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# Information theoretic approaches to single cell gene regulatory network inference

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## Abstract

Single cell transcriptomic data present new challenges and opportunities for understanding the dynamics of gene expression. Biological heterogeneity from cell to cell reveals statistical relationships between genes in unprecedented detail, but the relationships are frequently non-linear and co-factor-dependent. Information theory provides measures that quantify the dependence between variables without making assumptions about the nature of the dependence; these include the pairwise measure, mutual information, and its multivariate generalization, partial information decomposition (PID). Using PID, we develop PIDC, a network inference algorithm designed for single cell data, which finds the most important relationships between pairs of genes by examining their dependencies within a multivariate context. We implement PIDC and several widely-used information-based algorithms in a software package - `NetworkInference.jl` - using the Julia programming language. The speed of our package improves on existing network inference software and allows us to compare the performance of different algorithms on many single cell datasets with ease. We show that PIDC outperforms other methods on both simulated single cell data and single cell transcriptomic data from differentiating stem cells, and we use `NetworkInference.jl` to investigate which aspects of a network inference algorithm contribute to its success.

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