

Pathway-VisualiseR: An Interactive Web Application for Visualising Gene Networks

Göknur Giner and Alexandra Garnham

10-12th July 2019

useR2019



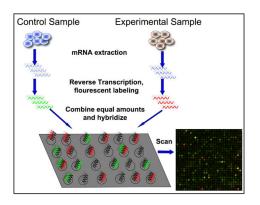


Motivation

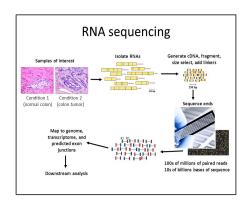
The traditional biological research approaches were used to study **one gene** or a few genes at a time.

Nowadays it is possible to measure the changes and the regulation of **genome-wide** genes under certain biological conditions.

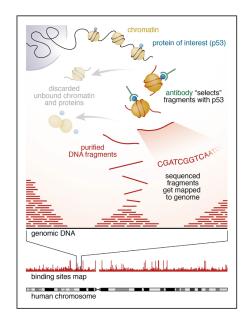
Microarray



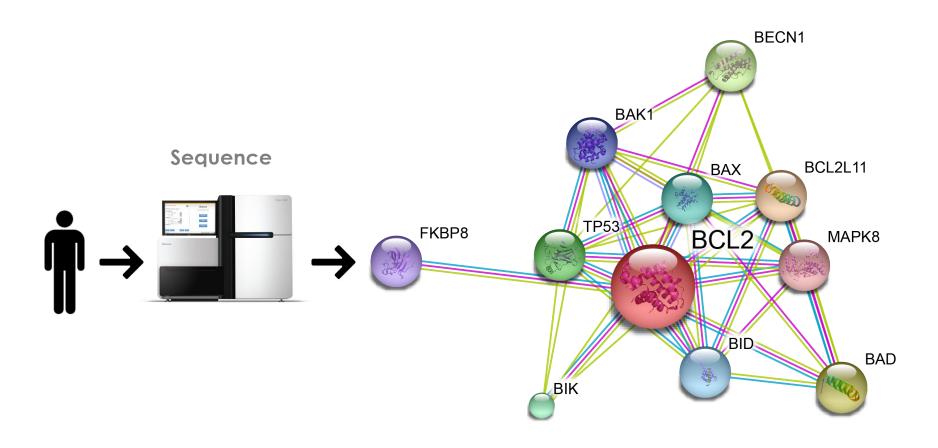
RNA-Seq



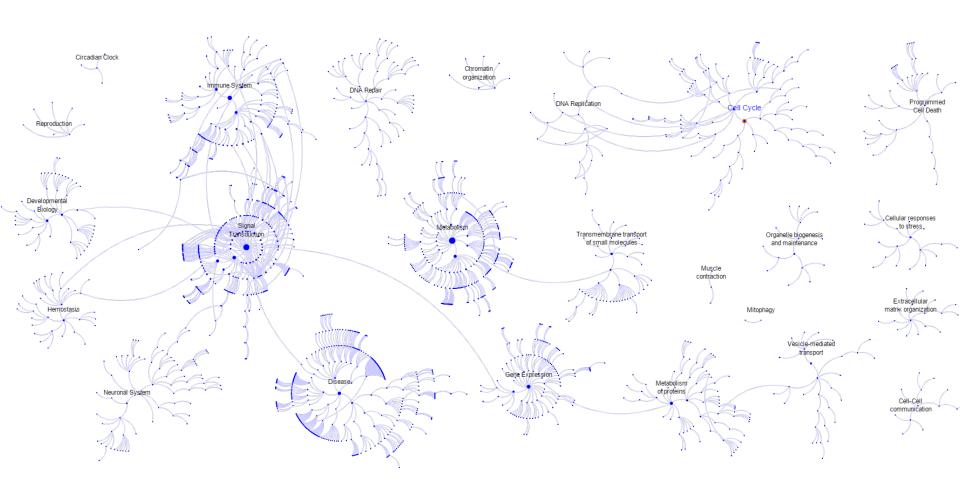
ChIP-Seq



Set of Genes As a Focus of Biological Research



Pathways for Human



Pathway-Visualiser

Pathway-Visualiser constructs these pathways for a given set of genes.







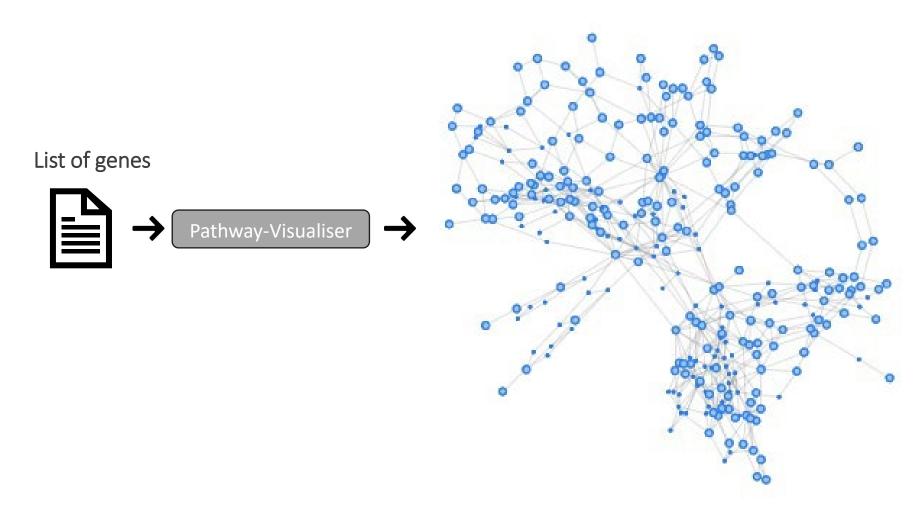








Build the Entire Network



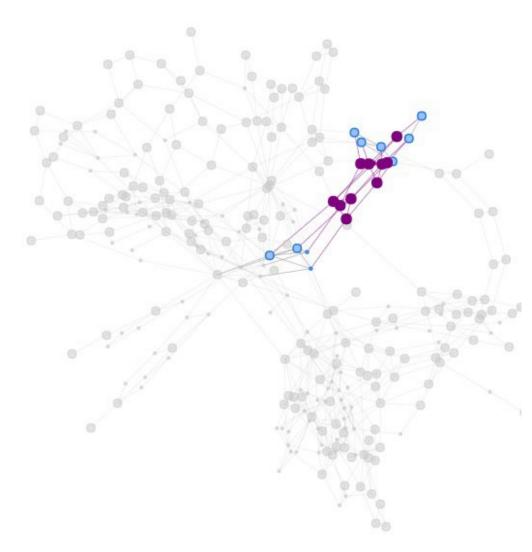
Significant Gene Ontologies that includes the input list of genes

Highlight the Selected GO Terms

Pathway-Visualiser is interactive.

Purple nodes are the pathways of interest selected by the user.

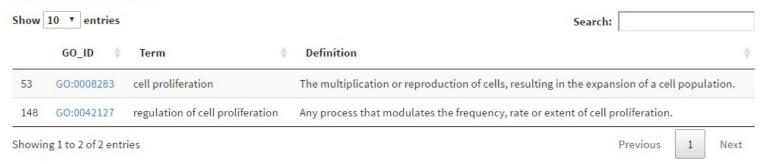
Blue nodes are the periphery pathways.



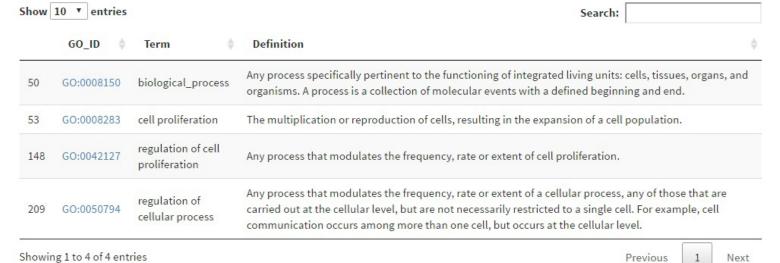
The network of selected pathways

Table of GO Terms for Selected Nodes

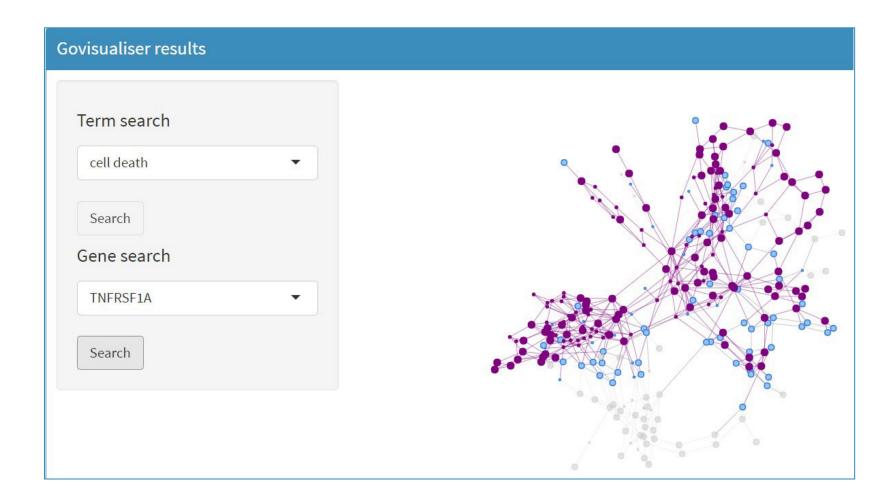
Selected Term



Periphery Terms



GO Terms with Inquired Gene



Acknowledgements



Bioinformatics Division

Gordon Smyth Melissa Davis



Contributing to Australian Scholarship & Science

For providing financial support to travel to useR2019!

Thanks for Listening ©

Any Questions?





Acknowledgements



Bioinformatics Division

Gordon Smyth Melissa Davis



Contributing to Australian Scholarship & Science

For providing financial support to travel to useR2019!

Thanks for Listening ©

Any Questions?



