CSCI x490 Algorithms for Computational Biology

Lecture Note 4 (by Liming Cai)

April 21, 2016

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Probabilistic models



Probabilistic models

• Characterization of data observable from a system

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Probabilistic models

- Characterization of data observable from a system
- Expression of uncertainty of data with probability theory

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- Automatic learning of the system from data
- Computational inference/prediction of unknown

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1. Parameter Re-estimation for HMMs

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2. SCFG for Co-evolution

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• parameter estimation (given G, and data D)

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 $\theta^* = \arg \max_{\theta} P(\theta|D)$

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1. Parameter Re-estimation for HMMs

- HMM (and profile HMM) (introduced) topology G: states and transitions parameter θ: probability distributions for emissions and transitions
- parameter estimation (given G, and data D)

 $\theta^* = \arg\max_{\theta} P(\theta|D)$

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• How to compute $P(D, e|\theta_{old})$ and $P(D|\theta_{old})$?

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• Let sequence $x \in D$, and π represents any path in HMM,

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• Let sequence $x \in D$, and π represents any path in HMM, then

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The algorithm to compute $\sum_{\pi} P(x, \pi | \theta_{old})$ is Forward Algorithm.

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where position j partitions the sequence x into two segments $x_{[1,.j]}$ and $x_{[j+1..n]}$.

To compute

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To compute

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Backward Algorithm computes for suffixes instead of prefixes.

Examples of event e in a profile HMM (with begin and end states B and E);

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- etc..

Summary of parameter re-estimation for HMMs from given data ${\it D}$

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$$P(e|\theta_{new}) = \frac{P(D, e|\theta_{old})}{P(D|\theta_{old})}$$

where $P(D|\theta_{old}) = \sum\limits_{x \in D} P(x|\theta_{old})$ that can be computed with Forward

and $P(D, e|\theta_{old}) = \sum_{x \in D} P(x, e|\theta_{old})$ that can be computed with both Forward and Backward.

• iterate the above steps until $\frac{|P(D|\theta_{new}) - P(D|\theta_{old})|}{P(D|\theta_{old})} < \Delta$. for a given constant Δ .

Called Forward-backward algorithm.

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2. Stochastic context-free grammar

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2. Stochastic context-free grammar

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2. Stochastic context-free grammar

• an extension of HMM;

2. Stochastic context-free grammar

- an extension of HMM;
- with a capability to model correlation and coevolution;

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2. Stochastic context-free grammar

- an extension of HMM;
- with a capability to model correlation and coevolution;

• correlation patterns are limited.



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We can use a different notation for the HMM.



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We can use a different notation for the HMM.

• $Begin \to eM_1$, $e \in \{a, c, g, t\}$



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We can use a different notation for the HMM.

• $Begin \to eM_1, e \in \{a, c, g, t\}$ $Begin \to eI_0$



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We can use a different notation for the HMM.

• $Begin \to aM_1$, $Begin \to cM_1$, $Begin \to gM_1$, $Begin \to tM_1$



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• $Begin \rightarrow aM_1$, $Begin \rightarrow cM_1$, $Begin \rightarrow gM_1$, $Begin \rightarrow tM_1$ $Begin \rightarrow aI_0$, $Begin \rightarrow cI_0$, $Begin \rightarrow gI_0$, $Begin \rightarrow tI_0$ $Begin \rightarrow D_1$



We can use a different notation for the HMM.

• $Begin \rightarrow aM_1$, $Begin \rightarrow cM_1$, $Begin \rightarrow gM_1$, $Begin \rightarrow tM_1$ $Begin \rightarrow aI_0$, $Begin \rightarrow cI_0$, $Begin \rightarrow gI_0$, $Begin \rightarrow tI_0$ $Begin \rightarrow D_1$

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• $M_i \to eM_{i+1}$ $M_i \to eI_i$ $M_i \to D_{i+1}$



sequence *acggt*

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sequence acggt

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• $Begin \rightarrow aM_1, \ldots$



sequence acggt

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• $Begin \rightarrow aM_1, \ldots$

•
$$M_i \rightarrow aM_{i+1}$$
, $M_i \rightarrow aI_i$, $I_i \rightarrow aM_{i+1}$
 $M_i \rightarrow cM_{i+1}$, $M_i \rightarrow cI_i$, $I_i \rightarrow cM_{i+1}$
 $M_i \rightarrow tM_{i+1}$, $M_i \rightarrow gI_i$, $I_i \rightarrow gM_{i+1}$
 $M_i \rightarrow tM_{i+1}$, $M_i \rightarrow tI_i$, $I_i \rightarrow tM_{i+1}$, for $i = 1, 2, 3$
 $M_4 \rightarrow End$



sequence acggt

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• $Begin \rightarrow aM_1, \ldots$

•
$$M_i \rightarrow aM_{i+1}$$
, $M_i \rightarrow aI_i$, $I_i \rightarrow aM_{i+1}$
 $M_i \rightarrow cM_{i+1}$, $M_i \rightarrow cI_i$, $I_i \rightarrow cM_{i+1}$
 $M_i \rightarrow tM_{i+1}$, $M_i \rightarrow gI_i$, $I_i \rightarrow gM_{i+1}$
 $M_i \rightarrow tM_{i+1}$, $M_i \rightarrow tI_i$, $I_i \rightarrow tM_{i+1}$, for $i = 1, 2, 3$
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sequence acggt

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$$M_i \rightarrow aM_{i+1}$$
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 $M_i \rightarrow cM_{i+1}$, $M_i \rightarrow cI_i$, $I_i \rightarrow cM_{i+1}$
 $M_i \rightarrow tM_{i+1}$, $M_i \rightarrow gI_i$, $I_i \rightarrow gM_{i+1}$
 $M_i \rightarrow tM_{i+1}$, $M_i \rightarrow tI_i$, $I_i \rightarrow tM_{i+1}$, for $i = 1, 2, 3$
 $M_4 \rightarrow End$

we use rules to produce *acggt*:

Begin



sequence acggt

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• $Begin \rightarrow aM_1, \ldots$

$$\begin{array}{lll} \bullet & M_i \rightarrow a M_{i+1}, & M_i \rightarrow a I_i, & I_i \rightarrow a M_{i+1} \\ & M_i \rightarrow c M_{i+1}, & M_i \rightarrow c I_i, & I_i \rightarrow c M_{i+1} \\ & M_i \rightarrow t M_{i+1}, & M_i \rightarrow g I_i, & I_i \rightarrow g M_{i+1} \\ & M_i \rightarrow t M_{i+1}, & M_i \rightarrow t I_i, & I_i \rightarrow t M_{i+1}, & \text{for } i = 1, 2, 3 \\ & M_4 \rightarrow End \end{array}$$

we use rules to produce *acggt*:

 $Begin \Rightarrow aM_1$



sequence acggt

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• $Begin \rightarrow aM_1, \ldots$

$$\begin{array}{lll} \bullet & M_i \rightarrow a M_{i+1}, & M_i \rightarrow a I_i, & I_i \rightarrow a M_{i+1} \\ & M_i \rightarrow c M_{i+1}, & M_i \rightarrow c I_i, & I_i \rightarrow c M_{i+1} \\ & M_i \rightarrow t M_{i+1}, & M_i \rightarrow g I_i, & I_i \rightarrow g M_{i+1} \\ & M_i \rightarrow t M_{i+1}, & M_i \rightarrow t I_i, & I_i \rightarrow t M_{i+1}, & \text{for } i = 1, 2, 3 \\ & M_4 \rightarrow End \end{array}$$

we use rules to produce *acggt*:

 $Begin \Rightarrow aM_1 \Rightarrow acM_2$



sequence acggt

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• $Begin \rightarrow aM_1, \ldots$

$$\begin{array}{lll} \bullet & M_i \rightarrow a M_{i+1}, & M_i \rightarrow a I_i, & I_i \rightarrow a M_{i+1} \\ & M_i \rightarrow c M_{i+1}, & M_i \rightarrow c I_i, & I_i \rightarrow c M_{i+1} \\ & M_i \rightarrow t M_{i+1}, & M_i \rightarrow g I_i, & I_i \rightarrow g M_{i+1} \\ & M_i \rightarrow t M_{i+1}, & M_i \rightarrow t I_i, & I_i \rightarrow t M_{i+1}, & \text{for } i = 1, 2, 3 \\ & M_4 \rightarrow End \end{array}$$

$$Begin \Rightarrow aM_1 \Rightarrow acM_2 \Rightarrow acgI_2$$



sequence acggt

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• $Begin \rightarrow aM_1, \ldots$

•
$$M_i \rightarrow aM_{i+1}$$
, $M_i \rightarrow aI_i$, $I_i \rightarrow aM_{i+1}$
 $M_i \rightarrow cM_{i+1}$, $M_i \rightarrow cI_i$, $I_i \rightarrow cM_{i+1}$
 $M_i \rightarrow tM_{i+1}$, $M_i \rightarrow gI_i$, $I_i \rightarrow gM_{i+1}$
 $M_i \rightarrow tM_{i+1}$, $M_i \rightarrow tI_i$, $I_i \rightarrow tM_{i+1}$, for $i = 1, 2, 3$
 $M_4 \rightarrow End$

$$Begin \Rightarrow aM_1 \Rightarrow acM_2 \Rightarrow acgI_2 \Rightarrow acggM_3$$



sequence acggt

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• $Begin \rightarrow aM_1, \ldots$

•
$$M_i \rightarrow aM_{i+1}$$
, $M_i \rightarrow aI_i$, $I_i \rightarrow aM_{i+1}$
 $M_i \rightarrow cM_{i+1}$, $M_i \rightarrow cI_i$, $I_i \rightarrow cM_{i+1}$
 $M_i \rightarrow tM_{i+1}$, $M_i \rightarrow gI_i$, $I_i \rightarrow gM_{i+1}$
 $M_i \rightarrow tM_{i+1}$, $M_i \rightarrow tI_i$, $I_i \rightarrow tM_{i+1}$, for $i = 1, 2, 3$
 $M_4 \rightarrow End$

$$Begin \Rightarrow aM_1 \Rightarrow acM_2 \Rightarrow acgI_2 \Rightarrow acggM_3 \Rightarrow acggtM_4$$



sequence *acggt*

• $Begin \to aM_1, \ldots$

•
$$M_i \rightarrow aM_{i+1}$$
, $M_i \rightarrow aI_i$, $I_i \rightarrow aM_{i+1}$
 $M_i \rightarrow cM_{i+1}$, $M_i \rightarrow cI_i$, $I_i \rightarrow cM_{i+1}$
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 $M_i \rightarrow tM_{i+1}$, $M_i \rightarrow tI_i$, $I_i \rightarrow tM_{i+1}$, for $i = 1, 2, 3$
 $M_4 \rightarrow End$

we use rules to produce *acggt*:

 $Begin \Rightarrow aM_1 \Rightarrow acM_2 \Rightarrow acgI_2 \Rightarrow acggM_3 \Rightarrow acggtM_4 \Rightarrow acggtEnd$



sequence *acggt*

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Called a derivation



sequence *acggt*

• $Begin \to aM_1, \ldots$

•
$$M_i \rightarrow aM_{i+1}$$
, $M_i \rightarrow aI_i$, $I_i \rightarrow aM_{i+1}$
 $M_i \rightarrow cM_{i+1}$, $M_i \rightarrow cI_i$, $I_i \rightarrow cM_{i+1}$
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 $M_4 \rightarrow End$

we use rules to produce *acggt*:

 $Begin \Rightarrow aM_1 \Rightarrow acM_2 \Rightarrow acgI_2 \Rightarrow acggM_3 \Rightarrow acggtM_4 \Rightarrow acggtEnd$

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Called a derivation \iff a path in HMM.

Notes on the rules:



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Notes on the rules:

• Rules are grammar rules

Notes on the rules:

• Rules are grammar rules (also called rewriting rules)

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- \bullet Rules like $A \rightarrow aB$ and $A \rightarrow C$ are regular grammar rules

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(日) (同) (三) (三) (三) (○) (○)

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- a sequence may have more than one derivation;
- one of the derivations of the sequence is of the max probability;
- letters on the sequence are derived one at a time, independently;
- Can rules be designed to model complex relationships among letters?

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Consider rules for RNA sequences
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Consider rules for RNA sequences

• $H_i \to a H_{i+1} u$

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•
$$H_i \rightarrow aH_{i+1}u$$

 $H_i \rightarrow uH_{i+1}a$
 $H_i \rightarrow cH_{i+1}g$
 $H_i \rightarrow gH_{i+1}c$

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$$\bullet \begin{array}{l} H_i \rightarrow a H_{i+1} u \\ H_i \rightarrow u H_{i+1} a \\ H_i \rightarrow c H_{i+1} g \\ H_i \rightarrow g H_{i+1} c \\ H_i \rightarrow L_i \end{array}$$

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Consider rules for RNA sequences

$$\bullet \ \ H_i \rightarrow a H_{i+1} u \\ H_i \rightarrow u H_{i+1} a \\ H_i \rightarrow c H_{i+1} g \\ H_i \rightarrow g H_{i+1} c \\ H_i \rightarrow L_i$$

 $L_i \rightarrow aL_{i+1}$

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$$\label{eq:higher} \bullet \ H_i \rightarrow a H_{i+1} u \\ H_i \rightarrow u H_{i+1} a \\ H_i \rightarrow c H_{i+1} g \\ H_i \rightarrow g H_{i+1} c \\ H_i \rightarrow L_i$$

$$\begin{array}{l} L_i \rightarrow aL_{i+1} \\ L_i \rightarrow cL_{i+1} \\ L_i \rightarrow gL_{i+1} \\ L_i \rightarrow uL_{i+1} \end{array}$$

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•
$$H_i \rightarrow aH_{i+1}u$$

 $H_i \rightarrow uH_{i+1}a$
 $H_i \rightarrow cH_{i+1}g$
 $H_i \rightarrow gH_{i+1}c$
 $H_i \rightarrow L_i$
 $L_i \rightarrow aL_{i+1}$

$$L_i \rightarrow dL_{i+1}$$

$$L_i \rightarrow cL_{i+1}$$

$$L_i \rightarrow gL_{i+1}$$

$$L_i \rightarrow uL_{i+1}$$

$$L_i \rightarrow \epsilon$$

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•
$$H_i \rightarrow aH_{i+1}u$$

 $H_i \rightarrow uH_{i+1}a$
 $H_i \rightarrow cH_{i+1}g$
 $H_i \rightarrow gH_{i+1}c$
 $H_i \rightarrow L_i$
 $L_i \rightarrow aL_{i+1}$
 $L_i \rightarrow gL_{i+1}$
 $L_i \rightarrow uL_{i+1}$
 $L_i \rightarrow uL_{i+1}$
 $L_i \rightarrow e$ (empty)

Consider rules for RNA sequences

•
$$H_i \rightarrow aH_{i+1}u$$

 $H_i \rightarrow uH_{i+1}a$
 $H_i \rightarrow cH_{i+1}g$
 $H_i \rightarrow gH_{i+1}c$
 $H_i \rightarrow L_i$
 $L_i \rightarrow aL_{i+1}$
 $L_i \rightarrow cL_{i+1}$
 $L_i \rightarrow gL_{i+1}$

 $L_i \to uL_{i+1}$ $L_i \to \epsilon \quad \text{(empty)}$

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Consider rules for RNA sequences

•
$$H_i \rightarrow aH_{i+1}u$$

 $H_i \rightarrow uH_{i+1}a$
 $H_i \rightarrow cH_{i+1}g$
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• a derivation an RNA sequence that folds into a stem-loop

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RNA secondary structure examples:



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• nesting, parallel patterns are context-free, while

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- nesting, parallel patterns are context-free, while
- crossing patterns are not!

Illustration of context-free grammar derivation:



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Illustration of context-free grammar derivation:



• Context-free grammar derivation is a tree (because of simultaneous emissions)

Illustration of CFG derivation again:



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(A CFG applied on the same sequence with two alternative syntactic structures)

Stochastic context-free grammar (SCFG):

• Probability distributions are associated with grammar rules

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$$X, \quad \sum\limits_{X \to \alpha} Prob(X \to \alpha) = 1$$

• Every syntax structure of a sequence is associated with a probability.

 $\pi_A: \underline{S} \Rightarrow_1 \underline{a\underline{S}b} \Rightarrow_1 \underline{a\underline{S}bb} \Rightarrow_3 \underline{aab\underline{S}bb} \Rightarrow_4 \underline{aababb} = x$ $\pi_B: \underline{S} \Rightarrow_6 \underline{SS} \Rightarrow_1 \underline{a\underline{S}bS} \Rightarrow_4 \underline{aab\underline{S}} \Rightarrow_1 \underline{aaba\underline{S}b} \Rightarrow_5 \underline{aababb} = x$

 $Prob(\pi_A, x) = 0.4 \times 0.4 \times 0.1 \times 0.1 = 0.016$ $Prob(\pi_B, x) = 0.2 \times 0.4 \times 0.1 \times 0.4 \times 0.1 = 0.0032$

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[Sakakibara et al, 1994, Eddy and Durbin 1994,

Rivas et al, 2012]

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- much smaller set of resolved 3D structures (in contrast to proteins or reported RNA secondary structures)
- tertiary interactions were not understood until recently



(Leontis et al, 2003; Zirbel et al, 2009. 12 base-base, 10 base-phosphate, and 10 base-ribose families)
All nucleotide interactions of a tRNA (excluding stacking)



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• gray relation is context-free;

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- gray relation is context-free;
- purple relation is context-sensitive.

All nucleotide interactions of a tRNA (excluding stacking)



- gray relation is context-free;
- purple relation is context-sensitive.
- We need a higher-order model for such complex relations!

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3. Markov networks and learning

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• Compute joint probability distribution P(X) from observed random variables $X = \langle X_1, \dots, X_n \rangle$

Example 1: molecule residues forming structure

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• Compute joint probability distribution P(X) from observed random variables $X = \langle X_1, \dots, X_n \rangle$

Example 1: molecule residues forming structure

Example 2: gene networks from expression data

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 $\bullet \ P(X)$ is a n^{th} order distribution, difficult to compute

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molecular structure is defined over their joint distribution, involving multi-body interactions.

Markov network model approximates multi-body interactions with pairwise interactions.

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Questions to answer:

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• What does $P_G(X)$ look like

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Questions to answer:

• What does $P_G(X)$ look like even a Markov graph G is given?

• How to measure the difference between $P_G(X)$ and P(X)?

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- How to measure the difference between $P_G(X)$ and P(X)?
- Can we compute G and $P_G(X)$ efficiently?

The framework of Chow and Liu 1968:

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• to measure difference between two distributions P(X) and $P_G(X)$) with D_{KL} , Kullback-Leibler divergence;

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- If non-tree topology is desired
 - 1. the problem becomes computationally intractable;
 - 2. relying on heuristics.

Assume we have a Markov tree T for variable $X=\{X_1,\ldots,X_n\}$ with with a root X_1

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- \bullet tree topology is completely determined by $\pi,$ the parent information e.g., $\pi(6)=3$
- $P_T(X) = P(X_1) \prod_{i=2}^n P(X_i | X_{\pi(i)})$
- Minimizing $D_{KL}(P(X), P_T(X))$ would tell us what T should be.

Kullback-Leilber divergence:

$$D_{KL}((P(X), P_T(X))) = \sum_{x} P(x) \log_2 \frac{P(x)}{P_T(x)}$$

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is the **mutual information** between X_i and $X_{\pi(i)}$.

Such Markovtree T can be found with the following steps:

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- edge (i, j) has weight $I(X_i, X_j)$, for every pair of i, j;
- find a maximum spanning tree T of G_X ; (max spanning tree has the same algorithm as min spanning tree)



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Formulated complete graph:



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