

Project Title: A new approach for covariance selection models for the inference of gene regulatory networks.

Project Description:

The inference, or 'reverse-engineering', of gene regulatory networks from expression data and the description of the complex dependency structures among genes are open issues in modern molecular biology. Several methods have been proposed to deal with this challenging problem, but there is no guarantee that the obtained estimator is positive definite. Furthermore, in many cases, one needs to capture some additional information on the setting of the problem.

We are developing a new regularized method of covariance selection for the inference of gene regulatory networks, to circumvent the problems raising when the number of observations n is smaller than the number of genes p with a new criterion that ensures the positive definiteness of the precision matrix and an inner-outer alternating direction method of multipliers as an efficient method for estimating it.

We compare the performance to three successful three approaches that provide alternative estimates of the inverse covariance matrix: (a) the 'PINV' method is based on the Moore–Penrose pseudoinverse, (b) the 'RCM' method performs correlation between regression residuals and (c) 'ℓ₂C' method maximizes a properly regularized log-likelihood function.

Duties/Activities: - Writing the code of the algorithm- Designing a set of experiments- Testing on small, medium and large gene, protein and metabolomics network. –Visualizing Graphs of the gene network on real and simulated data.

Required Skills: Knowledge on C or C+ or C++, Or Java, or R or Python.....

Learning Opportunities: learning R if the person is not fluent in R. - Learning some bioinformatics and computational biology tools. –Student or students is/are part of a manuscript based on these results to be submitted to a peer reviewed journal or conference.

Expected Team Size: i 1 or 2 students.

Mentors:

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