

ssemQr: Sparse Structural Equation Models based eQTL mapping

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In this vignette, we introduce the functionality of the `ssemQr` package to jointly implement eQTL-mapping and gene regulatory network (GRN) inference by gene expression and genetic perturbation data. To meet the space and time constraints in building this vignette within the `ssemQr` package, we are going to simulate gene expression and genetic perturbation data instead of using a real dataset. For this purpose, we will use function `randomeQTLdata` in `ssemQr` to generate simulated data, and then apply Sparse Structural Equation Models based eQTL mapping (SSEM-Q) to estimate the GRNs under two different conditions and their differential GRN. Also, please go to <https://github.com/Ivis4ml/ssemQr/tree/master/inst> for more large dataset analysis. In conclusion, this vignette is composed by three sections as follow,

- Simulating GRN and its corresponding cis-eQTL effects, effects of trans-eQTLs are mediated via gene-gene interaction of GRN.
- Estimating GRNs and cis-eQTL effect from the simulated gene expression data and genetic perturbation data
- Visualization

For user using package `ssemQr`, please cite the following article:

Xin Zhou and Xiaodong Cai. Joint eQTL mapping and Inference of Gene Regulatory Network Improves Power of Detecting both cis- and trans-eQTLs, *Bioinformatics*, submitted.

Simulating GRN and its corresponding cis-eQTL effects (Acyclic example)

We are going to simulate a GRN and its corresponding gene expression and genetic perturbation data in the following steps:

1. Load the necessary packages

```
library(ssemQr)
library(network)
> network: Classes for Relational Data
> Version 1.16.0 created on 2019-11-30.
> copyright (c) 2005, Carter T. Butts, University of California-Irvine
> Mark S. Handcock, University of California -- Los Angeles
> David R. Hunter, Penn State University
> Martina Morris, University of Washington
> Skye Bender-deMoll, University of Washington
> For citation information, type citation("network").
> Type help("network-package") to get started.
library(ggnetwork)
> Loading required package: ggplot2
library(igraph)
>
> Attaching package: 'igraph'
> The following objects are masked from 'package:network':
```

```

>
>      %c%, %s%, add.edges, add.vertices, delete.edges, delete.vertices,
>      get.edge.attribute, get.edges, get.vertex.attribute, is.bipartite,
>      is.directed, list.edge.attributes, list.vertex.attributes,
>      set.edge.attribute, set.vertex.attribute
> The following objects are masked from 'package:stats':
>
>      decompose, spectrum
> The following object is masked from 'package:base':
>
>      union
library(Matrix)

```

2. Simulate 20 genes expression data with a sparse directed acyclic graph (DAG) GRN. Set $\{cis\}$ -eQTLs ratio as 10% of neighboring SNPs, and 5% genes have no $\{cis\}$ -eQTLs

```

N = 100 # sample size
Ng = 20 # gene number
Nk = 20 * 3 # eQTL number
Ns = 15 / Ng # sparsity of GRN
sigma2 = 0.01 # sigma2
Es = 0.1 # sparsity of  $\{cis\}$ -eQTL
set.seed(123)
data = randomeQTLdata(n = N, p = Ng, k = Nk, sparse = Ns, sqtl = Es, intercept = 5, sigma2 = sigma2, es = Es)

```

Based on the mediation mechanism assumption, the eQTL-eGene associations are classified into two categories; cis-eQTLs and trans-eQTLs. The effects of trans-eQTLs are mediated by the GRN, which can be represented as series $\mathbf{BF} + \mathbf{B}^2\mathbf{F} + \dots + \mathbf{B}^n\mathbf{F}$. If $\rho(\mathbf{B}) \leq 1$, the effects of trans-eQTLs can be represented as $(\mathbf{I} - \mathbf{B})^{-1}\mathbf{F} - \mathbf{F}$.

```

Fw = (solve(diag(Ng) - data$Vars$B) %*% data$Vars$F)
Ftrans = sum(Fw[data$Vars$F == 0] != 0)

```

- Finally, 60 cis-eQTLs-eGene, 114 trans-eQTLs-eGene association simulated.
- Summary of GRN and QTLs

```

rownames(data$Vars$B) = colnames(data$Vars$B) = rownames(data$Vars$F) = rownames(data$Data$Y)
colnames(data$Vars$F) = rownames(data$Data$X)
GE = get.edgelist(graph.adjacency(t(data$Vars$B) != 0))
QE = which(t(data$Vars$F) != 0, arr.ind = TRUE)
QE[,2] = rownames(data$Vars$F)[QE[,2]]
QE[,1] = rownames(QE)
GRN = network(rbind(GE, QE), matrix.type = "edgelist", directed = TRUE)
plot(GRN, displaylabels = TRUE, label.cex = 0.5, vertex.col = rep(c(2, 5), times = c(length(unique(QE[,1])), length(unique(QE[,2])))))

```

Implementing eQTL-mapping and GRN inference with simulated gene expression data and genetic perturbation data

1. Simulated gene expression

```

head(data$Data$Y)
>      [,1]      [,2]      [,3]      [,4]      [,5]      [,6]
> g_00001 -6.038139  0.6443969 -1.3587065  1.091444 -1.226743 -5.57685969
> g_00002 23.383864 14.2227603 14.3115817 14.989256 13.997098  5.21653112
> g_00003 12.965449  1.4776122  8.8602495  9.539895  5.740746 -0.56314204
> g_00004  8.680858 -0.3154836 12.2303879 11.590797 12.984470 -0.09114854

```



```

> g_00004 4.338571 2.8609885 8.757427 14.513295 8.692028 13.4417498 14.060510
> g_00005 6.188368 -1.1023432 6.052601 8.653607 8.081071 6.0791392 9.228961
> g_00006 9.382513 -2.0088045 9.399975 10.093147 9.257986 9.9098151 13.353713
>           [,39]      [,40]      [,41]      [,42]      [,43]      [,44]
> g_00001 -3.0060822 -1.134171 -12.6736888 -5.8349892 -1.8656431 -2.024858
> g_00002  0.1108343  9.061710  7.6852113 14.1420419  5.7148266 11.469324
> g_00003 -10.7957793  0.114919 -0.2166458  0.3976376 -4.9987882  8.874392
> g_00004  9.9425633  8.027816 10.4379657  7.8836556  0.5374723  7.193962
> g_00005  0.7059098  6.058761 -1.7728103 14.2017676  5.9692886 -1.930270
> g_00006  5.2615153  5.603717  4.8875901 10.1416156  5.1692746  4.855222
>           [,45]      [,46]      [,47]      [,48]      [,49]      [,50]      [,51]
> g_00001 -1.933522 3.867380 -1.925601 -2.226472  5.3090633  1.916836 -2.4231929
> g_00002 14.335534 7.587169 15.314490  8.195370 16.2872207  9.750388 10.9504148
> g_00003  0.604662 4.121844  2.117166  1.632544  0.9915105  2.751724  0.5667139
> g_00004  6.492399 9.981586  7.526914  1.554155  7.1437187 15.267246 10.2864788
> g_00005  1.298690 6.208491  1.418061  8.508896  3.7537718 -1.281104  9.3633607
> g_00006  5.648892 2.027159  1.435545  9.479543  1.7009150  1.663106  9.3399113
>           [,52]      [,53]      [,54]      [,55]      [,56]      [,57]      [,58]
> g_00001 -3.5473039 -4.393693  0.3921614  3.890589 -6.726872  5.942963 -1.053999
> g_00002 11.9620802 11.437627 11.1966680 10.351887 13.469142 16.155706 17.443236
> g_00003 -3.8307753  8.890505 -1.6812782  5.005066  4.777561  5.095566 15.108740
> g_00004 -0.3620542 12.871005  8.8236845 10.618419  6.444955 15.573605 12.087122
> g_00005 13.3969300  8.587354 14.1236456  6.266269  6.283303  3.813854  1.322333
> g_00006  6.3972207 -2.669502  9.4935484  5.512256  2.081688 -1.938316  5.738951
>           [,59]      [,60]      [,61]      [,62]      [,63]      [,64]
> g_00001 -11.195599 -5.768291  5.060398  8.7749914  4.056718 -11.7286004
> g_00002 -5.246004 11.652374  8.216822 16.4001093 15.751575  7.8079298
> g_00003 -4.083751  2.027858 -3.299455 -3.0149797  2.986897 -0.6390034
> g_00004 13.043358  6.707587  9.393615  4.5066203  9.444174 -3.0088597
> g_00005  3.259035 11.069753  1.240651 -0.3639891 -1.114934  7.8536911
> g_00006  1.992011  6.235394  6.058027  1.6109180  1.644187  5.5773164
>           [,65]      [,66]      [,67]      [,68]      [,69]      [,70]
> g_00001 -2.978133 -1.950763  4.502137  0.7128866 -1.7423517  0.6437823
> g_00002 14.146234 12.269135 13.572292 -2.7733150  0.7019292 14.1809632
> g_00003 -2.376841  3.047890  4.381545 -11.8750191 -9.5438658 -0.7949477
> g_00004  9.285481 13.710103  9.359436  2.3853670  9.9105672 15.1429150
> g_00005  6.109719  5.575372  6.161236  9.3143839  3.1989699 11.0601977
> g_00006  6.130370  5.667780  5.667409 10.0227647  5.4201123  1.9883107
>           [,71]      [,72]      [,73]      [,74]      [,75]      [,76]
> g_00001  3.204284  8.126654 -1.544988 -1.31803901 -1.433919  1.384086
> g_00002  2.631195  7.206733  6.423605 12.86863858  9.010747  7.645500
> g_00003 -6.985166 -11.300990 -5.791771  0.02377311 -4.602436 -8.878113
> g_00004  6.096830  1.121800 -4.578092  2.19404512  8.410683  7.535253
> g_00005  3.937240 -1.680335  5.628887  7.72330860  9.407079  6.069205
> g_00006  1.172539  9.417599 -2.518401  9.68875483  5.797374  9.848149
>           [,77]      [,78]      [,79]      [,80]      [,81]      [,82]
> g_00001  0.3878227  1.2264747  4.304476 -2.5372381 -1.112774 -7.923377
> g_00002  6.7227010  8.9927746 18.558877  9.2040634  7.421554 -5.127343
> g_00003  2.1070564 -8.6819711  4.701564 -0.3407032  3.681131 -14.115413
> g_00004  6.1500404 -0.7263027 13.323989  9.8980301 18.602395  5.700684
> g_00005  5.3864538  8.5552216  6.055221  8.6557686  9.357022  8.065133
> g_00006  9.8118246 10.2990689  8.943252 13.6588664  1.819483  5.856623
>           [,83]      [,84]      [,85]      [,86]      [,87]      [,88]

```

```

> g_00001 -4.249496 -0.4036571 -2.701486 -13.104847 -1.5264872 -7.6580429
> g_00002 10.003278 6.1962004 9.266007 14.269113 14.2560830 -0.5561409
> g_00003 3.918818 -0.7920674 3.193766 10.098628 -3.1187153 -4.9693846
> g_00004 11.438041 3.6336251 6.713172 -1.260435 -0.2156557 7.6892550
> g_00005 3.848850 2.9987655 4.584526 12.796822 -1.6794919 13.4044095
> g_00006 1.116631 4.7920443 1.116494 5.417585 1.6985779 10.2497881
>          [,89]      [,90]      [,91]      [,92]      [,93]      [,94]      [,95]
> g_00001 -1.615780 -5.119185 4.237222 2.229065 -0.2066921 2.0818405 1.716663
> g_00002 15.671043 11.592149 4.913900 8.238007 10.0928720 15.3091971 17.123965
> g_00003 -1.424904 1.213970 -1.772840 -7.786742 -0.2133384 0.4061676 6.721378
> g_00004 7.337562 6.691697 8.422380 7.081328 5.0635455 9.0410206 6.427174
> g_00005 6.115046 13.685374 3.914024 14.170359 -1.8505320 11.7049881 11.114235
> g_00006 5.659739 13.888826 5.589979 9.821148 1.5750276 5.6813180 5.707217
>          [,96]      [,97]      [,98]      [,99]      [,100]
> g_00001 0.8116527 -0.5738103 3.401589 4.173171 1.525293
> g_00002 13.5271154 9.3686685 18.328054 11.029991 5.203210
> g_00003 4.8479400 -1.5629534 5.037280 0.806792 -2.476404
> g_00004 7.6497027 7.8937133 10.206356 14.258247 11.295805
> g_00005 -1.8487619 8.0275200 11.730174 6.002121 7.047583
> g_00006 1.5968447 13.8801314 6.025969 1.343257 1.869980

```

2. Simulated eQTL's genotype

```

head(data$Data$X)
>          [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12] [,13]
> rs_00001    1    2    1    2    1    0    1    2    0    2    1    2    1
> rs_00002    1    2    1    2    1    0    0    2    0    1    1    2    0
> rs_00003    1    2    1    2    1    0    0    2    0    1    0    2    0
> rs_00004    1    2    1    2    1    0    0    2    0    1    0    2    1
> rs_00005    1    2    1    2    1    0    0    2    0    1    0    2    1
> rs_00006    1    2    2    2    1    0    0    2    0    1    0    2    1
>          [,14] [,15] [,16] [,17] [,18] [,19] [,20] [,21] [,22] [,23] [,24]
> rs_00001    1    2    1    0    1    0    1    1    2    0    1
> rs_00002    1    2    1    1    1    0    1    1    2    1    1
> rs_00003    1    2    1    1    1    0    1    1    2    1    1
> rs_00004    1    2    1    1    1    0    1    1    2    1    1
> rs_00005    1    2    1    1    1    0    1    1    2    1    1
> rs_00006    1    2    1    1    1    0    1    2    2    1    2
>          [,25] [,26] [,27] [,28] [,29] [,30] [,31] [,32] [,33] [,34] [,35]
> rs_00001    0    0    1    2    2    2    2    1    2    0    1
> rs_00002    0    0    1    1    1    2    2    1    2    0    1
> rs_00003    0    0    1    1    1    2    2    1    2    0    1
> rs_00004    0    0    0    1    1    2    2    1    2    0    1
> rs_00005    0    0    0    1    1    2    2    1    2    0    1
> rs_00006    0    0    0    1    1    2    2    1    2    0    1
>          [,36] [,37] [,38] [,39] [,40] [,41] [,42] [,43] [,44] [,45] [,46]
> rs_00001    1    2    2    1    1    0    1    1    1    1    1
> rs_00002    1    2    2    1    1    0    1    1    1    1    2
> rs_00003    1    2    2    1    1    0    1    2    1    1    2
> rs_00004    1    2    2    1    1    0    1    2    1    1    2
> rs_00005    1    2    2    1    1    0    1    2    1    1    2
> rs_00006    1    2    2    1    1    0    1    1    0    1    2
>          [,47] [,48] [,49] [,50] [,51] [,52] [,53] [,54] [,55] [,56] [,57]
> rs_00001    1    0    2    1    1    0    0    2    2    1    2

```

```

> rs_00002    1    0    2    1    1    0    0    2    2    1    2
> rs_00003    1    0    2    1    1    0    0    2    2    1    2
> rs_00004    1    0    2    1    1    0    0    2    2    1    2
> rs_00005    1    0    2    1    1    0    0    2    2    1    2
> rs_00006    1    0    2    1    1    0    0    2    2    1    2
>             [,58] [,59] [,60] [,61] [,62] [,63] [,64] [,65] [,66] [,67] [,68]
> rs_00001    1    0    0    2    2    2    1    1    0    2    1
> rs_00002    1    0    0    2    2    2    1    1    0    2    1
> rs_00003    0    0    0    2    1    2    1    1    0    2    1
> rs_00004    0    0    0    2    1    2    0    1    0    2    1
> rs_00005    0    0    0    2    1    2    0    1    0    2    2
> rs_00006    0    0    0    2    1    2    0    1    0    2    2
>             [,69] [,70] [,71] [,72] [,73] [,74] [,75] [,76] [,77] [,78] [,79]
> rs_00001    1    1    1    2    2    2    1    1    2    2    1
> rs_00002    1    1    1    2    2    2    1    1    2    2    1
> rs_00003    1    1    1    2    2    2    1    1    2    2    1
> rs_00004    1    1    1    2    2    2    1    1    2    1    1
> rs_00005    1    1    1    2    2    2    1    1    2    1    1
> rs_00006    1    1    1    2    2    2    1    1    2    1    1
>             [,80] [,81] [,82] [,83] [,84] [,85] [,86] [,87] [,88] [,89] [,90]
> rs_00001    2    2    0    1    2    0    0    0    1    1    1
> rs_00002    1    2    0    1    2    0    0    0    1    1    1
> rs_00003    1    2    0    1    2    0    0    1    1    1    1
> rs_00004    1    2    0    1    2    0    0    2    0    2    1
> rs_00005    1    2    0    1    2    1    0    2    0    2    1
> rs_00006    1    2    0    1    2    1    0    2    0    2    1
>             [,91] [,92] [,93] [,94] [,95] [,96] [,97] [,98] [,99] [,100]
> rs_00001    2    1    1    1    0    0    0    0    1    2
> rs_00002    1    1    1    1    0    0    0    0    1    2
> rs_00003    1    1    1    1    0    0    0    0    1    2
> rs_00004    1    1    1    1    0    0    0    0    1    1
> rs_00005    1    2    1    1    0    0    0    0    1    1
> rs_00006    1    2    1    1    0    0    0    0    1    1

```

3. `data$Data$Sk` stores each genes' nearby SNPs' indices, which is the candidate pool of cis-eQTL mapping filtered by distance constraint

```

head(data$Data$Sk)
> [[1]]
> [1]  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] 26 27 28 29 30
>
> [[2]]
> [1] 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55
> [26] 56 57 58 59 60
>
> [[3]]
> [1] 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85
> [26] 86 87 88 89 90
>
> [[4]]
> [1] 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109
> [20] 110 111 112 113 114 115 116 117 118 119 120
>

```

```

> [[5]]
> [1] 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139
> [20] 140 141 142 143 144 145 146 147 148 149 150
>
> [[6]]
> [1] 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169
> [20] 170 171 172 173 174 175 176 177 178 179 180

```

Initialization of ssemQr by ridge regression

We implement our ssemQr by the observed gene expression data and genetic perturbations data that stored in `data$Data`, and it is initialized by ridge regression, the l_2 norm penalty's hyperparameter γ is selected by 10-fold cross-validation.

```

X      = data$Data$X
Y      = data$Data$Y
Sk     = data$Data$Sk
gamma = cv.ridgeRegression(X, Y, Sk, ngamma = 10, nfold = 10, data$Vars$n, data$Vars$p, data$Vars$q)
> [1] 6.3522569 5.5227972 4.0958865 3.2110817 2.7474365 2.5828221 2.7211478
> [8] 2.9769015 3.1492752 3.2105083 5.7272243 5.0210032 3.6719598 2.7018944
> [15] 2.1070388 1.7704783 1.7814009 1.9559592 2.0864278 2.1340119 5.4678958
> [22] 4.8710421 3.6079306 2.5510549 1.8257179 1.2503900 0.9952741 0.9987344
> [29] 1.0577530 1.0845648 5.5440533 4.9976447 3.7695414 2.6425265 1.8496802
> [36] 1.1585370 0.7021353 0.5110323 0.4918077 0.5002854 5.6419720 5.1101398
> [43] 3.8880463 2.7263598 1.9061438 1.1825437 0.6673229 0.3835734 0.3035372
> [50] 0.2981736 5.6761598 5.1476984 3.9263664 2.7547164 1.9271808 1.1965676
> [57] 0.6710365 0.3720622 0.2783720 0.2693739 5.6844648 5.1567396 3.9355293
> [64] 2.7615720 1.9323839 1.2003088 0.6729144 0.3720001 0.2769582 0.2676446
> [71] 5.6863030 5.1587372 3.9375507 2.7630881 1.9335405 1.2011542 0.6733817
> [78] 0.3721399 0.2769240 0.2676184 5.6867013 5.1591697 3.9379883 2.7634166
> [85] 1.9337912 1.2013378 0.6734843 0.3721751 0.2769236 0.2676269 5.6867872
> [92] 5.1592630 3.9380827 2.7634874 1.9338454 1.2013773 0.6735065 0.3721844
> [99] 0.2769253 0.2675866
fit0   = ridgeRegression(X, Y, Sk, gamma[1], gamma[2], data$Vars$n, data$Vars$p, data$Vars$q, trans = F)

```

Run ssemQr algorithm for data

Then, we chose the `fit0` object from ridge regression as intialization, and implement the `ssemQr` algorithm, BIC is used to select optimal hyperparameters λ, ρ , where `nlambda` is the number of candidate lambda values for l_1 regularized term, and `nrho` is the number of candidate rho values for fused lasso regularized term.

```

fitOpt = opt.SSEMiPALM(X = X, Y = Y, B = fit0$B, F = fit0$F, Sk = Sk, sigma2 = fit0$sigma2,
                      nlambda = 10, nrho = 10, p = data$Vars$p, wt = TRUE)
> SSEM@lambda = 111.536547, rho = 74.290336
> SSEM@lambda = 51.770679, rho = 74.290336
> SSEM@lambda = 24.029821, rho = 74.290336
> SSEM@lambda = 11.153655, rho = 74.290336
> SSEM@lambda = 5.177068, rho = 74.290336
> SSEM@lambda = 2.402982, rho = 74.290336
> SSEM@lambda = 1.115365, rho = 74.290336
> SSEM@lambda = 0.517707, rho = 74.290336
> SSEM@lambda = 0.240298, rho = 74.290336
> SSEM@lambda = 0.111537, rho = 74.290336

```



```

> SSEM@lambda = 267.267555, rho = 34.482519
> SSEM@lambda = 124.054610, rho = 34.482519
> SSEM@lambda = 57.581049, rho = 34.482519
> SSEM@lambda = 26.726756, rho = 34.482519
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> SSEM@lambda = 381.269630, rho = 0.742903
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> SSEM@lambda = 82.142052, rho = 0.742903

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> SSEM@lambda = 38.126963, rho = 0.742903
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> SSEM@lambda = 1.814032, rho = 0.074290
> SSEM@lambda = 0.841999, rho = 0.074290
> SSEM@lambda = 0.390821, rho = 0.074290
fitQtl = SSEMiPALM(X = X, Y = Y, B = fit0$B, F = fit0$F, Sk = Sk, sigma2 = fit0$sigma2,
  lambda = fitOpt$lambda, rho = fitOpt$rho,
  Wb = 1 / abs(fit0$B), Wf = 1 / abs(fit0$F),
  p = data$Vars$p, maxit = 1000, trans = TRUE, strict = TRUE)
> SSEMQ      niter = 1,  relerr = 0.953770, logLik = 5634.438145
> SSEMQ      niter = 2,  relerr = 0.354811, logLik = 4463.149911
> SSEMQ      niter = 3,  relerr = 0.142849, logLik = 3087.634889
> SSEMQ      niter = 4,  relerr = 0.057526, logLik = 2537.623961
> SSEMQ      niter = 5,  relerr = 0.021952, logLik = 2444.238039
> SSEMQ      niter = 6,  relerr = 0.008531, logLik = 2271.852885
> SSEMQ      niter = 7,  relerr = 0.009151, logLik = 2044.442995
> SSEMQ      niter = 8,  relerr = 0.009271, logLik = 1849.003795
> SSEMQ      niter = 9,  relerr = 0.007953, logLik = 1718.129885
> SSEMQ      niter = 10, relerr = 0.006245, logLik = 1637.257199
> SSEMQ      niter = 11, relerr = 0.004701, logLik = 1580.825947
> SSEMQ      niter = 12, relerr = 0.003572, logLik = 1534.437267

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> SSEQM      niter = 15,      relerr = 0.002848, logLik = 1424.261764
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> SSEQM      niter = 213,      relerr = 0.000005, logLik = 1293.970982
> SSEQM      niter = 214,      relerr = 0.000005, logLik = 1293.971014
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> SSEQM      niter = 217,      relerr = 0.000004, logLik = 1293.971154
> SSEQM      niter = 218,      relerr = 0.000004, logLik = 1293.971212
> SSEQM      niter = 219,      relerr = 0.000004, logLik = 1293.971275
> SSEQM      niter = 220,      relerr = 0.000004, logLik = 1293.971343
> SSEQM      niter = 221,      relerr = 0.000004, logLik = 1293.971415
> SSEQM      niter = 222,      relerr = 0.000004, logLik = 1293.971489
> SSEQM      niter = 223,      relerr = 0.000004, logLik = 1293.971567
> SSEQM      niter = 224,      relerr = 0.000004, logLik = 1293.971647

```

```

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> SSEQM      niter = 226,      relerr = 0.000003, logLik = 1293.971811
> SSEQM      niter = 227,      relerr = 0.000003, logLik = 1293.971895
> SSEQM      niter = 228,      relerr = 0.000003, logLik = 1293.971979
> SSEQM      niter = 229,      relerr = 0.000003, logLik = 1293.972064
> SSEQM      niter = 230,      relerr = 0.000003, logLik = 1293.972148
> SSEQM      niter = 231,      relerr = 0.000003, logLik = 1293.972230
> SSEQM      niter = 232,      relerr = 0.000003, logLik = 1293.972312
> SSEQM      niter = 233,      relerr = 0.000003, logLik = 1293.972391
> SSEQM      niter = 234,      relerr = 0.000003, logLik = 1293.972467
> SSEQM      niter = 235,      relerr = 0.000003, logLik = 1293.972539
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> SSEQM      niter = 237,      relerr = 0.000002, logLik = 1293.972672
> SSEQM      niter = 238,      relerr = 0.000002, logLik = 1293.972731
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> SSEQM      niter = 243,      relerr = 0.000002, logLik = 1293.972953
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> SSEQM      niter = 266,      relerr = 0.000002, logLik = 1293.972615
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> SSEQM      niter = 276,      relerr = 0.000002, logLik = 1293.972077
> SSEQM      niter = 277,      relerr = 0.000002, logLik = 1293.972021

```


[illegible]


```

> SSEQM      niter = 331,      relerr = 0.000001, logLik = 1293.970559
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> SSEQM      niter = 337,      relerr = 0.000001, logLik = 1293.970563
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> SSEQM      niter = 340,      relerr = 0.000001, logLik = 1293.970570
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> SSEQM      niter = 344,      relerr = 0.000001, logLik = 1293.970582
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> SSEQM      niter = 348,      relerr = 0.000001, logLik = 1293.970597
> SSEQM      niter = 349,      relerr = 0.000001, logLik = 1293.970601
> SSEQM      niter = 350,      relerr = 0.000001, logLik = 1293.970604
> SSEQM      niter = 351,      relerr = 0.000001, logLik = 1293.970608
> SSEQM      niter = 352,      relerr = 0.000001, logLik = 1293.970612
> SSEQM      niter = 353,      relerr = 0.000001, logLik = 1293.970615
> SSEQM      niter = 354,      relerr = 0.000001, logLik = 1293.970619
> SSEQM      niter = 355,      relerr = 0.000001, logLik = 1293.970622
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> SSEQM      niter = 366,      relerr = 0.000001, logLik = 1293.970654
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> SSEQM      niter = 368,      relerr = 0.000001, logLik = 1293.970658
> SSEQM      niter = 369,      relerr = 0.000001, logLik = 1293.970659

```

Comparing our estimated cis-QTL and GRN with ground truth

```

cat("Power of estimated GRN = ", fssemR:::TPR(fitQtl$B, data$Vars$B))
> Power of estimated GRN = 1
cat("FDR of estimated GRN = ", fssemR:::FDR(fitQtl$B, data$Vars$B))
> FDR of estimated GRN = 0
cat("Power of estimated cis-eQTL =", fssemR:::TPR(fitQtl$F, data$Vars$F))
> Power of estimated cis-eQTL = 1
cat("FDR of estimated cis-eQTL =", fssemR:::FDR(fitQtl$F, data$Vars$F))
> FDR of estimated cis-eQTL = 0

```

Based on these 4 metrics, we can get the performance of `ssemQr` in cis-eQTL identification and GRN

estimation.

Comparing estimated trans-eQTL

```
Ftrans = (solve(diag(Ng) - fitQtl$B) %*% fitQtl$F)
Ftrue = (solve(diag(Ng) - data$Vars$B) %*% data$Vars$F)
PRcurve = calcPR(Ftrans, Ftrue)[-1,]
ggplot(PRcurve, aes(x = recall, y = precision)) + geom_point(size = 0.5) + geom_path() + labs(x = "Recall", y = "Precision")
```

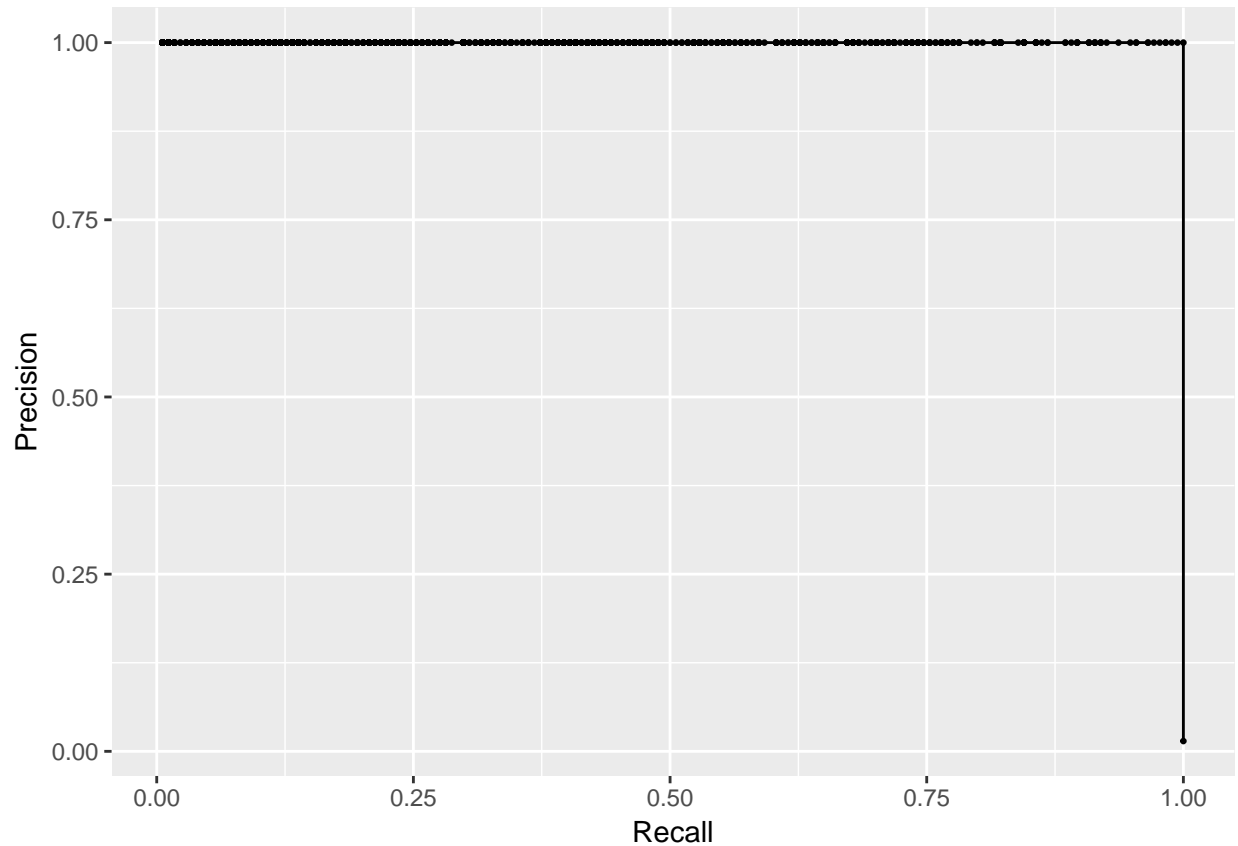


Figure 2: PR curve of trans-eQTL

Estimated GRN and eQTL visualization

```
rownames(fitQtl$B) = colnames(fitQtl$B) = rownames(fitQtl$F) = rownames(data$Data$Y)
colnames(fitQtl$F) = rownames(data$Data$X)
GE = get.edgelist(graph.adjacency(t(fitQtl$B) != 0))
QE = which(t(fitQtl$F) != 0, arr.ind = TRUE)
QE[,2] = rownames(fitQtl$F)[QE[,2]]
QE[,1] = rownames(QE)
GRN = network(rbind(GE, QE), matrix.type = "edgelist", directed = TRUE)
plot(GRN, displaylabels = TRUE, label.cex = 0.5, vertex.col = rep(c(2, 5), times = c(length(unique(QE[,1])), length(unique(QE[,2])))))
```

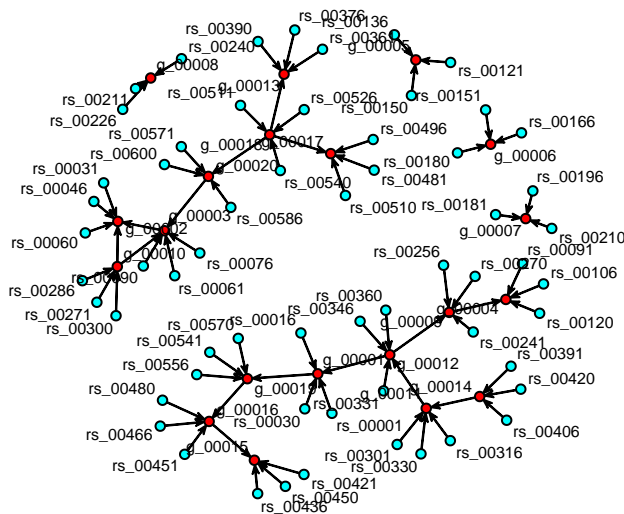


Figure 3: GRN QTL Network

Session Information

```
sessionInfo()
> R version 3.4.0 (2017-04-21)
> Platform: x86_64-pc-linux-gnu (64-bit)
> Running under: Ubuntu 14.04.6 LTS
>
> Matrix products: default
> BLAS: /usr/lib64/microsoft-r/3.4/lib64/R/lib/libRblas.so
> LAPACK: /usr/lib64/microsoft-r/3.4/lib64/R/lib/libRlapack.so
>
> locale:
>  [1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
>  [3] LC_TIME=en_US.UTF-8      LC_COLLATE=en_US.UTF-8
>  [5] LC_MONETARY=en_US.UTF-8  LC_MESSAGES=en_US.UTF-8
>  [7] LC_PAPER=en_US.UTF-8     LC_NAME=C
>  [9] LC_ADDRESS=C             LC_TELEPHONE=C
> [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
>
> attached base packages:
> [1] stats      graphics  grDevices  utils      datasets  methods   base
>
> other attached packages:
> [1] Matrix_1.2-14      igraph_1.2.2      ggnetwork_0.5.1
> [4] ggplot2_2.2.1      network_1.16.0    ssemQr_0.1.0
> [7] RevoUtilsMath_10.0.0
>
> loaded via a namespace (and not attached):
> [1] Rcpp_1.0.3          sna_2.5           RSpectra_0.16-0
> [4] plyr_1.8.5          compiler_3.4.0    pillar_1.4.3.9001
> [7] iterators_1.0.9     tools_3.4.0       digest_0.6.23
> [10] evaluate_0.14       tibble_3.0.1.9000 lifecycle_0.2.0.9000
> [13] gtable_0.3.0        lattice_0.20-35   pkgconfig_2.0.3
> [16] rlang_0.4.5.9000    foreach_1.4.4     ggrepel_0.8.1
```

```

> [19] yaml_2.2.1           parallel_3.4.0       mvtnorm_1.0-8
> [22] xfun_0.12            coda_0.19-3         fssemR_0.1.6
> [25] stringr_1.4.0        knitr_1.28          RevoUtils_10.0.4
> [28] vctrs_0.2.99.9011    stabs_0.6-3         glmnet_2.0-8
> [31] grid_3.4.0           R6_2.4.1            rARPACK_0.11-0
> [34] qtl_1.45-11          rmarkdown_2.1       farver_2.0.3.9000
> [37] magrittr_1.5         scales_1.1.0.9000   codetools_0.2-15
> [40] htmltools_0.4.0      ellipsis_0.3.0.9000 MASS_7.3-49
> [43] colorspace_1.4-1     labeling_0.3         stringi_1.4.5
> [46] lazyeval_0.2.2       munsell_0.5.0       statnet.common_4.1.4
> [49] crayon_1.3.4

```