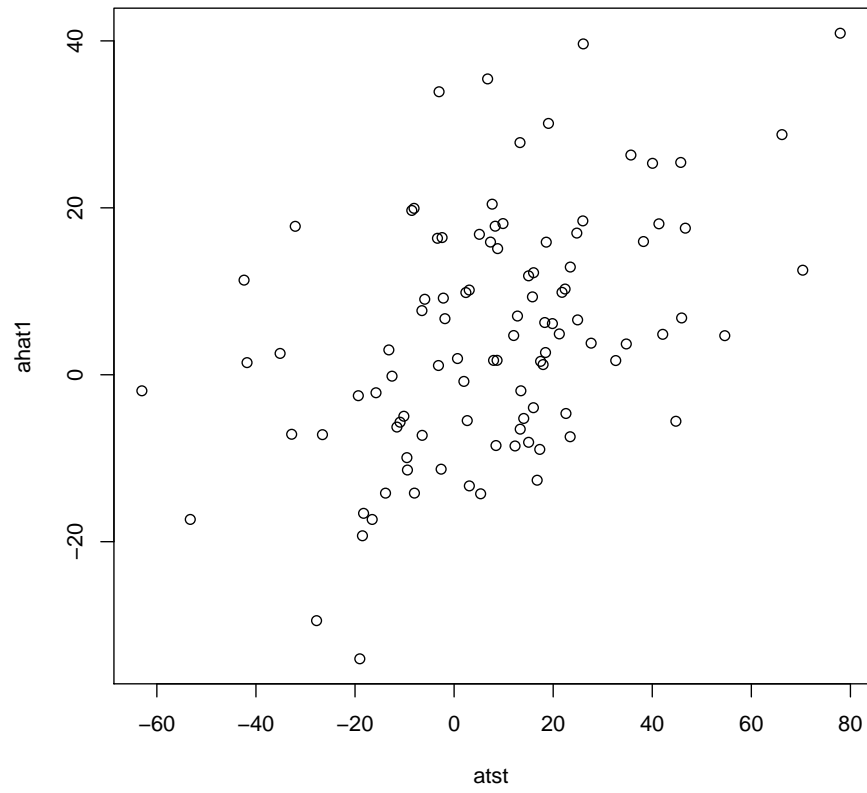
##          [,1]
## [1,] 0.4555

ahat2 = sol2[1] + Ztst %*% sol2[-1]
(cor(atst, ahat2))

##          [,1]
## [1,] 0.435

plot(atst, ahat1)

```



```
plot(atst, ahat2)
```

