Inferring cancer pathways from Retroviral Insertional Mutagenesis Screens

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Summary

In this study, 100 splenic tumors - that were induced by retroviral insertional mutagenesis are expression profiled, resulting in a dataset for which both the initiating events (the viral integration sites) as well as the consequent expression profiles are available.

To capture complex associations that arise due to interaction among insertion target genes, we infer small Boolean logic networks that explicitly incorporate operators to model the potential parallel alternatives ('or-' and 'exclusive-or' gates) as well as the potential cooperation between mutations ('and' gates).



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