

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) 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 it 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. Identification of trans-eQTLs via Joint eQTL mapping and inference of Gene Regulatory Network Bioinformatics, submitted.

Simulating GRN and it 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 1.13.0.1 created on 2015-08-31.
> 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, e

```

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]),

```

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_00005  6.166067 13.5259890 -0.3794916 14.182132 -1.131211 -1.69599359

```



```

> g_00005 3.791205 6.188368 -1.1023432 6.052601 8.653607 8.081071
> g_00006 1.227683 9.382513 -2.0088045 9.399975 10.093147 9.257986
>      [,37]      [,38]      [,39]      [,40]      [,41]      [,42]
> g_00001 6.7238047 4.203827 -3.0060822 -1.134171 -12.6736888 -5.8349892
> g_00002 10.4952372 13.883943 0.1108343 9.061710 7.6852113 14.1420419
> g_00003 -0.2475049 7.121438 -10.7957793 0.114919 -0.2166458 0.3976376
> g_00004 13.4417498 14.060510 9.9425633 8.027816 10.4379657 7.8836556
> g_00005 6.0791392 9.228961 0.7059098 6.058761 -1.7728103 14.2017676
> g_00006 9.9098151 13.353713 5.2615153 5.603717 4.8875901 10.1416156
>      [,43]      [,44]      [,45]      [,46]      [,47]      [,48]
> g_00001 -1.8656431 -2.024858 -1.933522 3.867380 -1.925601 -2.226472
> g_00002 5.7148266 11.469324 14.335534 7.587169 15.314490 8.195370
> g_00003 -4.9987882 8.874392 0.604662 4.121844 2.117166 1.632544
> g_00004 0.5374723 7.193962 6.492399 9.981586 7.526914 1.554155
> g_00005 5.9692886 -1.930270 1.298690 6.208491 1.418061 8.508896
> g_00006 5.1692746 4.855222 5.648892 2.027159 1.435545 9.479543
>      [,49]      [,50]      [,51]      [,52]      [,53]      [,54]
> g_00001 5.3090633 1.916836 -2.4231929 -3.5473039 -4.393693 0.3921614
> g_00002 16.2872207 9.750388 10.9504148 11.9620802 11.437627 11.1966680
> g_00003 0.9915105 2.751724 0.5667139 -3.8307753 8.890505 -1.6812782
> g_00004 7.1437187 15.267246 10.2864788 -0.3620542 12.871005 8.8236845
> g_00005 3.7537718 -1.281104 9.3633607 13.3969300 8.587354 14.1236456
> g_00006 1.7009150 1.663106 9.3399113 6.3972207 -2.669502 9.4935484
>      [,55]      [,56]      [,57]      [,58]      [,59]      [,60]
> g_00001 3.890589 -6.726872 5.942963 -1.053999 -11.195599 -5.768291
> g_00002 10.351887 13.469142 16.155706 17.443236 -5.246004 11.652374
> g_00003 5.005066 4.777561 5.095566 15.108740 -4.083751 2.027858
> g_00004 10.618419 6.444955 15.573605 12.087122 13.043358 6.707587
> g_00005 6.266269 6.283303 3.813854 1.322333 3.259035 11.069753
> g_00006 5.512256 2.081688 -1.938316 5.738951 1.992011 6.235394
>      [,61]      [,62]      [,63]      [,64]      [,65]      [,66]
> g_00001 5.060398 8.7749914 4.056718 -11.7286004 -2.978133 -1.950763
> g_00002 8.216822 16.4001093 15.751575 7.8079298 14.146234 12.269135
> g_00003 -3.299455 -3.0149797 2.986897 -0.6390034 -2.376841 3.047890
> g_00004 9.393615 4.5066203 9.444174 -3.0088597 9.285481 13.710103
> g_00005 1.240651 -0.3639891 -1.114934 7.8536911 6.109719 5.575372
> g_00006 6.058027 1.6109180 1.644187 5.5773164 6.130370 5.667780
>      [,67]      [,68]      [,69]      [,70]      [,71]      [,72]
> g_00001 4.502137 0.7128866 -1.7423517 0.6437823 3.204284 8.126654
> g_00002 13.572292 -2.7733150 0.7019292 14.1809632 2.631195 7.206733
> g_00003 4.381545 -11.8750191 -9.5438658 -0.7949477 -6.985166 -11.300990
> g_00004 9.359436 2.3853670 9.9105672 15.1429150 6.096830 1.121800
> g_00005 6.161236 9.3143839 3.1989699 11.0601977 3.937240 -1.680335
> g_00006 5.667409 10.0227647 5.4201123 1.9883107 1.172539 9.417599
>      [,73]      [,74]      [,75]      [,76]      [,77]      [,78]
> g_00001 -1.544988 -1.31803901 -1.433919 1.384086 0.3878227 1.2264747
> g_00002 6.423605 12.86863858 9.010747 7.645500 6.7227010 8.9927746
> g_00003 -5.791771 0.02377311 -4.602436 -8.878113 2.1070564 -8.6819711
> g_00004 -4.578092 2.19404512 8.410683 7.535253 6.1500404 -0.7263027
> g_00005 5.628887 7.72330860 9.407079 6.069205 5.3864538 8.5552216
> g_00006 -2.518401 9.68875483 5.797374 9.848149 9.8118246 10.2990689
>      [,79]      [,80]      [,81]      [,82]      [,83]      [,84]
> g_00001 4.304476 -2.5372381 -1.112774 -7.923377 -4.249496 -0.4036571

```

```

> g_00002 18.558877 9.2040634 7.421554 -5.127343 10.003278 6.1962004
> g_00003 4.701564 -0.3407032 3.681131 -14.115413 3.918818 -0.7920674
> g_00004 13.323989 9.8980301 18.602395 5.700684 11.438041 3.6336251
> g_00005 6.055221 8.6557686 9.357022 8.065133 3.848850 2.9987655
> g_00006 8.943252 13.6588664 1.819483 5.856623 1.116631 4.7920443
>          [,85]      [,86]      [,87]      [,88]      [,89]      [,90]
> g_00001 -2.701486 -13.104847 -1.5264872 -7.6580429 -1.615780 -5.119185
> g_00002 9.266007 14.269113 14.2560830 -0.5561409 15.671043 11.592149
> g_00003 3.193766 10.098628 -3.1187153 -4.9693846 -1.424904 1.213970
> g_00004 6.713172 -1.260435 -0.2156557 7.6892550 7.337562 6.691697
> g_00005 4.584526 12.796822 -1.6794919 13.4044095 6.115046 13.685374
> g_00006 1.116494 5.417585 1.6985779 10.2497881 5.659739 13.888826
>          [,91]      [,92]      [,93]      [,94]      [,95]      [,96]
> g_00001 4.237222 2.229065 -0.2066921 2.0818405 1.716663 0.8116527
> g_00002 4.913900 8.238007 10.0928720 15.3091971 17.123965 13.5271154
> g_00003 -1.772840 -7.786742 -0.2133384 0.4061676 6.721378 4.8479400
> g_00004 8.422380 7.081328 5.0635455 9.0410206 6.427174 7.6497027
> g_00005 3.914024 14.170359 -1.8505320 11.7049881 11.114235 -1.8487619
> g_00006 5.589979 9.821148 1.5750276 5.6813180 5.707217 1.5968447
>          [,97]      [,98]      [,99]      [,100]
> g_00001 -0.5738103 3.401589 4.173171 1.525293
> g_00002 9.3686685 18.328054 11.029991 5.203210
> g_00003 -1.5629534 5.037280 0.806792 -2.476404
> g_00004 7.8937133 10.206356 14.258247 11.295805
> g_00005 8.0275200 11.730174 6.002121 7.047583
> g_00006 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]
> rs_00001    1    2    1    2    1    0    1    2    0    2    1    2
> rs_00002    1    2    1    2    1    0    0    2    0    1    1    2
> rs_00003    1    2    1    2    1    0    0    2    0    1    0    2
> rs_00004    1    2    1    2    1    0    0    2    0    1    0    2
> rs_00005    1    2    1    2    1    0    0    2    0    1    0    2
> rs_00006    1    2    2    2    1    0    0    2    0    1    0    2
>          [,13] [,14] [,15] [,16] [,17] [,18] [,19] [,20] [,21] [,22] [,23]
> rs_00001    1    1    2    1    0    1    0    1    1    2    0
> rs_00002    0    1    2    1    1    1    0    1    1    2    1
> rs_00003    0    1    2    1    1    1    0    1    1    2    1
> rs_00004    1    1    2    1    1    1    0    1    1    2    1
> rs_00005    1    1    2    1    1    1    0    1    1    2    1
> rs_00006    1    1    2    1    1    1    0    1    2    2    1
>          [,24] [,25] [,26] [,27] [,28] [,29] [,30] [,31] [,32] [,33] [,34]
> rs_00001    1    0    0    1    2    2    2    2    1    2    0
> rs_00002    1    0    0    1    1    1    2    2    1    2    0
> rs_00003    1    0    0    1    1    1    2    2    1    2    0
> rs_00004    1    0    0    0    1    1    2    2    1    2    0
> rs_00005    1    0    0    0    1    1    2    2    1    2    0
> rs_00006    2    0    0    0    1    1    2    2    1    2    0
>          [,35] [,36] [,37] [,38] [,39] [,40] [,41] [,42] [,43] [,44] [,45]
> rs_00001    1    1    2    2    1    1    0    1    1    1    1
> rs_00002    1    1    2    2    1    1    0    1    1    1    1

```

```

> rs_00003      1      1      2      2      1      1      0      1      2      1      1
> rs_00004      1      1      2      2      1      1      0      1      2      1      1
> rs_00005      1      1      2      2      1      1      0      1      2      1      1
> rs_00006      1      1      2      2      1      1      0      1      1      0      1
>               [,46] [,47] [,48] [,49] [,50] [,51] [,52] [,53] [,54] [,55] [,56]
> rs_00001      1      1      0      2      1      1      0      0      2      2      1
> rs_00002      2      1      0      2      1      1      0      0      2      2      1
> rs_00003      2      1      0      2      1      1      0      0      2      2      1
> rs_00004      2      1      0      2      1      1      0      0      2      2      1
> rs_00005      2      1      0      2      1      1      0      0      2      2      1
> rs_00006      2      1      0      2      1      1      0      0      2      2      1
>               [,57] [,58] [,59] [,60] [,61] [,62] [,63] [,64] [,65] [,66] [,67]
> rs_00001      2      1      0      0      2      2      2      1      1      0      2
> rs_00002      2      1      0      0      2      2      2      1      1      0      2
> rs_00003      2      0      0      0      2      1      2      1      1      0      2
> rs_00004      2      0      0      0      2      1      2      0      1      0      2
> rs_00005      2      0      0      0      2      1      2      0      1      0      2
> rs_00006      2      0      0      0      2      1      2      0      1      0      2
>               [,68] [,69] [,70] [,71] [,72] [,73] [,74] [,75] [,76] [,77] [,78]
> rs_00001      1      1      1      1      2      2      2      1      1      2      2
> rs_00002      1      1      1      1      2      2      2      1      1      2      2
> rs_00003      1      1      1      1      2      2      2      1      1      2      2
> rs_00004      1      1      1      1      2      2      2      1      1      2      1
> rs_00005      2      1      1      1      2      2      2      1      1      2      1
> rs_00006      2      1      1      1      2      2      2      1      1      2      1
>               [,79] [,80] [,81] [,82] [,83] [,84] [,85] [,86] [,87] [,88] [,89]
> rs_00001      1      2      2      0      1      2      0      0      0      1      1
> rs_00002      1      1      2      0      1      2      0      0      0      1      1
> rs_00003      1      1      2      0      1      2      0      0      1      1      1
> rs_00004      1      1      2      0      1      2      0      0      2      0      2
> rs_00005      1      1      2      0      1      2      1      0      2      0      2
> rs_00006      1      1      2      0      1      2      1      0      2      0      2
>               [,90] [,91] [,92] [,93] [,94] [,95] [,96] [,97] [,98] [,99]
> rs_00001      1      2      1      1      1      0      0      0      0      1
> rs_00002      1      1      1      1      1      0      0      0      0      1
> rs_00003      1      1      1      1      1      0      0      0      0      1
> rs_00004      1      1      1      1      1      0      0      0      0      1
> rs_00005      1      1      2      1      1      0      0      0      0      1
> rs_00006      1      1      2      1      1      0      0      0      0      1
>               [,100]
> rs_00001      2
> rs_00002      2
> rs_00003      2
> rs_00004      1
> rs_00005      1
> rs_00006      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] 24 25 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
> [24] 54 55 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
> [24] 84 85 86 87 88 89 90
>
> [[4]]
> [1] 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107
> [18] 108 109 110 111 112 113 114 115 116 117 118 119 120
>
> [[5]]
> [1] 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137
> [18] 138 139 140 141 142 143 144 145 146 147 148 149 150
>
> [[6]]
> [1] 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167
> [18] 168 169 170 171 172 173 174 175 176 177 178 179 180

```

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 = 100, nfold = 10, data$Vars$n, data$Vars$p, data$Vars$q)
> [1] 6.3522574 6.2507156 6.1439930 6.0324521 5.9165073 5.7966113 5.6732394
> [8] 5.5468767 5.4180058 5.2870996 5.1546170 5.0210037 4.8866971 4.7521324
> [15] 4.6177527 4.4840154 4.3513991 4.2204045 4.0915513 3.9653680 3.8423790
> [22] 3.7230828 3.6079310 3.4973031 3.3914844 3.2906459 3.1948307 3.1039484
> [29] 3.0177765 2.9359721 2.8580894 2.7836054 2.7119483 2.6425268 2.5747611
> [36] 2.5081078 2.4420822 2.3762762 2.3103690 2.2441320 2.1774298 2.1102152
> [43] 2.0425208 1.9744459 1.9061441 1.8378049 1.7696424 1.7018774 1.6347289
> [50] 1.5684012 1.5030821 1.4389350 1.3761012 1.3147002 1.2548290 1.1965683
> [57] 1.1399806 1.0851192 1.0320220 0.9807181 0.9312308 0.8835738 0.8377552
> [64] 0.7937793 0.7516502 0.7113628 0.6729146 0.6363108 0.6015428 0.5686167
> [71] 0.5375372 0.5083024 0.4809286 0.4554202 0.4317874 0.4100311 0.3901532
> [78] 0.3721385 0.3559648 0.3415844 0.3289407 0.3179365 0.3084878 0.3004579
> [85] 0.2937241 0.2881442 0.2835858 0.2798914 0.2769299 0.2746041 0.2727766
> [92] 0.2713580 0.2702884 0.2694663 0.2688706 0.2683959 0.2681146 0.2678791
> [99] 0.2677509 0.2675926
fit0   = ridgeRegression(X, Y, Sk, gamma, data$Vars$n, data$Vars$p, data$Vars$q, trans = FALSE, sparse = FALSE)

```

Run ssemQr algorithm for data

Then, we chose the `fit0` object from ridge regression as initialization, 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$sigma2,
                      nlambdas = 7, nrho = 7, p = data$Vars$p, wt = TRUE)
> SSEMiPALM@lambda = 51.870637, rho = 74.290202
> SSEMiPALM@lambda = 16.402936, rho = 74.290202
> SSEMiPALM@lambda = 5.187064, rho = 74.290202
> SSEMiPALM@lambda = 1.640294, rho = 74.290202
> SSEMiPALM@lambda = 0.518706, rho = 74.290202
> SSEMiPALM@lambda = 0.164029, rho = 74.290202
> SSEMiPALM@lambda = 0.051871, rho = 74.290202
> SSEMiPALM@lambda = 273.633043, rho = 23.492625
> SSEMiPALM@lambda = 86.530366, rho = 23.492625
> SSEMiPALM@lambda = 27.363304, rho = 23.492625
> SSEMiPALM@lambda = 8.653037, rho = 23.492625
> SSEMiPALM@lambda = 2.736330, rho = 23.492625
> SSEMiPALM@lambda = 0.865304, rho = 23.492625
> SSEMiPALM@lambda = 0.273633, rho = 23.492625
> SSEMiPALM@lambda = 325.878545, rho = 7.429020
> SSEMiPALM@lambda = 103.051844, rho = 7.429020
> SSEMiPALM@lambda = 32.587854, rho = 7.429020
> SSEMiPALM@lambda = 10.305184, rho = 7.429020
> SSEMiPALM@lambda = 3.258785, rho = 7.429020
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> SSEMiPALM@lambda = 0.325879, rho = 7.429020
> SSEMiPALM@lambda = 335.101519, rho = 2.349262
> SSEMiPALM@lambda = 105.968405, rho = 2.349262
> SSEMiPALM@lambda = 33.510152, rho = 2.349262
> SSEMiPALM@lambda = 10.596840, rho = 2.349262
> SSEMiPALM@lambda = 3.351015, rho = 2.349262
> SSEMiPALM@lambda = 1.059684, rho = 2.349262
> SSEMiPALM@lambda = 0.335102, rho = 2.349262
> SSEMiPALM@lambda = 323.162488, rho = 0.742902
> SSEMiPALM@lambda = 102.192952, rho = 0.742902
> SSEMiPALM@lambda = 32.316249, rho = 0.742902
> SSEMiPALM@lambda = 10.219295, rho = 0.742902
> SSEMiPALM@lambda = 3.231625, rho = 0.742902
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> SSEMiPALM@lambda = 318.851306, rho = 0.234926
> SSEMiPALM@lambda = 100.829636, rho = 0.234926
> SSEMiPALM@lambda = 31.885131, rho = 0.234926
> SSEMiPALM@lambda = 10.082964, rho = 0.234926
> SSEMiPALM@lambda = 3.188513, rho = 0.234926
> SSEMiPALM@lambda = 1.008296, rho = 0.234926
> SSEMiPALM@lambda = 0.318851, rho = 0.234926
> SSEMiPALM@lambda = 332.715189, rho = 0.074290
> SSEMiPALM@lambda = 105.213781, rho = 0.074290
> SSEMiPALM@lambda = 33.271519, rho = 0.074290
> SSEMiPALM@lambda = 10.521378, rho = 0.074290
> SSEMiPALM@lambda = 3.327152, rho = 0.074290
> SSEMiPALM@lambda = 1.052138, rho = 0.074290
> SSEMiPALM@lambda = 0.332715, 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 = 0.895967,  logLik = 6150.677191
> SSEMQ      niter = 2,  relerr = 0.354813,  logLik = 5278.927954
> SSEMQ      niter = 3,  relerr = 0.160027,  logLik = 4261.989548
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> SSEMQ      niter = 5,  relerr = 0.034103,  logLik = 3493.288094
> SSEMQ      niter = 6,  relerr = 0.015237,  logLik = 3334.760204
> SSEMQ      niter = 7,  relerr = 0.009916,  logLik = 3094.711895
> SSEMQ      niter = 8,  relerr = 0.010957,  logLik = 2827.542307
> SSEMQ      niter = 9,  relerr = 0.010488,  logLik = 2590.033975
> SSEMQ      niter = 10, relerr = 0.008996,  logLik = 2410.652824
> SSEMQ      niter = 11, relerr = 0.007299,  logLik = 2284.873273
> SSEMQ      niter = 12, relerr = 0.005846,  logLik = 2194.234866
> SSEMQ      niter = 13, relerr = 0.004800,  logLik = 2125.252899
> SSEMQ      niter = 14, relerr = 0.004179,  logLik = 2072.940685
> SSEMQ      niter = 15, relerr = 0.003847,  logLik = 2029.122534
> SSEMQ      niter = 16, relerr = 0.003559,  logLik = 1991.412641
> SSEMQ      niter = 17, relerr = 0.003283,  logLik = 1961.926872
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```

[illegible]


```

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```

```

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> SSEQM      niter = 373,      relerr = 0.000001, logLik = 1874.476207
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> SSEQM      niter = 398,      relerr = 0.000001, logLik = 1874.476214

```

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")

```

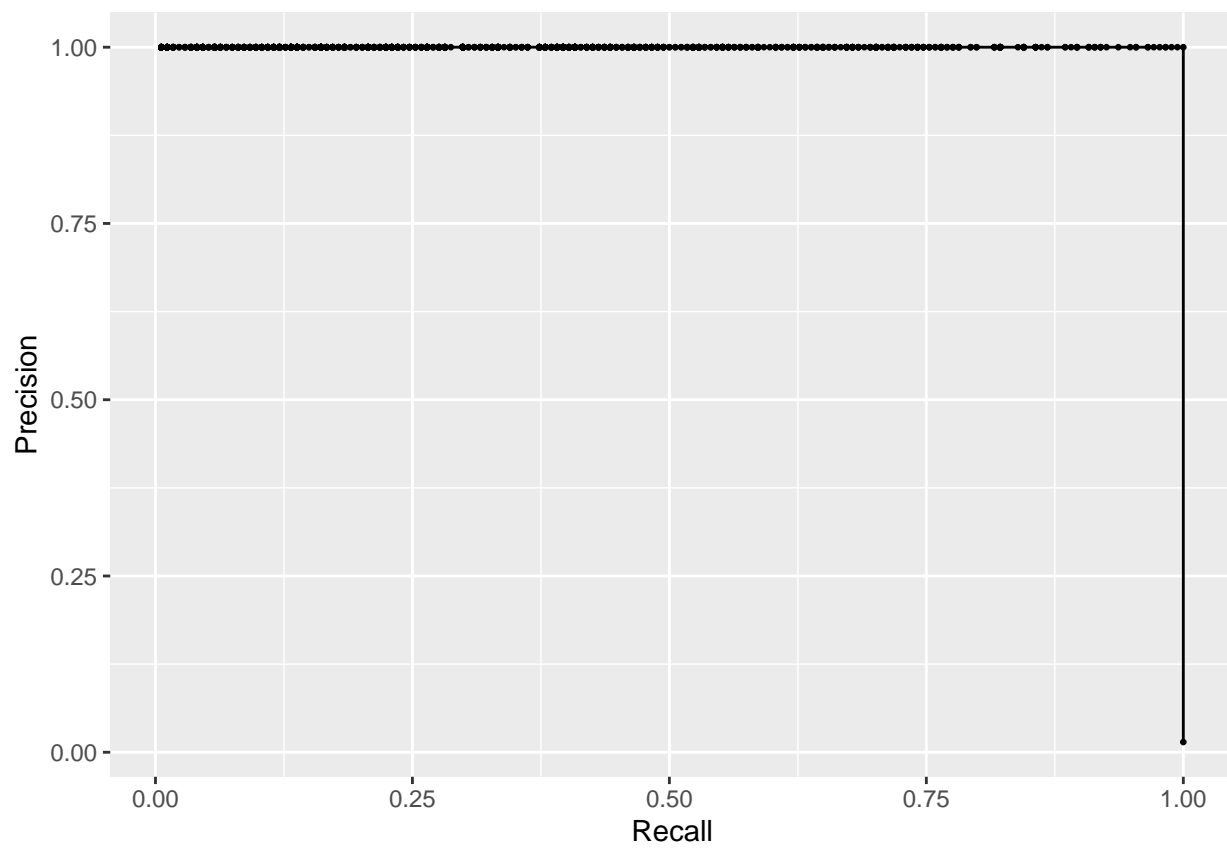



Figure 2: PR curve of trans-eQTL

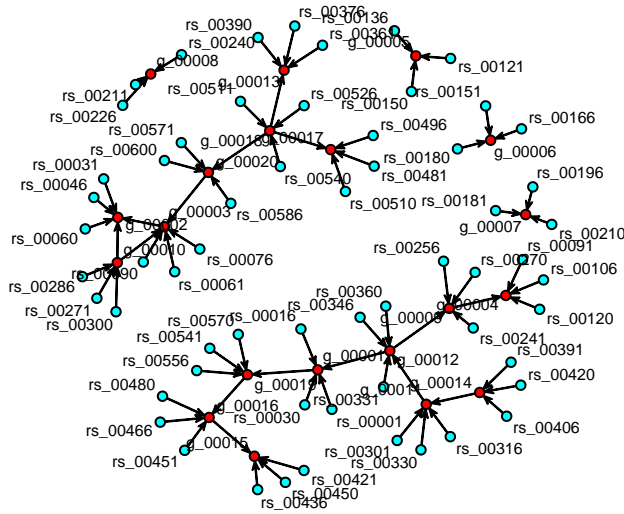


Figure 3: GRN QTL Network

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]),
```

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_3.2.1.9000    network_1.13.0.1      ssemQr_0.1.0
> [7] RevoUtilsMath_10.0.0
>
> loaded via a namespace (and not attached):
> [1] RevoUtils_10.0.4      tidyselect_0.2.5      xfun_0.4
> [4] purrr_0.3.0           sna_2.4               lattice_0.20-35
> [7] colorspace_1.4-0      vctrs_0.2.0.9007      htmltools_0.3.6
> [10] yaml_2.2.0            rlang_0.4.2.9000      pillar_1.4.2.9001
> [13] glue_1.3.0            withr_2.1.2           plyr_1.8.4
> [16] foreach_1.4.4         lifecycle_0.1.0.9000  stringr_1.3.1
> [19] munsell_0.5.0         gtable_0.2.0          mvtnorm_1.0-8
> [22] codetools_0.2-15      coda_0.19-2           evaluate_0.12
> [25] labeling_0.3          knitr_1.21            fssemR_0.1.6
> [28] parallel_3.4.0        rARPACK_0.11-0        Rcpp_1.0.0
> [31] scales_1.1.0.9000     lobstr_1.1.1          farver_2.0.1.9000
> [34] RSpectra_0.12-0       digest_0.6.18         stringi_1.2.4
> [37] dplyr_0.8.99.9000     ggrepel_0.8.0         grid_3.4.0
> [40] tools_3.4.0           magrittr_1.5          glmnet_2.0-16
> [43] tibble_2.99.99.9010   crayon_1.3.4          pkgconfig_2.0.2
> [46] zeallot_0.0.3         MASS_7.3-49           assertthat_0.2.0
> [49] rmarkdown_1.11        iterators_1.0.9       statnet.common_4.1.4
> [52] qtl_1.44-9            R6_2.2.2              compiler_3.4.0

```