

Regulatory network inference on developmental and evolutionary lineages

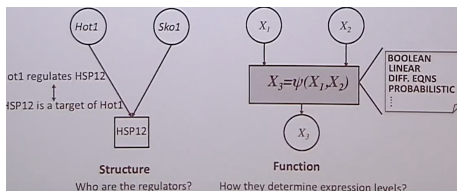
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<https://qdata.github.io/deep2Read>

A Regulatory Network

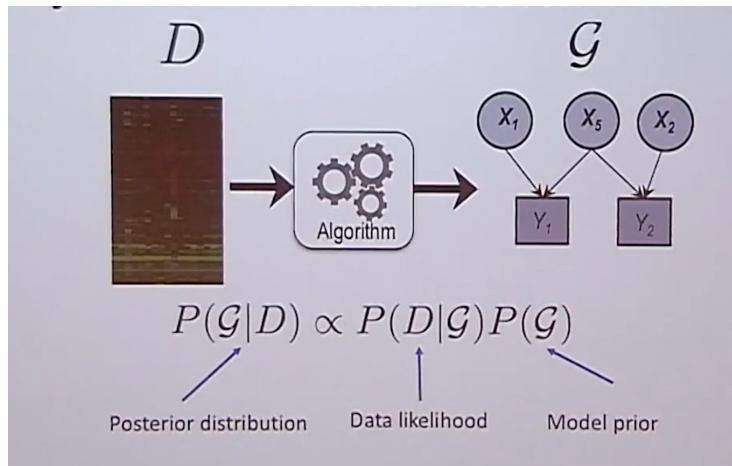
- TFs that affect gene expression level.
- Represented as *directed* graphs from TFs to target gene.
- Aim is to find the edges that exist.



Ways to infer networks

- Experimental
 - ChIP ChIP
 - Knock Out : knock down a TF and measure genome wide expression levels
 - DNase ATAC Seq + Sequence Specific Motifs
- Computational
 - Supervised: Train a classifier and run on target pairs
 - Unsupervised : Use gene expression data
 - Gene Level: more precise
 - Module Level : more interpretable

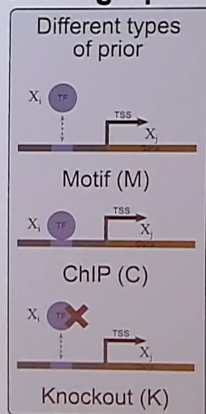
Bayesian formulation of Network Inference



$$P(G) = \prod_{X_i \rightarrow X_j \in G} P(X_i \rightarrow X_j) \prod_{X_i \rightarrow X_j \notin G} 1 - P(X_i \rightarrow X_j)$$

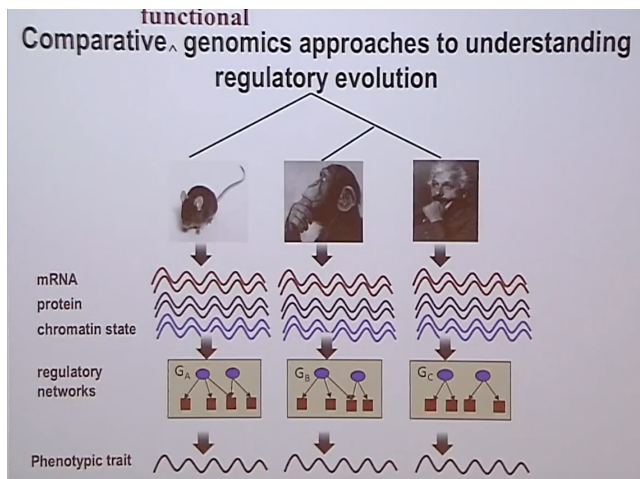
Defining prior distribution of the graph

$$P(X_i \rightarrow X_j) = \frac{1}{1 + \exp(-(\beta^S + \beta^M w_{ij}^M + \beta^C w_{ij}^C + \beta^K w_{ij}^K))}$$

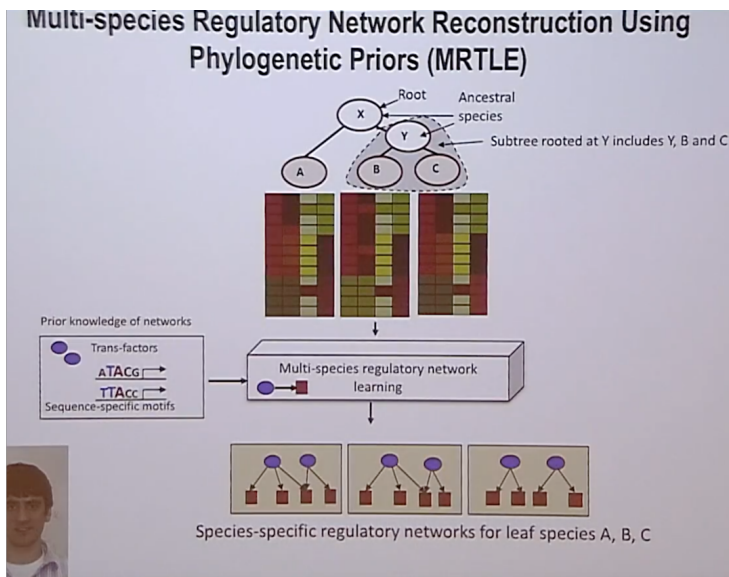


Part 2: Multi Species Network Inference

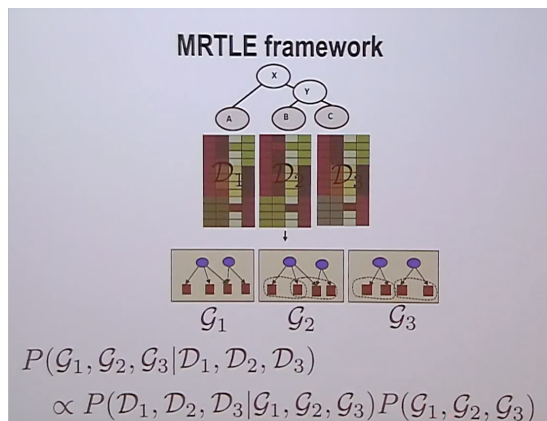
Multi task Regulatory Network Inference: Changes in regulation affect change in phenotype



Part 2: Multi Species Network Inference



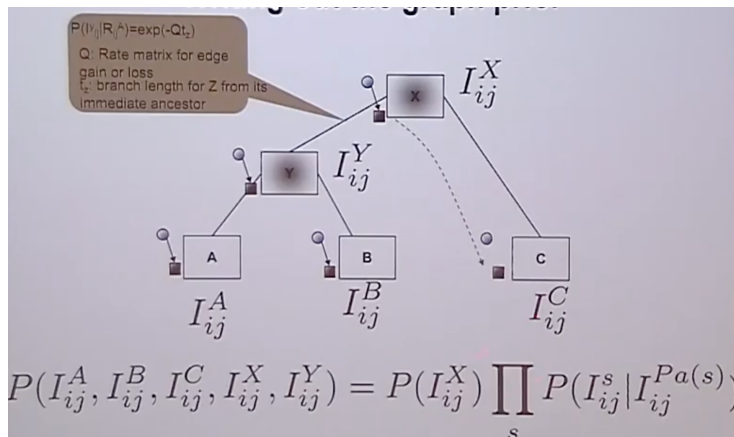
3 Datasets, 3 Graphs for example



- Treat $P(D_1, D_2, D_3 | G_1, G_2, G_3)$ independently
- Incorporate phylogenetic prior through $P(G_1, G_2, G_3)$

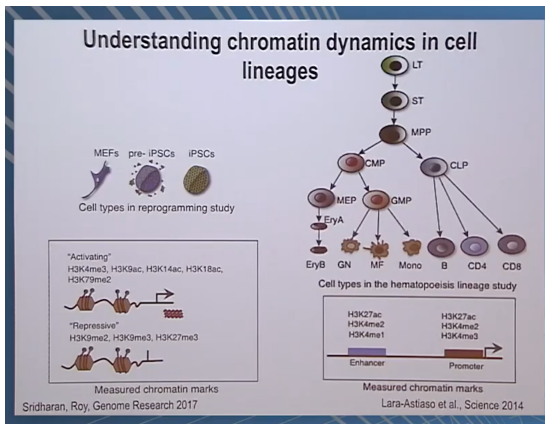
MRTLE

- phylogeny tree is an undirected network
- assume independence over edges

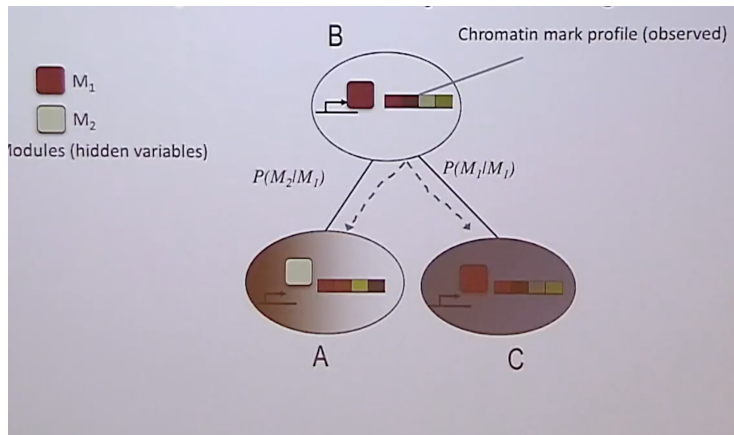


Part 3: Chromatin Dynamics in Cell Lineages

- Chromatin State of each genomic loci
- Module: set of loci with similar chromatin state
- identify how modules(chunks of genome) change from one cell type to another



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