

AFRICAN CENTERS OF EXCELLENCE IN BIOINFORMATICS

KAMPALA, UGANDA

Gene Regulatory Networks 1



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Computational Genomics
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Bachelor in biochemistry @NUS
Ph.D in stem cell biology @NUS
Postdoc in neurodegeneration, single cell
biology @JHU
Bioinformatician @ NIH

Recent projects

- Single cell analysis of cancer stem cells
- Single cell analysis of immune response in lung cancer
- Bulk RNA-seq on irradiation, HIV blood samples
- PLEASE JOIN THE DISCUSSION

Today's Instructor

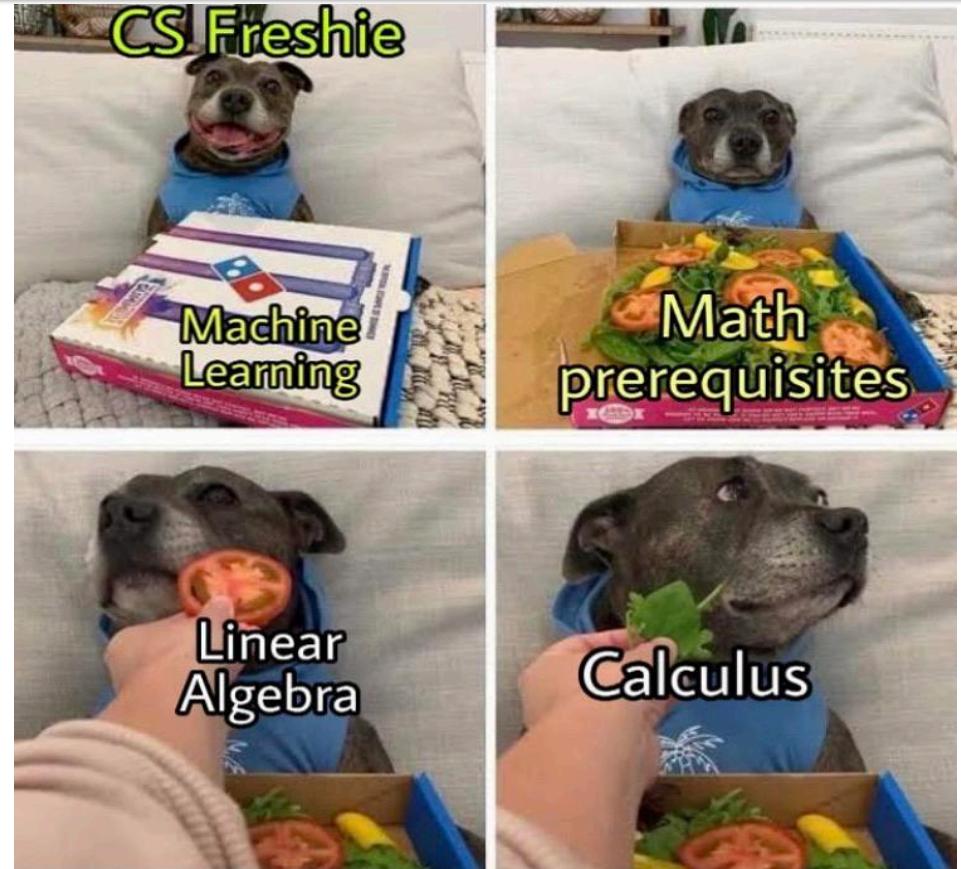
- Bioinformatics and Computational Biosciences Branch (BCBB), NIAID
- National Institutes of Health, Bethesda, MD USA.
- Contact our team via email:
 - Github: https://github.com/niaid/Gene_Regulatory_Networks
 - Instructors: zhuy16@nih.gov
 - Server: ssh <username@137.63.194.9>,
`/home/bcbb_teaching_files/`
 - Googledoc, <https://tinyurl.com/zhu-GRN>
 - Email: bioinformatics@niaid.nih.gov
 - Linkedin: <https://tinyurl.com/zhu-linkedin>

Personal experience: learning bioinformatics

- Sounds Nice
- A lot of difficulties
- Luckily...

Bachelor and PhD in Biology
Postdoc training in neuroscience
Studied Single-cell RNA-seq

Key question today:
How to discovery regulatory connections and key
players from a crowd of thousands of genes.



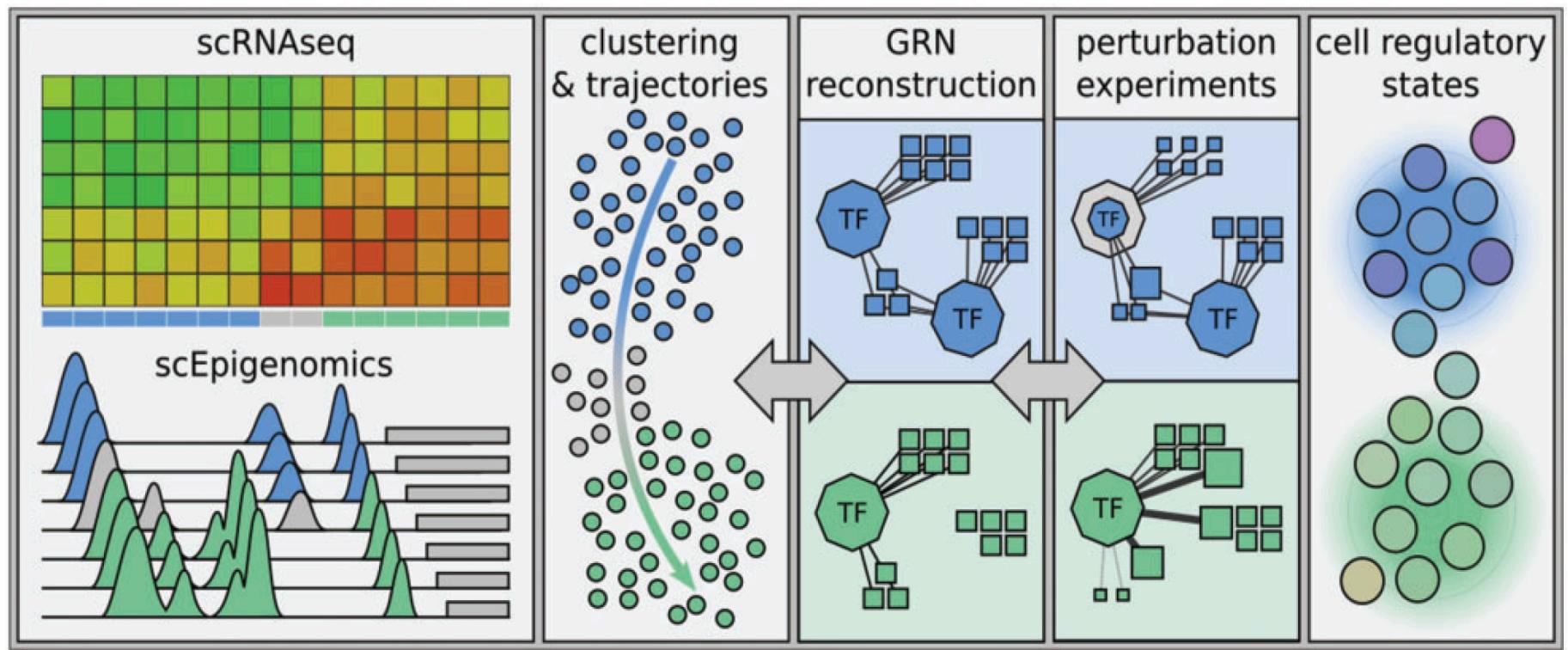




Objectives: achieve a general overview of GRN

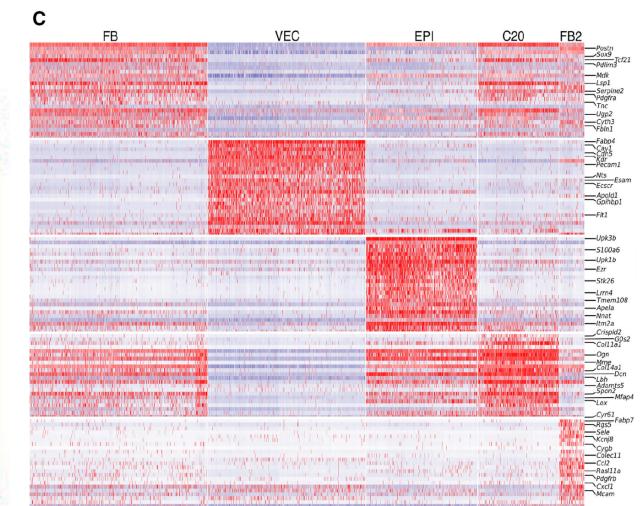
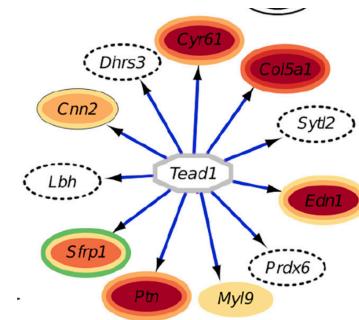
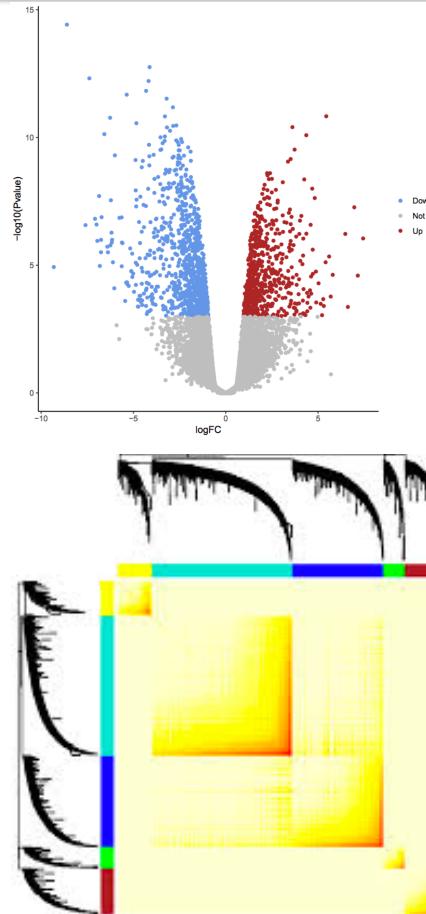
- Biological rational
- Theoretical bases of theories, intuitions and tools.
- Practical demonstration
- Links to further resources in case needed
- A discussion, not a lecture

A workflow of a transcriptomic study



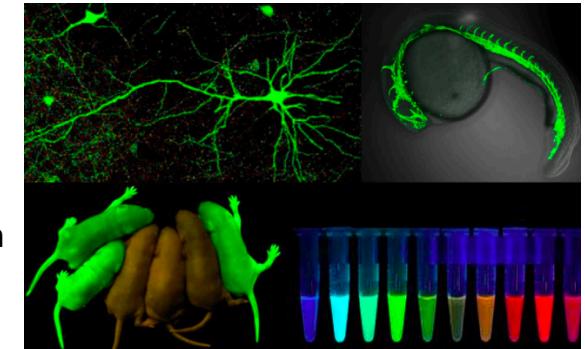
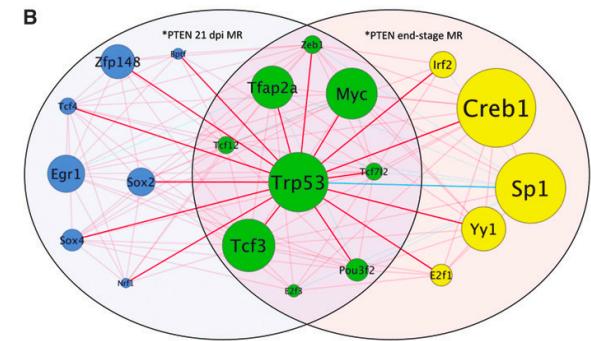
Prerequisite: identify a group of genes

- How to get a set of interesting genes?
 - Differential expression analysis
 - Clustering
 - WGCNA--Weighted Gene Co-expression Network Analysis
 - Dynamic tree cutting.



Why study gene regulatory network

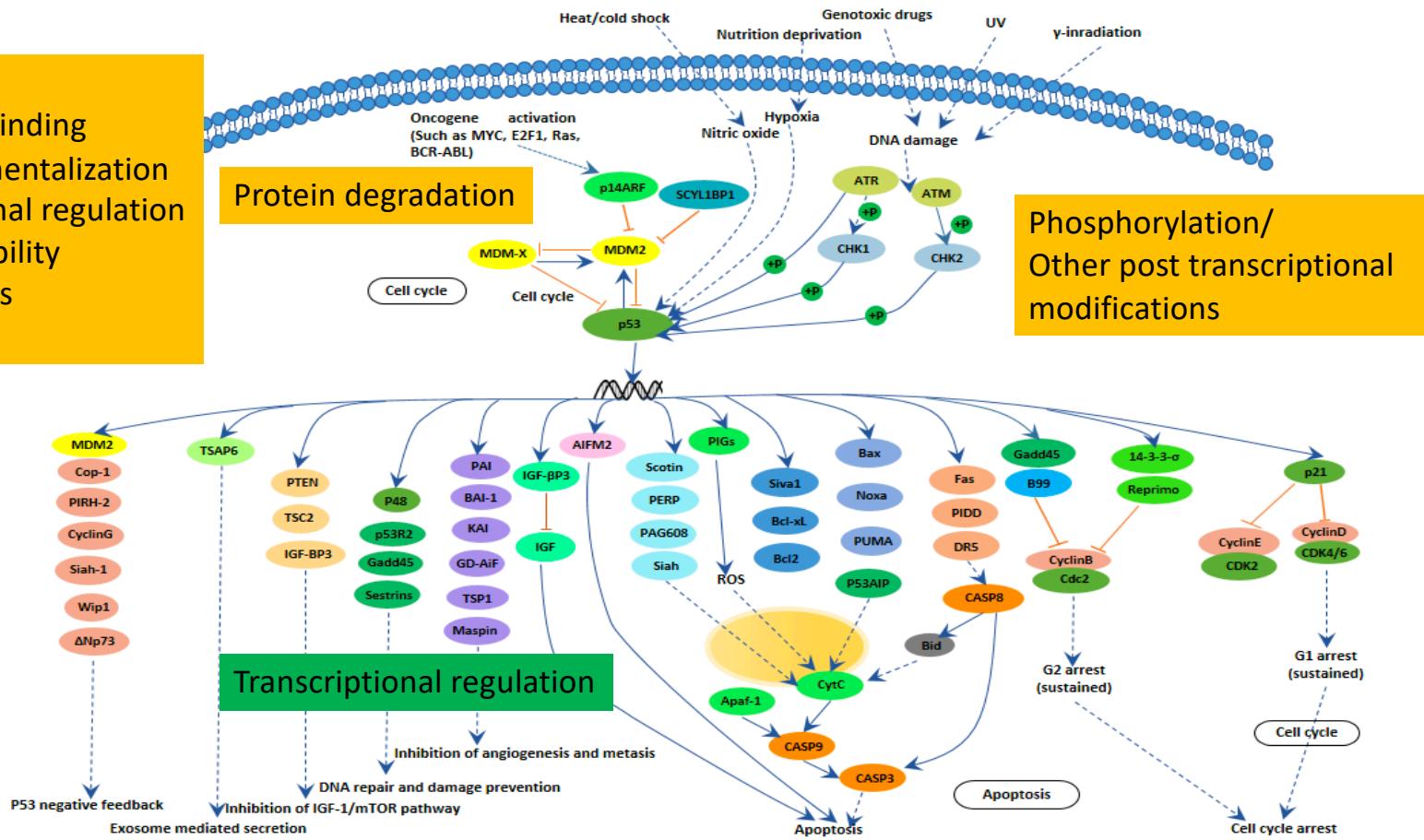
- Why
 - High throughput are usually screening procedure for key players
 - Gene lists of few hundreds do not tell internal relationship between genes.
 - Regulatory information is hidden in the statistical relationships
 - Important down-stream prove is usually costly, tediously and risky
 - Need to have meaningful hypothesis to test
- Format
 - Prerequisites: well defined list of genes of interest
 - Output: a network contains the statistical relationship of all genes.
- Aims
 - Finding key candidate genes/master regulators for validation.
- Challenges
 - Data are massive, and mostly static that do not reflect dynamic regulation
 - Relationships can take various forms, linear or non-linear
 - Statistical inference



Expensive, tedious, time consuming, complicated

A side note: GRN is only a subset of cellular network

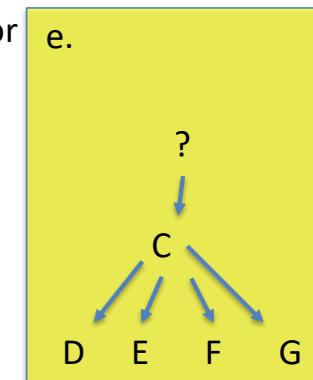
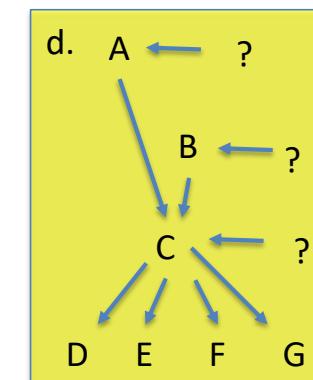
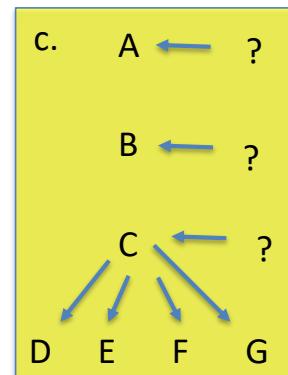
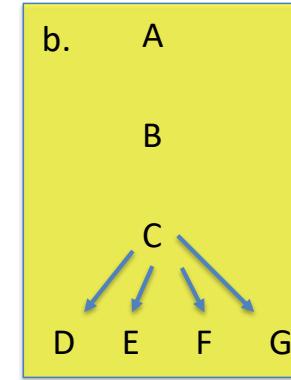
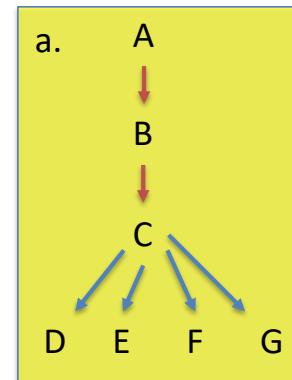
Others
 Cofactor binding
 Compartmentalization
 Translational regulation
 mRNA stability
 Epigenetics
 ...





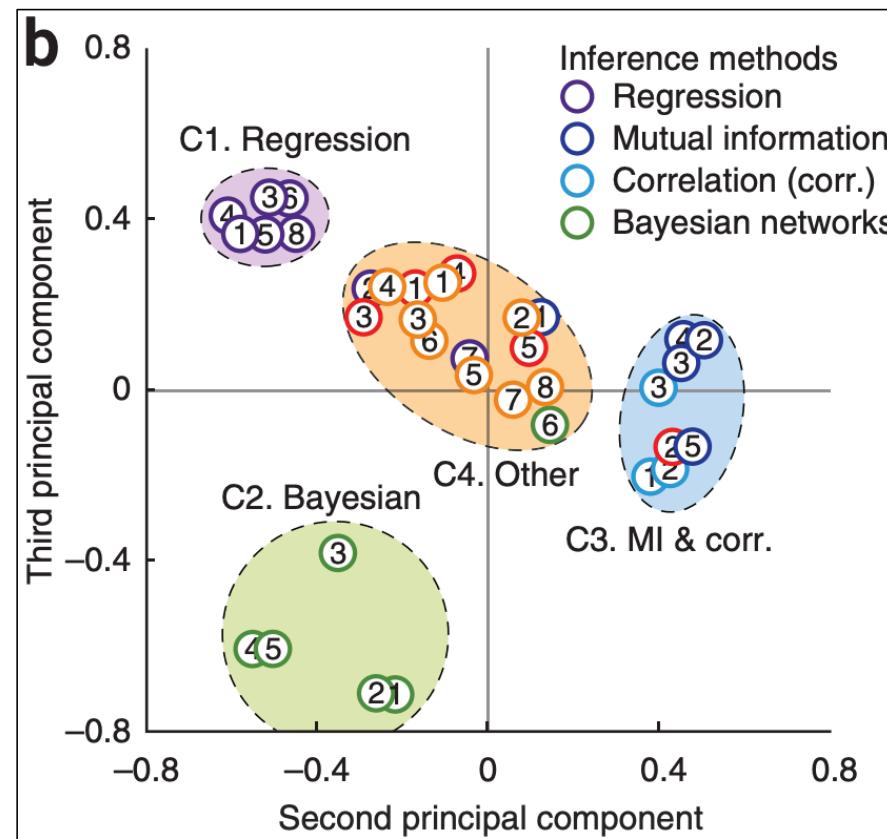
A schematic illustration on the difference

- (a) a conventional structure of intracellular signaling
- (b) Biochemical link will be invisible in GRN.
- (c) Other regulators kicks in
- (d) Upstream factors may be independent from each other in the transcriptional RGN.
- (e) Upstream factors may be invisible.



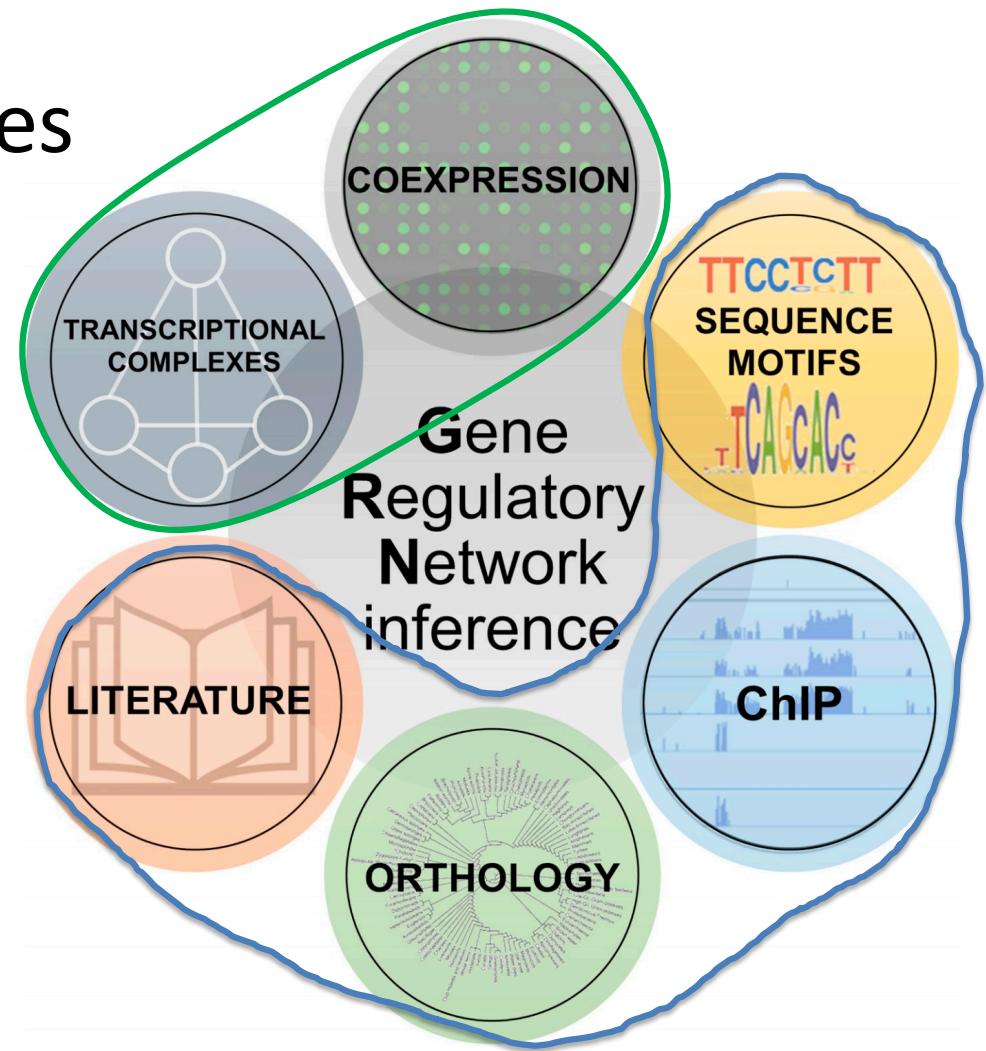
or

DREAM5– Network Inference Challenge (2010)



Computational Strategies

- Infer network through expression patterns based on linear/non-linear relationship between genes.
 - Linear relationships
 - Mutual information—linear/non-linear statistic relationships
 - Bayesian network /Bayes Net
 - Regression tree + random forest
- Predicting master regulators through promoter sequences
 - cis-Target and iRegulon
- Combinatory approach
 - SCENIC



Mercatelli et al., 2019

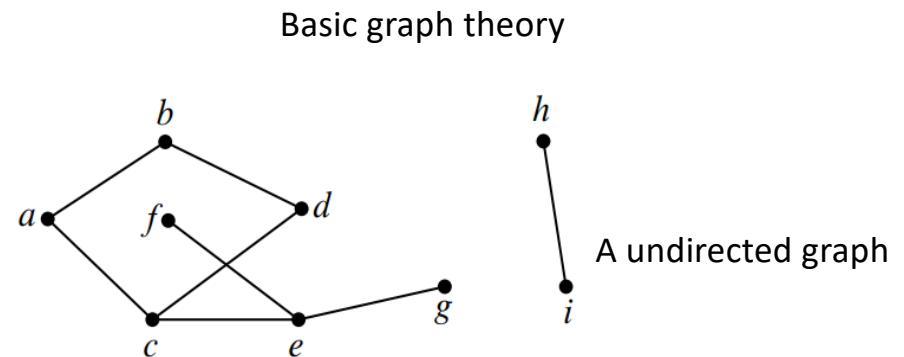
Overview of Tools in GRN inference

Software	ARACNE	NetworkInference /PIDC	bnlearn	Genie3	iRegulon	SCENIC
semantics	Mutual information	Partial Information decomposition	Bayes theory	Random Forest, Regression tree	Promoter and TF binding sequence, database	Combination of regression and promoter sequence
years published	2006	2017	2009	2010	2014	2017
No. of cited	2179	82	894	658	337	265
FullName/explanation	Algorithm for the Reconstruction of Accurate Cellular Networks	Using proportional unique contribution (PUC) to a target gene	Bayes net structure and parameter learning, causality	GEnet Network Inference with Ensemble of trees	reverse-engineer the transcriptional regulatory network with regulatory sequence analysis	single-cell regulatory network inference and clustering
Implementation	GUI (geWorkbench)	Julia	R	R	GUI (Cytoscape)	R, Python
type of experiment	Microarray, bulk RNA-seq	Single cell data	General	single cell data	a list of gene names	single cell data
input format	csv	csv	csv	csv	a list	csv/loom file
output	network file	network file	directed network file	network file	network file/binding sequences	network file/heatmap

Graph/network theory

--What are we estimating

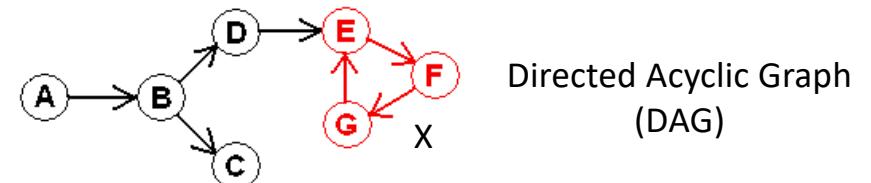
- Graph (network) theory
 - Vertex (Vertices)/nodes
 - Genes
 - Edges
 - Undirected graph
 - ARACNE, PIDC
 - Directed Acyclic Graph (DAG)
 - Bayes net
 - Edge weights



The graph in Figure 5.1 is expressed mathematically as $G = (V, E)$, where:

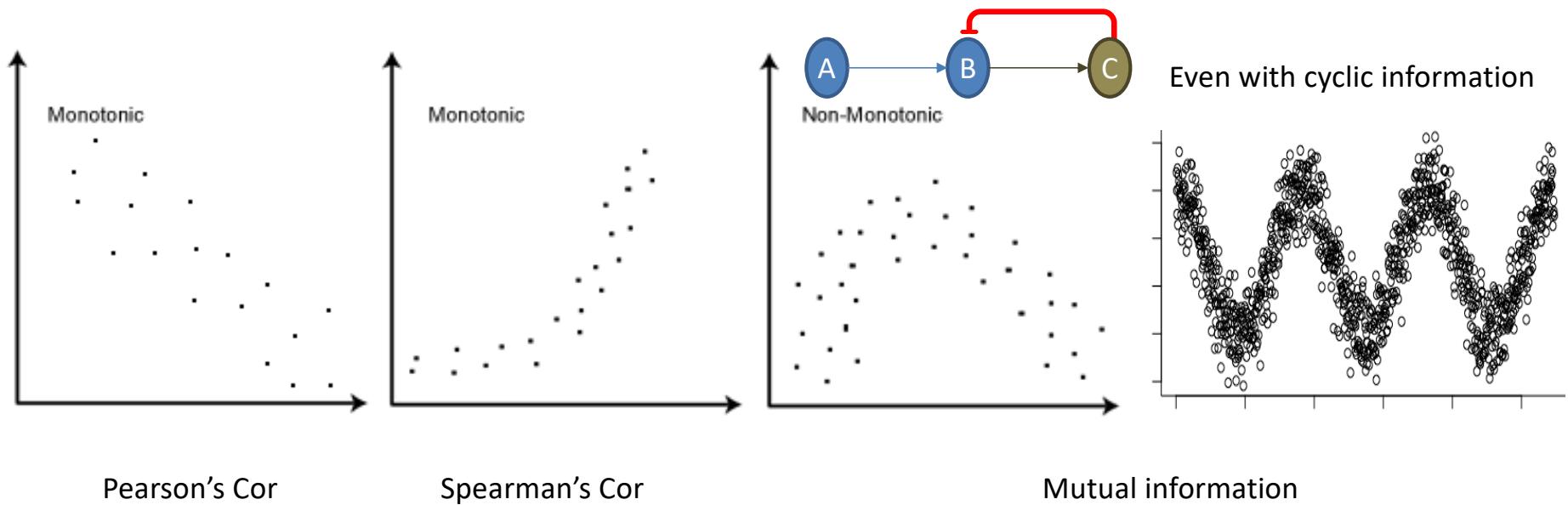
$$V = \{a, b, c, d, e, f, g, h, i\} \text{ Vertex/node}$$

$$E = \{\{a, b\}, \{a, c\}, \{b, d\}, \{c, d\}, \{c, e\}, \{e, f\}, \{e, g\}, \{h, i\}\}.$$

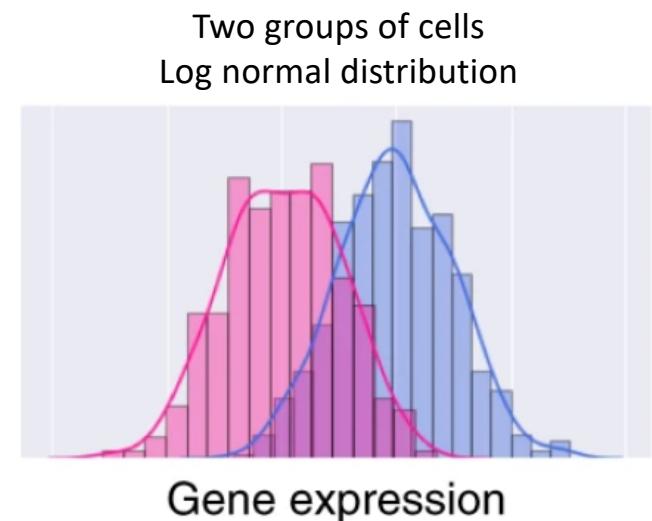
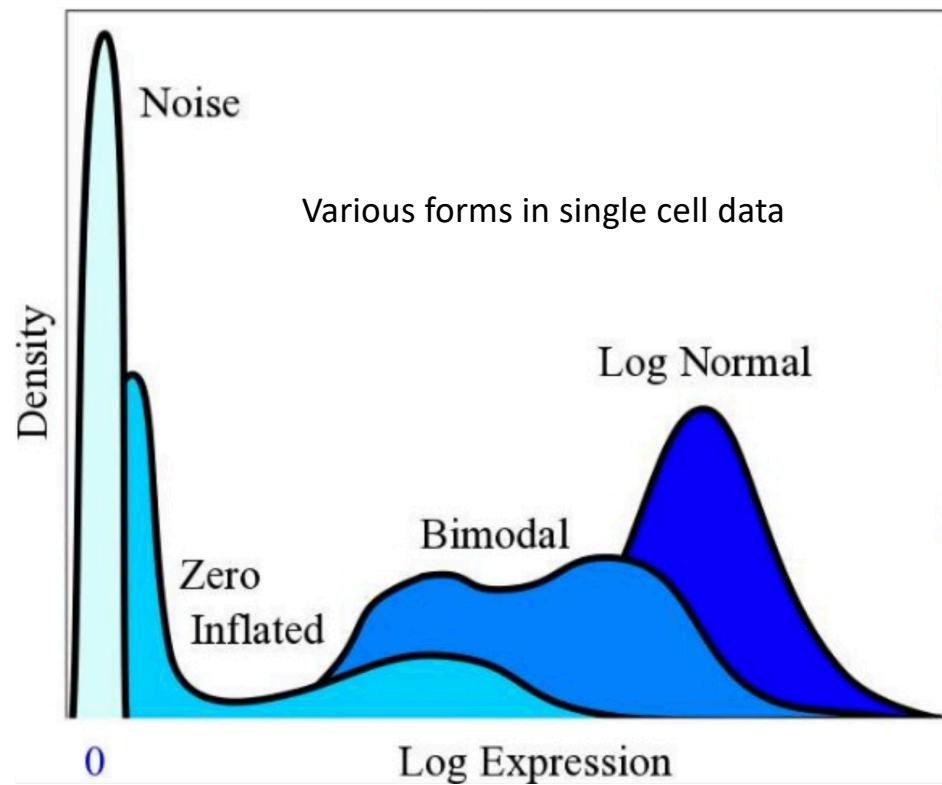


Types of statistical relationship

- Pearson's correlation, low computational complexity, and their capability of inferring genome-wide networks even when a relatively low number of samples ($n = 50$) is available
- Spearman's correlation, rank based, no assumption on normal distribution
- Mutual information, any statistical relationship. But requires N to be sufficient for approximation.



Various types of distributions of gene expression

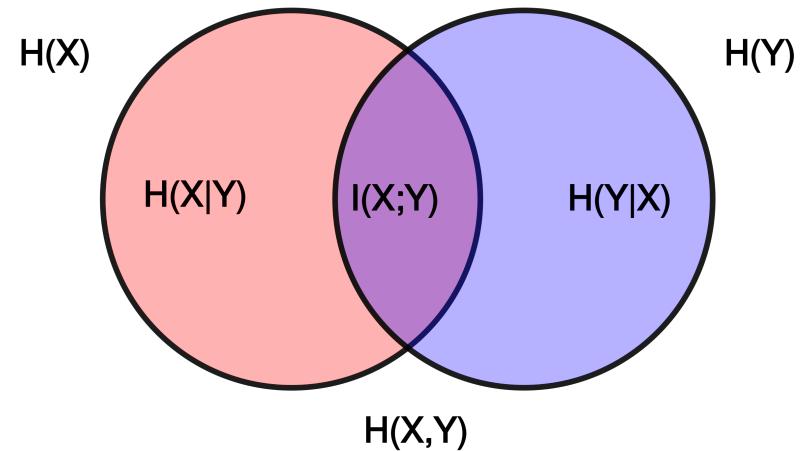


<https://www.slideshare.net/TimothyTickle/introduction-to-singlecell-rnaseq>



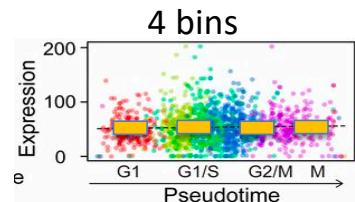
Information theory

- Entropy,
 - Statistical information of a random variable can be calculated as Shannon's entropy
 - Statistical relationship (overlap) between two random variables can be calculated as mutual information



Shannon's Entropy—measure of information content. (Not the entropy in physics)

- Example:
 - Gene1,
 - Probability of gene expression at the G0 is 100% because all states average the same
 - Gene2,
 - Probability of gene expressed at high level, $2/4=50\%$
 - at low level, $2/4=50\%$



$$H_1 = \frac{1}{1} \times \log_2(1/1) + \text{same} + \text{same} + \text{same} = 0 \text{ bits}$$

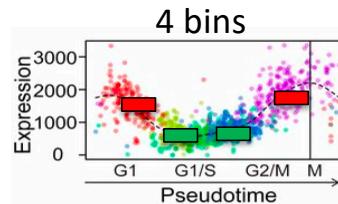
$$H = \sum_{i=1}^n p_i \times \log_2\left(\frac{1}{p_i}\right)$$

All the surprises you have got = entropy

How many times this event happen

That's why the unit is 'bits'.

How surprise this event is. In another word, how rare is the event.



$$H_2 = \frac{1}{(50\%)} \times \log_2(1/(50\%)) + \frac{1}{(50\%)} \times \log_2(1/(50\%)) + \text{same} + \text{same} = 2 \times 4 = 8 \text{ bits}$$

Mutual Information

- $H(X)$, $H(Y)$ are the information contents for X and Y .
- $I(X;Y)$ is the mutual information of X and Y .

All the information you have got = entropy

Observed joint probability

Mutual information

$$MI_{ij} = \sum_{x_i} \sum_{x_j} p(x_i, x_j) \log_2 \frac{p(x_i, x_j)}{p(x_i)p(x_j)}$$

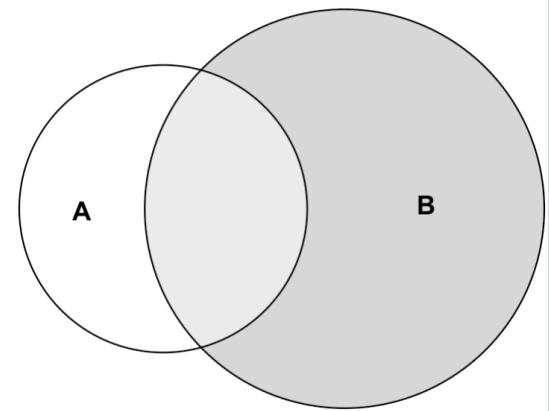
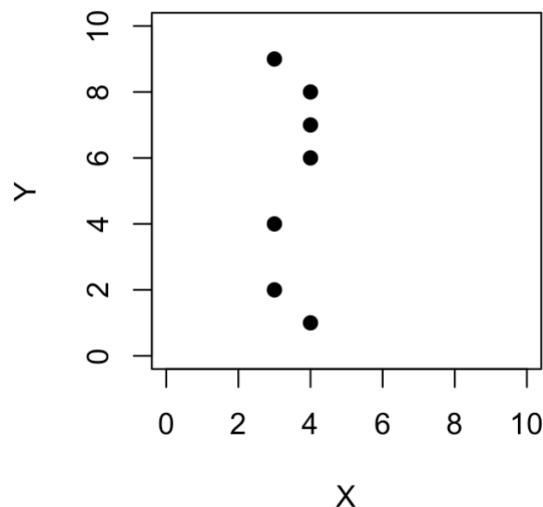
Equal to joint probability assuming x_i, x_j co-occur purely by chance.

The Venn diagram shows two overlapping circles. The left circle is labeled $H(X)$ and contains the region $H(X|Y)$. The right circle is labeled $H(Y)$ and contains the region $H(Y|X)$. The overlapping region between the two circles is labeled $I(X;Y)$.

An example

```
X=c(4,3,4,3,4,3,4)  
Y=c(1,4,6,2,7,9,8)  
plot(X,Y)
```

```
#install.packages("infotheo")  
library(infotheo)  
entropy(X)  
entropy(Y)  
mutinformation(X,Y)  
#install.packages("eulerr")  
library(eulerr)  
fit <- euler(c(A = entropy(X), B = entropy(Y), "A&B" = mutinformation(X,Y)))  
plot(fit)
```



Breaking indirect connection, by DPI

Data processing inequality (DPI), to remove indirect interaction

$$x_i \rightarrow x_j \rightarrow x_k,$$

then,

$$I(x_i, x_k) \leq \min \{ I(x_i, x_j), I(x_j, x_k) \}$$

If i and k are not directly connected,
the correlation of them will not be
high as a direct connection.

Illustration of how the mutual information is calculated with 3 variables

<https://www.youtube.com/watch?v=3iplfAfGzI>

Notes on running ARACNE

geWorkbench will have ARACNE by default

http://wiki.c2b2.columbia.edu/workbench/index.php/Download_and_Installation

What data to use for ARACNE

The Bcell-100.exp as an expression file

http://wiki.c2b2.columbia.edu/workbench/index.php/Tutorial - Data#Tutorial_data_files

The HG_U95Av2.na36.annot.csv is the most updated version instead of the

- The HG_U95Av2.na36.annot.csv
- The file need registration on thermofisher website!!!

Troublesome

The layout of the geWorkbench is different from the video,

1. The project file cannot be created
2. The window looks different as well, no sub-division of windows at the bottom.



Discussion on ARACNE

- Early and most widely used GRN software
- Straightforward concept of mutual information
- Processing inequality to break indirect linkages
- Too slow, newer implementation may be useful



Demonstration on ARACNE in geWorkstation

Bioinformatics, 2016 Jul 15;32(14):2233-5. doi: 10.1093/bioinformatics/btw216. Epub 2016 Apr 23.

ARACNe-AP: gene network reverse engineering through adaptive partitioning inference of mutual information.

Lachmann A¹, Giorgi FM¹, Lopez G¹, Califano A¹.

Author information

1 Department of Systems Biology, Columbia University, New York, NY, USA.

Abstract

The accurate reconstruction of gene regulatory networks from large scale molecular profile datasets represents one of the grand challenges of Systems Biology. The Algorithm for the Reconstruction of Accurate Cellular Networks (ARACNe) represents one of the most effective tools to accomplish this goal. However, the initial Fixed Bandwidth (FB) implementation is both inefficient and unable to deal with sample sets providing largely uneven coverage of the probability density space. Here, we present a completely new implementation of the algorithm, based on an Adaptive Partitioning strategy (AP) for estimating the Mutual Information. The new AP implementation (ARACNe-AP) achieves a dramatic improvement in computational performance (200x on average) over the previous methodology, while preserving the Mutual Information estimator and the Network inference accuracy of the original algorithm. Given that the previous version of ARACNe is extremely demanding, the new version of the algorithm will allow even researchers with modest computational resources to build complex regulatory networks from hundreds of gene expression profiles.

AVAILABILITY AND IMPLEMENTATION: A JAVA cross-platform command line executable and detailed usage guide are freely available on Sourceforge (<http://sourceforge.net/>)

CONTACT: califano@c2b2.columbia.edu

SUPPLEMENTARY INFORMATION: Supplementary data are available at Bioinfo

© The Author 2016. Published by Oxford University Press.

Bioinformatics, 2019 Jun 1;35(12):2165-2166. doi: 10.1093/bioinformatics/bty907.

SJARACNe: a scalable software tool for gene network reverse engineering from big data.

Khatamian A¹, Paull EO², Califano A², Yu J¹.

Author information

1 Department of Computational Biology, St. Jude Children's Research Hospital, Memphis, TN, USA.

2 Department of Systems Biology, Columbia University, New York, NY, USA.

Abstract

SUMMARY: Over the last two decades, we have observed an exponential increase in the number of generated array or sequencing-based transcriptomic profiles. Reverse engineering of biological networks from high-throughput gene expression profiles has been one of the grand challenges in systems biology. The Algorithm for the Reconstruction of Accurate Cellular Networks (ARACNe) represents one of the most effective and widely-used tools to address this challenge. However, existing ARACNe implementations do not efficiently process big input data with thousands of samples. Here we present an improved implementation of the algorithm, SJARACNe, to solve this big data problem, based on sophisticated software engineering. The new scalable SJARACNe package achieves a dramatic improvement in computational performance in both time and memory usage and implements new features while preserving the network inference accuracy of the original algorithm. Given that large-sampled transcriptomic data is increasingly available and ARACNe is extremely demanding for network reconstruction, the scalable SJARACNe will allow even researchers with modest computational resources to efficiently construct complex regulatory and signaling networks from thousands of gene expression profiles.

AVAILABILITY AND IMPLEMENTATION: SJARACNe is implemented in C++ (computational core) and Python (pipelining scripting wrapper, ≥3.6.1). It is freely available at <https://github.com/jyyulab/SJARACNe>.

SUPPLEMENTARY INFORMATION: Supplementary data are available at Bioinformatics online.

© The Author(s) 2018. Published by Oxford University Press.

<https://github.com/califano-lab/ARACNe-AP>



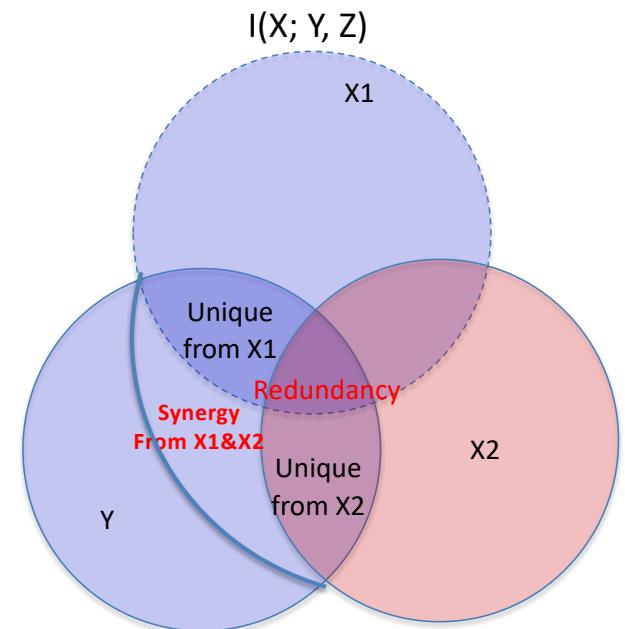
Method 2, Partial Information Decomposition



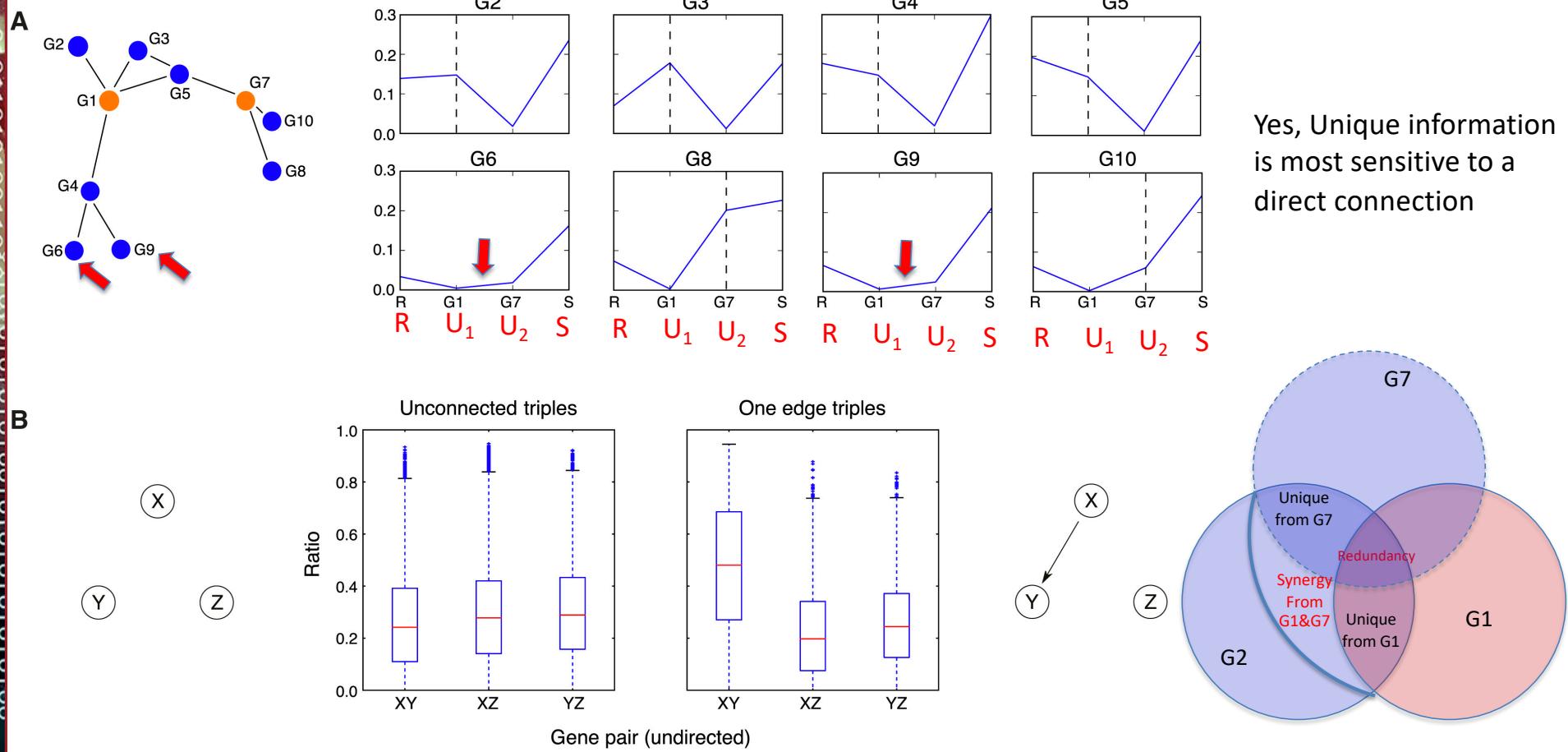
Information theory 2: Partial Information Decomposition

- Consider three variables X_1 , X_2 and Y
- Consider that Y is dependent on X_1, X_2
- The information from X_1 and X_2 that matches Y can be decomposed to 4 components (U_{X_1} , U_{X_2} , Redundancy and Synergy)

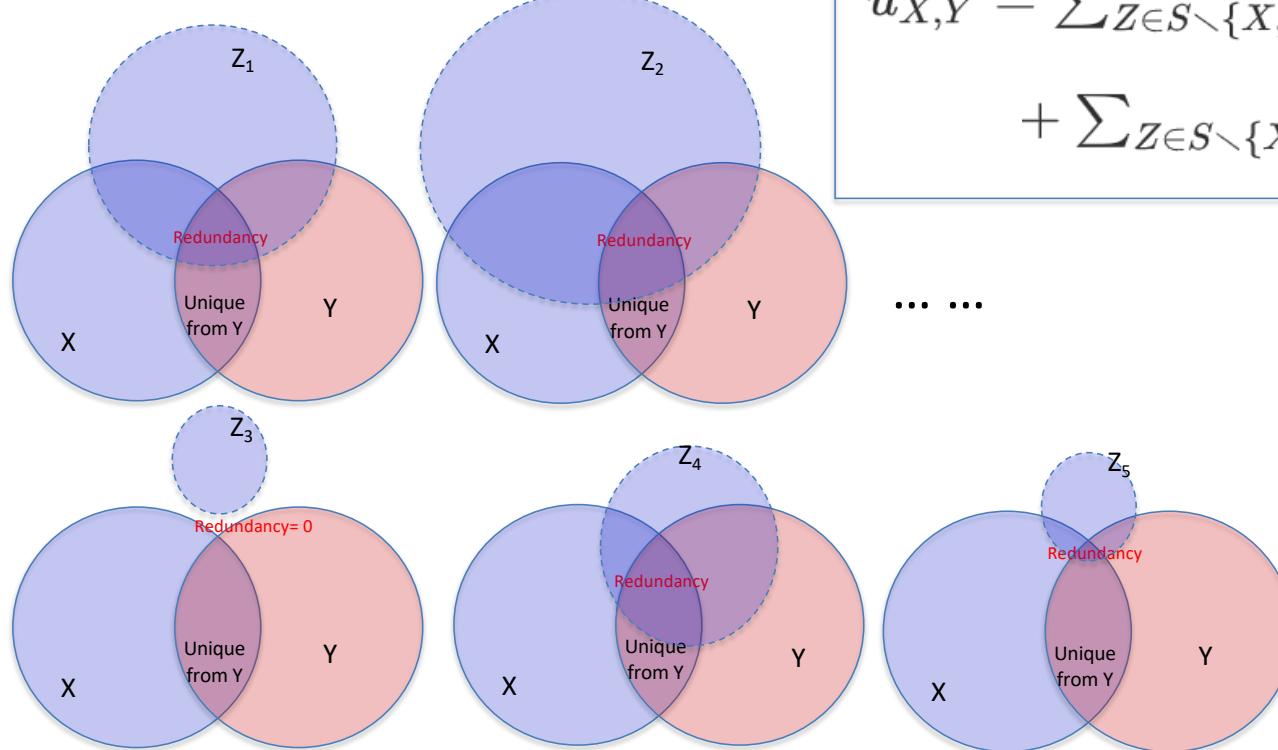
Information about Target Y provided by two sources X_1, X_2 .



Is any of these components an indicator of a network connection?

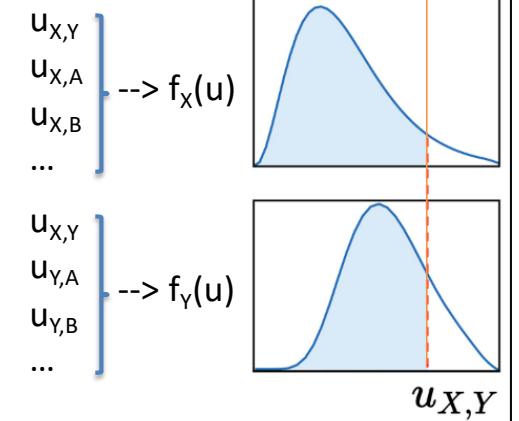


Proportional Unique Contribution



$$u_{X,Y} = \sum_{Z \in S \setminus \{X,Y\}} \frac{\text{Unique}_Z(X;Y)}{I(X;Y)} + \sum_{Z \in S \setminus \{X,Y\}} \frac{\text{Unique}_Z(Y;X)}{I(X;Y)}$$

... ...



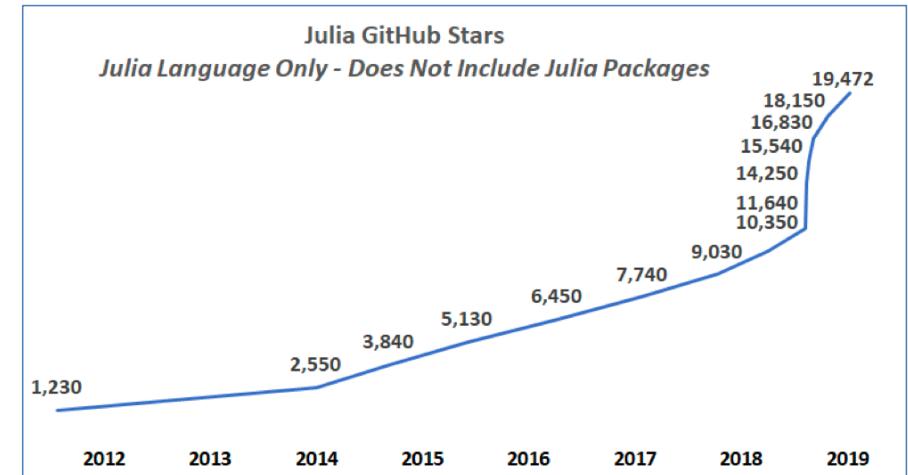
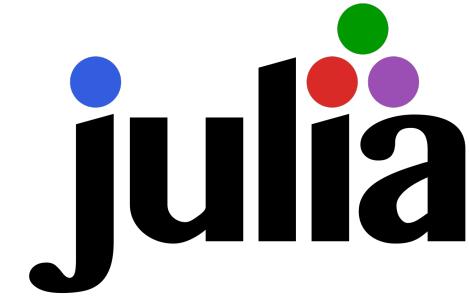


Discussion on NetworkInference

- Good at discovery of single edges, may systematically hind nodes with dense connections.
- Relatively new, not sufficiently validated.
- Easy to use in Julia, may need a HPC to run large data.
- Undirected, and no attempt is made to find the directionality of a regulation.

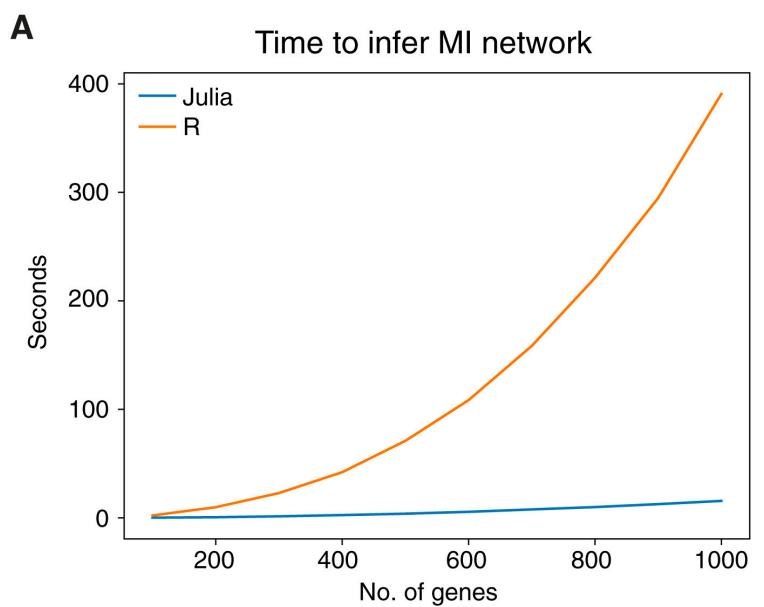
Julia-- A fresh approach to numerical computing

- A young language developed by researchers in MIT on 2012.
- Advantage, speed of C and intuitive as python.
- Use all the libraries developed for python.
- Disadvantage: changing fast, as versions upgrades.



Implementation in Julia

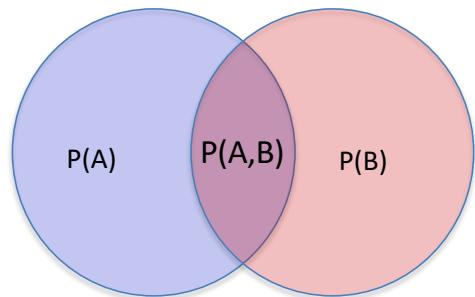
- Using NetworkInference, Julia
 - Install Julia
 - <https://julialang.org/downloads/>, download the binary file for Generic linux 64-bit
 - Install NetworkInference
 - Run examples





Demonstration on NetworkInference in Julia

Method 3, Bayes Net – conditional dependence



$$P(A, B) = P(A | B) * P(B) = P(B | A) * P(A)$$



Bayes's rule:

$$P(A | B) = \frac{P(B | A)P(A)}{P(B)}$$

Bayesian network – formulation

If A and B are independent

A= winter (yes 25%, no 75%)

B= happy (yes 50%, no 50%)



$$P(A) = 25\%$$

$$P(B) = 50\%$$

$$P(\text{winter, happy}) =$$

$$P(A,B) = 25\% * 50\% = 12.5\%$$

Right

How about if B dependent on A:

A= winter (yes 25% or no 75%)

B= cold weather (overall yes 25%, no 75%)



$$P(A) = 25\%$$

$P(B|A) = 100\%$ on winter and 0% on other seasons.

Overall 25%

The conditional probability of winter & cold is

$$P(A=\text{winter}, B=\text{cold}) = P(A)P(B) = 25\% * 25\% = 6.25\% \text{ wrong!}$$

$$P(\text{winter, cold}) =$$

$$P(A=\text{winter}; B=\text{cold}) = P(A)P(B|A) = 25\% * 100\% = 25\%$$

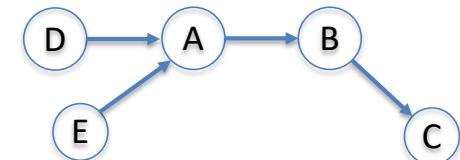
A= winter (yes or no 50% each)

B= cold weather (yes or no 100%)

C= wear sweater (yes or no, 50%)

D= month of a year

E= location on the earth

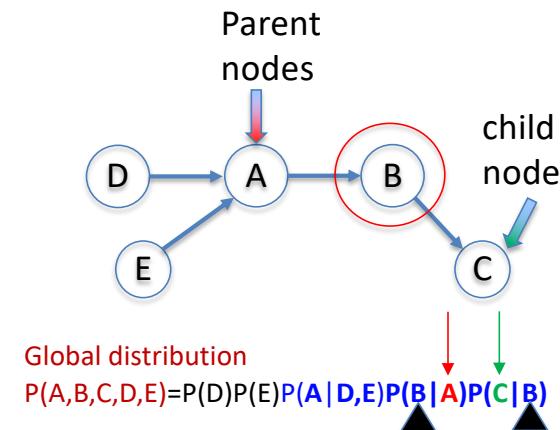
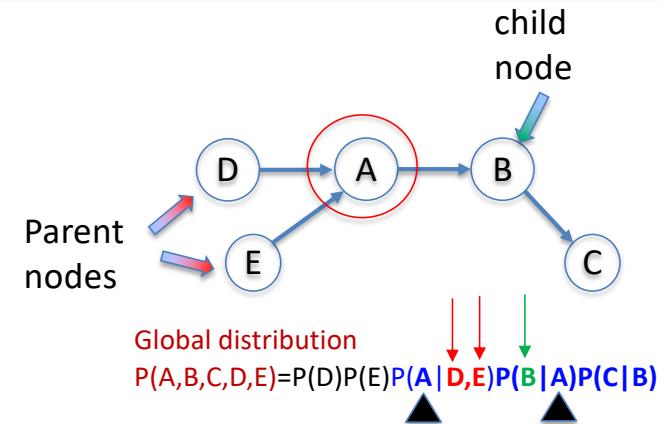


Global distribution

$$P(A, B, C, D, E) = P(D)P(E)P(A|D, E)P(B|A)P(C|B)$$

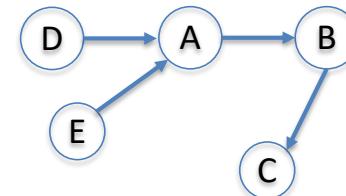
Parent nodes and child node

- To a given node
 - Conditional nodes (reasons or contributing factors) are called parents.
 - The consequent nodes are child nodes.



Curse of the dimensionality

- Complexity increases exponentially with respect to the
 - Number of bins each node can take.
 - Number of parent nodes that a node can have.
- Solutions
 - Bayesian net expression is already a great simplification, but far from enough.
 - Breaking a huge network containing thousands of nodes into conditionally independent units of Markov Blankets.



Global distribution

$$P(A,B,C,D,E) = P(D)P(E)P(A|D,E)P(B|A)P(C|B)$$

With binary values, Boolean

$$P(D)P(E)P(A|D,E)P(B|A)P(C|B)$$

Bayesian values: 2 +2 +8 +4 +4 =20

Without the network, requires $2^5=32$ instantiations

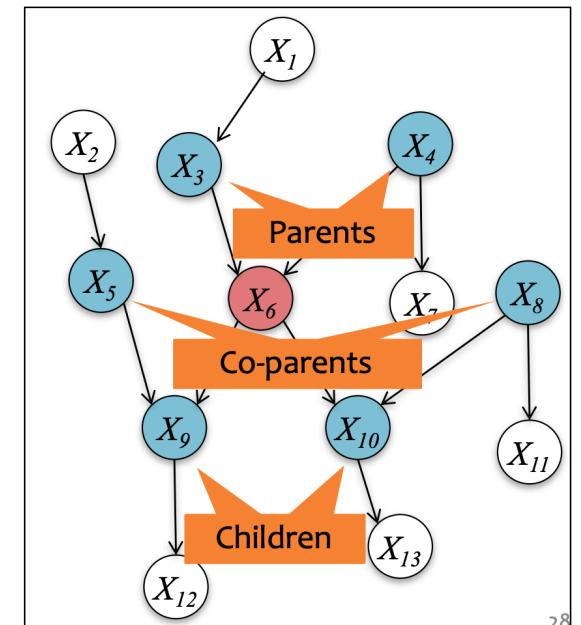
If each sample has 5 bins

Values to fully enumerate the distribution table: $5^5=1875$

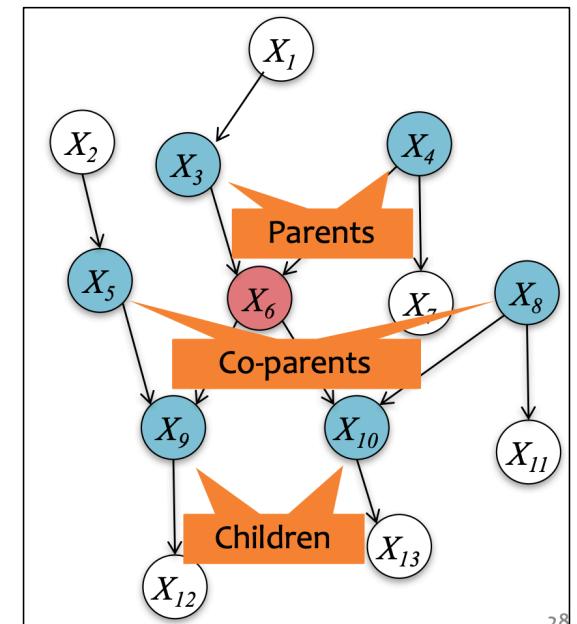
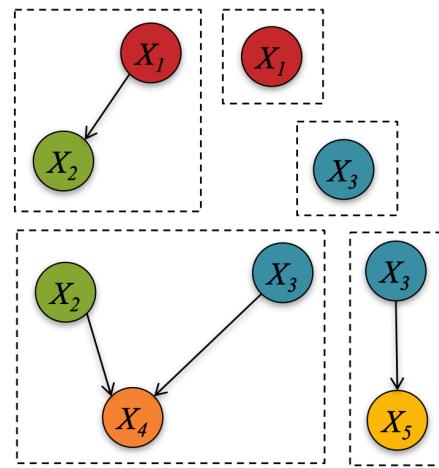
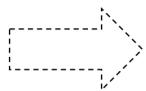
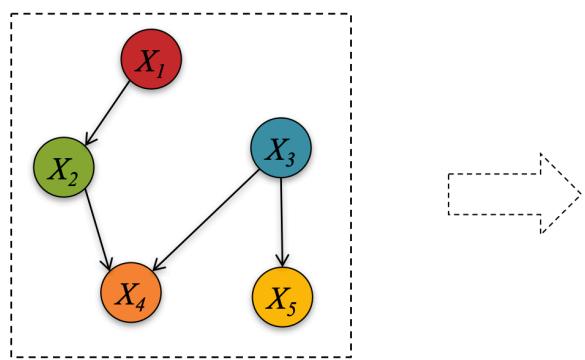
Enumerate the Bayesian network: $5 + 5 + 125 + 25 + 25 = 185$

Computation: how to break up a huge network to small local problems

- Optimization of the local variables
 - For computation purpose, you need to break a huge network into smaller pieces.
 - for a node in a graphical model, **Markov blanket** contains all the variables needed to do approximation, that shield the node from the rest of the network.
- Inferring the network/parameters can be done with 3 methods
 - Enumerate from the data, may overfit
 - Using maximum likelihood
 - Using expectation maximization

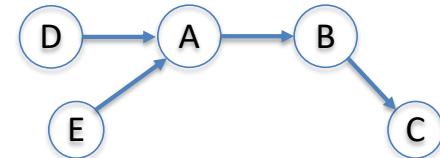


Decomposition of a Bayesian network



For gene expression data

- Objective: get the DAG network as the model of the gene regulatory relationships:
 - Component 1, the network structure
 - the connection, find parents of each node
 - the direction, how to assign causality
 - Component 2, the parameters
 - Conditional probabilities



Global distribution
 $P(A,B,C,D,E) = P(D)P(E)P(A|D,E)P(B|A)P(C|B)$

Probability of a model (M) given the data set (D).

The problem

Step 1

Step 2

$$\underbrace{P(\mathcal{M} \mid \mathcal{D}) = P(\mathcal{G}, \Theta \mid \mathcal{D})}_{\text{learning}} = \underbrace{P(\mathcal{G} \mid \mathcal{D})}_{\text{structure learning}} \cdot \underbrace{P(\Theta \mid \mathcal{G}, \mathcal{D})}_{\text{parameter learning}}$$

A set of edges
(graph, structure)
a set of conditional probabilities
(parameters)

Learn the network structure

- Divide the bayes net into two components
 - Θ , the conditional probabilities
 - \mathcal{G} , the structure
 - Can be decomposed to each node with parents (X_i and Π_{X_i}).

The problem Step 1 Step 2

$$P(\mathcal{M} | \mathcal{D}) = \underbrace{P(\mathcal{G}, \Theta | \mathcal{D})}_{\text{learning}} = \underbrace{P(\mathcal{G} | \mathcal{D})}_{\text{structure learning}} \cdot \underbrace{P(\Theta | \mathcal{G}, \mathcal{D})}_{\text{parameter learning}}$$

Probability of a model (M) given the data set (D).

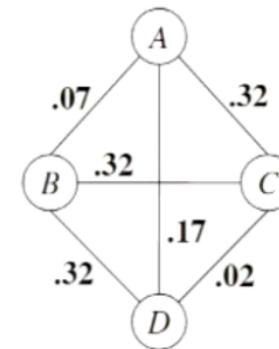
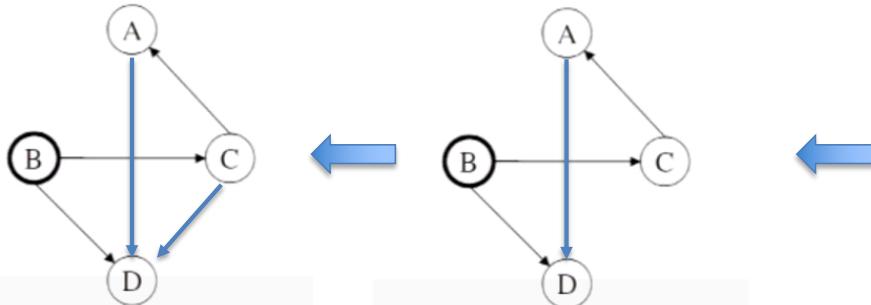
$$\begin{aligned} P(\mathcal{G} | \mathcal{D}) &\propto P(\mathcal{G}) P(\mathcal{D} | \mathcal{G}) = P(\mathcal{G}) \int P(\mathcal{D} | \mathcal{G}, \Theta) P(\Theta | \mathcal{G}) d\Theta. \\ &= P(\mathcal{G}) \prod_{i=1}^N \int P(X_i | \Pi_{X_i}, \Theta_{X_i}) P(\Theta_{X_i} | \Pi_{X_i}) d\Theta_{X_i}. \end{aligned}$$
$$\text{MI}_{\mathcal{D}}(X, U) \stackrel{\text{def}}{=} \sum_{x,u} \Pr_{\mathcal{D}}(x, u) \log \frac{\Pr_{\mathcal{D}}(x, u)}{\Pr_{\mathcal{D}}(x)\Pr_{\mathcal{D}}(u)}$$

Learning the graph basic

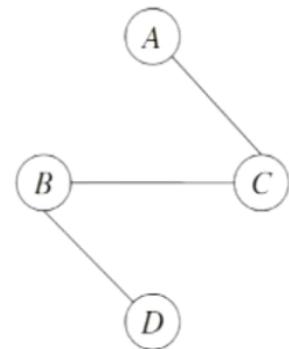
- Constructing a tree structure (each node can only have one parent node).
- Step 1, learning the Maximum Spanning Tree.
- Add direction through starting from a randomly node.
- The resulting directed graph will be used as seed for other algorithms.
- Optimization of a graph, a commonly used approach constrained on a penalty on the complexity ($||G||$) of the graph.

$$\text{Score}(G|\mathcal{D}) \stackrel{\text{def}}{=} \text{LL}(G|\mathcal{D}) - \underline{\psi(N) \cdot ||G||}$$

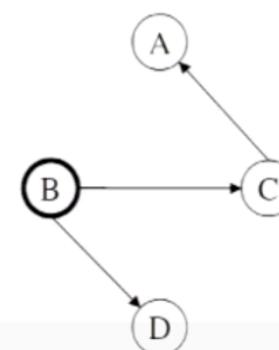
BIC score = Bayesian Information Criterion



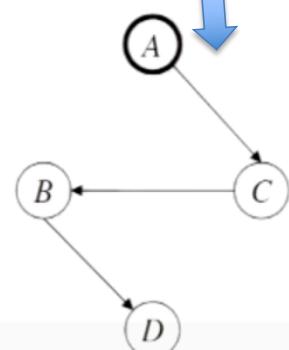
(a) mutual information graph



(b) maximum spanning tree



(c) maximum likelihood tree



(d) maximum likelihood tree

Induction of Causality algorithm

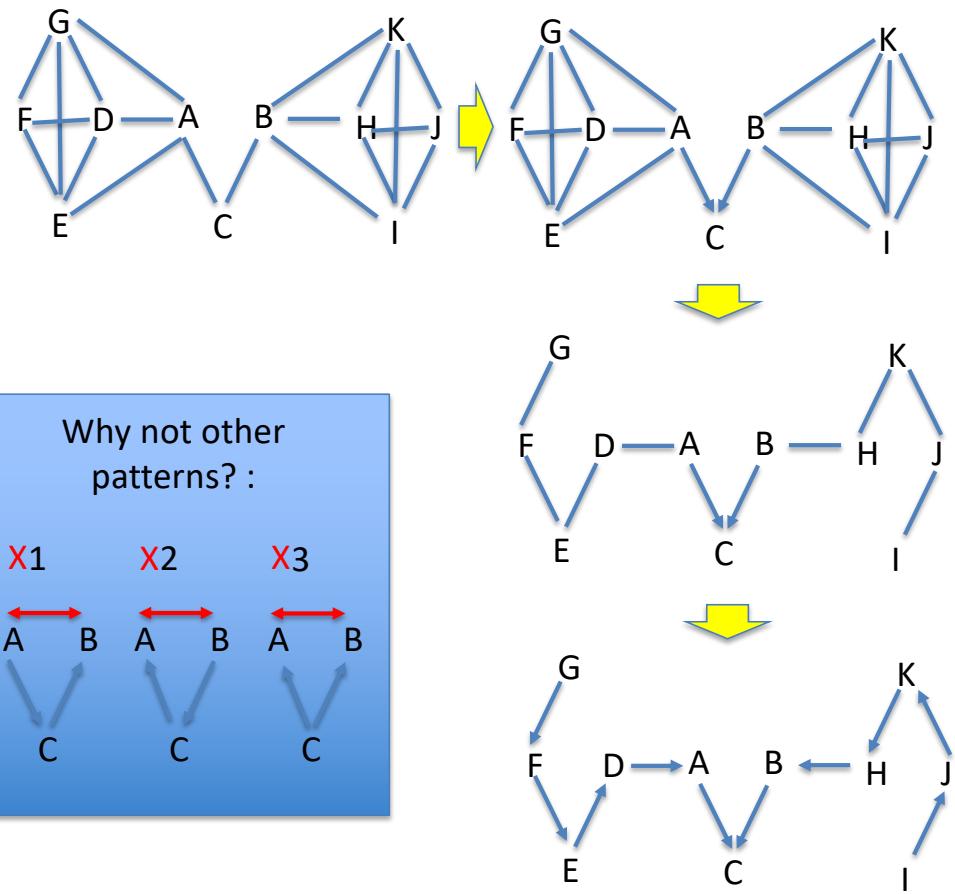
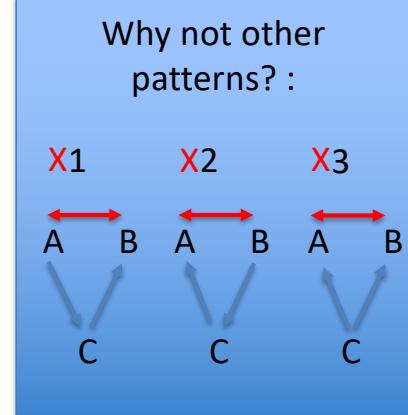
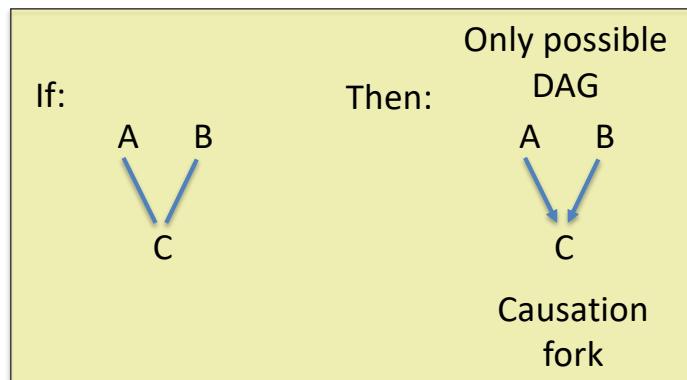
The Induction of Causality Algorithm:

If, these are true:

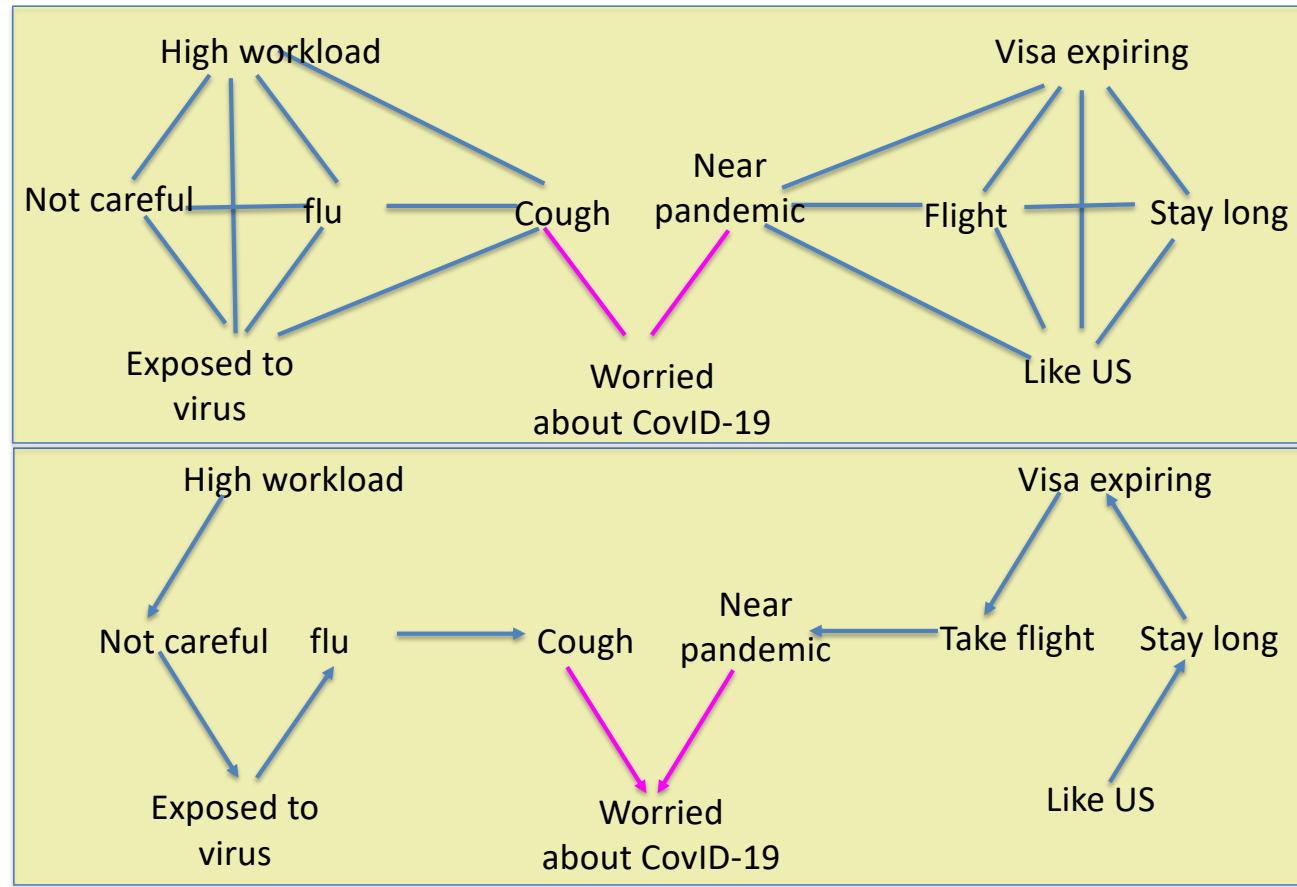
1. A, B are not connected through any other connection.
2. A, B has a common connection to C

Then:

The only possible connection is as draw in the Causation Fork, where C is the common target of A, B.



A concrete example





Demonstration of structural learning

- Bnlearn, <https://www.youtube.com/watch?v=4JkddqxGrO0>

Inference of network parameters – conditional probabilities

Log-likelihood decomposes into family-based components

Let G be a network structure and \mathcal{D} be a complete data set of size N . If $X|\mathbf{U}$ ranges over the families of structure G , then

$$\text{Objective function } \text{LL}(G|\mathcal{D}) = -N \sum_{X|\mathbf{U}} \text{ENT}_{\mathcal{D}}(X|\mathbf{U}),$$

where $\text{ENT}_{\mathcal{D}}(X|\mathbf{U})$ is the conditional entropy defined as follows:

$$\text{ENT}_{\mathcal{D}}(X|\mathbf{U}) = - \sum_{x|\mathbf{u}} \Pr_{\mathcal{D}}(x|\mathbf{u}) \log_2 \Pr_{\mathcal{D}}(x|\mathbf{u})$$

Decomposition is critical when learning network structure.

$$\theta^* = \operatorname{argmax}_{\theta} \text{L}(\theta|\mathcal{D}) \text{ iff } \theta^*_{x|\mathbf{u}} = \Pr_{\mathcal{D}}(x|\mathbf{u})$$



Steps of inferring the parameters in Bayesian network

Expectation Maximization

- Assign a set of random parameters θ^0 .
- Based on evidence samples, calculate the distribution of each sample.
- Go through all the samples.
- Construct the averaged distribution.
- Based on the averaged distribution, recalculate the set of parameters θ^1 .
- Repeat the previous step until θ^{K+1} and θ^K converges.

Using log-likelihood as a objective function to maximize

- Construct Log Likelihood formula.
- Use classical methods such as gradient decent to optimize the parameter with a assigned learning rate, to iterate and reach a local maximum.

Discussion on Bayesian Network

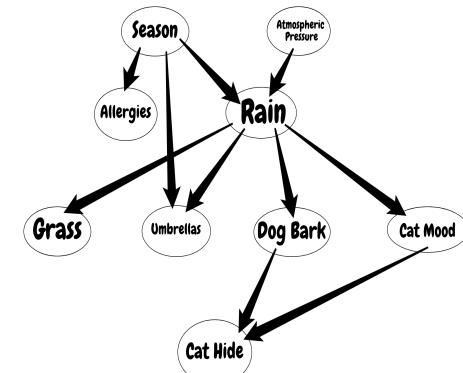
Pros

- Easy interpretation of result potentially with causality.
- Efficient software to calculate the skeleton of network.
- Integrated theory of causality theory, so the direction of regulation can be inferred.
- 2 rounds of pruning on edges so may mediate find better networks.

Cons

- Parameter learning requires large computation
- no efficient algorithm is available to calculate the Markov Blanket.

Combinatory approaches.



$$P(A | B) = \frac{P(B | A)P(A)}{P(B)}$$

Key reference

- Intuition understanding about entropy,
 - <https://www.youtube.com/watch?v=2s3aJfRr9gE>
- Calculation of mutual information using a concrete data sample.
 - <https://www.youtube.com/watch?v=3iplfAfGzI>
- CS262a: Learning and reasoning with Bayesian Networks Adnan Darwiche
 - 11a. Learning Parameters: Complete Data (Chapter 17)
 - <https://www.youtube.com/watch?v=gRVg0lZgLUG>
 - 11b. Learning Parameters: Incomplete Data (Chapter 17)
 - <https://www.youtube.com/watch?v=NDoHheP2ww4>
 - 12a. Learning Network Structure I (Chapter 17)
 - https://www.youtube.com/watch?v=RV2lInyq_bI
 - 12b. Learning Network Structure II (Chapter 17)
 - <https://www.youtube.com/watch?v=o-urnZRNnbY>
- Bnlearn <https://www.youtube.com/watch?v=4JkddqxGrO0>



Demonstration on bnlearn in R



Other resources

- GraphPlot, <http://juliagraphs.github.io/GraphPlot.jl/>
- Gamma distribution, <https://towardsdatascience.com/gamma-distribution-intuition-derivation-and-examples-55f407423840>
- `install.packages("igraph")`
- `install.packages("bnlearn")`
- `BiocManager::install("Rgraphviz")`
- iGraph for network analysis
<https://www.bioss.ac.uk/people/helen/igraphIntro.html>
- <https://www.r-bloggers.com/interactive-network-visualization-with-r/>



How to set up a tunel to server

- `install.packages('IRkernel') # Don't forget step 2/2!`
- `IRkernel::installspec()`
- `using Pkg`
- `Pkg.add("IJulia")`
- `user@local_machine$ ssh -N -L localhost:8888:localhost:8888
user@remote_mahcine`
- Paste this to the url to access the Julia – "localhost:1234"

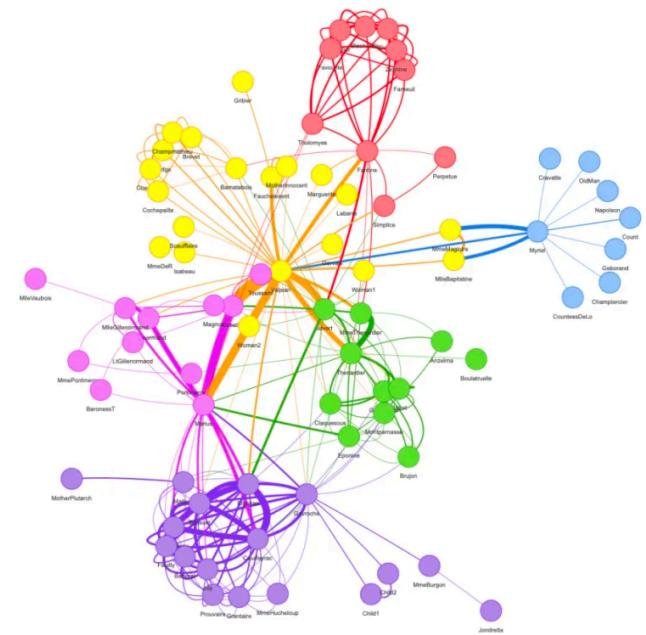


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- > tpm=read.table("S_GSE71485_Single TPM.txt",row.names=1,header=T)
 - > Tpm=tpm[rowMeans(tpm)>100,]
 - > write.table(Tpm,"S_GSE71485_Single TPM.txt")



Parameters in Bayesian network

$$P(A | B) = \frac{\text{likelihood prior}}{\text{posterior Evidence}}$$

$$P(\text{cold} | \text{winter}) = \frac{\text{posterior likelihood prior}}{\text{Evidence}} = \frac{P(\text{winter} | \text{cold})P(\text{cold})}{P(\text{winter})} = \frac{P(\text{winter} | \text{cold})P(\text{cold})}{P(\text{winter})} = \frac{100\% * 25\%}{25\%} = 100\%$$