

*Bayesian Decomposition Classification of the Project Normal Data Set*

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The process of development and maintenance of tissues is complex. Key genes have been identified that serve as master switches during development, regulating the expression of numerous other genes and guiding differentiation and the development of complex structures. Within cells comprising different tissue types, the genomic complements of genes remain the same, indicating that understanding of tissue differences requires an analysis at the functional rather than structural level. We have used a new version of the Bayesian Decomposition algorithm to identify tissue specific gene expression. The expression patterns identified in the analysis were analyzed in terms of the ontological information on the processes involving proteins encoded by the genes. The ontological information was retrieved from the Gene Ontology database with automated searching software. Tissue specific processes were identified, as well as processes related to multiple tissue types.