Using RQT, an R package for gene-level meta-analysis

Ilya Y. Zhbannikov

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1 Overview

Despite the recent advances of modern GWAS methods, it is still remains an important problem of addressing calculation an effect size and corresponding p-value for the whole gene rather than for single variant. We developed an R-package rqt, which offers gene-level GWAS meta-analysis. The package can be easily included into bioinformatics pipeline or used as stand-alone. Contact: ilya.zhbannikov@duke.edu for questions of usage the `rqt` or any other issues.

Below we provide several examples that show GWAS meta-analysis on gene-level layer.

1.1 Methods in brief

The workflow of gene-level meta analysis consists of the following steps: (i) reducing the number of predictors, thereby alleviating correlation problem in variants (accounting for LD); (ii) then the regression mod-el is fitted on the reduced dataset to obtain corresponding regression coefficient ("effect sizes"); (iii) these coefficients are then to be pooled into a total index representing a total gene-level effect size and corresponding statistics is calculated. P- and q- values are then calculated using this statistics from asymptotic approximation or permutation procedure; (iv) the final step is combining gene-level p-values calculated from each study with Fisher's combined probability method.

2 Data description

2.1 Single dataset

In `rqt` requires the following datasets: (i) `phenotype` (a `N` by 1) matrix (i.e. a vector); and (ii) `genotype` - an object of class `SummarizedExperiment` containing one assay: (a `N` by `M`) matrix, where `N` - is the total number of individuals in the study and `M` is the total number of genetic variants. Optionally, `rqt` can accept covariates, in form of `N` by `K` matrix, where `K` is the total number of covariates used in the study. Phenotype can be dichotomous (0/1, where 1 indicates control and 0 case).

2.2 Meta-analysis

In meta-analysis, `rqt` requires a list of `M` (`M` - number of datasets used in meta-analysis) and optionally it accepts covariates in form described above.

3 Examples

3.1 Gene-level analysis on a single dataset

3.2 Dichotomous phenotype

```
> library(rqt)
> data <- data.matrix(read.table(system.file("extdata/test.bin1.dat",
+                                            package="rqt"), header=TRUE))
> pheno <- data[,1]
> geno <- data[, 2:dim(data)[2]]
> colnames(geno) <- paste(seq(1, dim(geno)[2]))
> geno.obj <- SummarizedExperiment(geno)
> obj <- rqtClass(phenotype=pheno, genotype=geno.obj)
> res <- rQTest(obj, method="pca", out.type = "D")
> print(res)
```

```
Phenotype:
[1] 1 1 1 1 1 1
...

Genotype:
     1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28
[1,] 0 0 0 1 0 2 1 0 0  0  2  1  2  0  0  2  1  1  0  0  1  0  0  0  0  2  1  0
[2,] 1 0 1 0 0 1 0 0 0  0  0  0  1  0  0  0  2  1  2  1  0  1  0  0  0  2  1  1
[3,] 0 0 0 0 1 0 0 1 0  1  1  1  0  0  0  1  1  0  0  1  1  1  0  0  0  1  0  0
[4,] 0 0 1 0 1 0 0 1 1  0  0  0  1  0  0  0  1  0  0  2  0  1  0  0  0  1  0  2
[5,] 0 0 1 1 1 1 1 1 0  1  0  1  0  0  0  0  0  0  0  0  1  0  0  1  0  1  2  0
[6,] 0 0 1 1 1 0 0 1 0  1  1  0  1  0  0  2  0  0  1  0  1  1  0  0  0  2  0  0
     29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53
[1,]  1  0  0  0  0  0  0  1  1  0  0  1  0  0  1  0  0  0  0  1  1  0  0  0  1
[2,]  2  0  0  0  1  2  1  2  0  1  1  0  1  0  0  1  0  0  0  2  0  1  0  1  0
[3,]  0  0  0  0  0  1  1  1  2  2  0  0  0  1  0  1  0  2  1  1  1  0  0  0  1
[4,]  0  0  0  1  2  2  0  1  1  1  1  0  0  0  1  1  0  0  1  1  2  0  1  0  2
[5,]  0  0  0  0  1  1  0  0  1  1  0  0  2  2  0  0  0  1  2  1  0  0  0  0  1
[6,]  0  0  0  0  1  0  1  1  0  0  2  0  1  1  2  0  0  0  1  1  1  0  0  1  1
     54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78
[1,]  1  1  1  1  0  0  0  0  1  1  0  1  1  1  0  1  1  2  1  1  1  0  0  2  1
[2,]  2  1  0  1  0  0  0  1  0  1  2  2  1  1  0  1  0  1  0  0  0  0  1  1  2
[3,]  2  1  0  0  0  0  0  0  0  1  0  0  1  1  0  1  2  1  0  1  1  0  0  0  0
[4,]  1  1  0  0  0  0  2  1  0  1  0  0  2  1  0  0  1  1  1  0  0  0  0  0  1
[5,]  1  1  1  0  0  0  2  1  1  0  0  1  1  0  0  1  1  0  0  1  0  1  0  0  1
[6,]  0  1  1  0  0  0  0  0  0  0  1  2  1  1  0  0  0  0  0  1  1  1  1  1  1
     79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100
[1,]  1  1  0  1  1  0  1  1  0  0  0  1  0  1  1  0  0  0  1  0  1   1
[2,]  1  1  2  0  0  0  1  2  0  2  1  0  0  2  1  0  0  0  0  1  1   2
[3,]  1  1  0  0  0  0  2  0  0  2  0  0  0  0  1  1  0  0  1  2  0   0
[4,]  0  1  2  0  1  0  1  2  0  0  0  0  0  0  1  0  0  0  1  0  0   0
[5,]  0  2  0  1  0  0  2  0  0  0  0  1  0  0  1  0  0  1  1  2  1   1
[6,]  2  1  0  0  1  0  0  0  0  2  0  1  0  0  0  0  0  1  1  0  1   1
...

Covariates:
```

```
data frame with 0 columns and 0 rows


Results:

$Qstatistic
         Q1        Q2        Q3
1 0.9086994 0.9938212 0.9086994

$p.value
       p.Q1      p.Q2      p.Q3
1 0.3404597 0.9285409 0.5654533
```

3.3 Continuous phenotype

```
> library(rqt)
> data <- data.matrix(read.table(system.file("extdata/test.cont1.dat",
+                                            package="rqt"), header = TRUE))
> pheno <- data[,1]
> geno <- data[, 2:dim(data)[2]]
> colnames(geno) <- paste(seq(1, dim(geno)[2]))
> geno.obj <- SummarizedExperiment(geno)
> obj <- rqtClass(phenotype=pheno, genotype=geno.obj)
> res <- rQTest(obj, method="pca", out.type = "C")
> print(res)

Phenotype:
[1] 3.422452 2.457394 2.708564 4.589394 5.461723 4.438707
...

Genotype:
     1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28
[1,] 0 0 0 1 0 2 1 0 0  0  2  1  2  0  0  2  1  1  0  0  1  0  0  0  0  2  1  0
[2,] 1 0 1 0 0 1 0 0 0  0  0  0  1  0  0  0  2  1  2  1  0  1  0  0  0  2  1  1
[3,] 0 0 0 0 1 0 0 1 0  1  1  1  0  0  0  1  1  0  0  1  1  1  0  0  0  1  0  0
[4,] 0 0 1 0 1 0 0 1 1  0  0  0  1  0  0  0  1  0  0  2  0  1  0  0  0  1  0  2
[5,] 0 0 1 1 1 1 1 1 0  1  0  1  0  0  0  0  0  0  0  0  1  0  0  1  0  1  2  0
[6,] 0 0 1 1 1 0 0 1 0  1  1  0  1  0  0  2  0  0  1  0  1  1  0  0  0  2  0  0
     29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53
[1,]  1  0  0  0  0  0  0  1  1  0  0  1  0  0  1  0  0  0  0  1  1  0  0  0  1
[2,]  2  0  0  0  1  2  1  2  0  1  1  0  1  0  0  1  0  0  0  2  0  1  0  1  0
[3,]  0  0  0  0  0  1  1  1  2  2  0  0  0  1  0  1  0  2  1  1  1  0  0  0  1
[4,]  0  0  0  1  2  2  0  1  1  1  1  0  0  0  1  1  0  0  1  1  2  0  1  0  2
[5,]  0  0  0  0  1  1  0  0  1  1  0  0  2  2  0  0  0  1  2  1  0  0  0  0  1
[6,]  0  0  0  0  1  0  1  1  0  0  2  0  1  1  2  0  0  0  1  1  1  0  0  1  1
     54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78
[1,]  1  1  1  1  0  0  0  0  1  1  0  1  1  1  0  1  1  2  1  1  1  0  0  2  1
[2,]  2  1  0  1  0  0  0  1  0  1  2  2  1  1  0  1  0  1  0  0  0  0  1  1  2
[3,]  2  1  0  0  0  0  0  0  0  1  0  0  1  1  0  1  2  1  0  1  1  0  0  0  0
[4,]  1  1  0  0  0  0  2  1  0  1  0  0  2  1  0  0  1  1  1  0  0  0  0  0  1
[5,]  1  1  1  0  0  0  2  1  1  0  0  1  1  0  0  1  1  0  0  1  0  1  0  0  1
[6,]  0  1  1  0  0  0  0  0  0  0  1  2  1  1  0  0  0  0  0  1  1  1  1  1  1
```

```
     79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100
[1,]  1  1  0  1  1  0  1  1  0  0  0  1  0  1  1  0  0  0  1  0  1   1
[2,]  1  1  2  0  0  0  1  2  0  2  1  0  0  2  1  0  0  0  0  1  1   2
[3,]  1  1  0  0  0  0  2  0  0  2  0  0  0  0  1  1  0  0  1  2  0   0
[4,]  0  1  2  0  1  0  1  2  0  0  0  0  0  0  1  0  0  0  1  0  0   0
[5,]  0  2  0  1  0  0  2  0  0  0  0  1  0  0  1  0  0  1  1  2  1   1
[6,]  2  1  0  0  1  0  0  0  0  2  0  1  0  0  0  0  0  1  1  0  1   1
...

Covariates:
data frame with 0 columns and 0 rows


Results:

$Qstatistic
         Q1       Q2       Q3
1 0.2846585 2.389537 2.219594

$p.value
      p.Q1      p.Q2      p.Q3
1 0.593664 0.7022459 0.2561996
```

3.4 Preprocessing with Partial Least Square regression (PLS)

This method is used for continous outcome, i.e. out.type = "C".

```
> library(rqt)
> data <- data.matrix(read.table(system.file("extdata/test.cont1.dat",
+                                            package="rqt"), header = TRUE))
> pheno <- data[,1]
> geno <- data[, 2:dim(data)[2]]
> colnames(geno) <- paste(seq(1, dim(geno)[2]))
> geno.obj <- SummarizedExperiment(geno)
> obj <- rqtClass(phenotype=pheno, genotype=geno.obj)
> res <- rQTest(obj, method="pls", out.type = "C")
> print(res)

Phenotype:
[1] 3.422452 2.457394 2.708564 4.589394 5.461723 4.438707
...

Genotype:
     1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28
[1,] 0 0 0 1 0 2 1 0 0  0  2  1  2  0  0  2  1  1  0  0  1  0  0  0  0  2  1  0
[2,] 1 0 1 0 0 1 0 0 0  0  0  0  1  0  0  0  2  1  2  1  0  1  0  0  0  2  1  1
[3,] 0 0 0 0 1 0 0 1 0  1  1  1  0  0  0  1  1  0  0  1  1  1  0  0  0  1  0  0
[4,] 0 0 1 0 1 0 0 1 1  0  0  0  1  0  0  0  1  0  0  2  0  1  0  0  0  1  0  2
[5,] 0 0 1 1 1 1 1 1 0  1  0  1  0  0  0  0  0  0  0  0  1  0  0  1  0  1  2  0
[6,] 0 0 1 1 1 0 0 1 0  1  1  0  1  0  0  2  0  0  1  0  1  1  0  0  0  2  0  0
     29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53
[1,]  1  0  0  0  0  0  0  1  1  0  0  1  0  0  1  0  0  0  0  1  1  0  0  0  1
```

```
[2,]  2  0  0  0  1  2  1  2  0  1  1  0  1  0  0  1  0  0  0  2  0  1  0  1  0
[3,]  0  0  0  0  0  1  1  1  2  2  0  0  0  1  0  1  0  2  1  1  1  0  0  0  1
[4,]  0  0  0  1  2  2  0  1  1  1  1  0  0  0  1  1  0  0  1  1  2  0  1  0  2
[5,]  0  0  0  0  1  1  0  0  1  1  0  0  2  2  0  0  0  1  2  1  0  0  0  0  1
[6,]  0  0  0  0  1  0  1  1  0  0  2  0  1  1  2  0  0  0  1  1  1  0  0  1  1
     54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78
[1,]  1  1  1  1  0  0  0  0  1  1  0  1  1  1  0  1  1  2  1  1  1  0  0  2  1
[2,]  2  1  0  1  0  0  0  1  0  1  2  2  1  1  0  1  0  1  0  0  0  0  1  1  2
[3,]  2  1  0  0  0  0  0  0  0  1  0  0  1  1  0  1  2  1  0  1  1  0  0  0  0
[4,]  1  1  0  0  0  0  2  1  0  1  0  0  2  1  0  0  1  1  1  0  0  0  0  0  1
[5,]  1  1  1  0  0  0  2  1  1  0  0  1  1  0  0  1  1  0  0  1  0  1  0  0  1
[6,]  0  1  1  0  0  0  0  0  0  0  1  2  1  1  0  0  0  0  0  1  1  1  1  1  1
     79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100
[1,]  1  1  0  1  1  0  1  1  0  0  0  1  0  1  1  0  0  0  1  0  1   1
[2,]  1  1  2  0  0  0  1  2  0  2  1  0  0  2  1  0  0  0  0  1  1   2
[3,]  1  1  0  0  0  0  2  0  0  2  0  0  0  0  1  1  0  0  1  2  0   0
[4,]  0  1  2  0  1  0  1  2  0  0  0  0  0  0  1  0  0  0  1  0  0   0
[5,]  0  2  0  1  0  0  2  0  0  0  0  1  0  0  1  0  0  1  1  2  1   1
[6,]  2  1  0  0  1  0  0  0  0  2  0  1  0  0  0  0  0  1  1  0  1   1
...

Covariates:
data frame with 0 columns and 0 rows


Results:

$Qstatistic
         Q1       Q2       Q3
1 0.1910558 71.34471 16.59228

$p.value
       p.Q1         p.Q2       p.Q3
1 0.6620394 1.293491e-05 0.00011429
```

3.5 Preprocessing with Partial Least Square Discriminant Analysis (PLS-DA)

This method of data preprocessing is used for dichotomous outcome.

```
> library(rqt)
> data <- data.matrix(read.table(system.file("extdata/test.bin1.dat",
+                                            package="rqt"), header=TRUE))
> pheno <- data[,1]
> geno <- data[, 2:dim(data)[2]]
> colnames(geno) <- paste(seq(1, dim(geno)[2]))
> geno.obj <- SummarizedExperiment(geno)
> obj <- rqtClass(phenotype=pheno, genotype=geno.obj)
> res <- rQTest(obj, method="pls", out.type = "D", scale = TRUE)

PLS-DA
200 samples x 100 variables and 1 response
standard scaling of predictors and response(s)
```

```
      R2X(cum) R2Y(cum) Q2(cum) RMSEE pre ort pR2Y  pQ2
Total   0.0187    0.301  -0.292   0.2   1   0  0.8 0.55
<simpleError in model$scoreMN: $ operator not defined for this S4 class>
```

> print(res)

```
Phenotype:
[1] 1 1 1 1 1 1
...

Genotype:
     1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28
[1,] 0 0 0 1 0 2 1 0 0  0  2  1  2  0  0  2  1  1  0  0  1  0  0  0  0  2  1  0
[2,] 1 0 1 0 0 1 0 0 0  0  0  0  1  0  0  0  2  1  2  1  0  1  0  0  0  2  1  1
[3,] 0 0 0 0 1 0 0 1 0  1  1  1  0  0  0  1  1  0  0  1  1  1  0  0  0  1  0  0
[4,] 0 0 1 0 1 0 0 1 1  0  0  0  1  0  0  0  1  0  0  2  0  1  0  0  0  1  0  2
[5,] 0 0 1 1 1 1 1 1 0  1  0  1  0  0  0  0  0  0  0  0  1  0  0  1  0  1  2  0
[6,] 0 0 1 1 1 0 0 1 0  1  1  0  1  0  0  2  0  0  1  0  1  1  0  0  0  2  0  0
     29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53
[1,]  1  0  0  0  0  0  0  1  1  0  0  1  0  0  1  0  0  0  0  1  1  0  0  0  1
[2,]  2  0  0  0  1  2  1  2  0  1  1  0  1  0  0  1  0  0  0  2  0  1  0  1  0
[3,]  0  0  0  0  0  1  1  1  2  2  0  0  0  1  0  1  0  2  1  1  1  0  0  0  1
[4,]  0  0  0  1  2  2  0  1  1  1  1  0  0  0  1  1  0  0  1  1  2  0  1  0  2
[5,]  0  0  0  0  1  1  0  0  1  1  0  0  2  2  0  0  0  1  2  1  0  0  0  0  1
[6,]  0  0  0  0  1  0  1  1  0  0  2  0  1  1  2  0  0  0  1  1  1  0  0  1  1
     54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78
[1,]  1  1  1  1  0  0  0  0  1  1  0  1  1  1  0  1  1  2  1  1  1  0  0  2  1
[2,]  2  1  0  1  0  0  0  1  0  1  2  2  1  1  0  1  0  1  0  0  0  0  1  1  2
[3,]  2  1  0  0  0  0  0  0  0  1  0  0  1  1  0  1  2  1  0  1  1  0  0  0  0
[4,]  1  1  0  0  0  0  2  1  0  1  0  0  2  1  0  0  1  1  1  0  0  0  0  0  1
[5,]  1  1  1  0  0  0  2  1  1  0  0  1  1  0  0  1  1  0  0  1  0  1  0  0  1
[6,]  0  1  1  0  0  0  0  0  0  0  1  2  1  1  0  0  0  0  0  1  1  1  1  1  1
     79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100
[1,]  1  1  0  1  1  0  1  1  0  0  0  1  0  1  1  0  0  0  1  0  1   1
[2,]  1  1  2  0  0  0  1  2  0  2  1  0  0  2  1  0  0  0  0  1  1   2
[3,]  1  1  0  0  0  0  2  0  0  2  0  0  0  0  1  1  0  0  1  2  0   0
[4,]  0  1  2  0  1  0  1  2  0  0  0  0  0  0  1  0  0  0  1  0  0   0
[5,]  0  2  0  1  0  0  2  0  0  0  0  1  0  0  1  0  0  1  1  2  1   1
[6,]  2  1  0  0  1  0  0  0  0  2  0  1  0  0  0  0  0  1  1  0  1   1
...

Covariates:
data frame with 0 columns and 0 rows


Results:

$Qstatistic
  Q1 Q2 Q3
1 NA NA NA

$p.value
```

```
  p.Q1 p.Q2 p.Q3
1   NA   NA   NA
```

3.6 Using additional covariates

Quite often, researchers want to supply not only genetic data but also specific covariates, representic some physiological parameters or environment (for example, to evaluate hyphoteses of gene-environment interactions). In such cases, the package `rqt` can accept additional covariates, in form of `N` by `K` matrix, as provided below:

```
> library(rqt)
> data <- data.matrix(read.table(system.file("extdata/test.bin1.dat",
+                                            package="rqt"), header = TRUE))
> pheno <- data[,1]
> geno <- data[, 2:dim(data)[2]]
> colnames(geno) <- paste(seq(1, dim(geno)[2]))
> geno.obj <- SummarizedExperiment(geno)
> covars <- read.table(system.file("extdata/test.cova1.dat",package="rqt"),
+     header=TRUE)
> obj <- rqtClass(phenotype=pheno, genotype=geno.obj, covariates = covars)
> res <- rQTest(obj, method="pca", out.type = "D")
> print(res)

Phenotype:
[1] 1 1 1 1 1 1
...

Genotype:
     1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28
[1,] 0 0 0 1 0 2 1 0 0  0  2  1  2  0  0  2  1  1  0  0  1  0  0  0  0  2  1  0
[2,] 1 0 1 0 0 1 0 0 0  0  0  0  1  0  0  0  2  1  2  1  0  1  0  0  0  2  1  1
[3,] 0 0 0 0 1 0 0 1 0  1  1  1  0  0  0  1  1  0  0  1  1  1  0  0  0  1  0  0
[4,] 0 0 1 0 1 0 0 1 1  0  0  0  1  0  0  0  1  0  0  2  0  1  0  0  0  1  0  2
[5,] 0 0 1 1 1 1 1 1 0  1  0  1  0  0  0  0  0  0  0  0  1  0  0  1  0  1  2  0
[6,] 0 0 1 1 1 0 0 1 0  1  1  0  1  0  0  2  0  0  1  0  1  1  0  0  0  2  0  0
     29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53
[1,]  1  0  0  0  0  0  0  1  1  0  0  1  0  0  1  0  0  0  0  1  1  0  0  0  1
[2,]  2  0  0  0  1  2  1  2  0  1  1  0  1  0  0  1  0  0  0  2  0  1  0  1  0
[3,]  0  0  0  0  0  1  1  1  2  2  0  0  0  1  0  1  0  2  1  1  1  0  0  0  1
[4,]  0  0  0  1  2  2  0  1  1  1  1  0  0  0  1  1  0  0  1  1  2  0  1  0  2
[5,]  0  0  0  0  1  1  0  0  1  1  0  0  2  2  0  0  0  1  2  1  0  0  0  0  1
[6,]  0  0  0  0  1  0  1  1  0  0  2  0  1  1  2  0  0  0  1  1  1  0  0  1  1
     54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78
[1,]  1  1  1  1  0  0  0  0  1  1  0  1  1  1  0  1  1  2  1  1  1  0  0  2  1
[2,]  2  1  0  1  0  0  0  1  0  1  2  2  1  1  0  1  0  1  0  0  0  0  1  1  2
[3,]  2  1  0  0  0  0  0  0  0  1  0  0  1  1  0  1  2  1  0  1  1  0  0  0  0
[4,]  1  1  0  0  0  0  2  1  0  1  0  0  2  1  0  0  1  1  1  0  0  0  0  0  1
[5,]  1  1  1  0  0  0  2  1  1  0  0  1  1  0  0  1  1  0  0  1  0  1  0  0  1
[6,]  0  1  1  0  0  0  0  0  0  0  1  2  1  1  0  0  0  0  0  1  1  1  1  1  1
     79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100
[1,]  1  1  0  1  1  0  1  1  0  0  0  1  0  1  1  0  0  0  1  0  1   1
[2,]  1  1  2  0  0  0  1  2  0  2  1  0  0  2  1  0  0  0  0  1  1   2
```

```
[3,]  1  1  0  0  0  0  2  0  0  2  0  0  0  0  1  1  0  0  1  2  0   0
[4,]  0  1  2  0  1  0  1  2  0  0  0  0  0  0  1  0  0  0  1  0  0   0
[5,]  0  2  0  1  0  0  2  0  0  0  0  1  0  0  1  0  0  1  1  2  1   1
[6,]  2  1  0  0  1  0  0  0  0  2  0  1  0  0  0  0  0  1  1  0  1   1
...

Covariates:
          COV1
1 -0.612463927
2 -0.464158885
3  0.006153597
4 -0.732109468
5 -0.223530136
6 -0.744903822


Results:

$Qstatistic
        Q1       Q2       Q3
1 2.012625 3.761859 2.012625

$p.value
       p.Q1      p.Q2      p.Q3
1 0.1559952 0.8258796 0.2895166
```

4 Meta-analysis

```
> library(rqt)
> data1 <- data.matrix(read.table(system.file("extdata/phengen2.dat",
+                                             package="rqt"), skip=1))
> pheno <- data1[,1]
> geno <- data1[, 2:dim(data1)[2]]
> colnames(geno) <- paste(seq(1, dim(geno)[2]))
> geno.obj <- SummarizedExperiment(geno)
> obj1 <- rqtClass(phenotype=pheno, genotype=geno.obj)
> data2 <- data.matrix(read.table(system.file("extdata/phengen3.dat",
+                                             package="rqt"), skip=1))
> pheno <- data2[,1]
> geno <- data2[, 2:dim(data2)[2]]
> colnames(geno) <- paste(seq(1, dim(geno)[2]))
> geno.obj <- SummarizedExperiment(geno)
> obj2 <- rqtClass(phenotype=pheno, genotype=geno.obj)
> data3 <- data.matrix(read.table(system.file("extdata/phengen.dat",
+                                             package="rqt"), skip=1))
> pheno <- data3[,1]
> geno <- data3[, 2:dim(data3)[2]]
> colnames(geno) <- paste(seq(1, dim(geno)[2]))
> geno.obj <- SummarizedExperiment(geno)
> obj3 <- rqtClass(phenotype=pheno, genotype=geno.obj)
> res.meta <- rQTestMeta(list(obj1, obj2, obj3))
```

```
> print(res.meta)

$final.pvalue
[1] 0.01995627

$pvalueList
[1] 0.006016377 0.367634896 0.245240026

$df
[1] 6

$chi.comb
[1] 15.03891
```

5 Session information

```
> sessionInfo()

R version 3.3.2 (2016-10-31)
Platform: x86_64-apple-darwin13.4.0 (64-bit)
Running under: macOS Sierra 10.12.1

locale:
[1] C

attached base packages:
[1] parallel  stats4    stats     graphics  grDevices utils     datasets
[8] methods   base

other attached packages:
 [1] rqt_0.99.3                SummarizedExperiment_1.4.0
 [3] Biobase_2.34.0            GenomicRanges_1.26.1
 [5] GenomeInfoDb_1.10.1       IRanges_2.8.1
 [7] S4Vectors_0.12.1          BiocGenerics_0.20.0
 [9] ropls_1.6.2               plyr_1.8.4
[11] pls_2.5-0                 glmnet_2.0-5
[13] foreach_1.4.3             Matrix_1.2-7.1

loaded via a namespace (and not attached):
 [1] Rcpp_0.12.8        lattice_0.20-34    codetools_0.2-15   grid_3.3.2
 [5] zlibbioc_1.20.0    CCP_1.1            XVector_0.14.0     iterators_1.0.8
 [9] tools_3.3.2        CompQuadForm_1.4.2
```

6 References

References

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[2] Li, B. and Leal, S.M. (2008) Methods for Detecting Associations with Rare Vari-ants for Common Diseases: Application to Analysis of Sequence Data. The American Journal of Human Genetics, 83, 311-321.

[3] Liu D., Leal S. (2010) A Novel Adaptive Method for the Analysis of Next-Generation Sequencing Data to Detect Complex Trait Associations with Rare Variants Due to Gene Main Effects and Interactions, PLoS Genet., 6(10).

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[5] Lee, J., Kim, Y.J., Lee, J., T2D-Genes Consortium, Kim, B-J., Lee, S., Park T. (2016) Gene-set association tests for next-generation sequencing data, Bioinformatics, 32(17).

[6] Tibshirani, R. (1996) Regression shrinkage and selection via the lasso. J. Royal. Statist. Soc B., Vol. 58, No. 1, pages 267-288.