

Canadian Bioinformatics Workshops

www.bioinformatics.ca
bioinformaticsdotca.github.io



CC BY-SA 4.0 DEED

Attribution-ShareAlike 4.0 International

Canonical URL : <https://creativecommons.org/licenses/by-sa/4.0/>

[See the legal code](#)


You are free to:


Share — copy and redistribute the material in any medium or format for any purpose, even commercially.

Adapt — remix, transform, and build upon the material for any purpose, even commercially.

The licensor cannot revoke these freedoms as long as you follow the license terms.

Under the following terms:

 **Attribution** — You must give [appropriate credit](#), provide a link to the license, and [indicate if changes were made](#). You may do so in any reasonable manner, but not in any way that suggests the licensor endorses you or your use.

 **ShareAlike** — If you remix, transform, or build upon the material, you must distribute your contributions under the [same license](#) as the original.

No additional restrictions — You may not apply legal terms or [technological measures](#) that legally restrict others from doing anything the license permits.

Notices:

You do not have to comply with the license for elements of the material in the public domain or where your use is permitted by an applicable [exception or limitation](#).

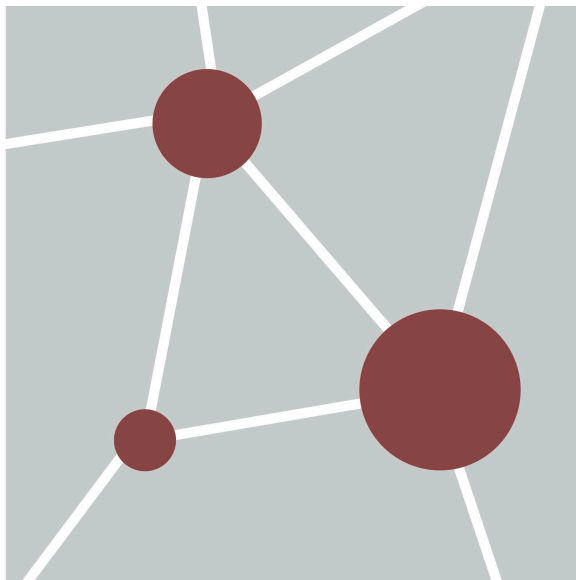
No warranties are given. The license may not give you all of the permissions necessary for your intended use. For example, other rights such as [publicity, privacy, or moral rights](#) may limit how you use the material.

More Depth on Pathway & Network Analysis

Reactome FI practical lab

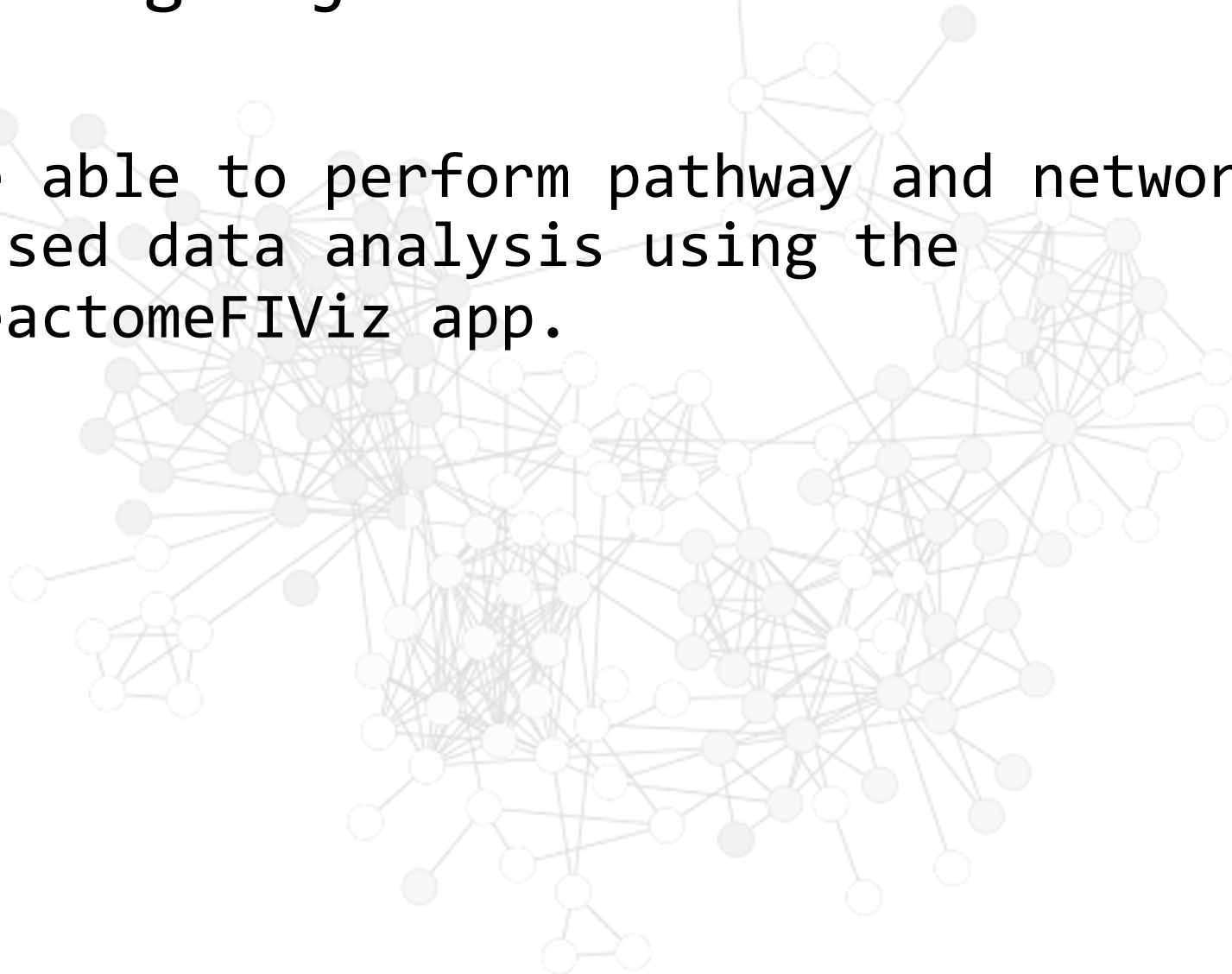


Veronique Voisin
Pathway and Network Analysis
June 26-28, 2024



Learning Objectives of Module

- Be able to perform pathway and network-based data analysis using the ReactomeFIViz app.



Major Features in ReactomeFIViz

The ReactomeFIViz app is designed to find pathways and network patterns related to cancer and other types of diseases.

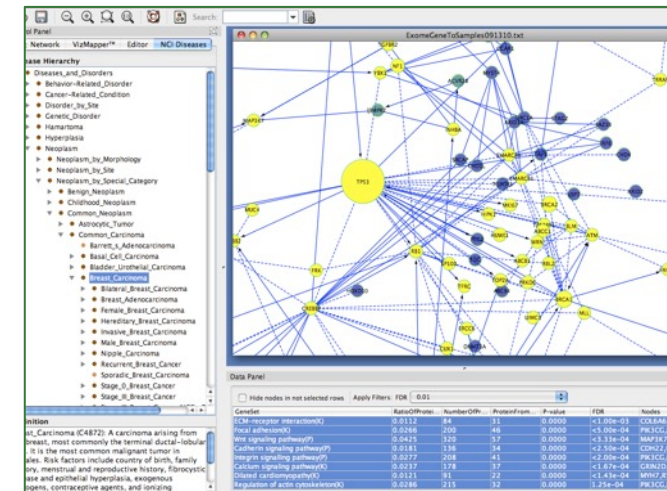
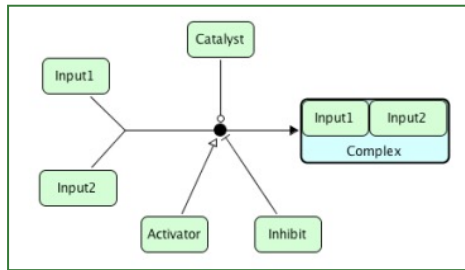
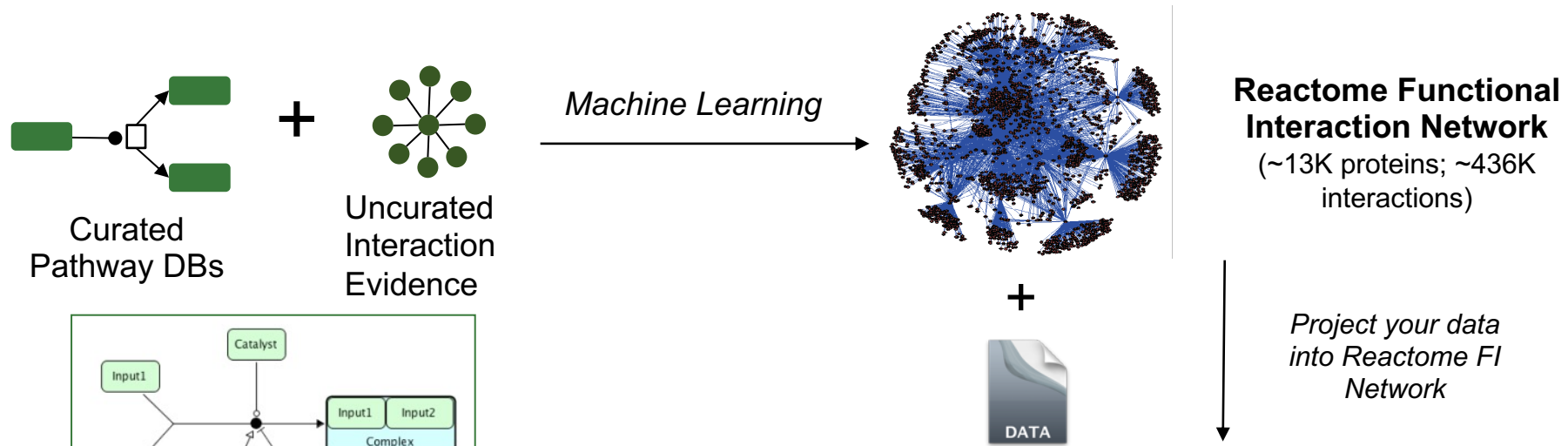
This app accesses **the Reactome pathways** stored in the database:

- help you to do **pathway enrichment analysis** for a set of genes
- visualize hit pathways using manually laid-out **pathway diagrams** directly in Cytoscape
- investigate functional relationships among genes in hit pathways.

The app can also access the **Reactome Functional Interaction (FI) network**:

- allows you to construct a **FI network** based on a set of genes, query the FI data source for the underlying evidence for the interaction
- build and **analyze network modules** of highly-interacting groups of genes
- perform functional **enrichment analysis** to annotate the modules
- expand the network by finding genes related to the experimental data set, and overlay with a variety of information sources such as **cancer gene index** annotations or **FDA-approved cancer drugs**.

Reactome Functional Interaction Network

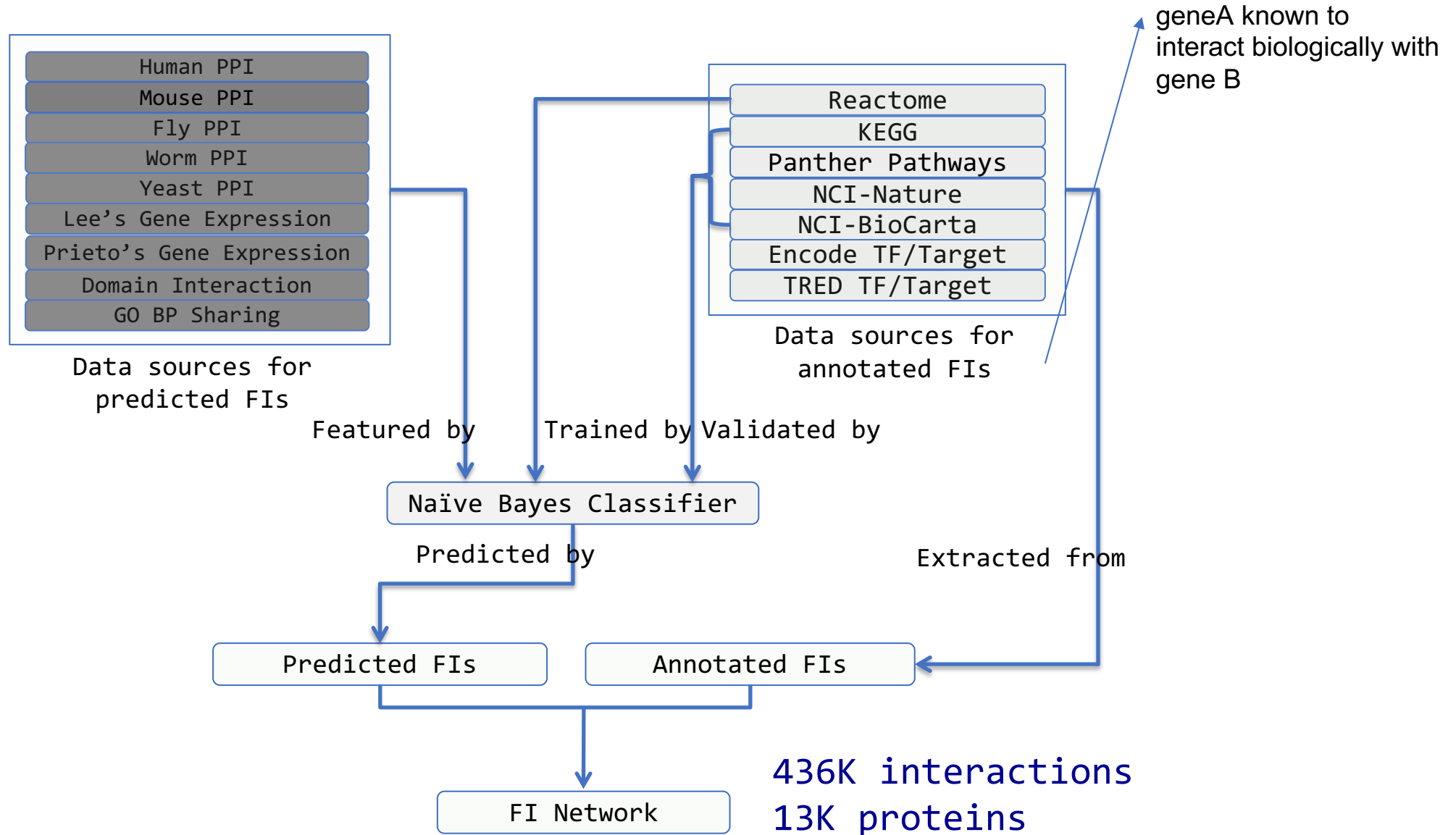


Cytoscape using ReactomeFIViz app

What is a Functional Interaction?

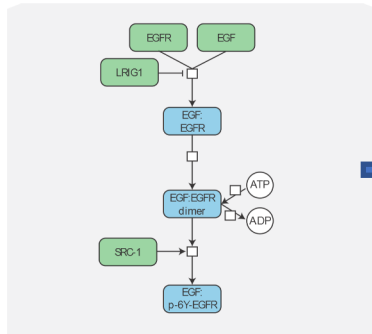
- Convert reactions in pathways into pair-wise relationships
- **Functional Interaction:** an interaction in which two proteins are involved in the same reaction as input, catalyst, activator and/or inhibitor, or as components in a complex

Construction of the FI Network

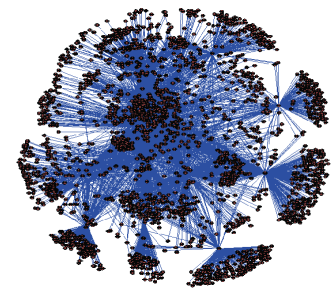
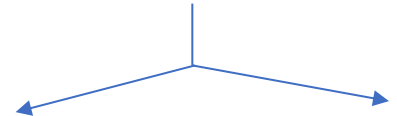
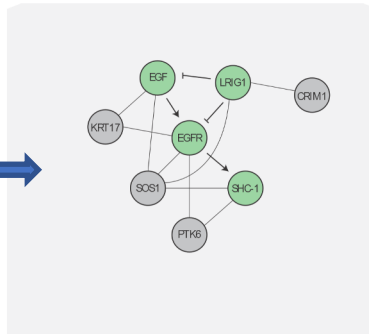


ReactomeFIViz (ReactomeFIPlugin): pathway AND network analysis

Pathway diagram



Network

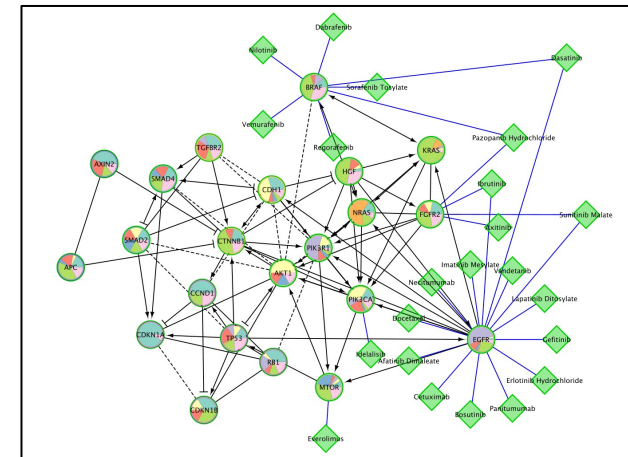
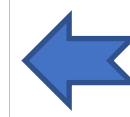


Reactome Functional Interaction Network

(~13K proteins; ~436K interactions)

Create a FI network

Your gene list



- Create a FI network using your gene list :
- Genes in your list will be connected by functional interactions.
- You can: further cluster your FI network to find protein complexes
- You can perform pathway analysis on the whole network.
- You can perform pathway analysis on the individual modules and it helps to add a biological label.
- You can add drug targets to the network.

- Browse the collections of the Reactome pathways
- Convert these pathways into a Cytoscape network

- Import your gene list.
- Reactome pathways enriched in your gene list will be returned.
- Genes that in your gene list will be highlighted in the pathway diagrams and network

Your gene list



And more...

Reactome: Collection of Pathways

The screenshot displays the Reactome web application interface. At the top, the session is titled "Session: New Session". The interface is divided into several panels:

- Control Panel:** Located on the left, it features a tree view of biological pathways. The "Cell Cycle" category is expanded, and "Cell Cycle Checkpoints" is selected. Below the tree, the "Selected Event Branch" is also set to "Cell Cycle" and "Cell Cycle Checkpoints".
- Diagram of Cell Cycle Checkpoints:** The main central panel displays a detailed pathway diagram. It shows the following components and interactions:
 - MCC:APC/C complex** (top node, light blue box) is inhibited by the **phosphorylated anaphase promoting complex (APC/C)** (light blue box).
 - The **phosphorylated anaphase promoting complex (APC/C)** is inhibited by the **hBUBR1:hBUB3:MAD2⁺:CDC20 complex** (light blue box).
 - The **hBUBR1:hBUB3:MAD2⁺:CDC20 complex** is formed from **BUB3** (green box) and **BUB1B** (green box).
 - BUB3** is inhibited by **CDC20** (green box).
 - MAD1L** (green box) is inhibited by the **Kinetochores Complex** (green box).
- Table Panel:** Located at the bottom, it contains a toolbar with icons for settings, pan, zoom, and other functions. Below the toolbar are tabs for "Node Table", "Edge Table", and "Network Table". A "Memory" indicator is visible in the bottom right corner.

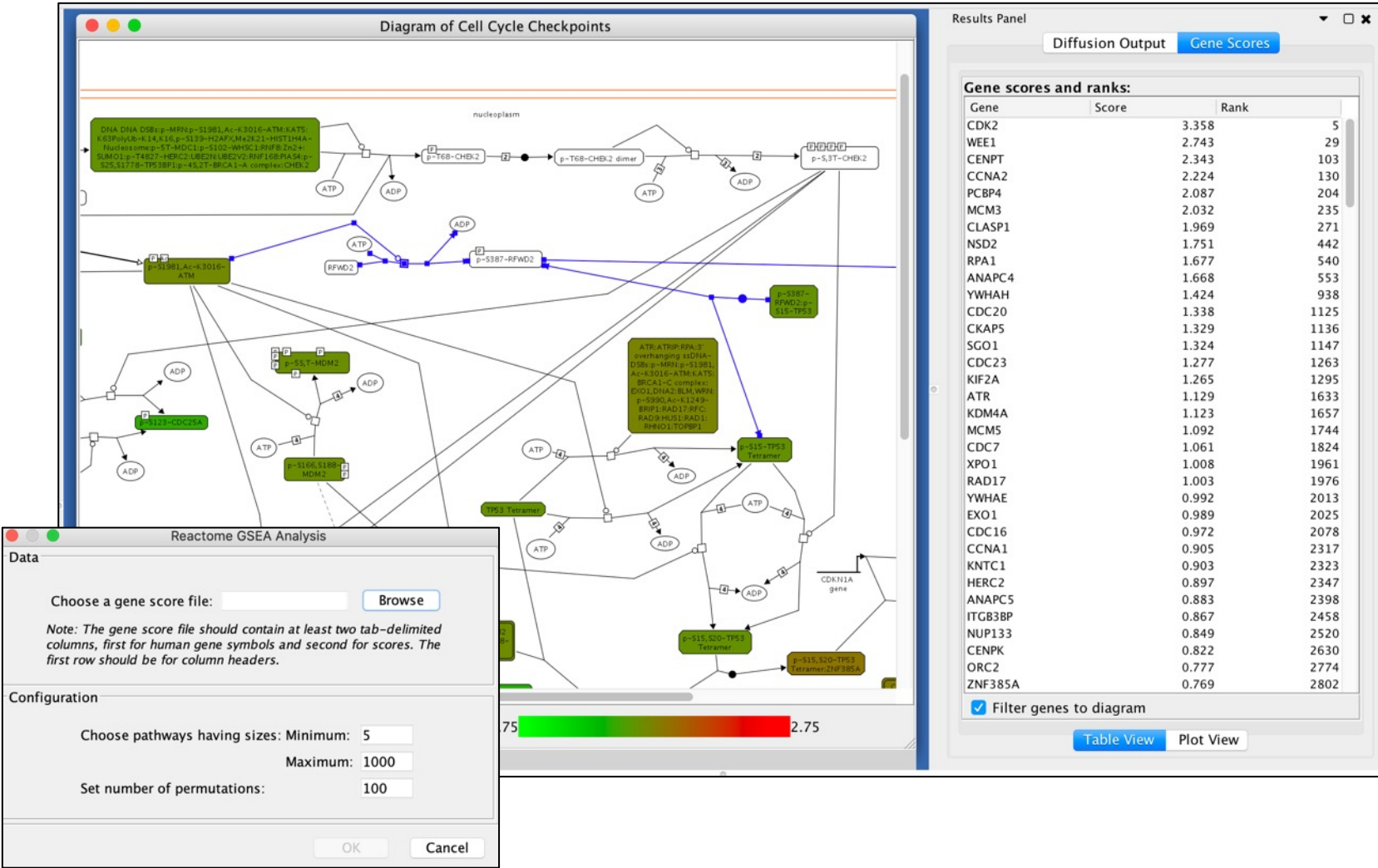
Pathway Enrichment Analysis (gene list) binomial test

The screenshot displays the Reactome software interface. The main window shows a pathway diagram titled "Diagram of Interleukin-7 signaling and JAK3 deficiency causes SCID (IL7R)". A context menu is open over the diagram, with "Analyze Pathway Enrichment" selected. A dialog box titled "Reactome Pathway Enrichment Analysis" is open, showing the "Gene Set Loading" section with a file named "hs_geneNames.txt" selected. Below the dialog, a "Table Panel" displays the results of the enrichment analysis, filtered by FDR 1.0.

ReactomePathway	RatioOfProteinPat...	NumberOfProteinIn...	ProteinFromGeneSet	P-value	FDR	HitGenes
Laminin interactions	0.0032	23	5	0.0111	0.0890	ITGA6,LAMC1,LAMB...
Activation of Rac	0.0011	8	3	0.0114	0.0911	ROBO1,SOS1,SLIT2
Interleukin-7 signali...	0.0011	8	3	0.0114	0.0911	IL7R,HGF,JAK1
CREB phosphorylati...	0.0021	15	4	0.0115	0.0917	GRIN2B,GRIN2A,AKA...
Mismatch Repair	0.0021	15	4	0.0115	0.0917	RPA1,POLD3,MLH1,...
M Phase	0.0315	225	22	0.0117	0.0937	KNTC1,NDE1,UBC,A...
GABA receptor activ...	0.0074	53	8	0.0124	0.0993	CABBR2,GNAT3,GAB...
Mitotic Prometaphase	0.0139	99	12	0.0131	0.1016	KNTC1,NDE1,PDSSB,...
Digestion of dietary ...	0.0004	3	2	0.0132	0.1016	MGAM,LCT
Mitotic Anaphase	0.0227	162	17	0.0136	0.1016	KNTC1,NDE1,UBC,A...
TGF-beta receptor s...	0.0022	16	4	0.0142	0.1016	UBC,PARD3,TGFB2,...

A binomial test uses sample data to determine if the population proportion of one level in a binary (or dichotomous) variable equals a specific claimed value.

Pathway Enrichment Analysis (ranked list) GSEA



Visualize Cancer Targetome in Reactome Pathways

The screenshot displays the Reactome pathway visualization interface. The main window shows a detailed network diagram titled "Diagram of Cell Cycle Checkpoints". The diagram features various nodes representing proteins and their phosphorylated states, such as CHEK2, p-53T-CHEK2, p-168-CHEK2 dimer, p-5317,5348-CHEK1, p-51981, and p-5387-RFWD2. Two cancer drugs, Bosutinib and Sunitinib Malate, are highlighted in red circles, with red lines indicating their interactions with several nodes in the network. A context menu is open over the diagram, listing various analysis and visualization options:

- Convert to FI Network
- Run Logic Model Analysis
- Remove Analysis Results
- Run Graphical Model Analysis
- Show Gene Level Analysis Results
- Show Observation
- Save Analysis Results
- Open Analysis Results
- Overlay Gene Scores
- Remove Gene Scores
- Fetch Cancer Drugs**
- Fetch DrugCentral Drugs
- Filter Drugs
- Load Mechismo Results
- Remove Mechismo Results
- Search Entities
- Search Reactions
- Export Diagram

The interface also includes a Control Panel on the left with a hierarchical tree of biological processes, a Table Panel at the bottom for data management, and a search bar at the top right.

Displaying Reactome Pathways in the FI Network View

The screenshot displays the FI Network View software interface. The main window shows a network diagram titled "FI Network for Diagram of Cell Cycle Checkpoints" with nodes like MAD1L1, BUB1B, CDC16, and various ANAPC proteins. The Control Panel on the left shows a Reactome pathway tree with "Mitotic Spindle Checkpoint" selected. The Table Panel at the bottom shows a list of gene names and their associated data.

Control Panel

Network Style Select Reactome

- Cell Cycle
 - Cell Cycle Checkpoints
 - G1/S DNA Damage Checkpoints
 - G2/M Checkpoints
 - Mitotic Spindle Checkpoint**
 - Cell Cycle, Mitotic
 - Chromosome Maintenance
 - Meiosis
 - Cell-Cell communication
 - Cellular responses to stress
 - Chromatin organization
 - Circadian Clock
 - Developmental Biology
 - DNA Repair
 - DNA Replication
 - Extracellular matrix organization
- Selected Event Branch
 - Cell Cycle
 - Cell Cycle Checkpoints
 - Mitotic Spindle Checkpoint**

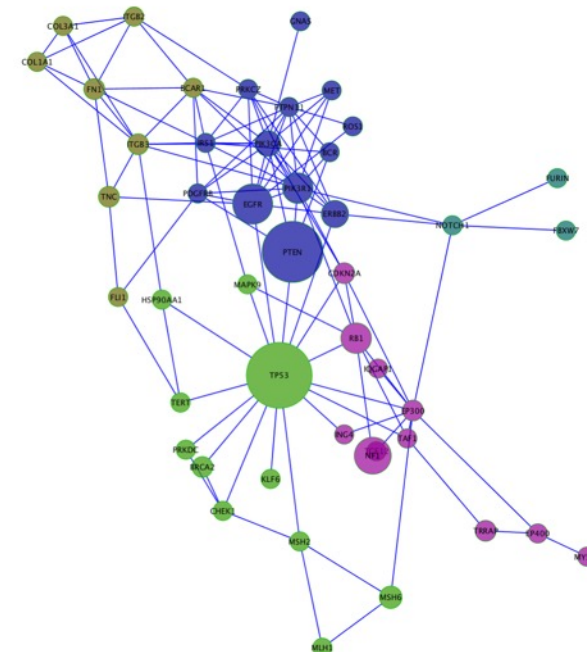
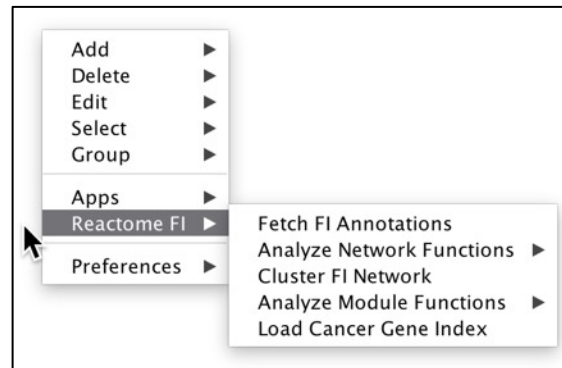
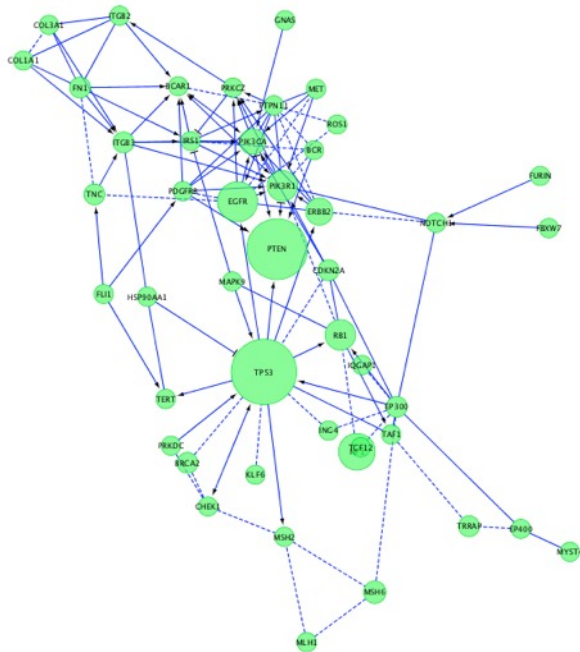
Table Panel

shared name	name	module	commonName	nodeToolTip	nodeLabel
BABAM1	BABAM1	BABAM1	BABAM1	BABAM1	BABAM1
BRCA1	BRCA1	BRCA1	BRCA1	BRCA1	BRCA1
PSMB1	PSMB1	PSMB1	PSMB1	PSMB1	PSMB1
PSME2	PSME2	PSME2	PSME2	PSME2	PSME2
HERC2	HERC2	HERC2	HERC2	HERC2	HERC2
HIST3H2BB	HIST3H2BB	HIST3H2BB	HIST3H2BB	HIST3H2BB	HIST3H2BB
PSME1	PSME1	PSME1	PSME1	PSME1	PSME1
HIST1H2BO	HIST1H2BO	HIST1H2BO	HIST1H2BO	HIST1H2BO	HIST1H2BO
KDM4B	KDM4B	KDM4B	KDM4B	KDM4B	KDM4B

Memory

Create and Cluster FI Network using a gene list

- Create the network
- Cluster the network
- Perform pathway analysis



File Formats to Create the FI Network

- Choose Plugins, Reactome FIs.

Simple Gene List

MSI2
PTPRT
PELO
SLC18A1
TACC2
FAM148B
PRC1
MSTN
ATP6V1G2
APOE
IMPA2
AGER
XPO5
MEST
RREB1
BAT1
WIP1

NCI MAF (mutation annotation file)

Hugo_Symbol	Entrez_Gene_Center	NCBI_Build	Chromosome	Start_position	End_position	Strand
BAI2	576 broad.mit.edu	36	1	31974808	31974808	+
LRRC41	10489 broad.mit.edu	36	1	46524584	46524584	+
C1orf173	127254 broad.mit.edu	36	1	74828082	74828082	+
SSX2IP	117178 broad.mit.edu	36	1	84900740	84900740	+
NTNG1	22854 broad.mit.edu	36	1	107668441	107668441	+
PGLYRP3	114771 broad.mit.edu	36	1	151541551	151541551	+
FCRL5	83416 broad.mit.edu	36	1	155783467	155783467	+
FBXO28	23219 broad.mit.edu	36	1	222388418	222388418	+
OR2M2	391194 broad.mit.edu	36	1	246410342	246410342	+
MKX	283078 broad.mit.edu	36	10	28063690	28063690	+
.....						

Variant_Classification	Variant_Type	Reference_Allele	Tumor_Seq_Allele1	Tumor_Seq_dbSNP_RS	dbSNP_Val_1	Tumor_Samp
Missense_Mutation	SNP	C	G	novel	none	TCGA-04-1331
Missense_Mutation	SNP	C	T	novel	none	TCGA-04-1331
Missense_Mutation	SNP	T	T	G	novel	TCGA-04-1331
Silent	SNP	A	A	G	novel	TCGA-04-1331
Missense_Mutation	SNP	G	G	A	novel	TCGA-04-1331
Missense_Mutation	SNP	G	G	T	novel	TCGA-04-1331
Missense_Mutation	SNP	A	A	C	novel	TCGA-04-1331
Missense_Mutation	SNP	A	A	T	novel	TCGA-04-1331
Missense_Mutation	SNP	G	G	A	novel	TCGA-04-1331
Missense_Mutation	SNP	C	C	A	novel	TCGA-04-1331

Matched_No	Match_Norm	Match_Norm	Tumor_Valid	Tumor_Valid	Match_Norm	Match_Norm	Verification	Validation_S	Mutation_Si	Sequencing	Sequence_Si	Validation_M_Score	BAM_File	Sequencer
TCGA-04-1331-10A-01W							Unknown	Unknown	Unknown	x	x		x
TCGA-04-1331-10A-01W							Unknown	Unknown	Unknown	x	x		x
TCGA-04-1331-10A-01W							Unknown	Unknown	Unknown	x	x		x
TCGA-04-1331-10A-01W							Unknown	Unknown	Unknown	x	x		x
TCGA-04-1331-10A-01W							Unknown	Unknown	Unknown	x	x		x
TCGA-04-1331-10A-01W							Unknown	Unknown	Unknown	x	x		x
TCGA-04-1331-10A-01W							Unknown	Unknown	Unknown	x	x		x
TCGA-04-1331-10A-01W							Unknown	Unknown	Unknown	x	x		x

Gene/Sample Number Pairs

Gene	Sample_Number	Samples
IFT88	1	TCGA-10-0937
TACC2	5	TCGA-24-2288;TCGA-09-1662;TCGA-13-0755;TCGA-13-0920;TCGA-24-2035
ADAD2	1	TCGA-24-1419
PODXL2	1	TCGA-24-2290
RTN3	1	TCGA-13-0726
TAD2A2B	1	TCGA-25-1313
CD274	1	TCGA-25-1627
SULF1	2	TCGA-24-2262;TCGA-09-2056
SYCP2	3	TCGA-24-1563;TCGA-61-2008;TCGA-24-1427
CD200R1L	1	TCGA-13-1488
RCBTB2	1	TCGA-61-2113
TOP2B	1	TCGA-13-0923
C1orf50	1	TCGA-25-2392
ATP9A	5	TCGA-25-1329;TCGA-04-1530;TCGA-24-2262;TCGA-10-0933;TCGA-13-0795
NUDT5	1	TCGA-61-2003
ZNF189	1	TCGA-24-2254
KCNB1	1	TCGA-23-1028
FERMT3	1	TCGA-24-1464
ZCCHC2	1	TCGA-61-1998
DDX18	1	TCGA-13-1509
TGM1	2	TCGA-24-0975;TCGA-25-1321
SAMD7	1	TCGA-09-2051
OR2F2	3	TCGA-13-0723;TCGA-24-2267;TCGA-25-2392
ZSWIM3	2	TCGA-24-1466;TCGA-23-1118
E1F2AK2	2	TCGA-59-2355;TCGA-24-1463
KIAA2018	4	TCGA-23-1024;TCGA-04-1367;TCGA-24-2288;TCGA-24-2289
.....		

Microarray (array) data file

gene	Sample 122	Sample 123	Sample 124	Sample 125	Sample 126	Sample 127	Sample 128	Sample 129	Sample 130
IFT88	1.433357937	0.749571365	0.204170171	1.376375723	0.049504161	0.912377692	0.464660294	0.106486375	0.40767808
KIF9	0.349692236	-0.093947168	-0.56890295	0.177455762	-0.30793794	-0.574121582	-0.772454492	0.850743799	0.19833291
CFP3	-0.628846878	-0.519774777	0.200101088	-0.38888256	-0.54931811	0.440059971	-0.247094525	1.421708617	
TACC2	0.985299156	-0.732555355	1.013646591	-0.057886422	0.730172249	0.554418157	1.280112472	0.463706367	0.956951722
C14orf132	1.249528811	0.104876045	0.524096007	-0.43464182	-1.528259113	-0.467450338	-0.715336925	-0.525776594	-1.06893985
RTN3	0.10643433	-0.286920286	-0.329065423	0.548958273	1.054699921	-0.827782882	-0.462525025	1.39888521	-0.588960437
PODXL2	-0.031430138	-0.390413822	-0.075387324	-0.412392415	0.085789024	-0.097365917	-0.053408731	-0.104692114	1.43380939
CORO1A	-0.247037235	0.664838693	-0.423713196	-0.001970579	0.488162732	-0.435111645	0.596447999	-0.463607768	0.055021666
RBM17	-0.360070659	-0.142165087	-0.233914802	0.018396914	-0.130696373	-0.394476802	-0.818819233	-0.692663375	0.993237633
WTF1	-0.768498156	-0.669419285	-0.763665041	-0.674252401	-0.618671571	-0.393931693	-0.906241952	-0.35285021	-0.538925163
SULF1	-0.863622291	1.588947769	0.272263522	-0.419487008	0.401966747	-0.081472544	-1.17805435	0.327289131	-0.21903657
SYCP2	-0.365259803	1.246319117	-0.107066702	0.891658263	0.914356558	0.091543376	-1.037696782	0.727095627	0.009262058
PHYH	-0.252934465	-0.340129465	0.084219531	-0.613340462	-1.85732245	0.479503528	0.22954453	-1.130697457	1.037551523
RCBTB2	-1.216044791	1.137367735	-0.741461602	0.636779988	-0.695953625	-0.46841374	-0.344892088	-0.130354482	-0.572431973
TOP2B	1.329376011	1.272684609	0.636481097	0.611284918	0.466406891	0.982928554	-0.749308731	0.397117399	0.050669942
SEC22B	-0.712050988	0.661526326	-0.33943161	0.917245507	0.427725933	0.413113408	-0.638988365	0.632301277	0.486176031
ATP9A	1.547427859	0.44411328	1.415509578	-0.14352465	0.540051896	0.510070468	-0.233468933	-0.149520936	-0.047584083
TGFB1	-0.782212802	-0.264862477	-0.123008356	0.027190126	-0.239829397	0.427719409	-0.77368442	0.110633726	1.270499777
NUDT5	-0.16643202	-0.117594702	0.072831699	-0.025664715	0.37488737	0.433985219	-0.898995959	0.020300278	0.112230265
VTI1B	1.252187159	0.515526231	0.073529674	0.770902019	-0.368466883	-1.684634408	0.191395423	0.967344934	2.116535981
RP56KB1	-0.387163384	0.639591396	-0.597648114	-0.392297158	0.932216509	1.563670699	-0.782463975	0.465043084	-0.674654723
RAPGEF4	0.202545341	0.240920292	0.106607963	1.564856103	0.557513638	-0.027704365	-0.651297319	-0.612922368	-1.178952896
PRO1596	-0.010044297	0.228155239	0.228155239	0.445509484	0.148635394	0.079718194	-0.376195587	0.138032748	0.03730761
KCNB1	0.093447081	-0.061401218	1.139678435	0.628377569	0.656531805	1.458927537	1.318156356	-0.469637643	0.346835207
ALDH9A1	0.702468807	-0.111692273	0.963729452	-1.181038168	-1.083849034	1.698904754	1.844724649	-0.038782325	-1.545587905
ZCCHC2	0.55864339	0.120590563	0.845270548	-0.479704052	0.477522496	-1.144895382	-0.39883158	-0.5323533	-0.095731821
LOC1274	-0.291416641	-0.264217345	0.134705668	-0.527143876	-0.07822271	-0.699406086	-0.971399049	-0.218885185	-0.146353728
DDX18	0.34967191	0.294984327	-1.00840307	1.015037505	0.140036175	0.076233995	-0.160745532	0.51373466	1.069725088

FI Results Display

The screenshot displays a software interface for network visualization. The main window is titled "LAC_genelist.txt" and shows a dense network graph with green circular nodes and black edges. A context menu is open over the graph, listing options: Add, Delete, Edit, Select, Group, Apps (highlighted), and Preferences. The "Apps" submenu is open, showing "Reactome FI" (highlighted) and other options: Fetch FI Annotations, Analyze Network Functions, Cluster FI Network, Analyze Module Functions, and Load Cancer Gene Index.

The Control Panel on the left shows the "Network" tab selected, with a table listing the loaded network:

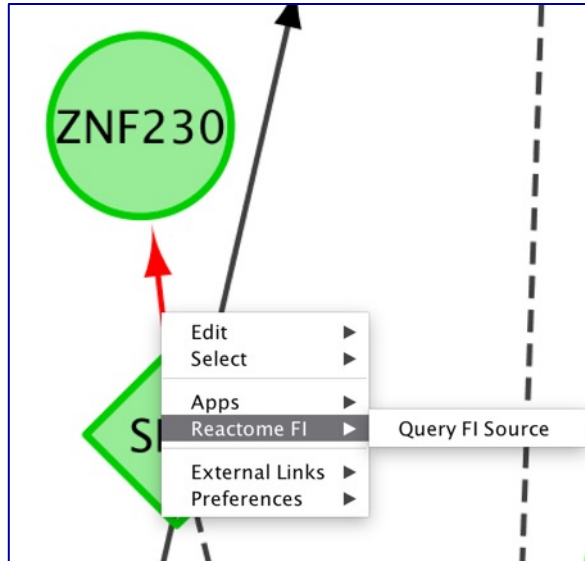
Network	Nodes	Edges
LAC_genelist.txt	238(0)	920(0)

The Table Panel at the bottom displays a table of node data:

shared name	name	module	commonName	nodeToolTip	nodeLabel	nodeType
ACTB	ACTB		ACTB	ACTB	ACTB	Gene
ITGAV	ITGAV		ITGAV	ITGAV	ITGAV	Gene
RAD21	RAD21		RAD21	RAD21	RAD21	Gene
YAP1	YAP1		YAP1	YAP1	YAP1	Gene
JUN	JUN		JUN	JUN	JUN	Gene
MAP2K7	MAP2K7		MAP2K7	MAP2K7	MAP2K7	Gene
FOS	FOS		FOS	FOS	FOS	Gene
UBC	UBC		UBC	UBC	UBC	Gene
USF1	USF1		USF1	USF1	USF1	Gene

- Constructed network is displayed in the Network View panel using an FI specific visual style

Query FI Source



Annotated FIs

Two overlapping windows showing interaction details for 'Interaction: SIX5 - ZNF230'. The top window, 'Interaction Info', has a 'Reactome Sources' tab with a table:

Reactome ID	Type	Data Source
6951674	TARGETED_INTERAC	ENCODE

A 'View Reactome Source' button is visible below the table. The bottom window, 'Reactome Instance View', shows the following details:

classType	TargetedInteraction
dbId	6951674
displayName	SIX5 ZNF230
dataSource	ENCODE
definition	ENCODE proximal_filtered TF/target interaction; supported by GO BP sharing
factor	SIX5
species	Homo sapiens
target	ZNF230

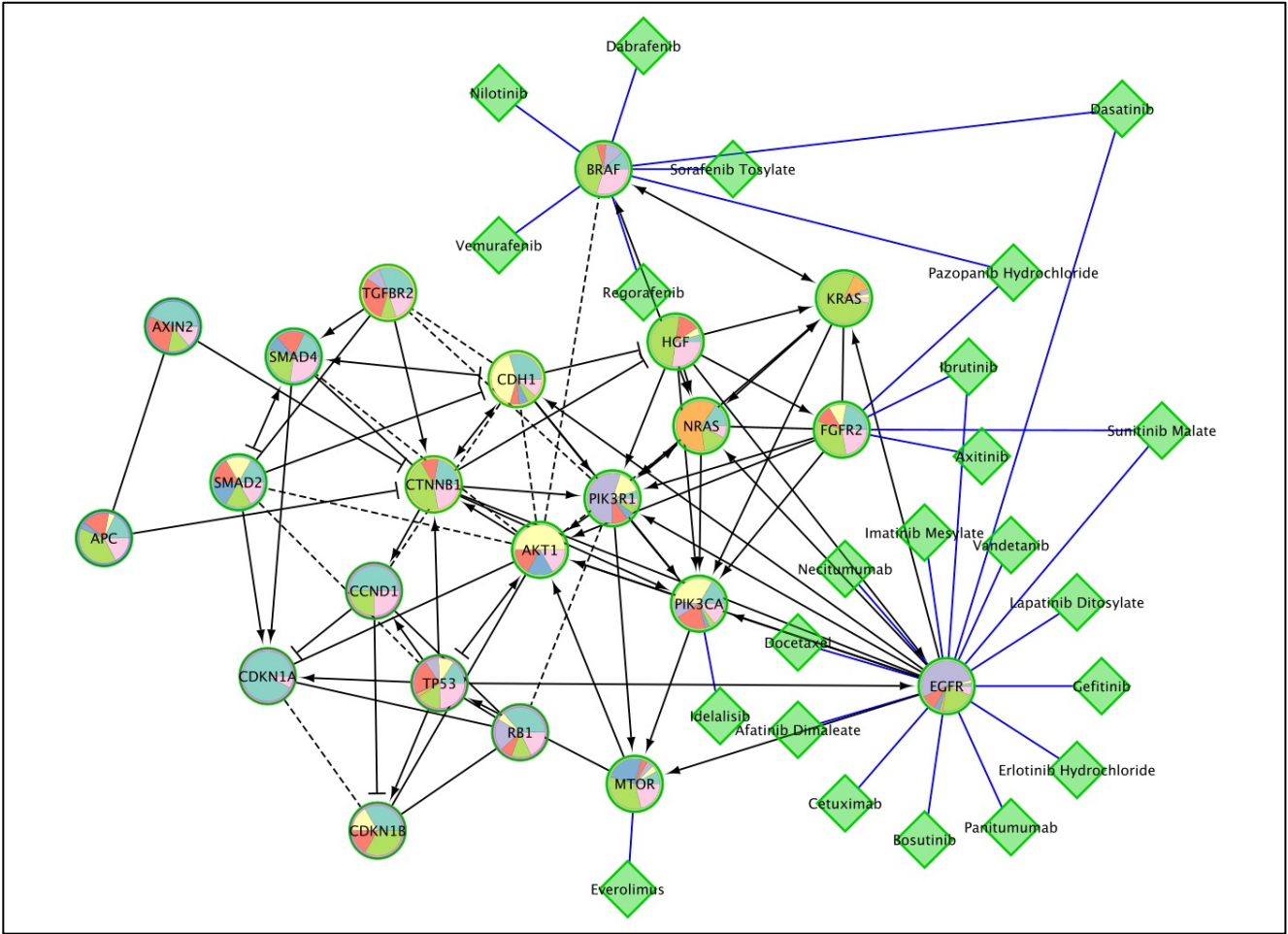
A 'Close' button is at the bottom of the 'Reactome Instance View' window.

Predicted FIs

A window titled 'Interaction Info' for 'Interaction: SNX4 - SNX6' with a 'Support Evidence' tab. It displays a table of evidence:

Predictor	Value
Human Interaction	true
Yeast Interaction	false
Fly Interaction	false
Worm Interaction	false
Mouse Interaction	false
Pavlidis Gene Exp	false
Carlos Gene Exp	false
PfamDomain Interaction	true
GO BP Sharing	true
Score	0.9642255584531738

Overlay FDR approved Cancer Drugs



Overlay Cancer Gene Index

- Load the NCI disease terms hierarchy in the left panel.
- Select a disease term in the tree to select all nodes that have this annotation or one of its sub-terms.

The screenshot displays the VizMapper software interface. On the left is the 'Control Panel' with a 'Disease Hierarchy' tree. The tree is expanded to 'Papillary_Breast_Neoplasm'. The center panel shows a network graph with nodes and edges. A context menu is open over the graph, listing options like 'Add', 'Edit', 'Select', 'Group', 'Nested Networks', 'Apps', 'Reactome FI', 'External Links', and 'Preferences'. The 'Reactome FI' option is highlighted, and a sub-menu is visible with options: 'Fetch FIs', 'Fetch Cancer Gene Index', 'Query Gene Card', 'Query Cosmic', and 'Analyze Nodes Functions'. The bottom panel is a 'Table Panel' showing a table of gene sets with columns for Module, GeneSet, RatioOfProteinIn..., NumberOfProtei..., ProteinFromMod..., P-value, FDR, and Nodes.

Module	GeneSet	RatioOfProteinIn...	NumberOfProtei...	ProteinFromMod...	P-value	FDR	Nodes
0	Bladder cancer(K)	0.0038	38	2	0.0063	2.026e-01	E2F3,CDKN2A
0	Lysosome(K)	0.0123	122	3	0.0065	1.906e-01	ARSG,NEU1,SCA...
0	HTLV-I infection...	0.0262	260	4	0.0084	2.256e-01	E2F3,CDKN2A,...
0	Validated trans...	0.0049	49	2	0.0103	2.498e-01	PMAIP1,CDKN2A
1	Focal adhesion(K)	0.0208	206	8	0.0000	<1.000e-03	TLN2,TNC,BCA...
1	Integrins in angi...	0.0047	47	4	0.0000	4.000e-03	BCAR1,PTK2B,I...
1	Type II diabetes...	0.0048	48	4	0.0000	2.667e-03	KCNJ11,PRKCE...
1	Signaling by EG...	0.0172	171	6	0.0000	3.000e-03	FGF9,LRIG1,SPR...
1	Endothelins(N)	0.0063	62	4	0.0001	4.400e-03	BCAR1,PTK2B,P...

Module Based Survival Analysis

- Discover Prognostic Signatures in Disease Module Datasets.
- Based on a server-side R script that runs either CoxPH or Kaplan-Meier survival analysis.
- Requires appropriate clinical data file.

Results Panel

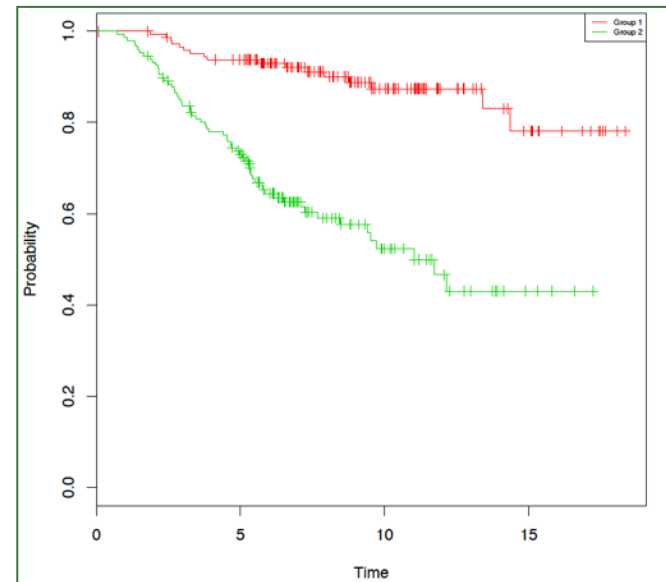
Survival Analysis

Analysis: Coxph (all modules)

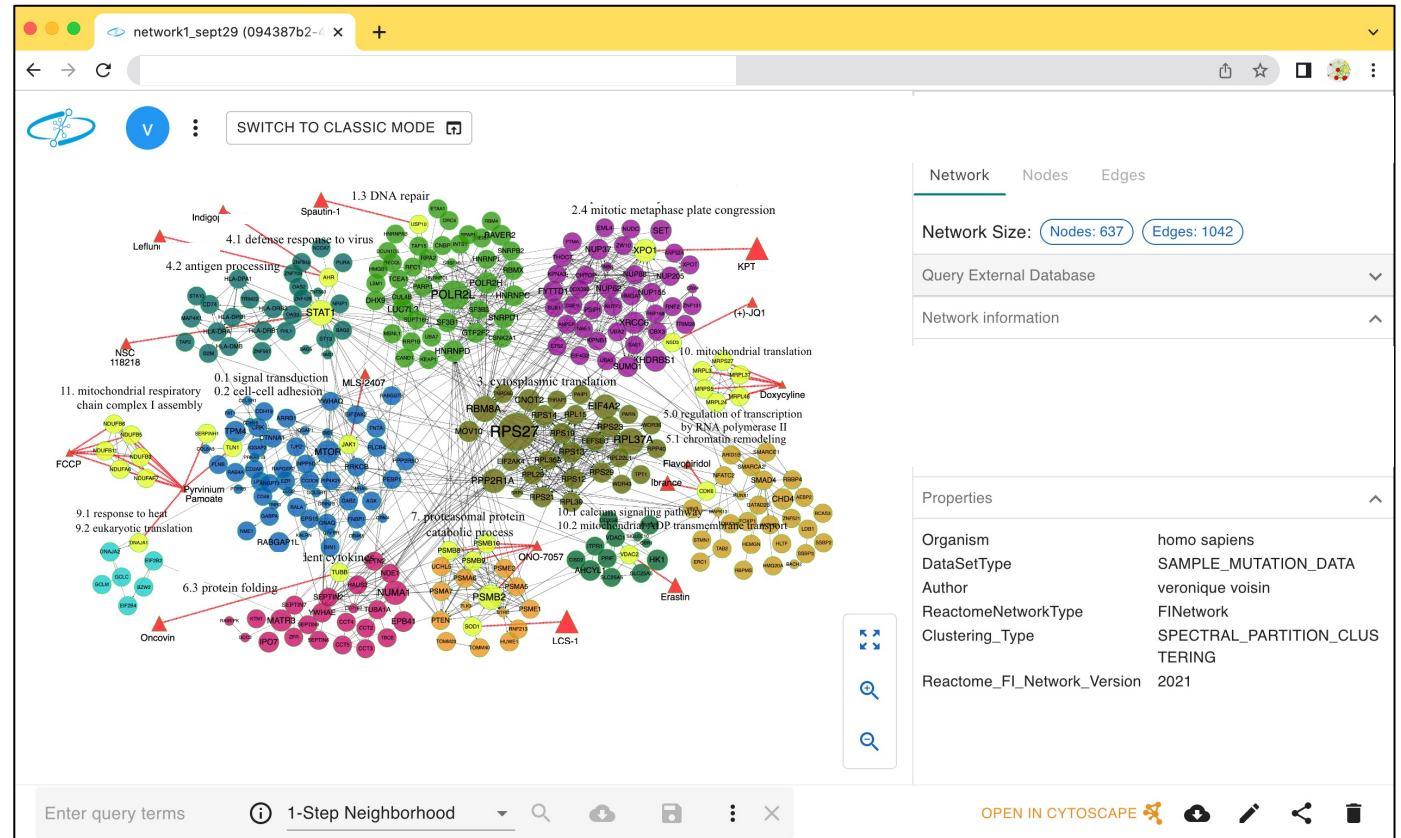
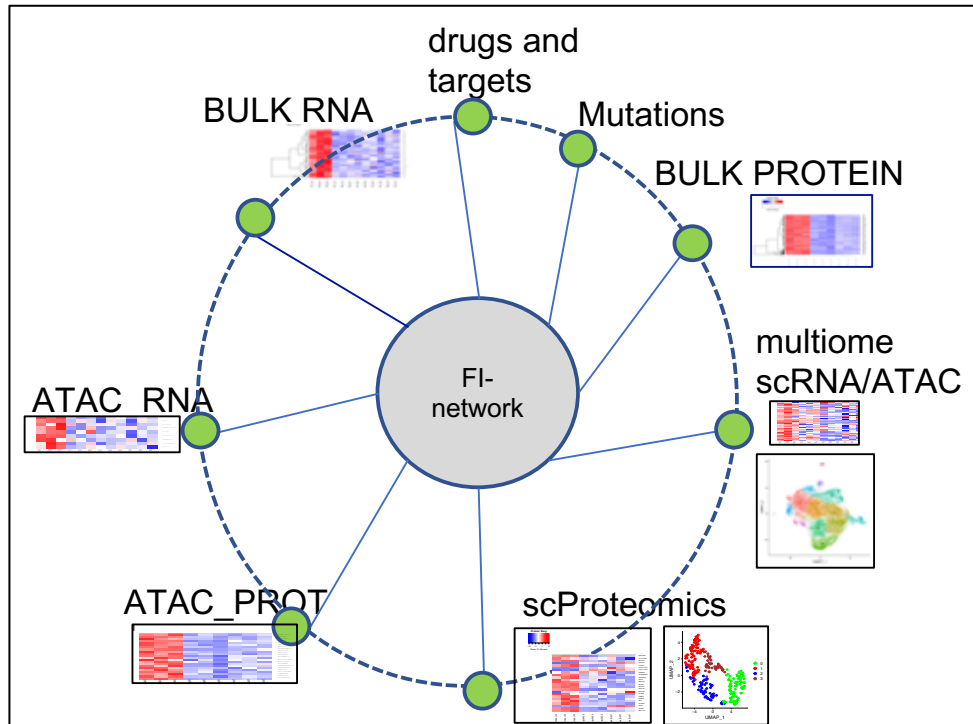
----Output----

Note: Click underlined modules in blue for single module-based analysis. You may not see any underlined module if all p-values > 0.05.

Module	Coefficient	P-value
<u>0</u>	<u>-0.6142421</u>	<u>0.0015</u>
<u>1</u>	<u>1.308675</u>	<u>2.7e-10</u>
<u>2</u>	<u>0.4908374</u>	<u>0.015</u>
3	0.3854999	0.071
4	0.1916897	0.38
<u>5</u>	<u>1.015691</u>	<u>4.4e-07</u>
6	-0.06630745	0.71
7	-0.01376751	0.94
8	0.4978022	0.053
<u>9</u>	<u>0.948809</u>	<u>3.8e-06</u>
<u>10</u>	<u>0.6773846</u>	<u>0.024</u>
11	0.09736692	0.61
<u>12</u>	<u>-0.6155788</u>	<u>0.00033</u>

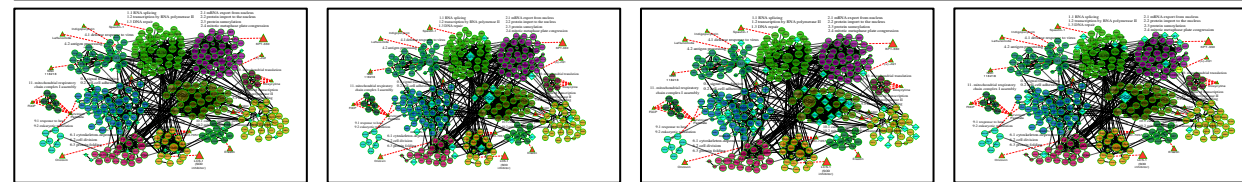


One example of use of Reactome FI VIZ



Get gene lists specific to a pure population extracted from the same experiment from different omics data:

- the omics lists have few direct overlaps but the genes might connect with each other if they are put in the same FI network.



scRNA

scPROT

ATAC

RNA

We are on a Coffee Break & Networking Session

Workshop Sponsors:



Canadian Centre for
Computational
Genomics



HPC4Health



GenomeCanada