```
235    resdat<-matrix(NA,nrow(new),length(phenotypes))
236    colnames(resdat)<-phenotypes
237
238    for (p in 1:length(phenotypes)){
239        assign(paste("lm", phenotypes[p], sep="_"),
240              lm(new[[phenotypes[p]]] ~ Age + Age2 +
241               center1 + center2 + center3 + center4 +
242                   center5 + center6 + center7 + center8 +
243                   center9 + center10 + center11 + center12 +
244                   center13 + center14 + center15 + center16 +
245                   center17 + center18 + center20 +
246                   center21 + Sex + Geno_batch, data=new,
247            na.action=na.exclude))
248        lmname<-paste("lm", phenotypes[p], sep="_")
249        lmobj<-get(lmname)
250        resdat[,p]<-resid(lmobj)
251    }
```

This code aimed to calculate the relationship between phenotypes and various factors such as age, centers, sex and geno_batch using linear regression model. The input data is a matrix, containing all the information for phenotype, age, centers, sex and geno_batch. Output are the residuals for phenotypes extracted from the linear regression model.