

Are gene networks always meaningful?

A. Gamot^{1,2}, N. Villa^{2,3}, L. Liaubet¹, F. Rossi⁴, G. Tosser-Klopp¹, P. Chere⁵, M. SanCristobal¹
¹INRA, ²Institut de Mathématiques de Toulouse, ³Université de Perpignan (IUT de Carcassonne), ⁴TELECOM ParisTech, ⁵Hendricks Genetics

Post analyses in transcriptomic studies become increasingly popular. Giving a biological meaning to a list of differentially expressed genes requires the use of tools such as gene networks. Several approaches are available in the literature for gene network reconstruction. Using gene expression only, the most famous approach is probably Gaussian networks. They are based on the partial correlation between gene expressions. The Eadgene Post-Analysis Workshop was an opportunity to test this approach on a SABRE/EADGENE data set, but the results were difficult to interpret (Jaffrezic and Tosser-Klopp, 2009, BMC Proceedings, in press). Two additional attempts are proposed here for a SABRE data set on folliculogenesis in pigs and on a eQTL design in pigs. Stability of gene network building is discussed according to sample size, simple simulations, and biological validation. It is shown that Gaussian networks are a useful tool for biological interpretation of a transcriptomic study, as far as the design is adapted. Then, the obtained network is analysed by the way of methods designed for clustering the vertices of a graph. We show that this methodology helps to emphasise the main structure of the network and provides simplified representations that are useful for the representation of the relations in the network.

Corresponding author: magali.san-cristobal@toulouse.inra.fr