

simple and multiple regression of the phenotype

Model specification

Here we define two models: a simple regression of SNP on phenotype, and a full model including available covariates. Both sample sex and site of ascertainment are natural categorical covariates. The encoding of the dosing regimen deserves some careful consideration. This can be treated as a continuous covariate, a categorical covariate, or perhaps some different altogether. Currently, I am treating it as a continuous variable. I am able to include it in fitting the SKAT-O model as an added benefit. We simply do not have the degrees of freedom necessary (i.e. number of samples) to include 33 dummy variables.

```
trans.fun <- log
basic.model <- trans.fun(ANC) ~ 1
full.model <- trans.fun(ANC) ~ sex + site + as.numeric(dose)
```

PGRNseq GWAS

Simple Regression

```
seq.reg.results <- mlreg(basic.model, seq.geno, trait="gaussian")
qqunif(seq.reg.results[, "P1df"])
title('PGRNseq Simple Linear Regression GWAS')
```

Multiple Regression

```
seq.reg.results <- mlreg(full.model, seq.geno, trait="gaussian")
qqunif(seq.reg.results[, "P1df"])
title('PGRNseq Multiple Linear Regression GWAS')
```

Exome chip GWAS

Simple Regression

```
exome.reg.results <- mlreg(basic.model, exome.geno, trait="gaussian")
qqunif(exome.reg.results[, "P1df"])
title('Exome chip Simple Linear Regression GWAS')
```

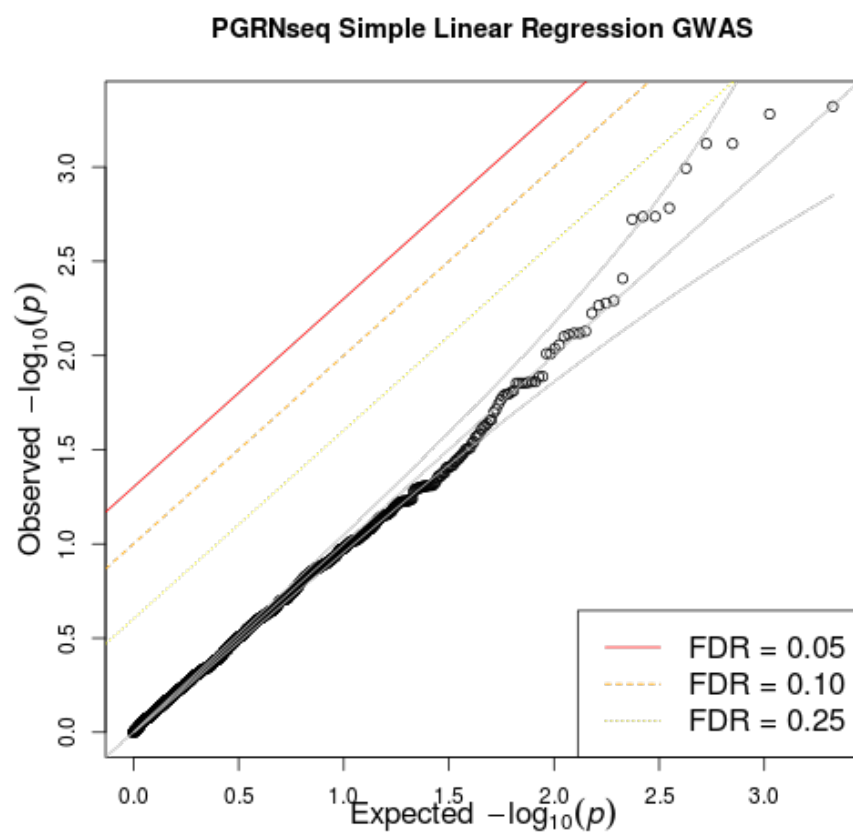


Figure 1: plot of chunk seq_simple_regression

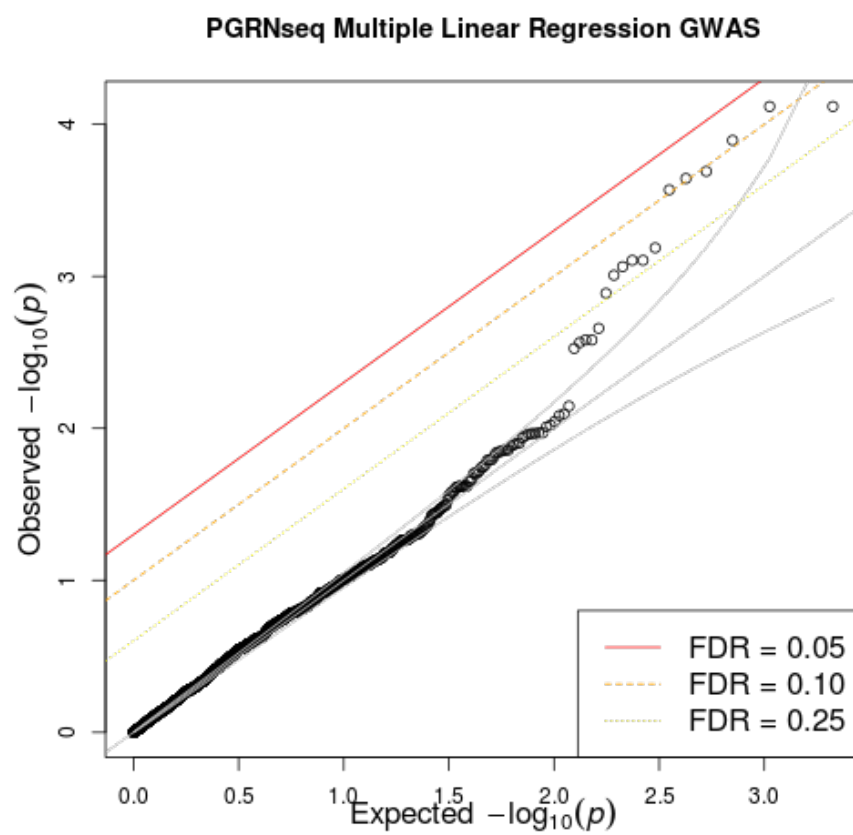


Figure 2: plot of chunk seq_multiple_regression

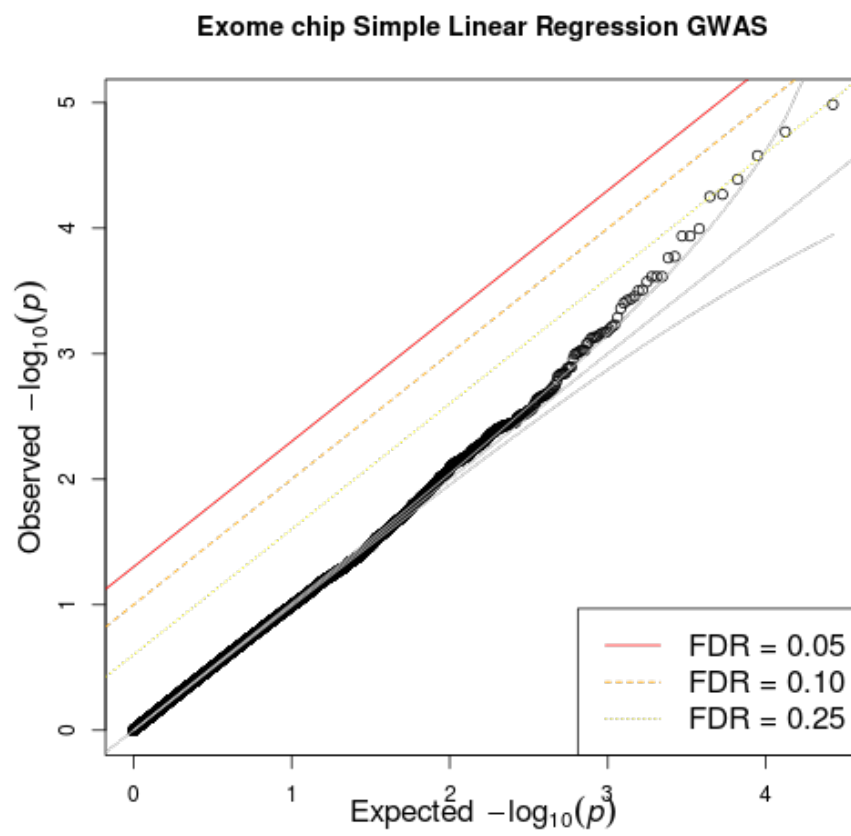


Figure 3: plot of chunk exome_simple_regression

Multiple Regression

```
exome.reg.results <- mlreg(full.model, exome.geno, trait="gaussian")
qqunif(seq.reg.results[, "P1df"])
title('Exome Chip Multiple Linear Regression')
```

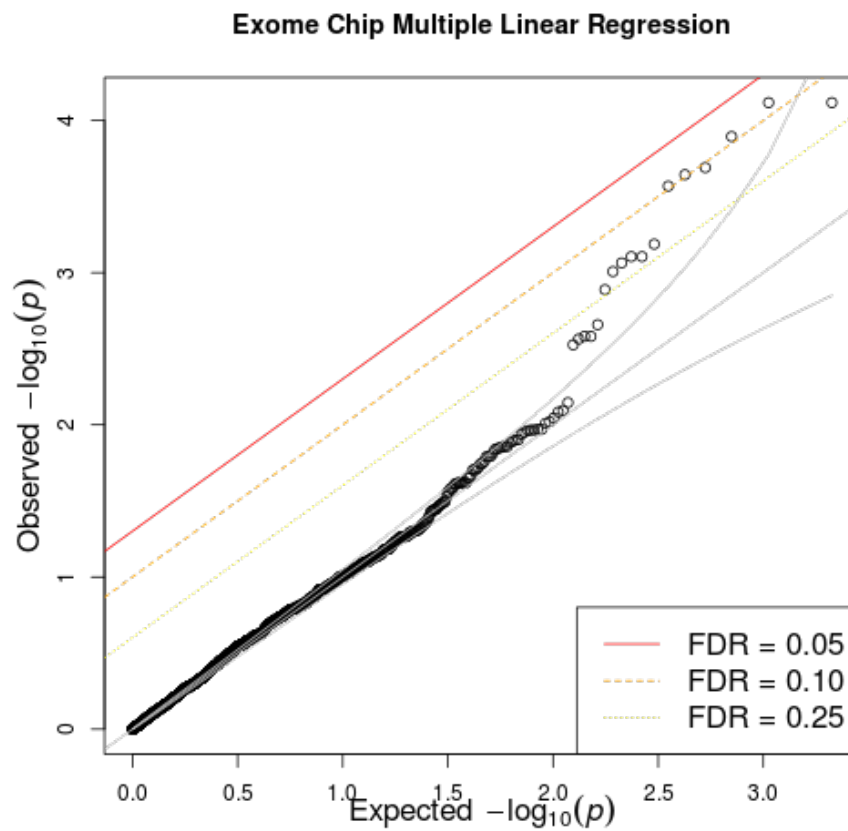


Figure 4: plot of chunk exome_multiple_regression

Known signals

UGT1A1*93: rs10929302
hg19 chr2:234,665,782 G/A
1000 Genomes allele frequencies:

A: 27%
G: 73%

```
rs10929302.res <- results(seq.reg.results)['chr2:234665782:G:A',]  
kable( rs10929302.res[,c('A1', 'A2', 'N', 'effB', 'se_effB', 'P1df')] )
```

	A1	A2	N	effB	se_effB	P1df														
chr2:234665782:G:A	T	G	151	-0.3253	0.1274	0.0107														