Estimation of covariance structure in high-dimensional setting using graphical lasso with application to gene expression data

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Background

A high dimensional setting is when the number of features/variables (p) are larger than the number of observations (n). In this setting the standard maximum likelihood estimated covariance matrix ($\hat{\Sigma}$) is singular and considering the expected value for the inverse of $\hat{\Sigma}$, using the properties of the Gaussian distribution [6]

$$E\left[\hat{\Sigma}^{-1}\right] = \psi\left(p, n\right)\Sigma^{-1}, \quad \psi\left(p, n\right) = \frac{n}{n-p-1} = \frac{1}{1-\frac{p-1}{n}}$$

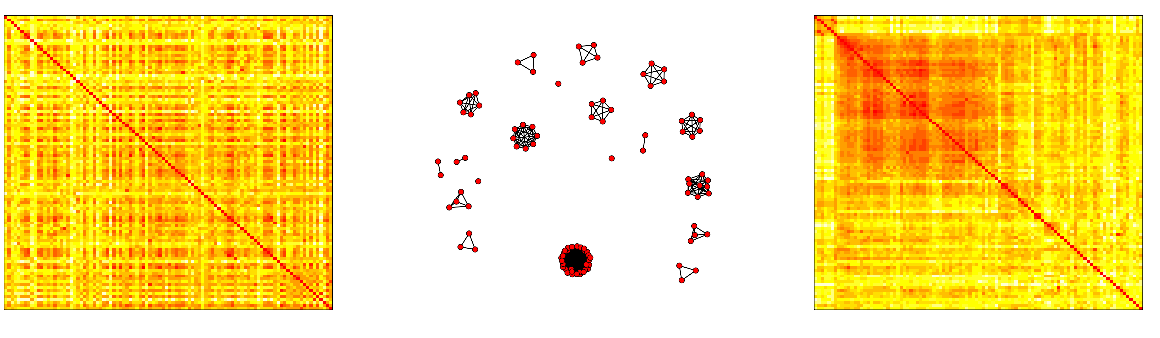
the effect of the relation between p and n for $\hat{\Sigma}^{-1}$ can be clearly seen. As Σ^{-1} is used in many statistical methods e.g. discriminant analysis and regression analysis it is essential to get reliable and non-biased estimates. Hence in recent years many methods for estimating Σ^{-1} in the high dimensional setting have been suggested, one of the most popular methods being the graphical lasso proposed by [10]. This method have been extended and improved by e.g. [4, 5, 3, 8]

Aim

The aim is to present existing graphical lasso methods for estimating covariance structure and to explore and compare these methods using both simulations and application of gene expression data.

Method

To explore the graphical lasso methods different covariance structures should generated according algorithms presented in e.g. [9, 2, 8]. Data will be simulated based on the different structures and then permuted. The performance of the graphical lasso methods to recover and identify true structure will be evaluated using true positive rates and false positive rates with regard to the estimated edges. Plotting the true positive rates against the false positive rates gives the receiver operating characteristic (ROC curve). Application to gene expression data will be to publicly available data such as [1, 7]



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