

# Tree-based mixtures: Application in epidemiology

Stéphane Robin

joint work with P. Barbillon, L. Schwaller

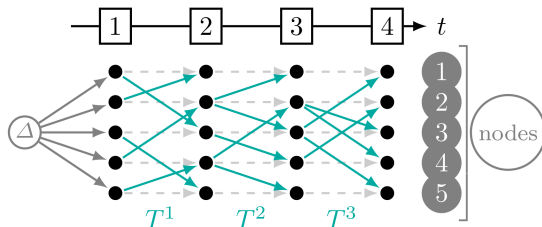
Sorbonne Université / LPSM

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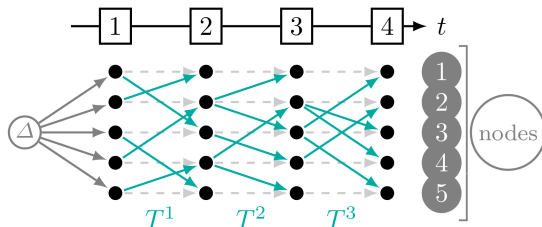
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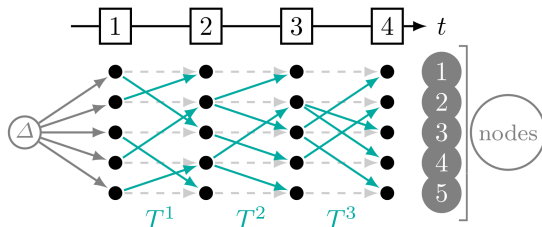


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**Assumption:** 'Contamination' spreads according to some 'social' network (not anybody can be 'contaminated' by anybody)

**Final aim:** Learn something about this network.

**For now:** Observe that the path of the 'epidemics' is a tree.

# Outline

Reminder on graphical models and trees

Tree shaped distributions and mixtures

Spread of an epidemics

## Graphical models

**Undirected graphical model** [Lau96]: the multivariate distribution  $p$  is *faithful* to the graph  $G$  iff

$$p(Y) \propto \prod_{C \in \mathcal{C}(G)} \psi_C(Y^C)$$

(i.e., iff  $p$  can be factorized according to the set  $\mathcal{C}(G)$  of maximal cliques of  $G$ )

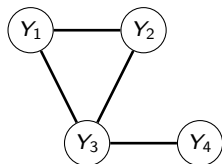
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**Example:**



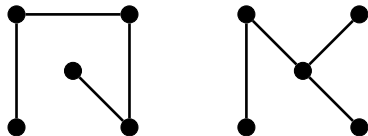
$$p(Y) \propto \psi_1(Y_1, Y_2, Y_3) \psi_2(Y_3, Y_4)$$

- ▶ Connected graph: all variables are dependent
- ▶  $Y_3 = \text{separator: } (Y_4 \perp (Y_1, Y_2)) \mid Y_3$

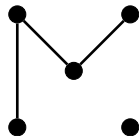
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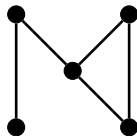
spanning trees



not spanning



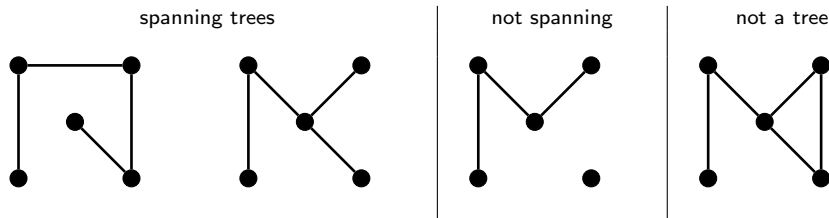
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**Tree-shaped graphical model:**  $p$  faithful to the spanning tree  $T$

$$\Leftrightarrow p(Y) \propto \prod_{(j,k) \in T} \psi_{jk}(Y_j, Y_k)$$

(cliques are only edges)

→ All variables are dependent (*spanning*) but few are conditionally dependent (*tree*)

## Maximum likelihood inference

Consider  $Y \sim p$ , faithful to  $T$ :

$$\log p_T(Y) = \sum_{(j,k) \in T} \log \psi_{jk}(Y_j, Y_k) + \text{cst}$$

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<sup>1</sup>Actually  $\psi_{jk}(Y_j, Y_k) = \rho(Y_j, Y_k) / (\rho(Y_j)\rho(Y_k))$ , so edge weight = mutual information

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Tree MLE. Finding

$$\hat{T} = \arg \max_{T \in \mathcal{T}} \log p_T(Y)$$

amounts to solve a **maximum spanning tree** problem, where edge  $(j, k)$  has weight

$$\log \hat{\psi}_{jk}(Y_j, Y_k)$$

(Chow & Liu algorithm<sup>1</sup>: [CL68])

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## Tree-based mixture

Mixture of tree-shaped distributions [MJ06,Kir07].

- ▶ Tree marginal distribution: product form

$$p(T) = B^{-1} \prod_{(j,k) \in T} \beta_{jk}, \quad B = \sum_{T \in \mathcal{T}} \prod_{(j,k) \in T} \beta_{jk}.$$

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- ▶ Tree conditional distribution: product form

$$p(T | Y) = C^{-1} \prod_{(j,k) \in T} w_{jk}(Y), \quad C = \sum_{T \in \mathcal{T}} \prod_{(j,k) \in T} w_{jk}(Y).$$

## Summing over trees

We need to sum over the set  $\mathcal{T}$  of spanning trees, but

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**Matrix-Tree Theorem (Kirchhoff)** [Cha82]. Let  $W = [w_{jk}]$  be a symmetric matrix with null diagonal and  $\Delta(W)$ , its Laplacian:

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2. and

$$[\Delta(W)]^{uv} = \sum_{T \in \mathcal{T}} \prod_{(j,k) \in T} w_{jk}$$

(i.e.:  $\sum_{T \in \mathcal{T}}$  can be computed at the price of a determinant:  $O(p^3)$ )

## Edge probability

We may not be interested in the whole (conditional) distribution of  $T$ , but rather on edge probabilities:

$$\Pr\{(j, k) \in T\} \quad \text{or} \quad \Pr\{(j, k) \in T \mid Y\}.$$

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**Theorem** [Kir07]. Denote  $W^{ab}$  the same matrix as  $W$  but setting  $w_{ab} = w_{ba} = 0$ , then

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- ▶ Gives access to  $\Pr\{(j, k) \notin T\}$  or  $\Pr\{(j, k) \in T\}$
- ▶ All  $[\Delta(W^{ab})]^{ab}$  can be computed at the price of one matrix inversion:  $O(p^3)$



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## Susceptible-Infected-Susceptible (SIS) model

Data.  $n$  times,  $p$  individuals

$$Y_{tj} = \begin{cases} 1 & \text{if individual } j \text{ is infected at time } t \\ 0 & \text{otherwise} \end{cases}$$

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**Model.** At each time  $t$ , each node  $k$

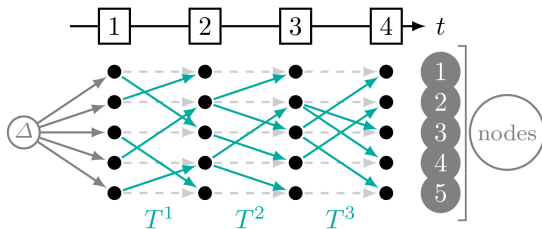
- ▶ picks up a parent  $j$  at time  $t - 1$  with probability  $\propto \beta_{jk}$  and,
- ▶ denoting  $\psi_{jk}^t = \Pr\{Y_{t+1,k} \mid Y_{t,k}, Y_{t,j}\}$ , it evolves according to

$\psi_{jk}^t$		$Y_{t+1,k} = 0$	$Y_{t+1,k} = 1$
		$Y_{t,k} = 1$	$Y_{t,j} = 1$
$Y_{t,k} = 1$	$Y_{t,j} = 0$	$e$	$1 - e$
$Y_{t,k} = 0$	$Y_{t,j} = 1$	$1 - c$	$c$
$Y_{t,k} = 0$	$Y_{t,j} = 0$	$1$	$0$

- ▶  $c$  = contamination rate
- ▶  $e$  = extinction rate (become susceptible again)

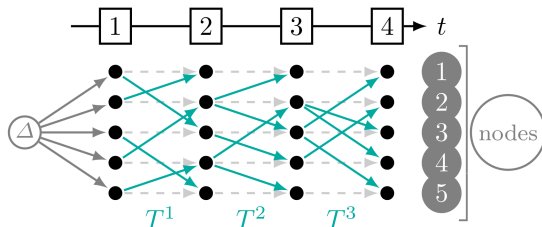
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Define  $\mathcal{T}_\Delta$  the set of oriented spanning tree

- ▶ over the nodes  $\Delta \cup \{(t, k) : 1 \leq t \leq n, 1 \leq k \leq p\}$ ,
- ▶ rooted in  $\Delta$ ,
- ▶ with edges connecting only time-adjacent nodes ( $j \neq k$ )

→  $\mathcal{T}_\Delta =$  set of spanning trees going 'forward' in time ( $|\mathcal{T}_\Delta| = (p-1)^{p(n-1)}$ )

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EM algorithm. Denote

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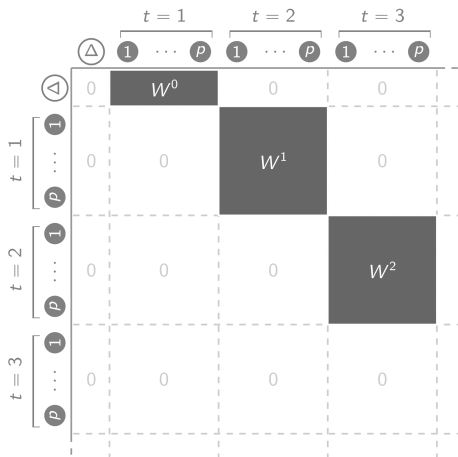
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Critical step = E step.

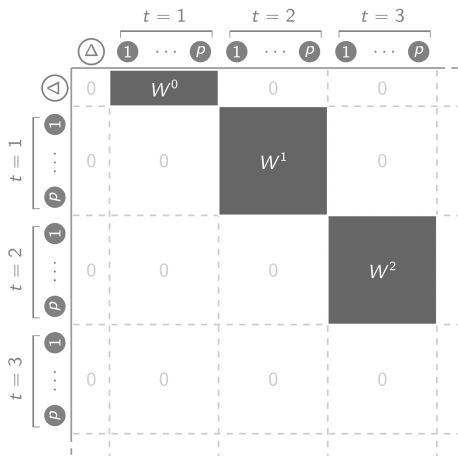
- ▶ We now need to sum over the (huge) set of rooted oriented trees  $\mathcal{T}_\Delta$ .
- ▶ Hopefully, a alternative version of the matrix-tree theorem enables to sum over all *directed* trees ( $W$  asymmetric) with given root [Cha82].

## An easy situation



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→ Laplacian  $\Delta(W)$   
is upper triangular

→ Matrix-tree theorem:

$$\Delta(W)^{00} = \prod_{t,j} \left( \sum_k \beta_{jk} \psi_{jk}^t \right)$$

→ computable in  $O(np^2)$

## In practice

### Edge probabilities:

$$\begin{array}{ll} \text{At a given time } t: & \Pr\{(j, k) \in T^t \mid Y\} \\ \text{At least in one time:} & \Pr\{\exists t : (j, k) \in T^t \mid Y\} \end{array}$$

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### Alternatives.

- ▶ Bayesian inference can be carried out for  $e$  and  $c$
- ▶ Iterating the EM steps does not improve the performances very much
- ▶ Observing multiple waves of the epidemics (even over a shortest time-range) improves the accuracy (see next)

## Simulation study

**Design:** Consider a graph  $G$  and launch the 'epidemics' along its edges.

**Method:** Predict if  $(j, k) \in G$  based on edge probability  $\Pr\{\exists t : (j, k) \in T^t \mid Y\}$ .

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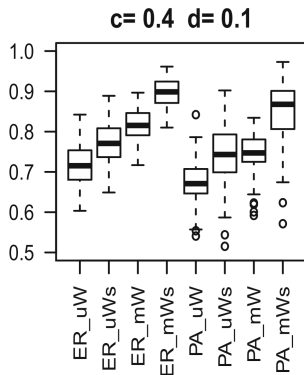
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**AUC:**



## Illustration: Seed exchange network

**Question:** decipher the social structure underlying seed exchanges between farmers

Telangana region (India) data:

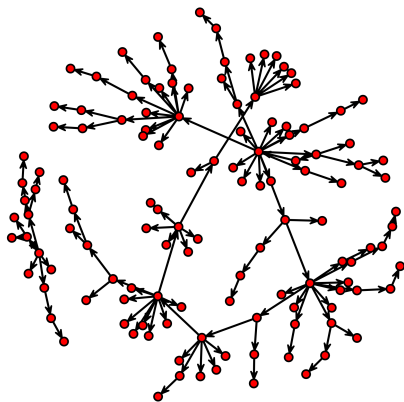
- ▶  $p = 127$  farmers
- ▶  $n = 3$  years
- ▶ 14 seed varieties (waves)

$Y_{ti}^h = 1$  if farmer  $i$  holds variety  $h$  at time  $t$ .

No symmetry assumption.

More exchanges

- ▶ within the same caste
- ▶ within the same village
- ▶ from younger to older



Most probable donor for each farmer

# Conclusion

## Tree shaped mixtures

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- ▶ 'Network' inference (= structure inference) [SRS19]
- ▶ Network comparison or network changes along time [SR17]
- ▶ Accounting for missing nodes ('actors') [RAR19,MRA20,MRA21]
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### Some questions

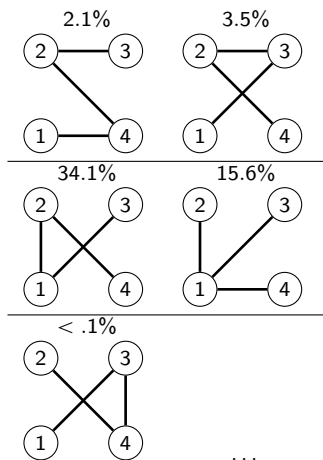
- ▶ Theoretical guaranties (e.g.: consistency of the estimated graph)?
- ▶ Numerical issues arising for large  $p$  or  $n$  (use tempering?)



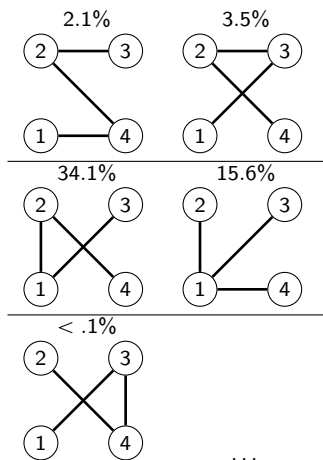
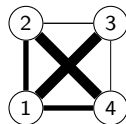
## References I

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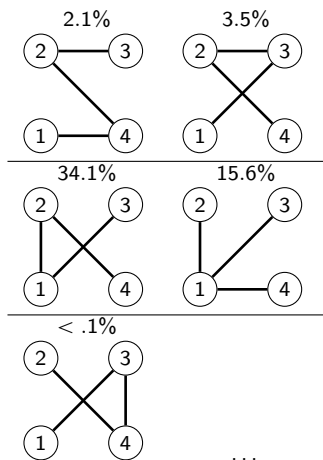
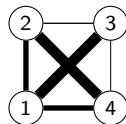
## 'Tree-averaging' principle

Tree conditional distribution.  $p(T|Y)$ 

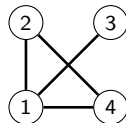
## 'Tree-averaging' principle

Tree conditional distribution.  $p(T|Y)$ Edge probabilities.  $\Pr\{(j, k) \in T \mid Y\}$ 

## 'Tree-averaging' principle

Tree conditional distribution.  $p(T|Y)$ Edge probabilities.  $\Pr\{(j, k) \in T \mid Y\}$ 

Most probable edges.



(not a tree) [SRS19]