A Model for Contextual Regulatory Controls and Identifying Molecular Contexts

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As the tumor must adjust its regulatory machinery away from the normal state to reliably provide proliferative signals and abrogate normal safeguards, its must achieve a new regulatory state different from the normal. Due to this tightly coordinated regulation, initiated by a set of regulatory components, the expression of those genes should show consistent patterns within the same type of cancer. Based on this assumption, we have developed a model to describe master-slave regulations and their dependency on cellular contexts, algorithms to identify genes that are most likely to be regulatory masters, and a set of genes whose transcriptional expression pattern is tightly regulated by those masters. We then went a step further to develop an algorithm to explore gene expression profile to mine possible putative molecular contexts that might be corresponding to some distinctive phenotypes such as tumor subtypes. The model and algorithms have been applied to previously published microarray data sets for a proof-of-principle study.