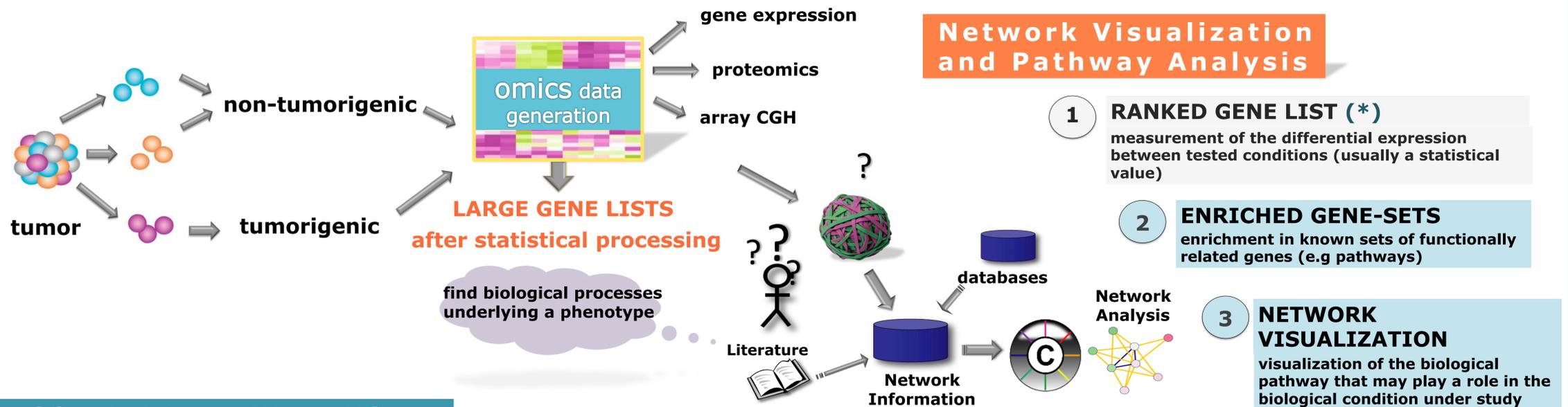


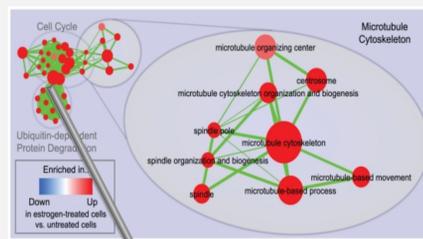
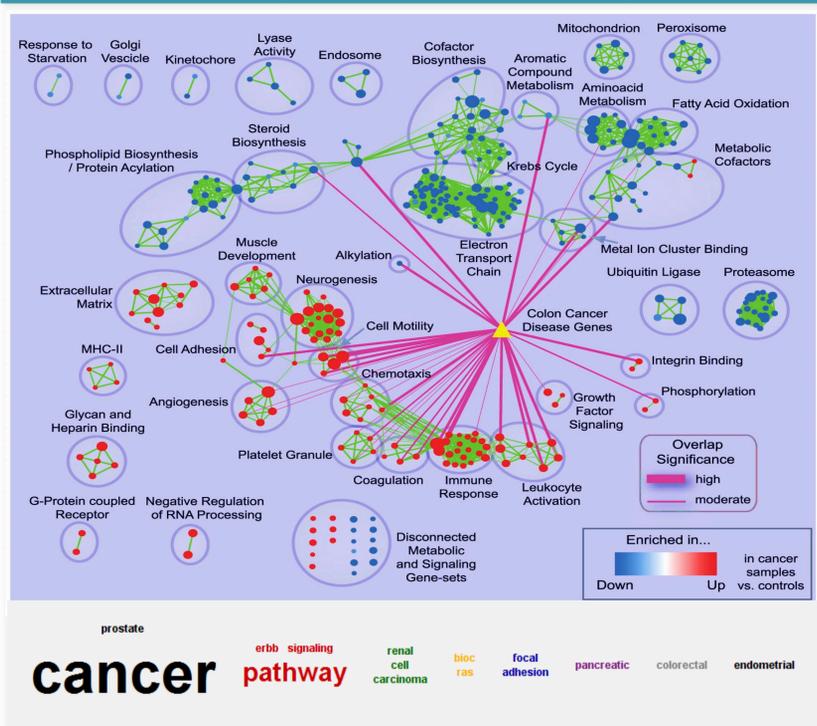
Veronique Voisin¹, Daniele Merico¹, Ruth Isserlin¹, Jayne Danska², John Dick³, Gary Bader¹

¹Donnelly Centre, ²SickKids, ³UHN

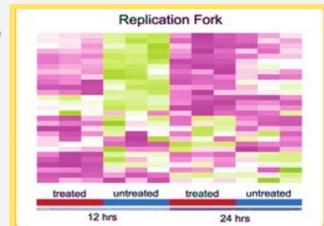
LARGE GENE LISTS ? | WE CAN HELP.



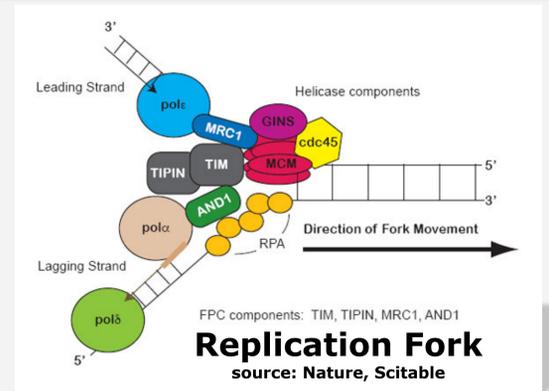
SOFTWARE WE USE: GSEA | CYTOSCAPE | ENRICHMENTMAP | WORDCLOUD | GENEMANIA



If Replication Fork does not function properly: increased risk of mutation and cancer



Shorter list of genes containing best targets



Identified candidate genes?



Back to the bench!

- shRNA
- over-expression
- specific inhibitors
- *in vivo* validation...



OUTCOME AND IMPLICATIONS:

- ❖ **DECREASE ANALYSIS TIME.**
- ❖ **EASE GENERATION OF NEW HYPOTHESES AND DESIGN OF NEW EXPERIMENTS.**
- ❖ **ULTIMATE GOAL: IDENTIFICATION OF THERAPEUTIC OR BIOMARKER CANDIDATES.**
- ❖ **Enrichment map: a network-based method for gene-set enrichment visualization and interpretation. MERICO ET AL. PLOS ONE. 2010 NOV 15;5(11).**

Information about the service:

- ❖ You can contact me at: veronique.voisin@utoronto.ca
- ❖ We have created a survey to assess your needs: please go to <http://www.surveymonkey.com/s/HZXD7VD>
- (*) **Standardized data input: only already statistically analyzed data in a correct format for GSEA analysis are accepted for pathway and network analysis**