

Cyni

*The Cytoscape Network Inference
(Cyni) toolbox for gene regulatory
network inference*



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Paris



Cytoscape

Cytoscape

- Open source platform for biological network data **integration, analysis, and visualization**
 - Free! (Open source, LPGL)
 - Developed and maintained by universities, companies, and research institutions
 - Expandable by Apps/Plugins

Cytoscape Workflow

VizMapper
Layouts

Filtering
Selection

Data
import

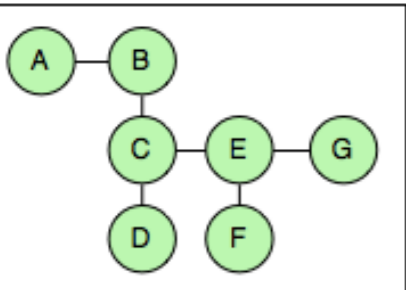
Data
export

Visualization

Human
analysis

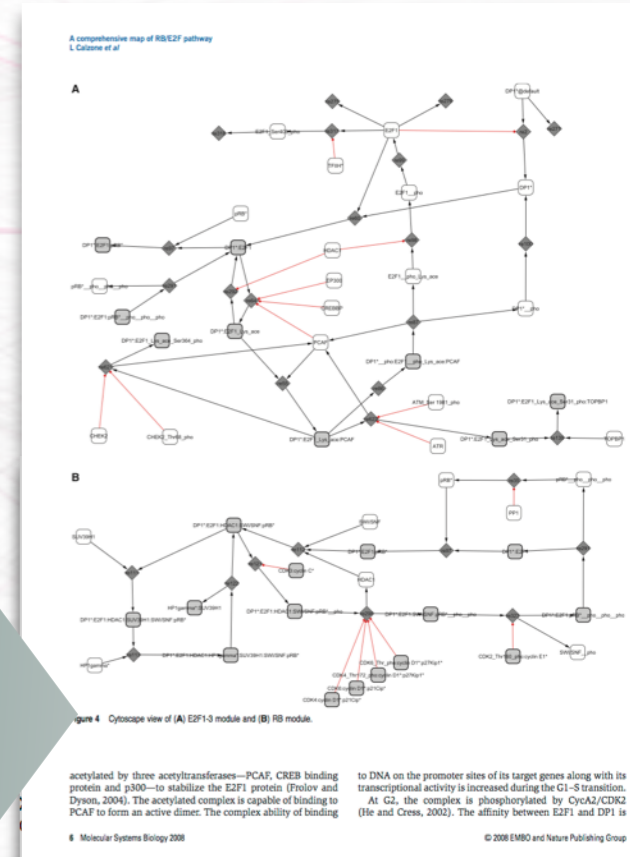
Computational
Analysis

Nodes and edges

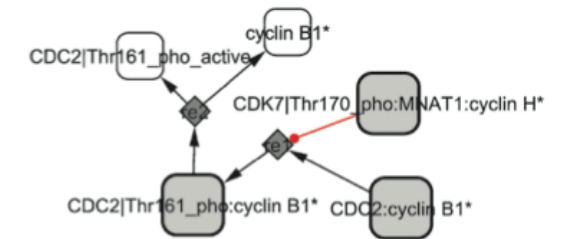


Attributes

	Numerical	Boolean
A	.1	true
B	.2	true
C	-.3	false
D	1.2	true
E	0.7	true
F	.1	false
G	1.3	false



Cytoscape (BiNoM) view



o Cytoscape. In Cytoscape, single proteins are represented by white squares and complexes

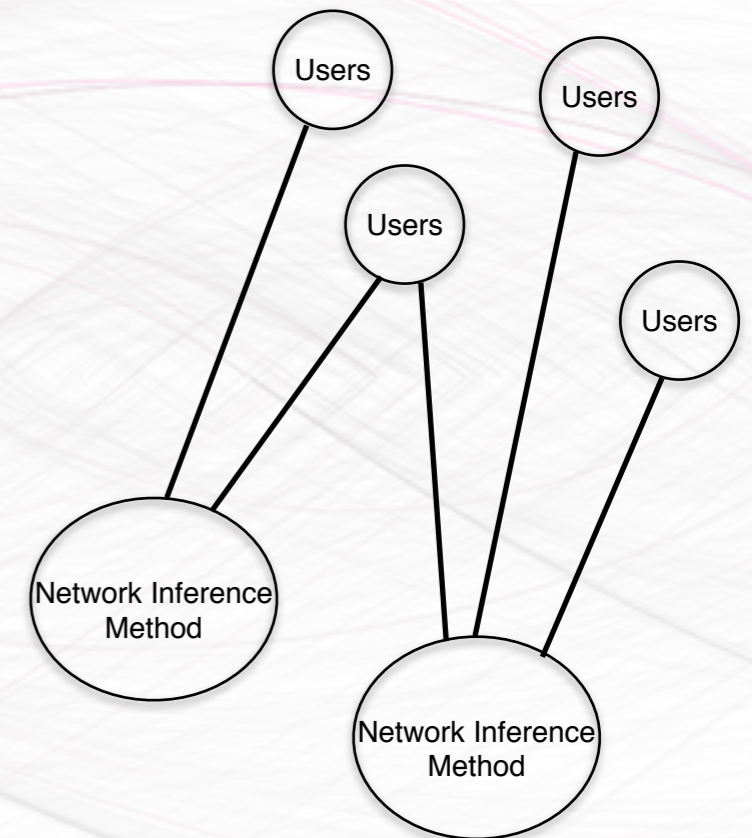


Paris, September 18, 2014

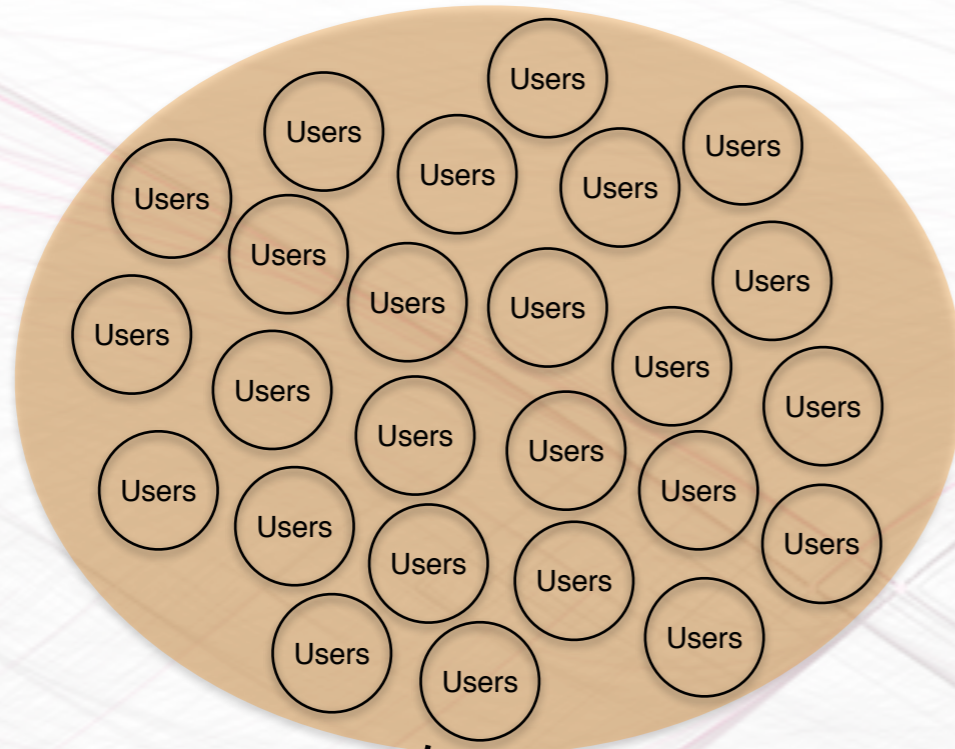


Why Cyni

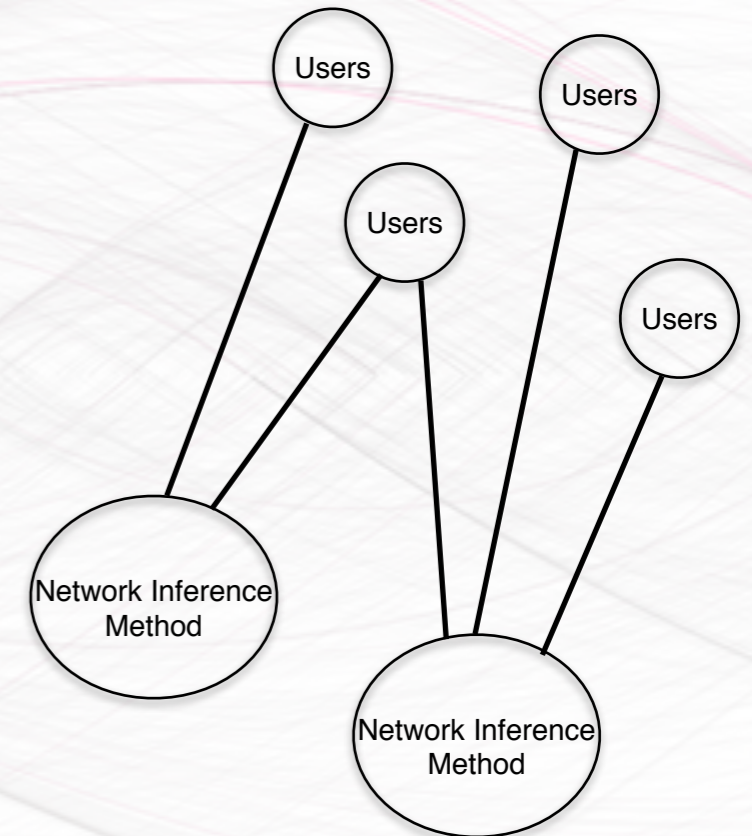
Why Cyni



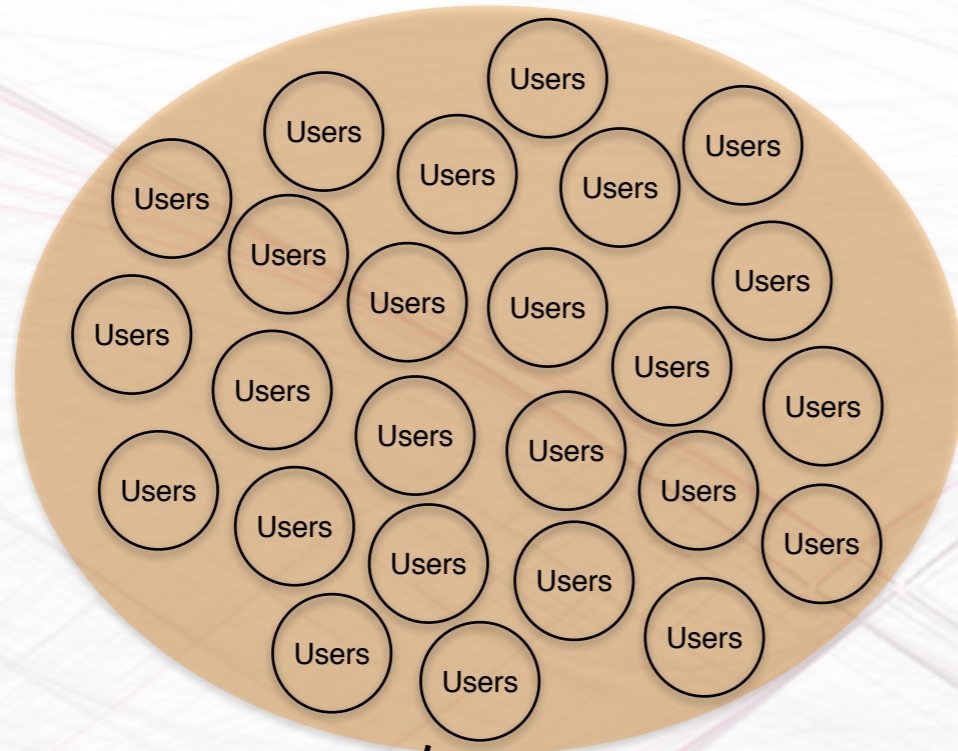
Why Cyni



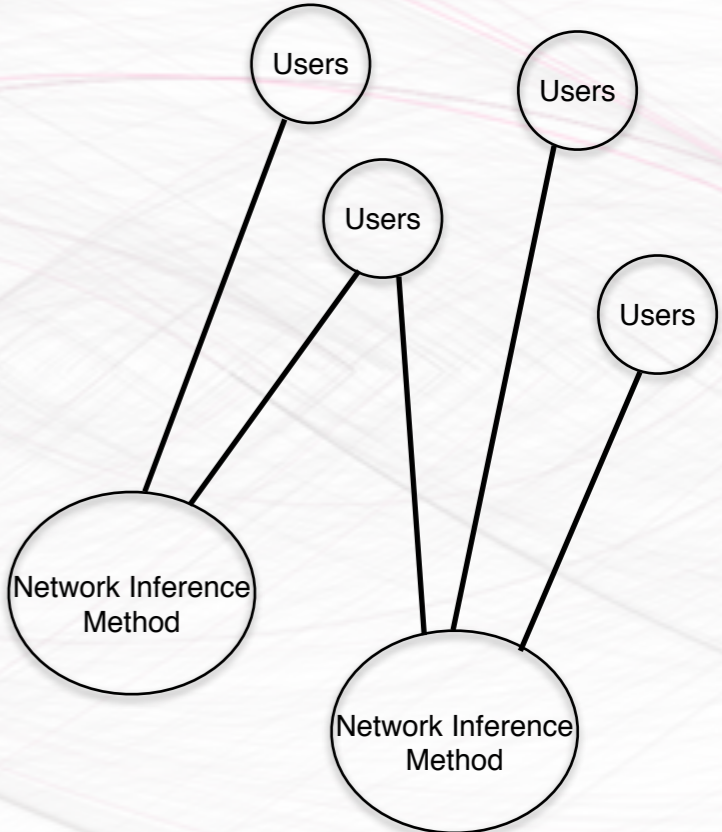
Cytoscape



Why Cyni

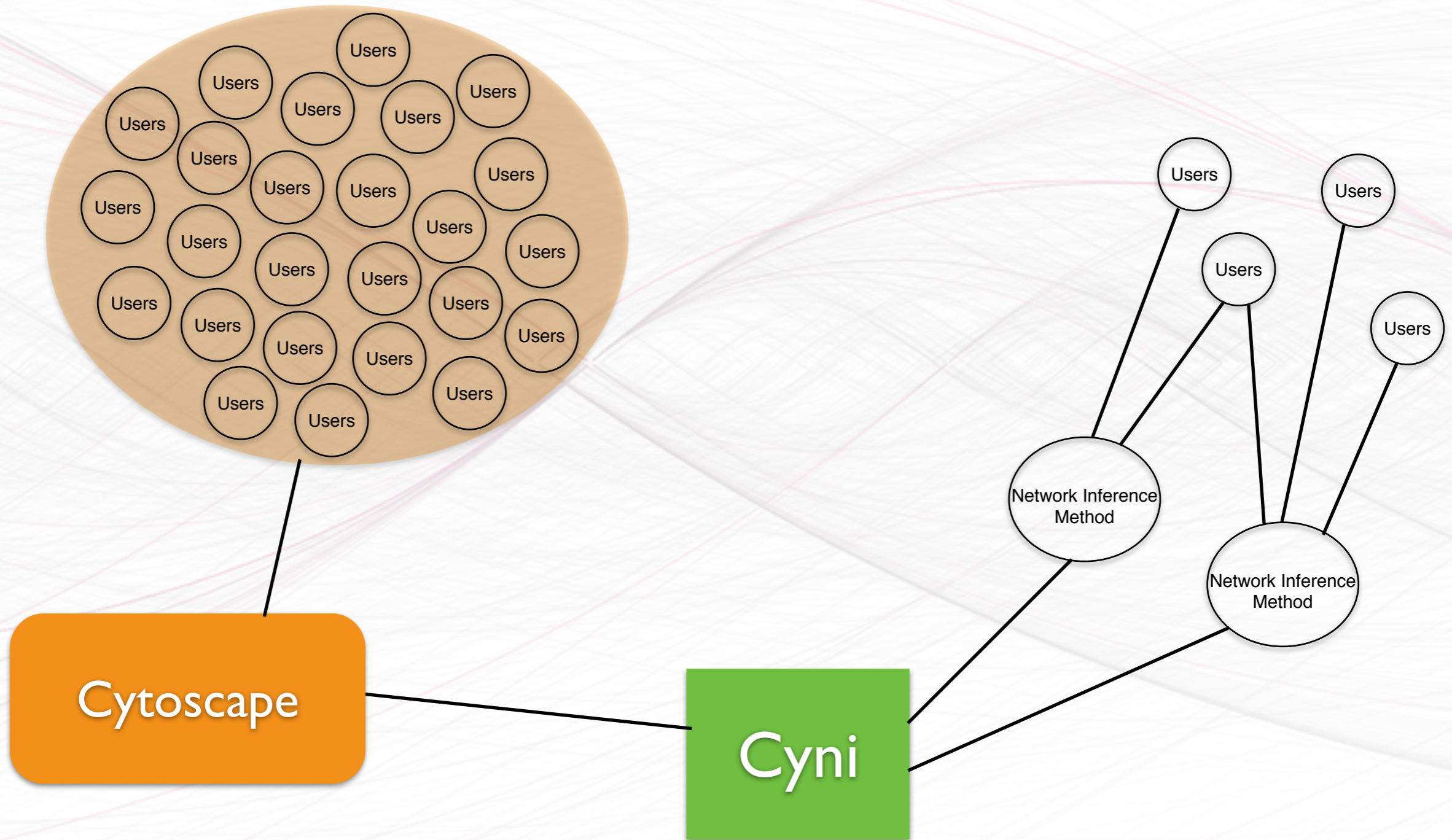


Cytoscape



Cyni

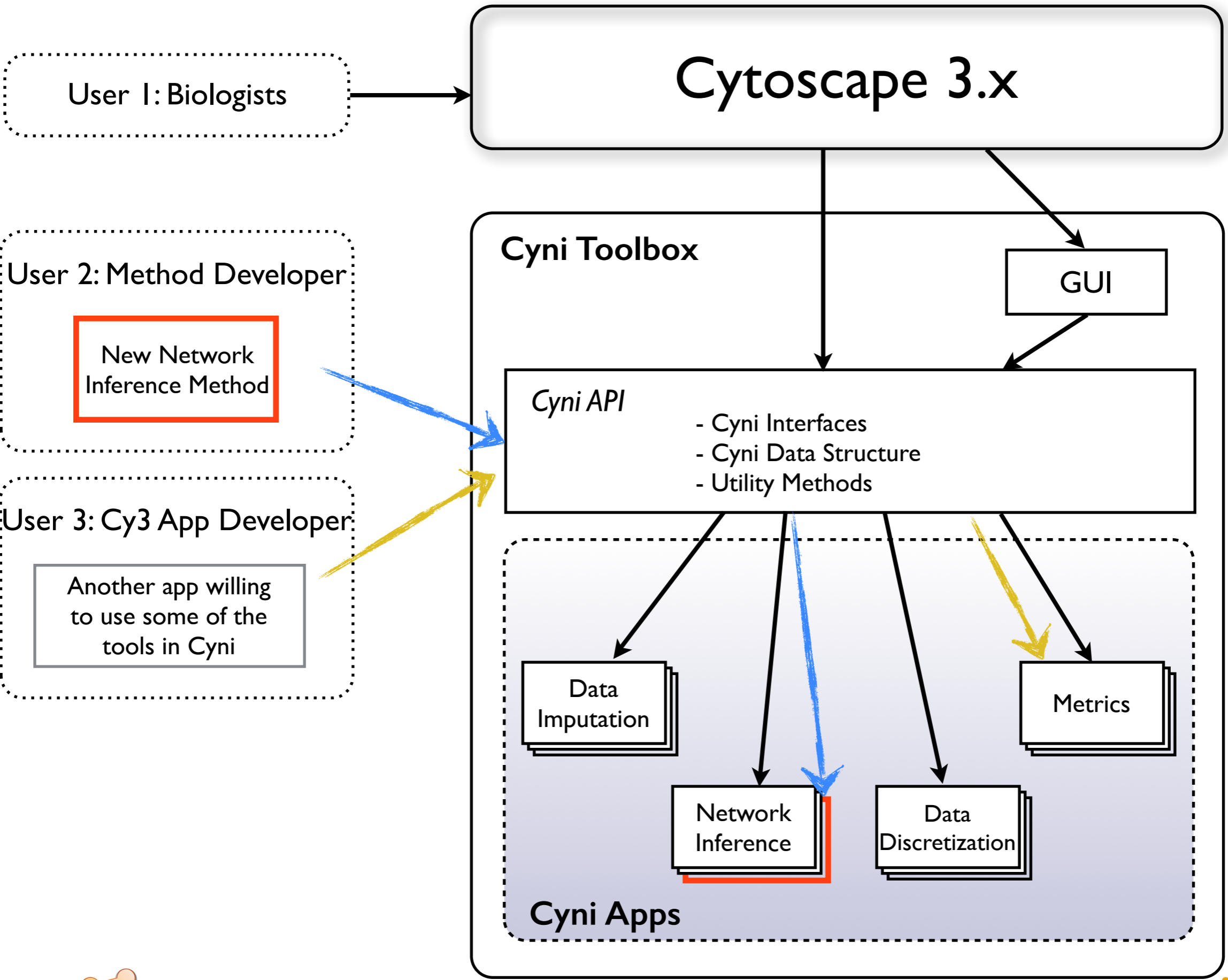
Why Cyni



Cyni Toolbox App

- To biologists:
 - Cyni is a collection of tools for network inference
- To bioinformaticians and inference researchers:
 - Cyni is a framework that supports and simplifies implementation of new network inference algorithms
- First 3.x app that exports functionality
- Cyni provides
 - Several commonly used network inference techniques
 - Data imputation and discretization techniques
 - Several known metrics (correlation, bayesian,...)
 - Documented API
 - Tutorials and sample code





How to get Cyni

- <http://apps.cytoscape.org/cynitoolbox>



Cyni Toolbox

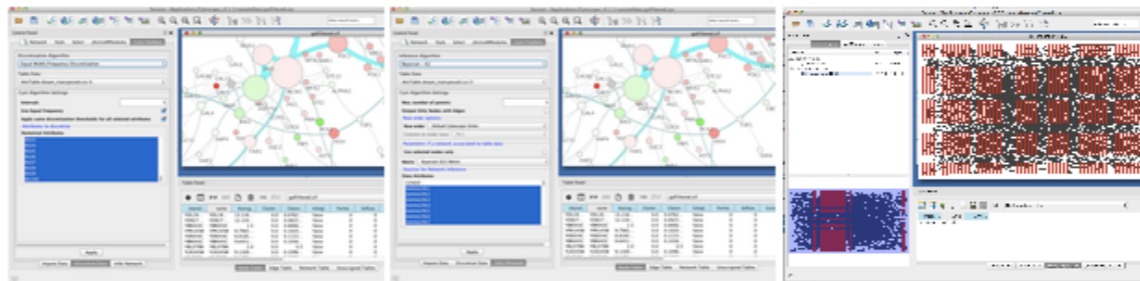
Cytoscape Network Inference Toolbox puts together several tools that allow inferring networks from bio data (Requires Cytoscape 3.1.x)

★★★★★ (22) 2660 downloads 3.0+

Details

Release History

Categories: [attribute generation](#), [bayesian networks](#), [data discretization](#), [data manipulation](#), [missing data estimation](#), [network generation](#), [network inference](#), [network learning](#)



Cytoscape Network Inference Toolbox (**Cyni**) is a new Cytoscape App that puts together several tools that allow inferring networks from biological data. Each of the tools can be used independently or together to perform several tasks.

The goal of Cyni is to make network inference more accessible to biologists by providing user-friendly solution as well as provide a framework to bio-informaticiens to develop and apply their new techniques. Data imputation and discretization techniques are provided along with several known inference algorithms to make this tool fully operational for any kind inference requirement. While data imputation and discretization techniques allow you modify Cytoscape tables, network inference algorithms produce a new network after applying the chosen technique.

Cyni provides:

CYTOSCAPE 3



Version 1.0.0.beta6

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Released 27 Jun 2014

Works with [Cytoscape 3.1](#)

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Cyni Toolbox

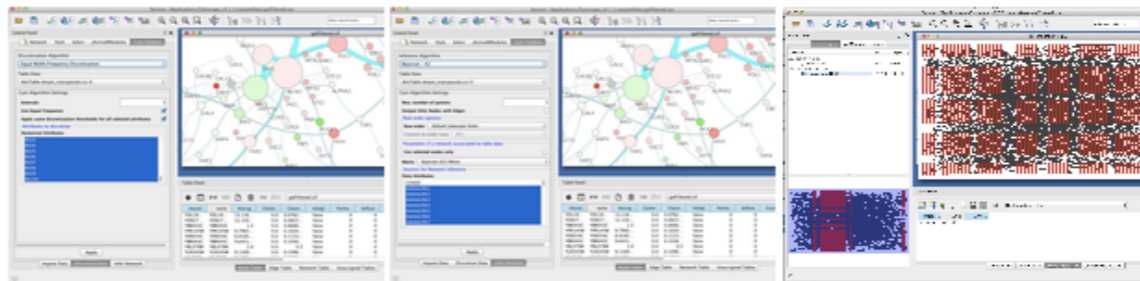
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How to use Cyni

Session: /Applications/Cytoscape_v3.1.1/sampleData/galFiltered.cys

Control Panel

Network | Style | Select | Cyni Toolbox

Inference Algorithm: Bayesian - K2

Table Data: galFiltered.sif default node

Cyni Algorithm Settings

Max. number of parents:

Output Only Nodes with Edges:

Row order options

Row order: Default Cytoscape Order

Column to order rows: SelfLoops

Parameters if a network associated to table data

Use selected nodes only:

Metric: Bayesian (K2) Metric

Sources for Network Inference

Data Attributes

- shared name
- name
- COMMON
- nominal.gal4RGexp
- nominal.gal80Rsig
- nominal.gal80Rexp

Apply

Impute Data | Discretize Data | Infer Network

galFiltered.sif

Table Panel

galFiltered.sif

shared...	name	Averag...	Cluster...	Closen...	IsSingl...	Partne...	SelfLo...	Eccent...	Stress	Degree
YDL19...	YDL19...	13.116...	0.0	0.0762...	false	0	0	26	0	1
YDR27...	YDR27...	12.120...	0.0	0.0825...	false	0	0	25	2722	2
YBR043C	YBR043C	1.5	0.0	0.6666...	false	0	0	2	0	1
YPR145W	YPR145W	9.7983...	0.0	0.1020...	false	0	0	18	0	1
YER054C	YER054C	8.8185...	0.0	0.1133...	false	0	0	19	11544	2
YBR045C	YBR045C	9.6451...	0.0	0.1036...	false	0	0	20	21474	3
YBL079W	YBL079W	2.0	0.0	0.5	false	0	0	3	0	1
YLR345W	YLR345W	9.1169...	0.0	0.1096...	false	0	0	19	0	1

Node Table | Edge Table | Network Table | Unassigned Tables

Memory: OK

How to use Cyni

The screenshot shows the Cytoscape v3.1.1 interface with the Cyni Toolbox highlighted in red. The main window displays a network graph titled 'galFiltered.sif' with nodes like MCM1, STE11, and SWI5. The Table Panel at the bottom shows a table of network metrics for various genes.

shared...	name	Averag...	Cluster...	Closen...	IsSingl...	Partne...	SelfLoo...	Eccent...	Stress	Degree
YDL19...	YDL19...	13.116...	0.0	0.0762...	false	0	0	26	0	1
YDR27...	YDR27...	12.120...	0.0	0.0825...	false	0	0	25	2722	2
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Data Attributes

- shared name
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- COMMON
- nominal.gal4RGexp
- nominal.gal80Rsig
- nominal.gal80Rexp

Impute Data | Discretize Data | Infer Network

galFiltered.sif

Table Panel

galFiltered.sif

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YDL19...	YDL19...	13.116...	0.0	0.0762...	false	0	0	26	0	1
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YBR043C	YBR043C	1.5	0.0	0.6666...	false	0	0	2	0	1
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Node Table | Edge Table | Network Table | Unassigned Tables

Memory: OK

How to use Cyni

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Inference Algorithm
Bayesian - K2

Table Data
galFiltered.sif default node

Cyni Algorithm Settings

Max. number of parents

Output Only Nodes with Edges

Row order options

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Column to order rows SelfLoops

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Metric Bayesian (K2) Metric

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galFiltered.sif

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Table Data: galFiltered.sif default node

Cyni Algorithm Settings

Max. number of parents: []

Output Only Nodes with Edges: []

Row order options

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Column to order rows: SelfLoops

Parameters if a network associated to table data

Use selected nodes only: []

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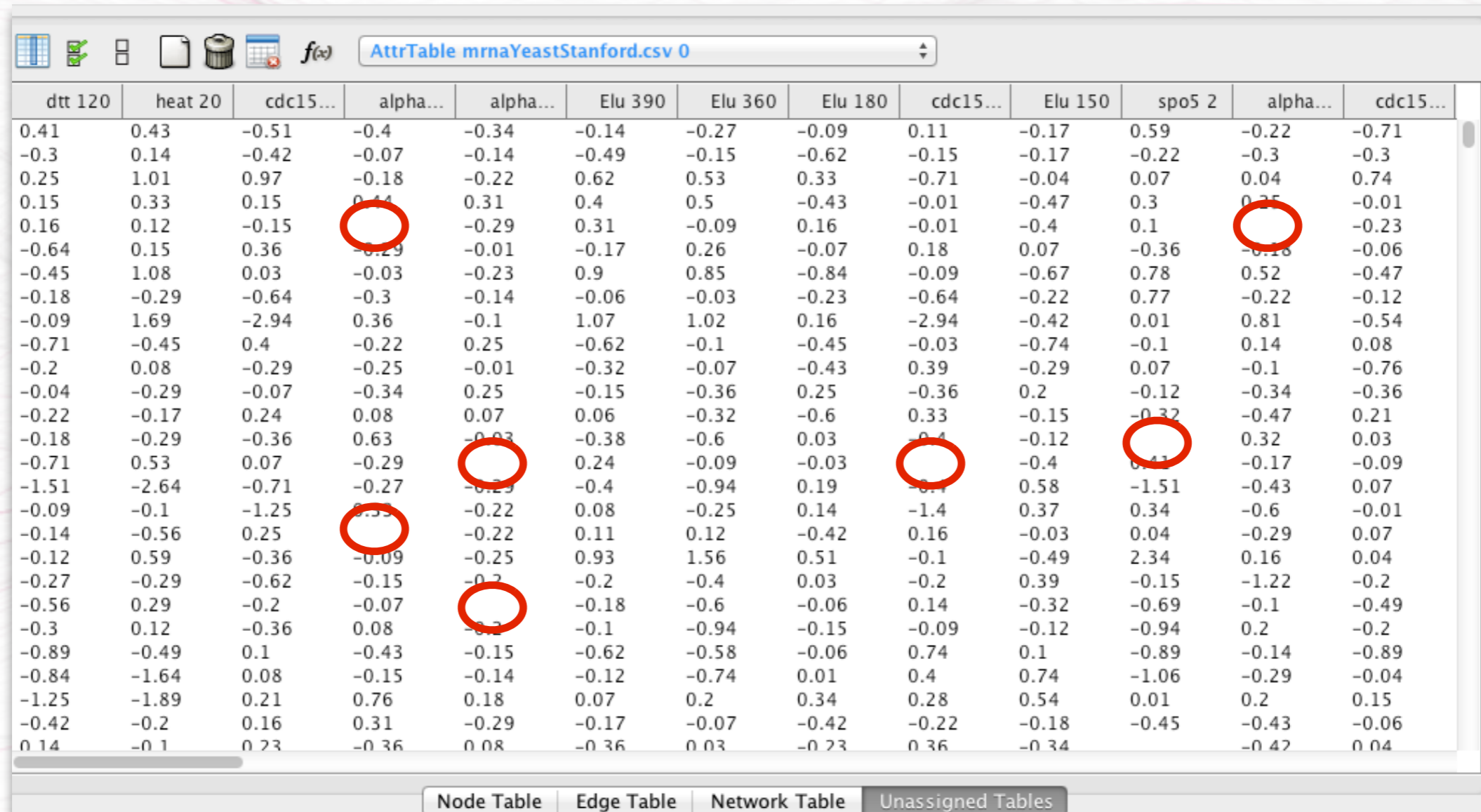
Memory: OK

Cyni Use case

Infer a network from gene expression data

Cyni Use case

Load Data



dt120	heat20	cdc15...	alpha...	alpha...	Elu390	Elu360	Elu180	cdc15...	Elu150	spo52	alpha...	cdc15...
0.41	0.43	-0.51	-0.4	-0.34	-0.14	-0.27	-0.09	0.11	-0.17	0.59	-0.22	-0.71
-0.3	0.14	-0.42	-0.07	-0.14	-0.49	-0.15	-0.62	-0.15	-0.17	-0.22	-0.3	-0.3
0.25	1.01	0.97	-0.18	-0.22	0.62	0.53	0.33	-0.71	-0.04	0.07	0.04	0.74
0.15	0.33	0.15	0.14	0.31	0.4	0.5	-0.43	-0.01	-0.47	0.3	0.25	-0.01
0.16	0.12	-0.15	-0.29	-0.29	0.31	-0.09	0.16	-0.01	-0.4	0.1	-0.18	-0.23
-0.64	0.15	0.36	-0.29	-0.01	-0.17	0.26	-0.07	0.18	0.07	-0.36	-0.18	-0.06
-0.45	1.08	0.03	-0.03	-0.23	0.9	0.85	-0.84	-0.09	-0.67	0.78	0.52	-0.47
-0.18	-0.29	-0.64	-0.3	-0.14	-0.06	-0.03	-0.23	-0.64	-0.22	0.77	-0.22	-0.12
-0.09	1.69	-2.94	0.36	-0.1	1.07	1.02	0.16	-2.94	-0.42	0.01	0.81	-0.54
-0.71	-0.45	0.4	-0.22	0.25	-0.62	-0.1	-0.45	-0.03	-0.74	-0.1	0.14	0.08
-0.2	0.08	-0.29	-0.25	-0.01	-0.32	-0.07	-0.43	0.39	-0.29	0.07	-0.1	-0.76
-0.04	-0.29	-0.07	-0.34	0.25	-0.15	-0.36	0.25	-0.36	0.2	-0.12	-0.34	-0.36
-0.22	-0.17	0.24	0.08	0.07	0.06	-0.32	-0.6	0.33	-0.15	-0.32	-0.47	0.21
-0.18	-0.29	-0.36	0.63	-0.03	-0.38	-0.6	0.03	-0.4	-0.12	-0.41	0.32	0.03
-0.71	0.53	0.07	-0.29	-0.29	0.24	-0.09	-0.03	-0.4	-0.4	0.41	-0.17	-0.09
-1.51	-2.64	-0.71	-0.27	-0.29	-0.4	-0.94	0.19	-0.4	0.58	-1.51	-0.43	0.07
-0.09	-0.1	-1.25	-0.29	-0.22	0.08	-0.25	0.14	-1.4	0.37	0.34	-0.6	-0.01
-0.14	-0.56	0.25	-0.09	-0.22	0.11	0.12	-0.42	0.16	-0.03	0.04	-0.29	0.07
-0.12	0.59	-0.36	-0.09	-0.25	0.93	1.56	0.51	-0.1	-0.49	2.34	0.16	0.04
-0.27	-0.29	-0.62	-0.15	-0.2	-0.2	-0.4	0.03	-0.2	0.39	-0.15	-1.22	-0.2
-0.56	0.29	-0.2	-0.07	-0.2	-0.18	-0.6	-0.06	0.14	-0.32	-0.69	-0.1	-0.49
-0.3	0.12	-0.36	0.08	-0.2	-0.1	-0.94	-0.15	-0.09	-0.12	-0.94	0.2	-0.2
-0.89	-0.49	0.1	-0.43	-0.15	-0.62	-0.58	-0.06	0.74	0.1	-0.89	-0.14	-0.89
-0.84	-1.64	0.08	-0.15	-0.14	-0.12	-0.74	0.01	0.4	0.74	-1.06	-0.29	-0.04
-1.25	-1.89	0.21	0.76	0.18	0.07	0.2	0.34	0.28	0.54	0.01	0.2	0.15
-0.42	-0.2	0.16	0.31	-0.29	-0.17	-0.07	-0.42	-0.22	-0.18	-0.45	-0.43	-0.06
0.14	-0.1	0.23	-0.36	0.08	-0.36	0.03	-0.23	0.36	-0.34	-0.42	-0.42	0.04

Cyni Use case

Load Data

The screenshot displays the Cyni software interface. At the top, there are tabs for 'Network', 'Style', 'Select', and 'Cyni Toolbox'. The main window is divided into several sections:

- Imputation Algorithm:** A dropdown menu set to 'BPCA Imputation'.
- Table Data:** A dropdown menu set to 'AttrTable mrnaYeastStanford.csv 0'.
- Cyni Algorithm Settings:**
 - Missing Value Definition:** A section with a dropdown menu set to 'By a single value'.
 - Single Value Selection:** A section with a text input field containing '999.0'.

On the left side, there is a table with two columns: 'dtt 120' and 'heat 20'. The table contains numerical values ranging from -1.51 to 0.41. On the right side, there is another table with two columns: 'ha...' and 'cdc15...'. The table contains numerical values ranging from -0.71 to 0.04. At the bottom of the window, there are tabs for 'Node Table', 'Edge Table', 'Network Table', and 'Unassigned Tables'.

Cyni Use case



AttrTable mrnaYeastStanford.csv 0

dt1 120	heat 20	cdc15...	alpha...	alpha...	Elu 390	Elu 360	Elu 180	cdc15...	Elu 150	spo5 2	alpha...	cdc15...
0.41	0.43	-0.51	-0.4	-0.34	-0.14	-0.27	-0.09	0.11	-0.17	0.59	-0.22	-0.71
-0.3	0.14	-0.42	-0.07	-0.14	-0.49	-0.15	-0.62	-0.15	-0.17	-0.22	-0.3	-0.3
0.25	1.01	0.97	-0.18	-0.22	0.62	0.53	0.33	-0.71	-0.04	0.07	0.04	0.74
0.15	0.33	0.15	0.14	0.31	0.4	0.5	-0.43	-0.01	-0.47	0.3	0.25	-0.01
0.16	0.12	-0.15	-0.1705	-0.29	0.31	-0.09	0.16	-0.01	-0.4	0.1	-0.2391	-0.23
-0.64	0.15	0.36	0.29	-0.01	-0.17	0.26	-0.07	0.18	0.07	-0.36	-0.18	-0.06
-0.45	1.08	0.03	-0.03	-0.23	0.9	0.85	-0.84	-0.09	-0.67	0.78	0.52	-0.47
-0.18	-0.29	-0.64	-0.3	-0.14	-0.06	-0.03	-0.23	-0.64	-0.22	0.77	-0.22	-0.12
-0.09	1.69	-2.94	0.36	-0.1	1.07	1.02	0.16	-2.94	-0.42	0.01	0.81	-0.54
-0.71	-0.45	0.4	-0.22	0.25	-0.62	-0.1	-0.45	-0.03	-0.74	-0.1	0.14	0.08
-0.2	0.08	-0.29	-0.25	-0.01	-0.32	-0.07	-0.43	0.39	-0.29	0.07	-0.1	-0.76
-0.04	-0.29	-0.07	-0.34	0.25	-0.15	-0.36	0.25	-0.36	0.2	-0.12	-0.34	-0.36
-0.22	-0.17	0.24	0.08	0.07	0.06	-0.32	-0.6	0.33	-0.15	-0.32	-0.47	0.21
-0.18	-0.29	-0.36	0.63	0.03	-0.38	-0.6	0.03	-0.4	-0.12	-0.0449	0.32	0.03
-0.71	0.53	0.07	-0.29	-0.2041	0.24	-0.09	-0.03	-0.1100	-0.4	0.41	-0.17	-0.09
-1.51	-2.64	-0.71	-0.27	-0.29	-0.4	-0.94	0.19	-0.4	0.58	-1.51	-0.43	0.07
-0.09	-0.1	-1.25	0.33	-0.22	0.08	-0.25	0.14	-1.4	0.37	0.34	-0.6	-0.01
-0.14	-0.56	0.25	-0.1879	-0.22	0.11	0.12	-0.42	0.16	-0.03	0.04	-0.29	0.07
-0.12	0.59	-0.36	-0.09	-0.25	0.93	1.56	0.51	-0.1	-0.49	2.34	0.16	0.04
-0.27	-0.29	-0.62	-0.15	0.2	-0.2	-0.4	0.03	-0.2	0.39	-0.15	-1.22	-0.2
-0.56	0.29	-0.2	-0.07	-0.0996	-0.18	-0.6	-0.06	0.14	-0.32	-0.69	-0.1	-0.49
-0.3	0.12	-0.36	0.08	0.2	-0.1	-0.94	-0.15	-0.09	-0.12	-0.94	0.2	-0.2
-0.89	-0.49	0.1	-0.43	-0.15	-0.62	-0.58	-0.06	0.74	0.1	-0.89	-0.14	-0.89
-0.84	-1.64	0.08	-0.15	-0.14	-0.12	-0.74	0.01	0.4	0.74	-1.06	-0.29	-0.04
-1.25	-1.89	0.21	0.76	0.18	0.07	0.2	0.34	0.28	0.54	0.01	0.2	0.15
-0.42	-0.2	0.16	0.31	-0.29	-0.17	-0.07	-0.42	-0.22	-0.18	-0.45	-0.43	-0.06
0.14	-0.1	0.23	-0.36	0.08	-0.36	0.03	-0.23	0.36	-0.34	-0.0631	-0.42	0.04

Cyni Use case



The screenshot displays the Cyni software interface with the following components:

- Network Panel:** A table with columns 'dtt 120', 'heat 20', and 'cdc'. It contains 20 rows of numerical data.
- Discretization Algorithm:** Set to 'Equal Width/Frequency Discretization'.
- Table Data:** Set to 'AttrTable mrnaYeastStanford.csv 0'.
- Cyni Algorithm Settings:**
 - Intervals: 5
 - Use Equal Frequency:
 - Apply same discretization thresholds for all selected attributes:
 - Attributes to discretize: A list of 'alpha' attributes (alpha 0, alpha 7, alpha 14, alpha 21, alpha 28, alpha 35, alpha 42, alpha 49) is shown in a blue selection box.
- Right Panel:** A table with columns 'spo5 2', 'alpha...', and 'cdc15...'. It contains 20 rows of numerical data. Two values are circled in red: '-0.2391' in the 'alpha...' column and '0449.' in the 'spo5 2' column.

Cyni Use case



AttrTable mrnaYeastStanford.csv 0

nomin...	nomin...	nomin...	nominal.Elu 330	nominal.Elu 360	nominal.Elu 390	nominal.Elu 60	nomi...
(-0.220...	(-0.450...	(-0.220...	(-0.22000,-0.013171)	(-0.45000,-0.22000)	(-0.22000,-0.013171)	(-0.22000,-0.013171)	(-0.450
(-0.450...	(-5.640...	(-0.220...	(-0.22000,-0.013171)	(-0.22000,-0.013171)	(-5.6400,-0.45000)	(-5.6400,-0.45000)	(-0.450
(0.2400...	(-0.013...	(0.2400...	(0.24000,5.8800)	(0.24000,5.8800)	(0.24000,5.8800)	(-0.013171,0.24000)	(-0.450
(-0.220...	(0.2400...	(-0.450...	(-0.013171,0.24000)	(0.24000,5.8800)	(0.24000,5.8800)	(0.24000,5.8800)	(0.2400
(-0.013...	(0.2400...	(-0.220...	(-0.013171,0.24000)	(-0.22000,-0.013171)	(0.24000,5.8800)	(-0.013171,0.24000)	(-5.640
(-0.013...	(-5.640...	(-5.640...	(0.24000,5.8800)	(0.24000,5.8800)	(-0.22000,-0.013171)	(-5.6400,-0.45000)	(-0.013
(-5.640...	(-0.220...	(-5.640...	(-0.45000,-0.22000)	(0.24000,5.8800)	(0.24000,5.8800)	(0.24000,5.8800)	(0.2400
(-0.450...	(-0.220...	(-0.220...	(-0.013171,0.24000)	(-0.22000,-0.013171)	(-0.22000,-0.013171)	(-0.22000,-0.013171)	(-0.450
(0.2400...	(0.2400...	(-0.013...	(0.24000,5.8800)	(0.24000,5.8800)	(0.24000,5.8800)	(-0.22000,-0.013171)	(0.2400
(-0.450...	(-5.640...	(-5.640...	(-0.22000,-0.013171)	(-0.22000,-0.013171)	(-5.6400,-0.45000)	(-5.6400,-0.45000)	(-5.640
(-0.450...	(-0.450...	(-0.450...	(-0.45000,-0.22000)	(-0.22000,-0.013171)	(-0.45000,-0.22000)	(-0.45000,-0.22000)	(-5.640
(-0.450...	(-0.450...	(-0.220...	(-5.6400,-0.45000)	(-0.45000,-0.22000)	(-0.22000,-0.013171)	(-0.45000,-0.22000)	(-0.450
(-0.450...	(-0.450...	(-0.450...	(-0.45000,-0.22000)	(-0.45000,-0.22000)	(-0.013171,0.24000)	(-0.45000,-0.22000)	(-5.640
(-0.220...	(0.2400...	(-0.450...	(-0.013171,0.24000)	(-5.6400,-0.45000)	(-0.45000,-0.22000)	(0.24000,5.8800)	(-0.013
(0.2400...	(-0.450...	(-0.450...	(0.24000,5.8800)	(-0.22000,-0.013171)	(-0.013171,0.24000)	(-0.45000,-0.22000)	(-0.220
(-0.013...	(-5.640...	(-0.013...	(-5.6400,-0.45000)	(-5.6400,-0.45000)	(-0.45000,-0.22000)	(-0.013171,0.24000)	(-0.013
(-0.013...	(-0.013...	(0.2400...	(-0.22000,-0.013171)	(-0.45000,-0.22000)	(-0.013171,0.24000)	(-0.013171,0.24000)	(0.2400
(-0.013...	(-0.450...	(-0.220...	(-0.22000,-0.013171)	(-0.013171,0.24000)	(-0.013171,0.24000)	(-0.45000,-0.22000)	(-0.450
(0.2400...	(0.2400...	(0.2400...	(0.24000,5.8800)	(0.24000,5.8800)	(0.24000,5.8800)	(0.24000,5.8800)	(0.2400
(-0.013...	(-0.220...	(0.2400...	(-0.22000,-0.013171)	(-0.45000,-0.22000)	(-0.22000,-0.013171)	(-0.013171,0.24000)	(0.2400
(-0.450...	(-5.640...	(-0.220...	(-0.45000,-0.22000)	(-5.6400,-0.45000)	(-0.22000,-0.013171)	(-5.6400,-0.45000)	(-0.450
(-0.450...	(-0.220...	(-0.220...	(-0.45000,-0.22000)	(-5.6400,-0.45000)	(-0.22000,-0.013171)	(-0.013171,0.24000)	(-0.013
(-0.450...	(-5.640...	(-0.450...	(-5.6400,-0.45000)	(-5.6400,-0.45000)	(-5.6400,-0.45000)	(-5.6400,-0.45000)	(-0.013
(0.2400...	(-5.640...	(-0.013...	(-5.6400,-0.45000)	(-5.6400,-0.45000)	(-0.22000,-0.013171)	(-0.22000,-0.013171)	(0.2400
(0.2400...	(-5.640...	(-0.450...	(0.24000,5.8800)	(-0.013171,0.24000)	(-0.013171,0.24000)	(-5.6400,-0.45000)	(-0.220
(-0.013...	(-5.640...	(-0.450...	(-0.013171,0.24000)	(-0.22000,-0.013171)	(-0.22000,-0.013171)	(-5.6400,-0.45000)	(-0.450
(-5.640...	(-0.450...	(-0.450...	(-5.6400,-0.45000)	(-0.013171,0.24000)	(-0.45000,-0.22000)	(-0.45000,-0.22000)	(-0.220

Node Table | Edge Table | Network Table | Unassigned Tables

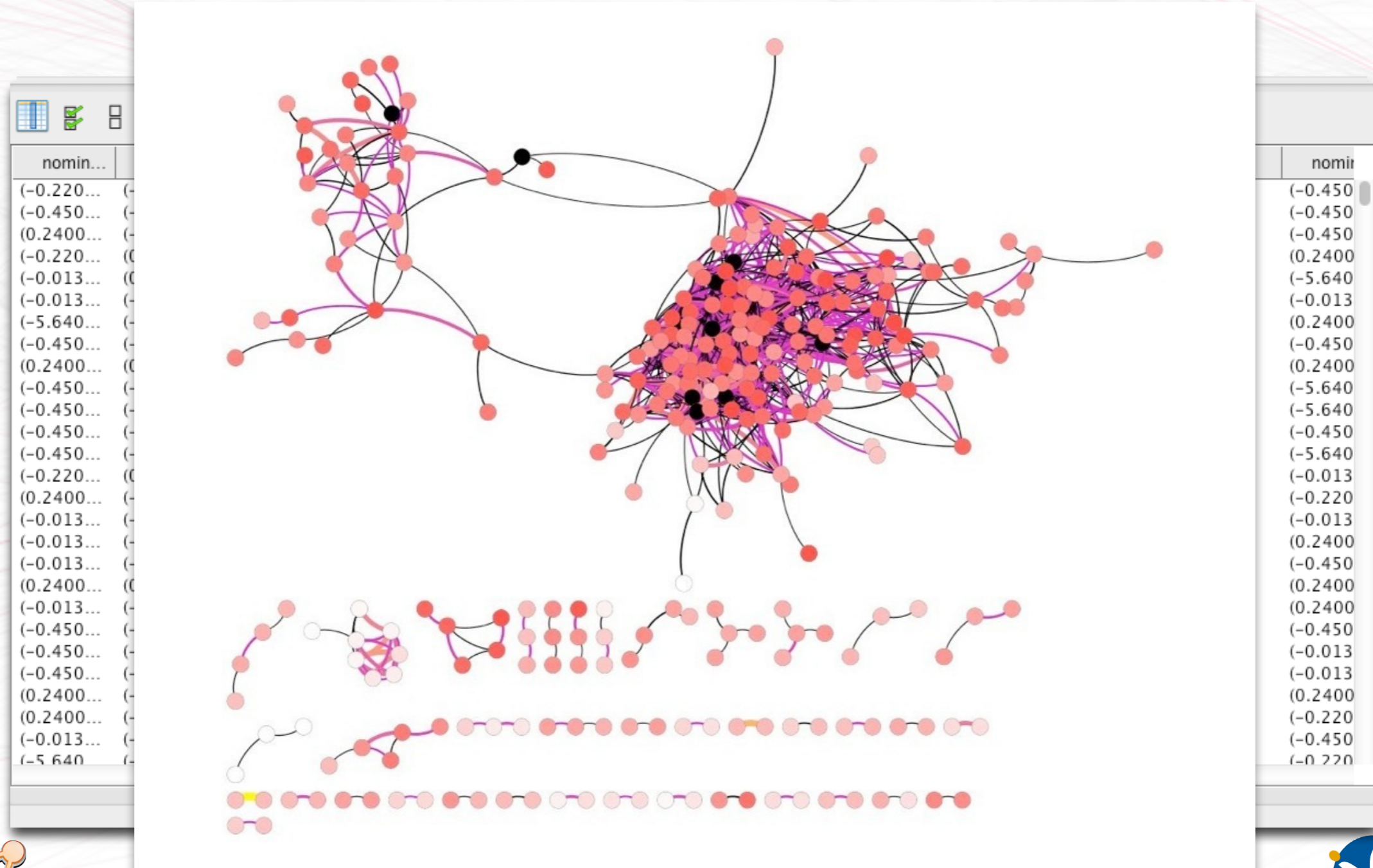
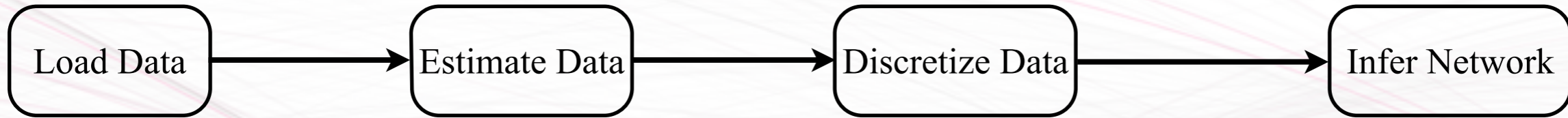
Cyni Use case



The screenshot displays the Cyni Toolbox interface within Cytoscape. The 'Inference Algorithm' is set to 'Mutual Information Inference'. The 'Table Data' dropdown is set to 'AttrTable mrnaYeastStanford.csv 0'. The 'Cyni Algorithm Settings' section includes a 'Threshold to add new edge' set to 0.6 and a checked option for 'Parameters if a network associated to table data'. The 'Sources for Network Inference' section shows a list of 'Data Attributes' under the 'ORF' category, including 'nominal.alpha 0', 'nominal.alpha 7', 'nominal.alpha 14', 'nominal.alpha 21', 'nominal.alpha 28', and 'nominal.alpha 35'. The background shows a data table with columns for 'nominal.alpha' and 'nominal.Elu 60'.

nominal.alpha	nominal.alpha	nominal.alpha	nominal.alpha
(-0.220000,-0.013171)	(-0.450000,-0.220000)	(-0.220000,-0.013171)	(-0.220000,-0.013171)
(-0.450000,-0.220000)	(-5.640000,-0.450000)	(-0.220000,-0.013171)	(-0.220000,-0.013171)
(0.240000,5.880000)	(-0.013171,0.240000)	(0.240000,5.880000)	(0.240000,5.880000)
(-0.220000,-0.013171)	(0.240000,5.880000)	(-0.450000,-0.220000)	(-0.013171,0.240000)
(-0.013171,0.240000)	(0.240000,5.880000)	(-0.220000,-0.013171)	(-0.013171,0.240000)
(-0.013171,0.240000)	(-5.640000,-0.450000)	(-5.640000,-0.450000)	(0.240000,5.880000)
(-5.640000,-0.450000)	(-0.220000,-0.013171)	(-5.640000,-0.450000)	(-0.450000,-0.220000)
(-0.450000,-0.220000)	(-0.220000,-0.013171)	(-0.220000,-0.013171)	(-0.013171,0.240000)
(0.240000,5.880000)	(0.240000,5.880000)	(-0.013171,0.240000)	(0.240000,5.880000)
(-0.450000,-0.220000)	(-5.640000,-0.450000)	(-5.640000,-0.450000)	(-0.220000,-0.013171)
(-0.450000,-0.220000)	(-0.450000,-0.220000)	(-0.450000,-0.220000)	(-0.450000,-0.220000)
(-0.450000,-0.220000)	(-0.450000,-0.220000)	(-0.220000,-0.013171)	(-5.640000,-0.450000)
(-0.450000,-0.220000)	(-0.450000,-0.220000)	(-0.450000,-0.220000)	(-0.450000,-0.220000)
(-0.220000,-0.013171)	(0.240000,5.880000)	(-0.450000,-0.220000)	(-0.013171,0.240000)
(0.240000,5.880000)	(-0.450000,-0.220000)	(-0.450000,-0.220000)	(0.240000,5.880000)
(-0.013171,0.240000)	(-5.640000,-0.450000)	(-0.013171,0.240000)	(-5.640000,-0.450000)
(-0.013171,0.240000)	(-0.013171,0.240000)	(0.240000,5.880000)	(-0.220000,-0.013171)
(-0.013171,0.240000)	(-0.450000,-0.220000)	(-0.220000,-0.013171)	(-0.220000,-0.013171)
(0.240000,5.880000)	(0.240000,5.880000)	(0.240000,5.880000)	(0.240000,5.880000)
(-0.013171,0.240000)	(-0.220000,-0.013171)	(0.240000,5.880000)	(-0.220000,-0.013171)
(-0.450000,-0.220000)	(-5.640000,-0.450000)	(-0.220000,-0.013171)	(-0.450000,-0.220000)
(-0.450000,-0.220000)	(-0.220000,-0.013171)	(-0.220000,-0.013171)	(-0.450000,-0.220000)
(-0.450000,-0.220000)	(-5.640000,-0.450000)	(-0.450000,-0.220000)	(-5.640000,-0.450000)
(0.240000,5.880000)	(-5.640000,-0.450000)	(-0.013171,0.240000)	(-5.640000,-0.450000)
(0.240000,5.880000)	(-5.640000,-0.450000)	(-0.450000,-0.220000)	(0.240000,5.880000)
(-0.013171,0.240000)	(-5.640000,-0.450000)	(-0.450000,-0.220000)	(-0.013171,0.240000)
(-5.640000,-0.450000)	(-0.450000,-0.220000)	(-0.450000,-0.220000)	(-5.640000,-0.450000)

Cyni Use case



First “Cyni Apps”

- ARACNE

BMC Bioinformatics



Proceedings

Open Access

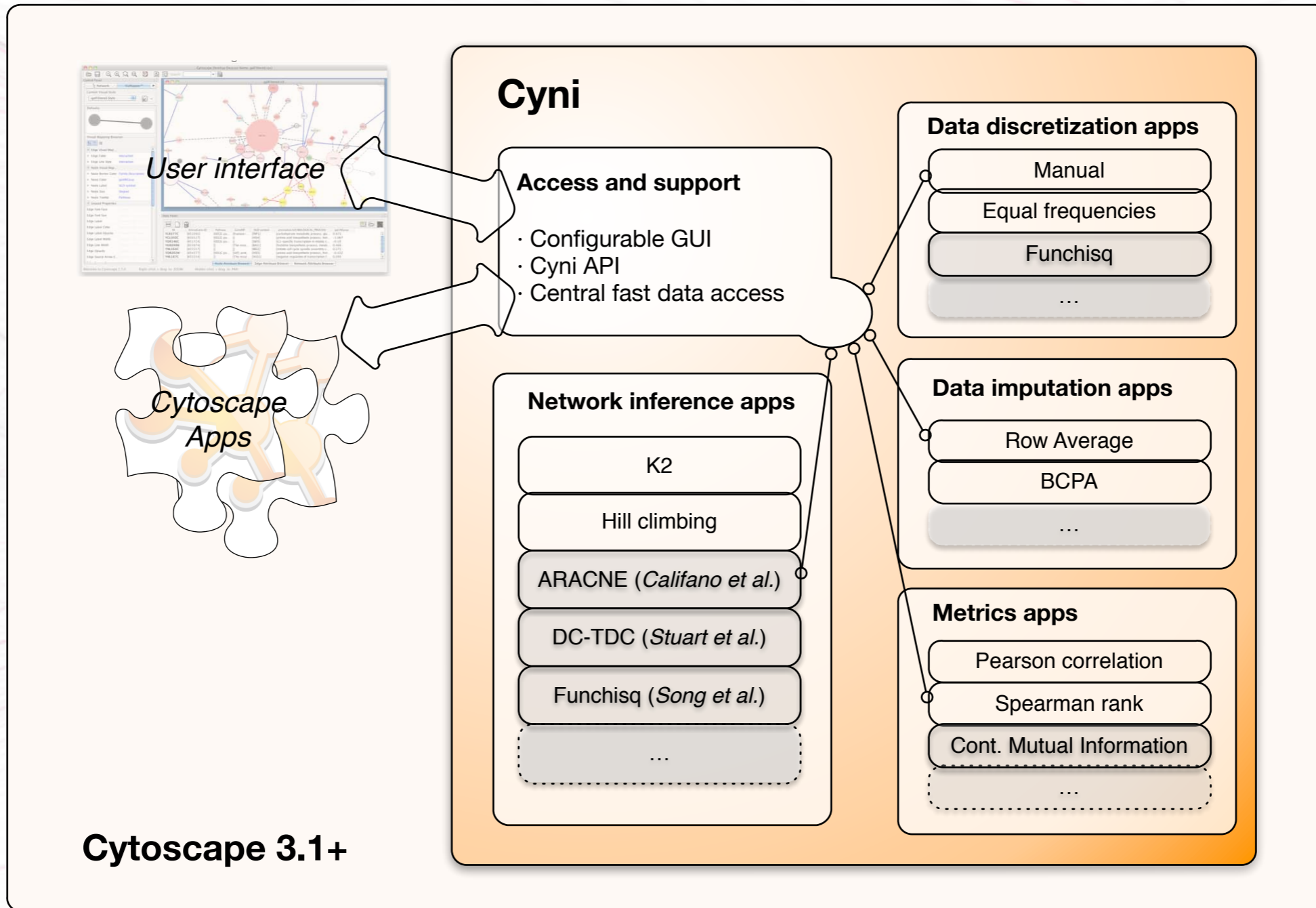
ARACNE: An Algorithm for the Reconstruction of Gene Regulatory Networks in a Mammalian Cellular Context

Adam A Margolin^{1,2}, Ilya Nemenman², Katia Basso³, Chris Wiggins^{2,4}, Gustavo Stolovitzky⁵, Riccardo Dalla Favera³ and Andrea Califano^{*1,2}

- DREAM 8 Breast Cancer SubChallenge 1 winners

- Stuart's Lab (UCSC): LASSO regression along with the use of prior biological knowledge by using a heat diffusion technique
- Song's Lab (NMSU): Discretization Gaussian mixture model along with a new non-constant functional chi-square metrics

Cyni Framework



Why your algorithm in Cyni?

- Friendly user interface
- Direct Cytoscape output visualization
- Access to a larger number of users through Cytoscape App Store
- Benchmarking system

Why your algorithm in Cyni?

- Friend
- Director
- Account
- Cytoscape
- Berlin

```
^Ccelery:Downloads oguitart$ java -jar -Xss4m -Xmx14848M aracne2.jar -m dx -i ~/angelica/temp/dream_transp
ed_aracneTest.csv -p 2e-11 -e 0.0 -t 0.0
Marker No: 1000 (1000 active), Array No: 100
Kernel width determined for this dataset: 0.1737676786204193
MI threshold determined for p=2.0E-11: 0.2292354044814858
[PARA] Input file: dream_transposed_aracneTest.csv
[PARA] Output file: dream_transposed_aracneTest_k0.174_t0.23_e0.0.adj
[PARA] Algorithm: FIXED_BANDWIDTH
[PARA] Mode: DISCOVERY
[PARA] Kernel width: 0.1737676786204193
[PARA] MI threshold: 0.2292354044814858
[PARA] MI threshold calculated from P-Value: 2.0E-11
[PARA] DPI tolerance: 0.0

10%, time: 62771
20%, time: 120564
30%, time: 170872
40%, time: 214810
50%, time: 251460
60%, time: 281133
70%, time: 306534
80%, time: 323610
90%, time: 334551
100%, time: 337939
Gene: 1000 Time: 337940
[NETWORK] Applying DPI ...
```

Why your algorithm in Cyni?

- Friendly user interface
- Direct Cytoscape integration
- Access to a large number of algorithms
- Cytoscape API
- Benchmarking

The screenshot shows the Cyni Control Panel interface. The 'Inference Algorithm' is set to 'ARACNE Algorithm'. The 'Table Data' is 'galFiltered.sif default node'. Under 'Cyni Algorithm Settings', 'Algorithm Definition' includes 'Aracne Mode' (Discovery), 'Mutual Information Algorithm Type' (Naive Bayes), and 'Mutual Information Steps' (6). 'Threshold Definition' shows 'Which threshold to use' (MI Threshold) and 'MI Threshold Definition' (Mutual Information Threshold: 0.5). 'Sources for Network Inference' lists 'Data Attributes' such as SelfLoops, TopologicalCoefficient, BetweennessCentrality, and gal4RGexp. The 'Table Panel' on the right shows a list of genes including GAL80, GAL11, GAL4, GCY1, HAP2, YDL19..., YDR27..., YBR043C, YPR145W, YER054C, YBR045C, YBL079W, YLR345W, and YLR345W.

Why your algorithm in Cyni?

- Friendly user interface
- Direct Cytoscape output visualization
- Access to a larger number of users through Cytoscape App Store
- Benchmarking system

Why your algorithm in Cyni?

- Friendly us
- Direct Cyto
- Access to Cytoscape
- Benchmark

```
File Path: ~/Downloads/dream_transposed_aracneTest_k0.174_t0.23_e0.0.adj
dream_transposed_aracneTest_k0.174_t0.23_e0.0.adj
1 > Input file      dream_transposed_aracneTest.csv
2 > ADJ file
3 > Output file    dream_transposed_aracneTest_k0.174_t0.23_e0.0.adj
4 > Algorithm      FIXED_BANDWIDTH
5 > Kernel width   0.1737676786204193
6 > No. bins       6
7 > MI threshold   0.2292354044814858
8 > MI P-value     2.0E-11
9 > DPI tolerance  0.0
10 > Correction     0.0
11 > Subnetwork file
12 > Hub probe
13 > Control probe
14 > Condition
15 > Percentage     0.35
16 > TF annotation
17 > Filter mean    0.0
18 > Filter CV      0.0
19 G4 G68 0.41765255
20 G14 G648 0.2877038
21 G16 G725 0.28323704 G779 0.28481848
22 G23 G517 0.32782376
23 G29 G109 0.29017115 G171 0.37597873 G259 0.25000112 G762 0.25419957 G890 0.33172792
24 G42 G68 0.42580094 G232 0.38303304
25 G45 G723 0.25590656
26 G47 G186 0.26458874
27 G49 G87 0.31255609
28 G63 G162 0.27760771 G518 0.23904986
29 G64 G94 0.24068346
30 G68 G4 0.41765255 G42 0.42580094 G141 0.41606366 G998 0.27828004
31 G73 G935 0.23190155
32 G75 G812 0.35670357
33 G77 G585 0.235077
34 G78 G252 0.26786838 G634 0.47017029
35 G83 G171 0.34168466
36 G87 G49 0.31255609 G507 0.25181004
37 G89 G988 0.3249307
38 G92 G770 0.24830698
39 G94 G64 0.24068346
40 G101 G274 0.27674308
41 G102 G707 0.29150621
42 G109 G29 0.29017115
43 G110 G770 0.45574345
44 G122 G131 0.29847346
```

Why your algorithm in Cyni?

The screenshot displays the Cyni software interface. On the left is the 'Control Panel' with various settings for the ARACNE algorithm. On the right is the 'ARACNE Inference 1' window showing a network graph with nodes labeled G4, G68, G14, G648, G16, G725, G779, G23, etc. Below the graph is a 'Table Panel' showing a table of results.

Control Panel Settings:

- Inference Algorithm: ARACNE Algorithm
- Table Data: AttrTable dream_transposed_aracneTest.csv 0
- Cyni Algorithm Settings:
 - Algorithm Definition:
 - Aracne Mode: Discovery
 - Mutual Information Algorithm Type: Fixed Bandwidth
 - Manual Kernel Width Definition: Kernel Width (0,1):
 - DPI Tolerance [0,1]:
 - Mutual Information Steps:
 - Hub/Transcription Factor Definition ▶
 - Threshold Definition:
 - Which threshold to use: P-Value Threshold
 - P-Value Threshold Definition: P-Value Threshold (0,1):
 - Sources for Network Inference ▼:
 - Data Attributes: RIL1, RIL2, RIL3, RIL4
- Buttons: Impute Data, Discretize Data, Infer Network

Table Panel:

shared...	name	GENEID	Affs	RIL1	RIL2	RIL3	RIL4	RIL5	RIL6	R
G4	G4	G4	gen4	1.0559...	1.2975...	1.6571...	1.4245...	1.4093...	2.0630...	1.454
G68	G68	G68	gen68	0.3235...	0.1968...	0.0581...	0.1578...	0.2001...	0.1140...	0.256
G14	G14	G14	gen14	0.9752...	1.7804...	1.0526...	1.4464...	2.3994...	2.7818...	1.948
G648	G648	G648	gen648	0.3089...	0.2242...	0.2716...	0.1161...	0.1194...	0.0952...	0.143
G16	G16	G16	gen16	0.0182...	0.0071...	0.0174...	0.0074...	0.0433...	0.0093...	0.017
G725	G725	G725	gen725	0.7729...	1.0295...	0.9233...	1.0820...	0.8222...	0.9082...	0.812
G779	G779	G779	gen779	5.79E-4	7.901E...	0.0014...	3.003E...	0.0046...	0.0011...	0.001
G23	G23	G23	gen23	0.3007...	0.2181...	0.4601...	0.0954...	0.1989...	0.1533...	0.196

Why your algorithm in Cyni?

The screenshot displays the Cyni software interface. On the left is the 'Control Panel' with various settings for the inference algorithm. On the right is the 'ARACNE Inference 1' window showing a network graph with red nodes and edges. Below the graph is the 'Table Panel' which contains a table of data attributes.

Control Panel Settings:

- Inference Algorithm: Bayesian - K2
- Table Data: galFiltered.sif default node
- Cyni Algorithm Settings:
 - Max. number of parents: [input field]
 - Output Only Nodes with Edges: [checkbox]
 - Row order options:
 - Row order: Default Cytoscape Order
 - Column to order rows: SelfLoops
 - Parameters if a network associated to table data:
 - Use selected nodes only: [checkbox]
 - Metric: Bayesian (K2) Metric
 - Sources for Network Inference:
 - Data Attributes:
 - shared name
 - name
 - COMMON
 - nominal.gal4RGexp
 - nominal.gal80Rsig
 - nominal.gal80Rexp

Table Panel Data:

shared...	name	GENEID	Affs	RIL1	RIL2	RIL3	RIL4	RIL5	RIL6	RIL7
G4	G4	G4	gen4	1.0559...	1.2975...	1.6571...	1.4245...	1.4093...	2.0630...	1.4546...
G68	G68	G68	gen68	0.3235...	0.1968...	0.0581...	0.1578...	0.2001...	0.1140...	0.2564...
G14	G14	G14	gen14	0.9752...	1.7804...	1.0526...	1.4464...	2.3994...	2.7818...	1.9483...
G648	G648	G648	gen648	0.3089...	0.2242...	0.2716...	0.1161...	0.1194...	0.0952...	0.1437...
G16	G16	G16	gen16	0.0182...	0.0071...	0.0174...	0.0074...	0.0433...	0.0093...	0.0171...
G725	G725	G725	gen725	0.7729...	1.0295...	0.9233...	1.0820...	0.8222...	0.9082...	0.8127...

Why your algorithm in Cyni?

- Friendly user interface
- Direct Cytoscape output visualization
- Access to a larger number of users through Cytoscape App Store
- Benchmarking system

Why your algorithm in Cyni?

Contents [hide]

- 1 Introduction
- 2 Application Download
- 3 Documentation and Support
- 4 Relevant Publications

Introduction

ARACNE (Algorithm for the Reconstruction of Accurate Cellular Networks), a novel algorithm, using microarray expression profiles, specifically designed to scale up to the complexity of regular mammalian cells, yet general enough to address a wider range of network deconvolution problems. This method uses an information theoretic approach to eliminate the vast majority of indirectly typically inferred by pairwise analysis.

On synthetic datasets ARACNE achieves extremely low error rates and significantly outperforms established methods, such as Relevance Networks and Bayesian Networks. Application to the of genetic networks in human B cells demonstrates ARACNE's ability to infer validated transcriptional targets of the c-MYC proto-oncogene.

Application Download

ARACNE2

[Usage.txt](#): This file is used by the native aracne2 binaries compiled from C++ source to provide ARACNE2 usage summary. Please copy this file to the same directory as the binary (This can be the entire source distribution is downloaded)

[aracne2.exe](#): PE32 executable for MS Windows (console) Intel 80386 32-bit

[aracne2](#): ELF 64-bit LSB executable, AMD x86-64, version 1 (SYSV), for GNU/Linux 2.6.9, dynamically linked (uses shared libs), for GNU/Linux 2.6.9, not stripped

[aracne2.macosx](#): Mach-O 64-bit executable x86_64

[aracne2.jar](#): Java executable jarfile

[ARACNE.src.tar.gz](#): C++ source only with Makefiles

[ARACNE-java.src.tar.gz](#): Java source only with ANT build file

[aracne.zip](#): Java Graphic User Interface (GUI) for loading adjacency matrices and drawing network diagrams using a built-in Cytoscape plugin. Please set a 'JAVA_HOME' environment variable to your JDK and use the launch_aracne scripts in the distribution to start the application



Paris, September 18, 2014



Why your algorithm in Cyni?

The screenshot displays the Cytoscape App Store interface. At the top, there is a navigation bar with the Cytoscape logo, the text "Cytoscape App Store", a "Submit an App" button, a dropdown menu currently showing "inference", and a "Sign In" button. On the left side, there is a sidebar with the heading "All Apps" and a "Categories" section. The categories listed are: network generation, online data import, data visualization, graph analysis, integrated analysis, clustering, utility, enrichment analysis, ontology analysis, pathway database, data integration, network analysis, local data import, scripting, layout, interaction database, and functional analysis. The main content area is titled "Tags" and shows "network inference" as the selected tag. Below this, the "Apps" section is displayed, sorted by "name" (indicated by an upward arrow). The apps listed are: ARACNE (Network inference algorithm to address a wide range of network), bayelviraApp (Learning and generation of Bayesian networks), CoNet (CoNet is a Cytoscape plugin that detects significant associations in), CyNetworkBMA (Infers gene regulatory networks from expression measurements), Cyni Toolbox (Cytoscape Network Inference Toolbox puts together several), and KDDN (Knowledge-fused Differential Dependency Network). Each app card includes a small icon, the app name, a brief description, and a "3.0+" rating badge.

Why your algorithm in Cyni?

- Friendly user interface
- Direct Cytoscape output visualization
- Access to a larger number of users through Cytoscape App Store
- Benchmarking system

Why your algorithm in Cyni?

- Friendly
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- Benchm

The screenshot shows the Cytoscape v3.1.1 interface. The 'Cyni' algorithm settings panel is open, displaying a list of algorithms: Dream8 DC_TDC Algorithm, Bayesian - Hill Climbing, Basic Correlation Inference, ARACNE Algorithm, Mutual Information Inference, and Bayesian - K2. The 'Bayesian - K2' algorithm is selected. Below the list, the 'Table Data' is set to 'galFiltered.sif default node'. The 'Cyni Algorithm Settings' section includes 'Max. number of parents' (empty), 'Output Only Nodes with Edges' (checked), 'Row order options' (Row order: Default Cytoscape Order, Column to order rows: SelfLoops), and 'Parameters if a network associated to table data' (Use selected nodes only: checked). The 'Metric' is set to 'Bayesian (K2) Metric'. The 'Sources for Network Inference' section shows 'Data Attributes' with a list of attributes: shared name, name, COMMON, nominal.gal4RGexp, nominal.gal80Rsig, and nominal.gal80Rexp. The 'Table Panel' at the bottom displays a table with columns: shared..., name, Averag..., Cluster..., Closen..., and IsSingl. The table contains data for various yeast genes.

shared...	name	Averag...	Cluster...	Closen...	IsSingl
YDL19...	YDL19...	13.116...	0.0	0.0762...	false
YDR27...	YDR27...	12.120...	0.0	0.0825...	false
YBR043C	YBR043C	1.5	0.0	0.6666...	false
YPR145W	YPR145W	9.7983...	0.0	0.1020...	false
YER054C	YER054C	8.8185...	0.0	0.1133...	false
YBR045C	YBR045C	9.6451...	0.0	0.1036...	false
YBL079W	YBL079W	2.0	0.0	0.5	false
YLR345W	YLR345W	9.1169...	0.0	0.1096...	false

Cyni Current Status

- Robust release available with first non beta API
- More than 2000 downloads
- ARACNE app already available in the App store and two more apps on the way
- Cyni paper submitted
- Cyni Apps need to be implemented in Java
 - Currently exploring options to support algorithms implemented in other programming languages like R or Python

Thank you!

- If it does not work for you, do not give up. Tell us why
- Please cite Cyni Algorithms and/or Cyni itself
- Questions: Welcome!