

# Canadian Bioinformatics Workshops

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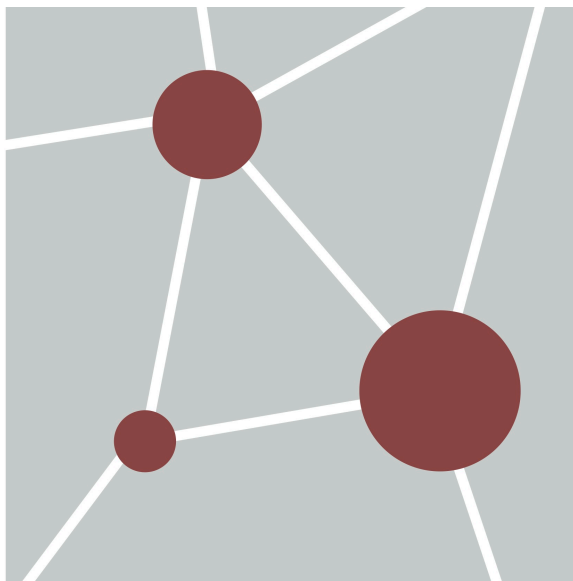
# More Depth on Pathway & Network Analysis

## Reactome FI practical lab

Veronique Voisin

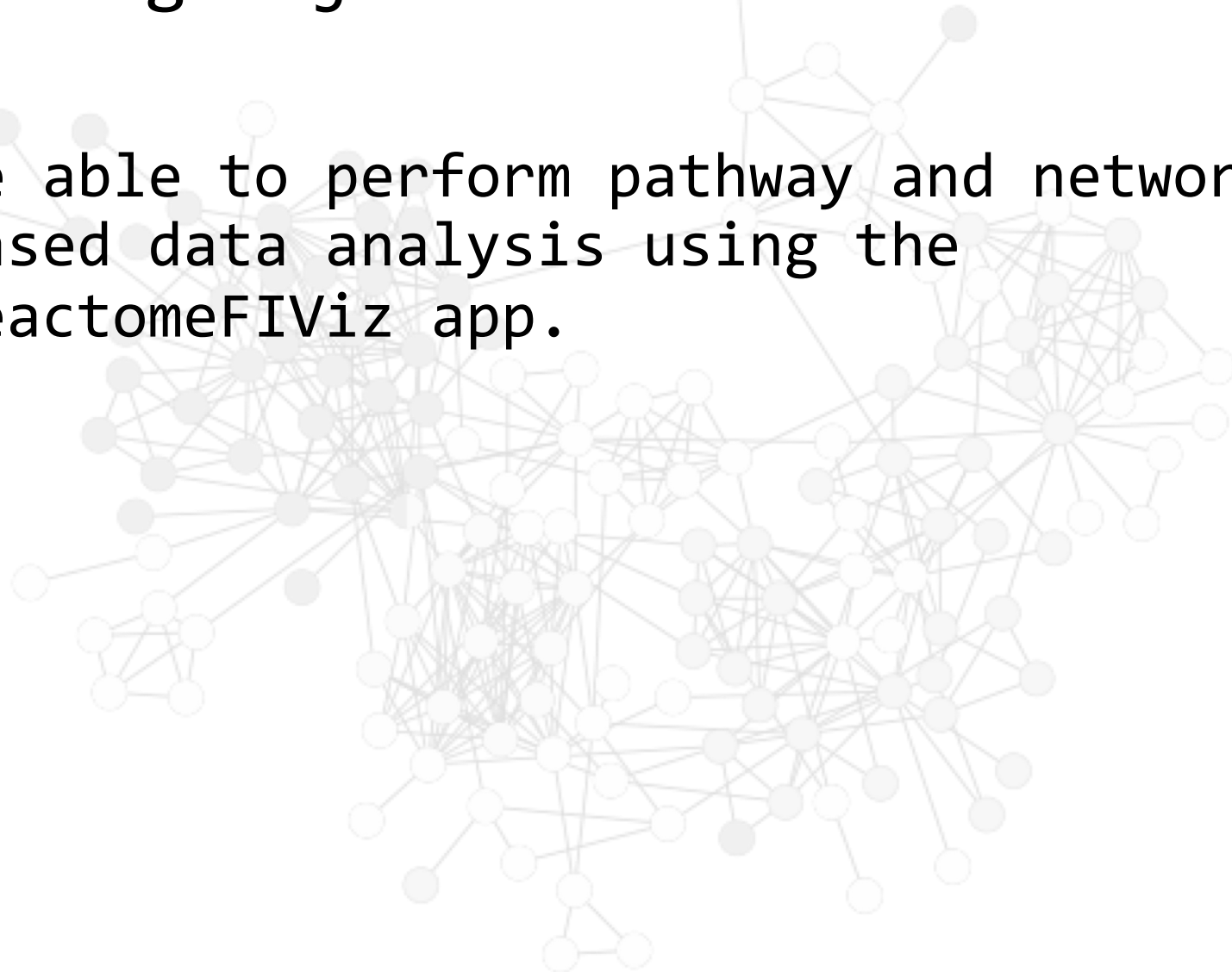
Pathway and Network Analysis

June 5-7, 2023



# 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.

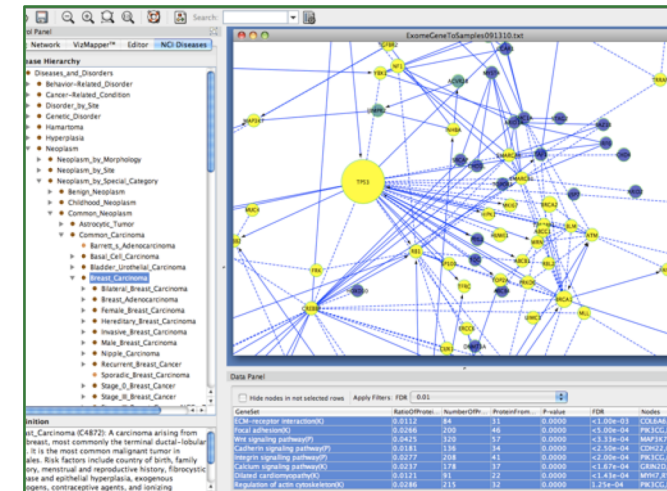
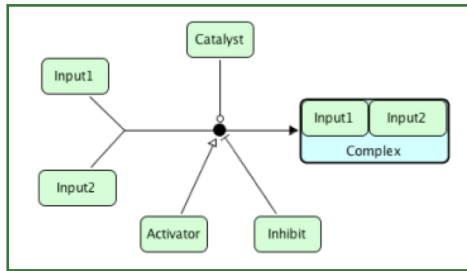
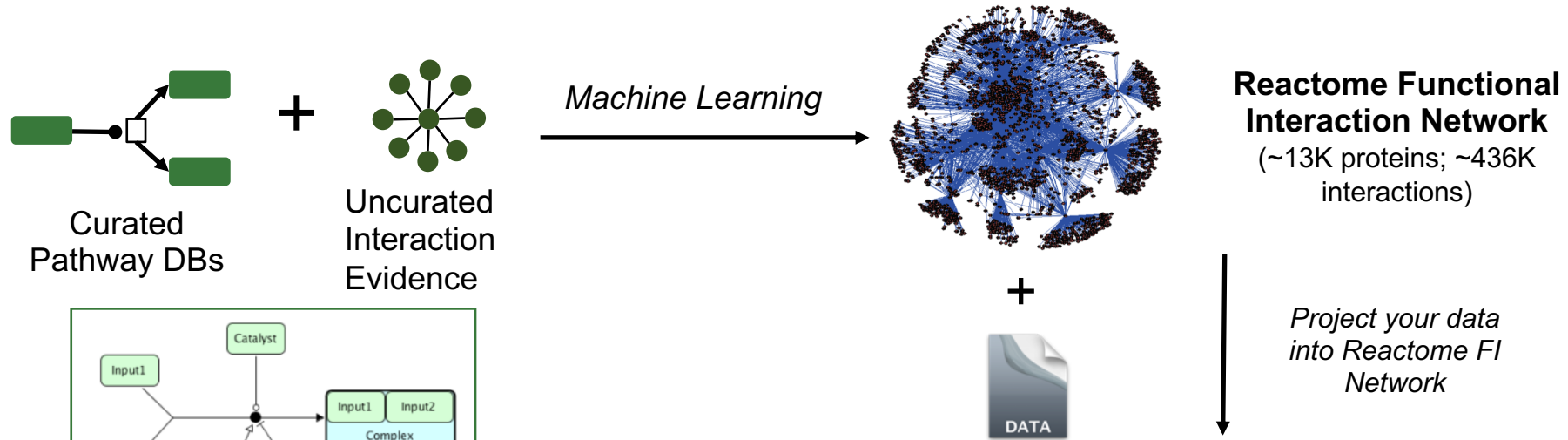
This app accesses **the Reactome pathways** stored in the database. It can:

- 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**. It can:

- 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

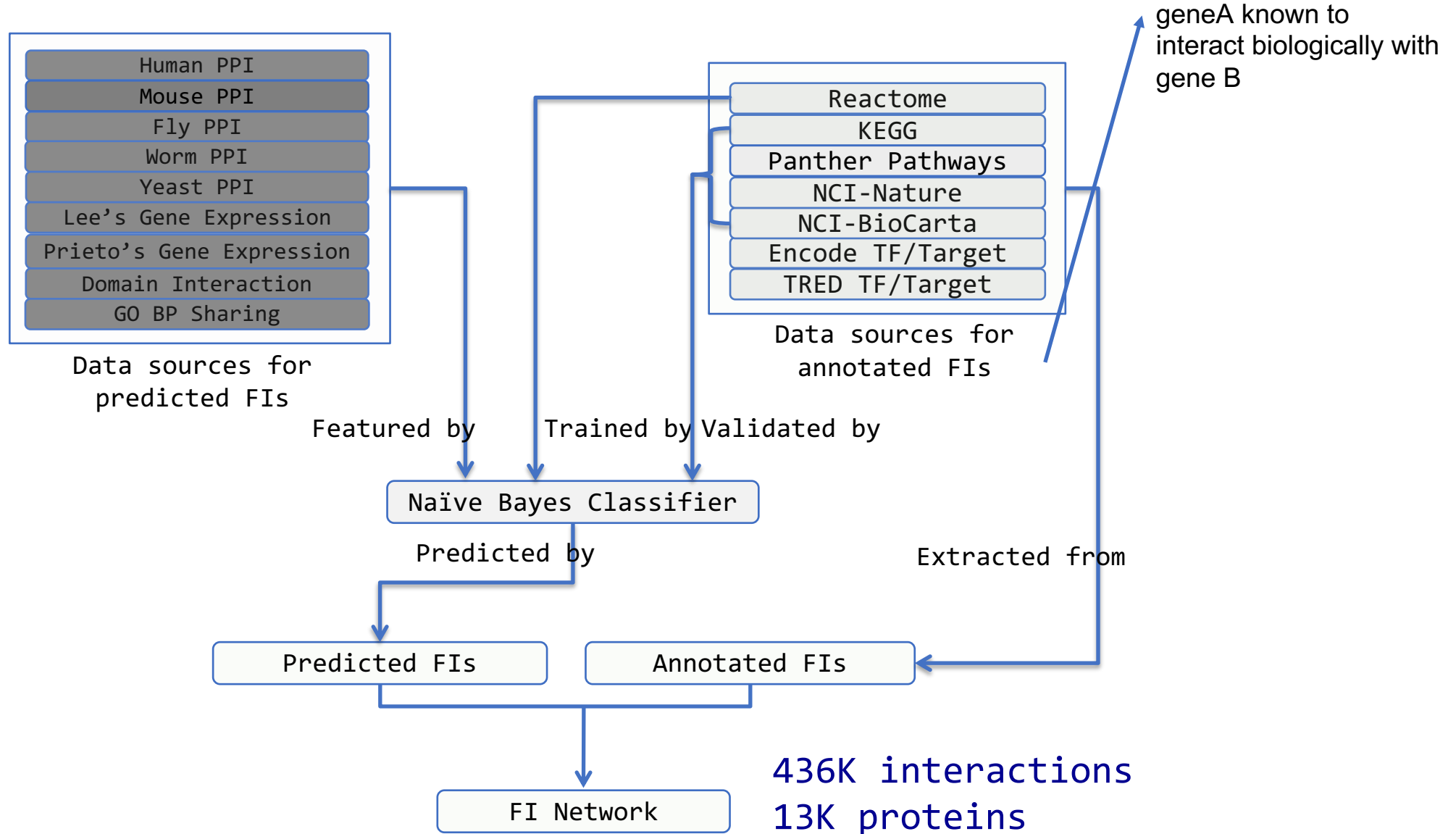


Cytoscape using ReactomeFIViz app

## What is a Functional Interaction?

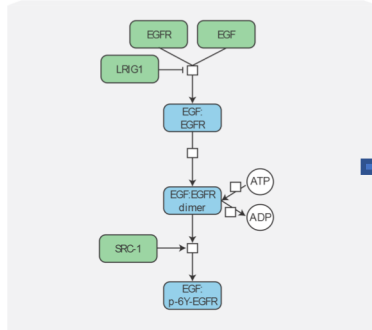
- Convert reactions in pathways into pair-wise relationships
- **Functional Interaction:** an interaction in which two proteins are involved in the same reaction as input, catalyst, activator and/or inhibitor, or as components in a complex

# Construction of the FI Network

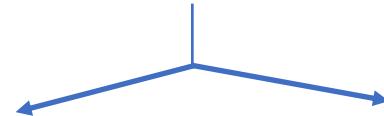
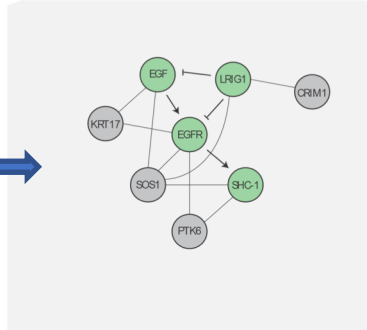


# ReactomeFIViz (ReactomeFIPlugin): pathway AND network analysis

Pathway diagram



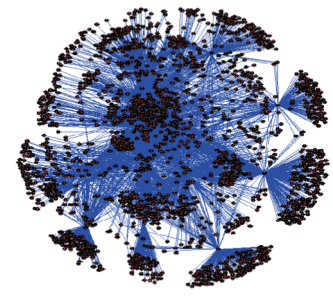
Network



Your gene list



- 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

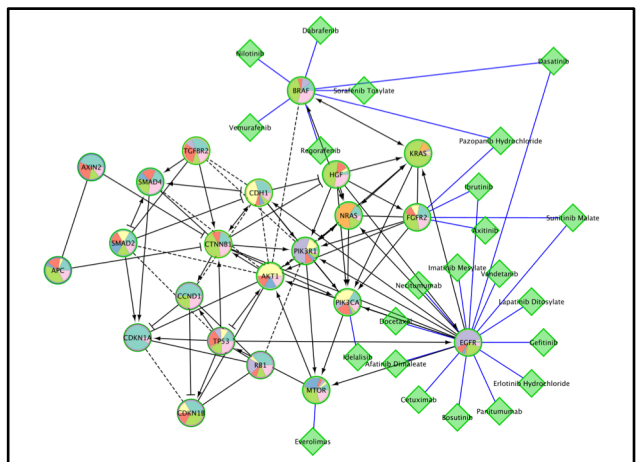


**Reactome Functional Interaction Network**  
(~13K proteins; ~436K interactions)

Your gene list



Create a FI network

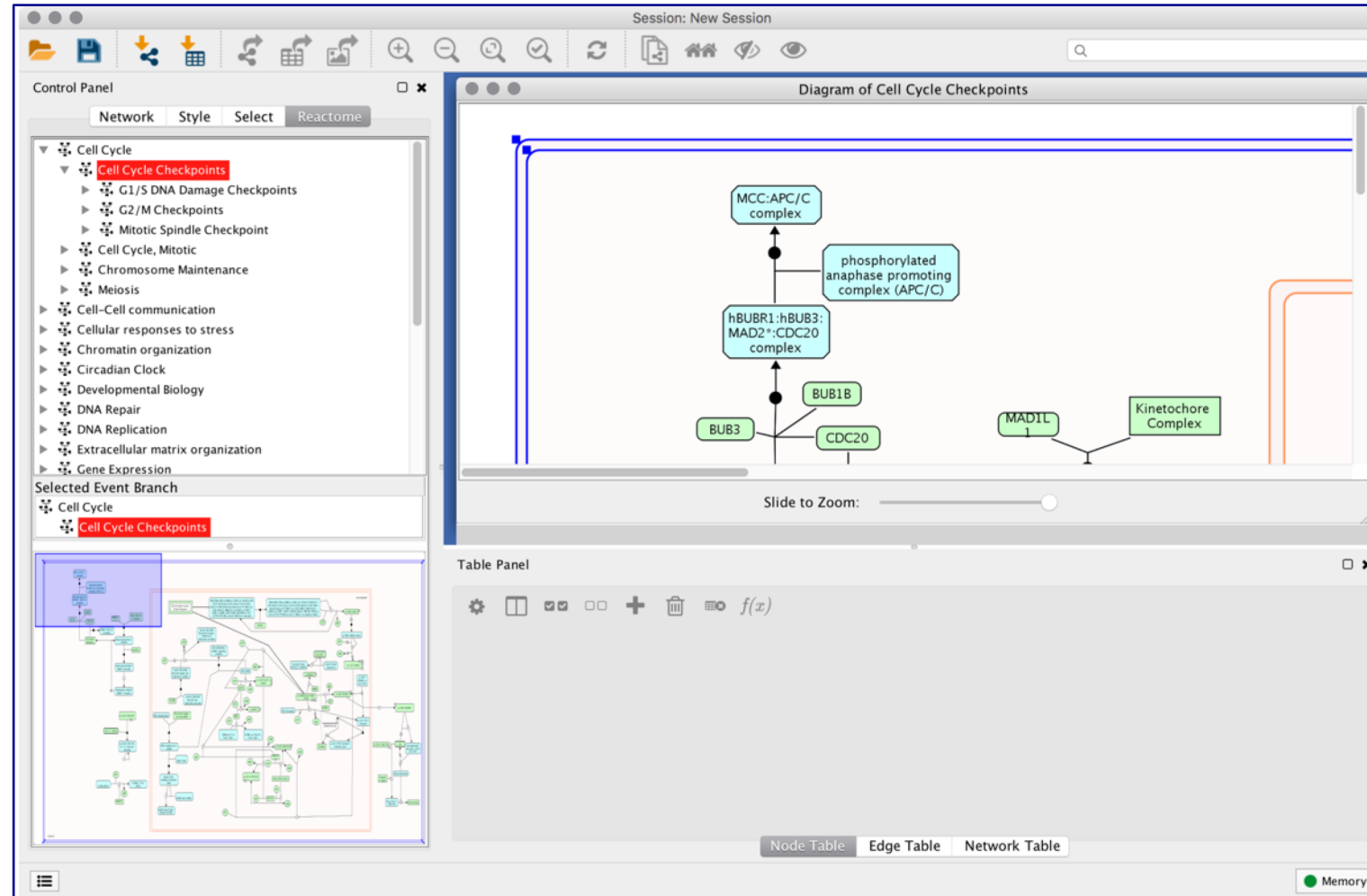


- Create a FI network using your gene list :
- Genes in your list will be connected by functional interactions.
- You can: further cluster your FI network to find protein complexes
- You can perform pathway analysis on the whole network.
- You can perform pathway analysis on the individual modules and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

And more...



# Reactome: Collection of Pathways



# Pathway Enrichment Analysis (gene list) binomial test

Control Panel

Network Style Select Reactome

FDR:  >=0.1  >=0.01  >=0.001  <0.001

- Interleukin-7 signaling (FDR: 0.091)
  - IL7 binds HGF(495-728)
  - IL7R binds JAK1
  - IL2RG binds JAK3
  - IL7 binds IL7R:JAK1
  - IL7:IL7R:JAK1 binds IL2RG
  - IL7R is phosphorylated on
  - IL7-p-Y449-IL7R:JAK1:IL2R
  - IL7-p-Y449-IL7R:JAK1:IL2R
  - IL7-p-Y449-IL7R:JAK1:IL2R
  - Interleukin-11 receptor alpha
  - Interleukin-11 receptor alpha
  - IL27 is a dimer of IL27A and IL
  - IL27 binds IL27RA:gp130
- Immune System (FDR: 0.291)
- Cytokine Signaling in Immune S
- Signaling by Interleukins (FDR: 0.091)
  - Interleukin-7 signaling (FDR: 0.091)

Selected Event Branch

Reactome Pathway Enrichment

Gene Set Loading

Choose a gene set file:

Specify file format:

- One gene per line
- Comma delimited (e.g. TP53, EGFR)
- Tab delimited (e.g. TP53 EGFR)

Table Panel

Apply Filters: 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	GABBR2,GNAT3,GAB...
Mitotic Prometaphase ...	0.0139	99	12	0.0131	0.1016	KNTC1,NDE1,PD55B,...
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,TGFBR2...

Node Table Edge Table Network Table Reactome Pathway Enrichment

Memory

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

The image displays the Reactome GSEA Analysis interface. The main window shows a detailed diagram of cell cycle checkpoints in the nucleoplasm, with various proteins and their interactions. A color scale at the bottom indicates gene scores from 75 (green) to 2.75 (red).

The Results Panel on the right shows the following table:

Gene	Score	Rank
CDK2	3.358	5
WEE1	2.743	29
CENPT	2.343	103
CCNA2	2.224	130
PCBP4	2.087	204
MCM3	2.032	235
CLASP1	1.969	271
NSD2	1.751	442
RPA1	1.677	540
ANAPC4	1.668	553
YWHAH	1.424	938
CDC20	1.338	1125
CKAP5	1.329	1136
SGO1	1.324	1147
CDC23	1.277	1263
KIF2A	1.265	1295
ATR	1.129	1633
KDM4A	1.123	1657
MCM5	1.092	1744
CDC7	1.061	1824
XPO1	1.008	1961
RAD17	1.003	1976
YWHAE	0.992	2013
EXO1	0.989	2025
CDC16	0.972	2078
CCNA1	0.905	2317
KNTC1	0.903	2323
HERC2	0.897	2347
ANAPC5	0.883	2398
ITGB3BP	0.867	2458
NUP133	0.849	2520
CENPK	0.822	2630
ORC2	0.777	2774
ZNF385A	0.769	2802

The configuration dialog box in the bottom left is titled "Reactome GSEA Analysis" and contains the following settings:

- Choose a gene score file: [Browse]
- Note: The gene score file should contain at least two tab-delimited columns, first for human gene symbols and second for scores. The first row should be for column headers.
- Choose pathways having sizes: Minimum: 5, Maximum: 1000
- Set number of permutations: 100

# Visualize Cancer Targetome in Reactome Pathways

Diagram of Cell Cycle Checkpoints

Control Panel

- Cell Cycle
  - Cell Cycle Checkpoints
    - G1/S DNA Damage Checkpoints
    - G2/M Checkpoints
      - G2/M DNA damage checkpoint
      - G2/M DNA replication checkpoint
      - Activation of ATR in response to replication stress
        - Stalling of DNA replication fork and RPA binding
        - Binding of ATR-ATRIP to the RPA-ssDNA complex
        - Recruitment of Rad17-RFC complex to DNA
        - Recruitment of the Rad9-Hus1-Rad1 complex to C
        - Loading of claspin onto DNA during replication or
        - Activation of claspin
        - Recruitment and activation of Chk1
        - Phosphorylation of Cdc25A at Ser-123 by Chk1
        - Phosphorylation of Cdc25C at Ser 216 by Chk1
        - GTSE1 binds TP53
        - GTSE1 promotes translocation of TP53 to the cytosol
        - GTSE1 facilitates proteasome-mediated degradation of
      - 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
    - Gene Expression
    - Hemostasis
    - Immune System
    - Mitophagy
    - Metabolism

Selected Event Branch

- Cell Cycle
  - Cell Cycle Checkpoints

Table Panel

Drag table files here

Node Table Edge Table

Memory

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

# Displaying Reactome Pathways in the FI Network View

The screenshot displays the FI Network View interface for a Reactome pathway. The main window shows a network diagram with nodes representing proteins and their interactions. A control panel on the left provides a hierarchical tree view of the pathway, with 'Mitotic Spindle Checkpoint' selected. Below the tree is a detailed diagram of the hBUBR1:hBUB3:MAD2::CDC20 complex and its interactions with BUB1B, BUB3, and CDC20. A table panel at the bottom lists various entities with columns for shared name, name, module, commonName, nodeToolTip, and nodeLabel. A context menu on the right offers options for network conversion, analysis, and visualization.

**Control Panel**

- Network
- Style
- Select
- Reactome

**Selected Event Branch**

- 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

**Table Panel**

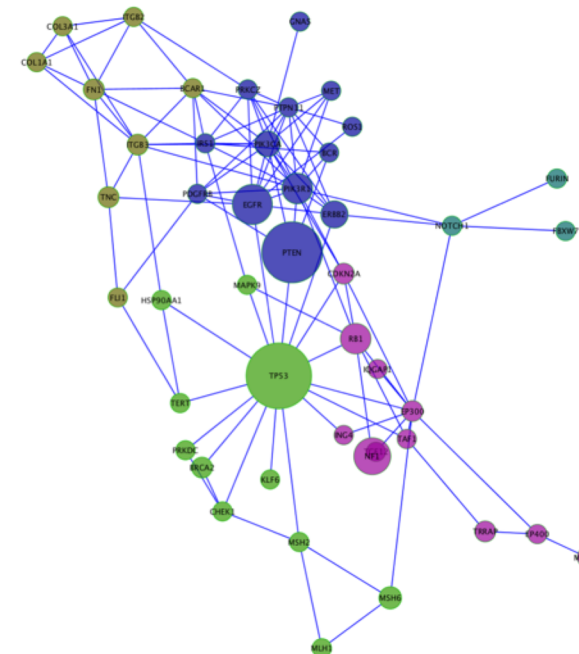
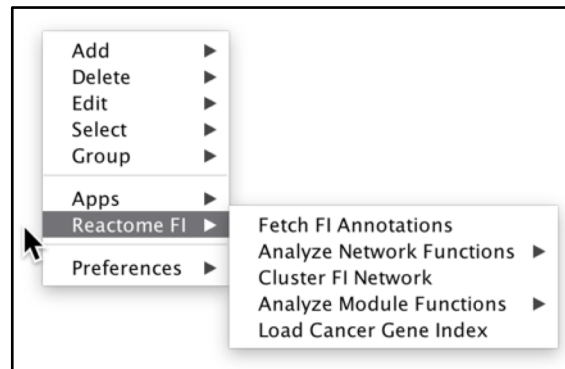
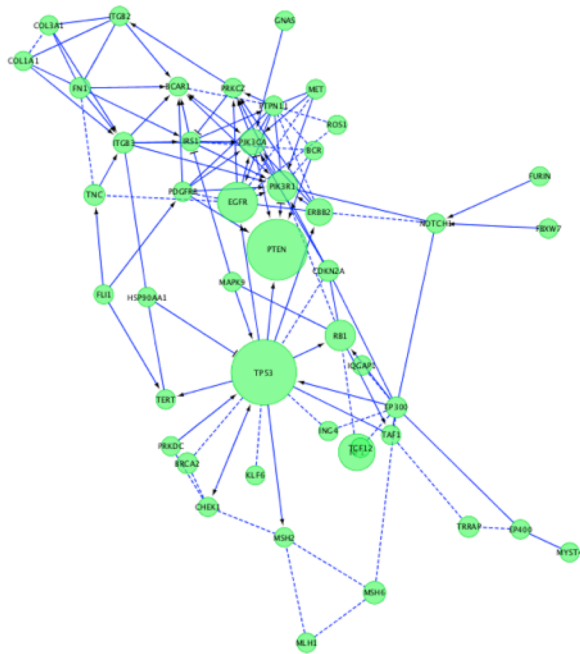
shared name	name	module	commonName	nodeToolTip	nodeLabel
BABAM1	BABAM1	BABAM1	BABAM1	BABAM1	BABAM1
BRCA1	BRCA1	BRCA1	BRCA1	BRCA1	BRCA1
PSMB1	PSMB1	PSMB1	PSMB1	PSMB1	PSMB1
PSME2	PSME2	PSME2	PSME2	PSME2	PSME2
HERC2	HERC2	HERC2	HERC2	HERC2	HERC2
HIST3H2BB	HIST3H2BB	HIST3H2BB	HIST3H2BB	HIST3H2BB	HIST3H2BB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

**Context Menu**

- 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

# 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

## 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
FERM13	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
.....		

## 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	+
LRRRC41	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

## 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	0.348692236	-0.093947168	-0.56890295	0.177455762	-0.30793794	-0.574121582	-0.772454492	0.850743799	0.19832391
CPFB3	-0.628846878	-0.519774777	0.200101088	-0.388882356	-0.44005917	-0.549131811	-0.44005917	-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	-0.01430138	-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	0.327289133	-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	-0.741461062	0.636779988	-0.695953625	-0.46841374	-0.344892088	-1.130354482	-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	-0.773868442	0.110633726	1.270499777
NUDT5	-0.166643202	-0.117594702	0.072831699	-0.025664715	0.37488737	0.433985219	-0.898995959	0.020300278	0.112230265
VT11B	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	-1.08384904	1.698904754	1.844724649	-0.038782325	-1.545587905
ZCCHC2	0.55864339	0.120590563	0.845270548	-0.479704052	0.477524096	-1.144895382	-0.39883158	0.5323533	-0.095731821
DDX1274	-0.291416641	-0.264217345	0.134705668	-0.527143876	-0.073822271	-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

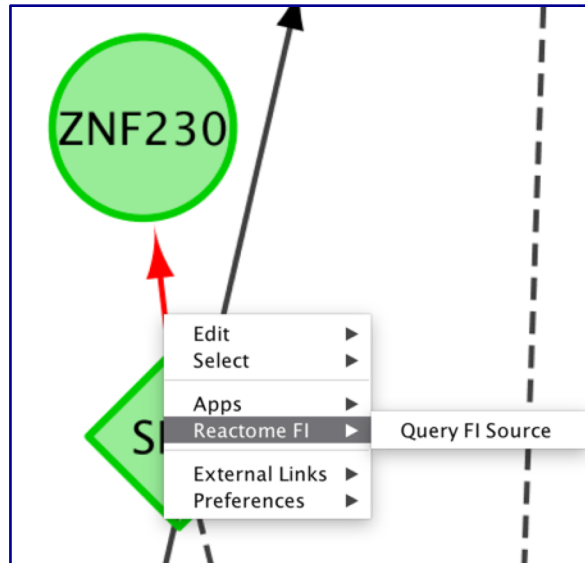
The screenshot displays a software interface for network visualization. The main window, titled "LAC\_genelist.txt", shows a dense network graph with green circular nodes and black edges. A "Control Panel" on the left lists the network "LAC\_genelist.txt" with 238 nodes and 920 edges. Below the graph is a "Table Panel" showing a table of node data. A red box highlights a context menu over the graph, with the "Reactome FI" option selected, opening a sub-menu with various analysis options.

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

Interaction Info  
Interaction: SIX5 - ZNF230

Reactome Sources

Reactome ID	Type	Data Source
6951674	TARGETED_INTERAC	ENCODE

View Reactome Source

Reactome Instance View

classType	TargetedInteraction
dbId	6951674
displayName	SIX5 ZNF230
dataSource	<a href="#">ENCODE</a>
definition	ENCODE proximal_filtered TF/target interaction; supported by GO BP sharing
factor	<a href="#">SIX5</a>
species	<a href="#">Homo sapiens</a>
target	<a href="#">ZNF230</a>

Close

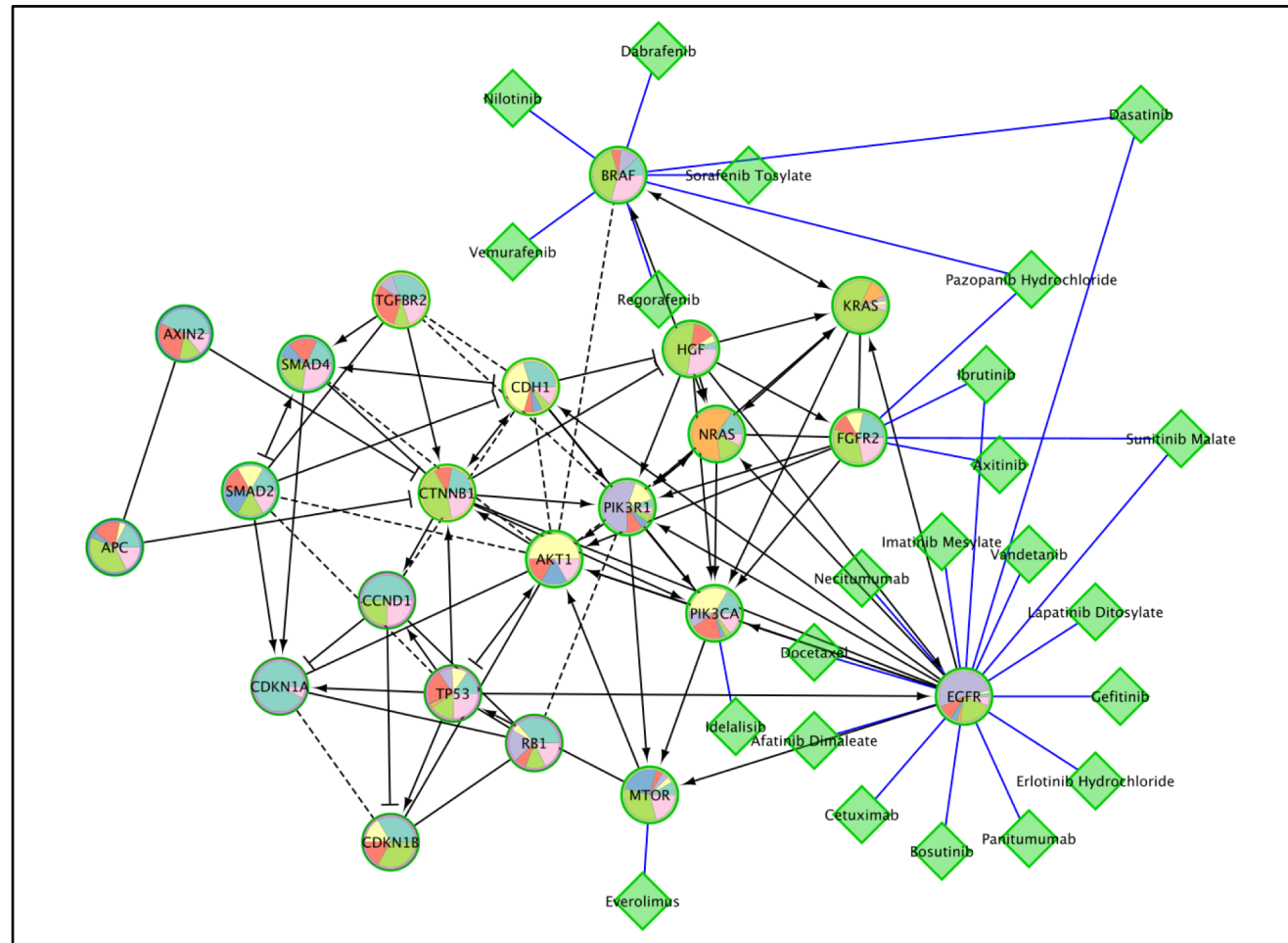
## Predicted FIs

Interaction Info  
Interaction: SNX4 - SNX6

Support 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, the 'Control Panel' shows a 'Disease Hierarchy' tree with 'Papillary\_Breast\_Neoplasm' selected. The main window shows a network diagram with nodes and edges. A context menu is open over a node, listing options like 'Add', 'Edit', 'Select', 'Group', 'Nested Networks', 'Apps', 'Reactome FI', 'External Links', and 'Preferences'. The 'Table Panel' at the bottom shows a table of modules and gene sets.

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-1 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

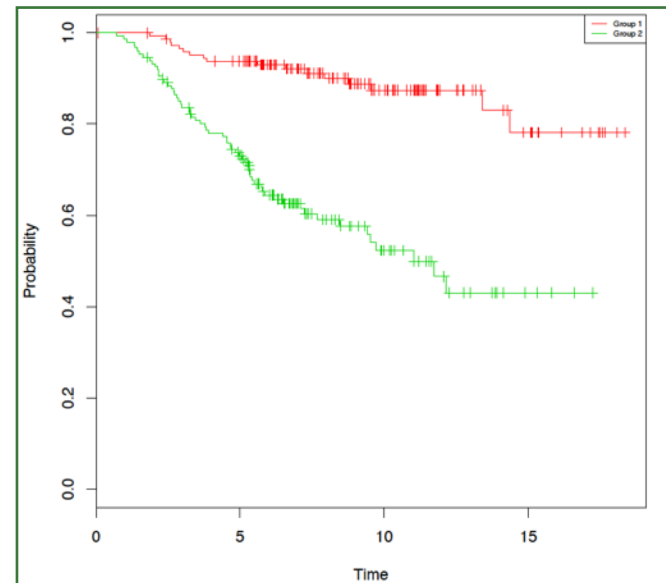
Survival Analysis

Analysis: Coxph (all modules)

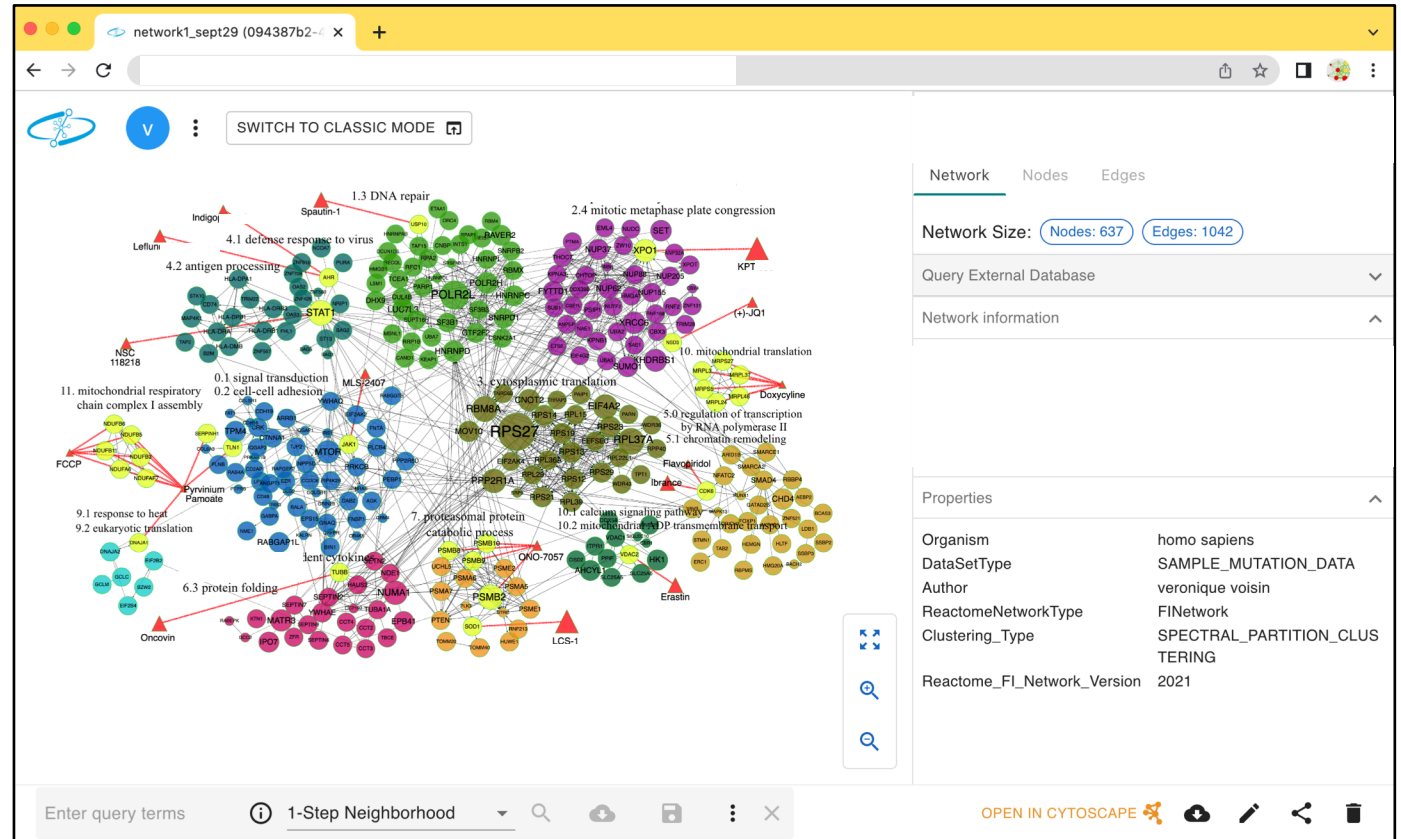
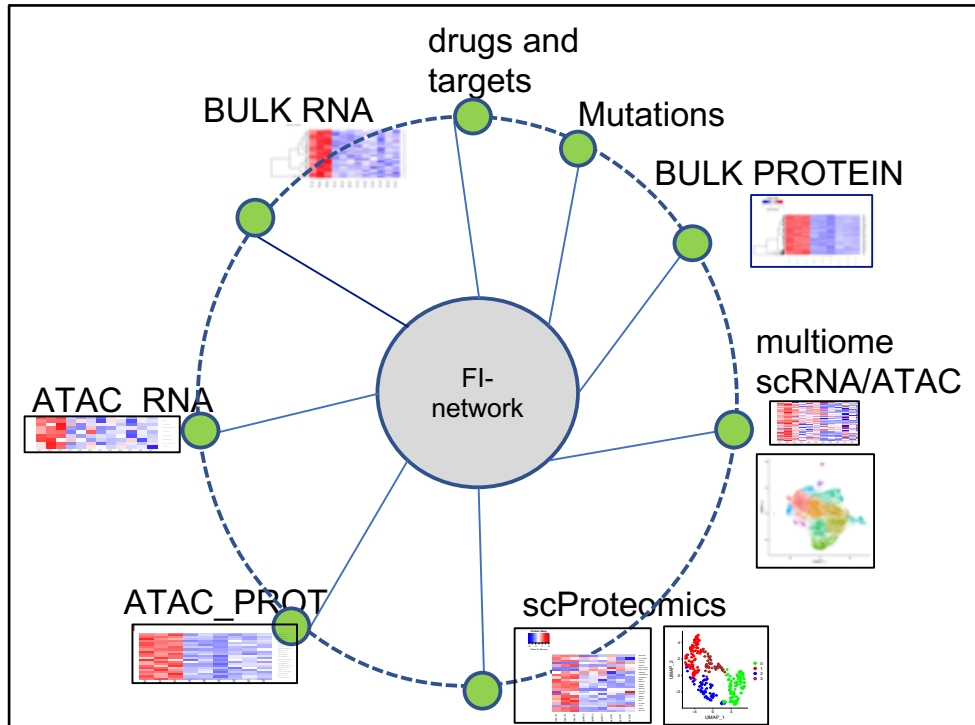
----Output----

*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>

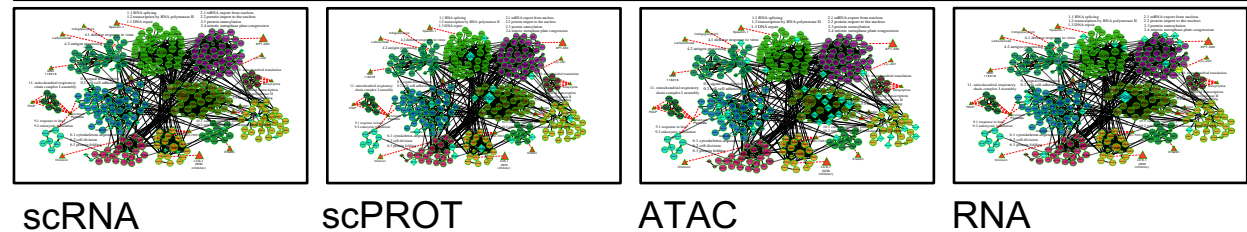


# One example of use of Reactome FI VIZ



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.



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