scalnet: Scalable network estimation with *L0* penalty

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1.Background

- Estimating a large and sparse precision matrix for genomic data has garnered substantial research attention for its direct application to classification analysis and graphical models.
- Most existing methods either use a lasso-type penalty that may lead to biased estimators or are computationally intensive, which prevents their application to very large graphs.

2. Method

- We propose using an *L*0 penalty to estimate an ultra-large precision matrix (*scalnetL0*), which includes two main procedures:
  1) convert the original problem into many small-scale linear regression problems.
  2) adopt an *L*0 penalty method to solve these linear regression problems.
- Software Installation from GitHub

```
devtools::install_github('BIG-S2/SCALNET')
```

3. Application

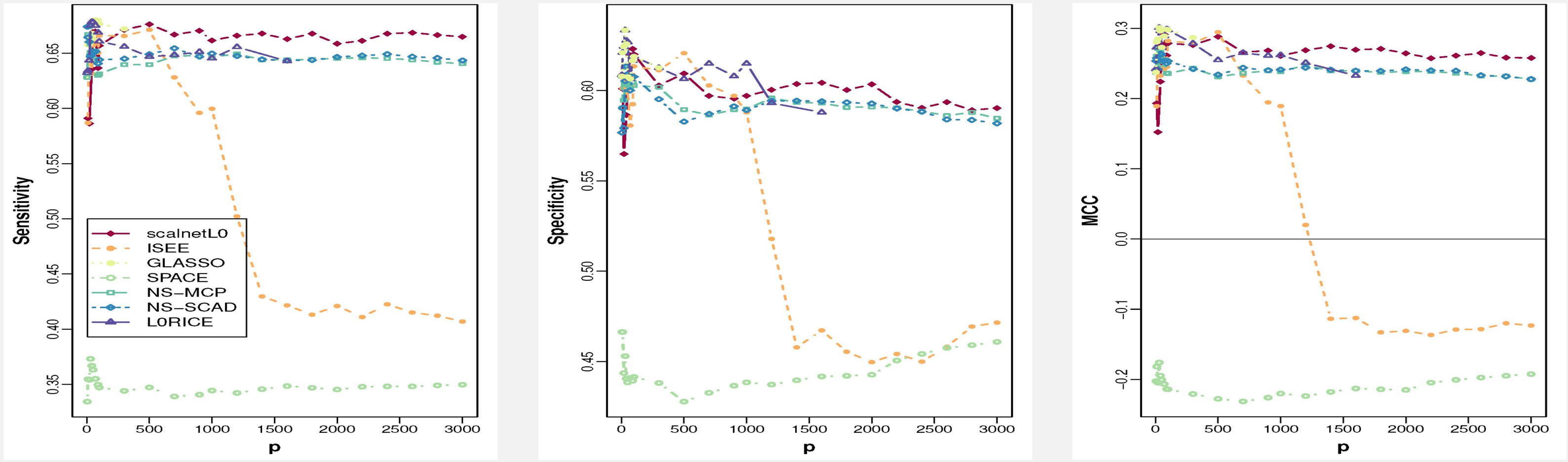
3.1. Linear Discriminant Analysis (LDA)

Using gene expression data, we perform a linear discriminant analysis for patients' survival times to predict whether individual patients with breast cancer will experience long or short survival times using their gene expression profiles.

3.2. Results

The *scalnetL0* can handle a larger number of genes than many existing methods (Figure 1).

Figure 1. Classification results for survival times in the TCGA breast cancer data, with the x-axis representing the number of expression profiles.



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5. Disclaimer The present study reflects the views of the authors and should not be constructed to represent the views or policies of the US Food and Drug Administration.