

# Stochastic Block Model for taxonomic identification in (meta)Barcoding

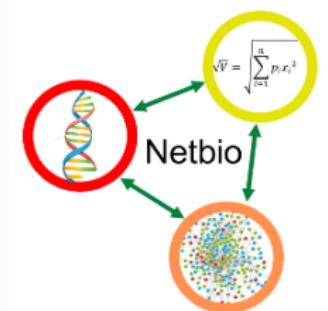
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# Scientific context

## Plant diversity



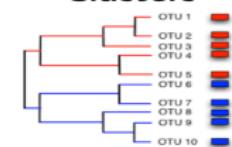
## Sequences

A large grid of text representing DNA sequences for 15 samples, with each row containing a sample ID and a sequence of characters.

## Dissimilarity matrix

$$\Rightarrow \begin{pmatrix} 0 & 2 & \dots & 3 \\ \vdots & 0 & \ddots & 11 \\ \vdots & \ddots & \ddots & 0 \\ 3 & \dots & \dots & 0 \end{pmatrix} \Rightarrow$$

## Clusters



Clade:	Magnoliids
Order:	Magnoliales
Family:	Myristicaceae
Genus:	<i>Myristica</i>



- Is there an agreement between botanical and molecular classifications on a coarse taxonomic level ?
- How to improve SBM model accuracy ?

# Summary

## 1 Agreement between botanical and molecular classifications

- Data set
- High taxonomic levels
- General approach
- Results

## 2 SBM model

- SBM Model parameters
- SBM possible estimation methods

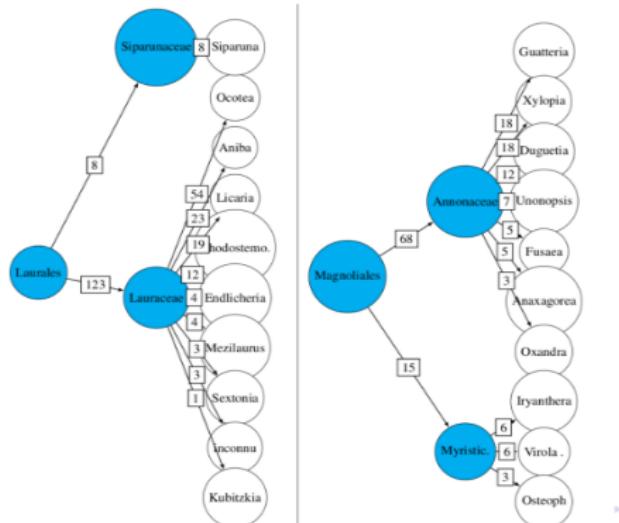
## 3 Tensor trains approximation for SBM estimation

- The idea
- How it works
- About marginals

# Agreement between botanical and molecular classifications

## Data set

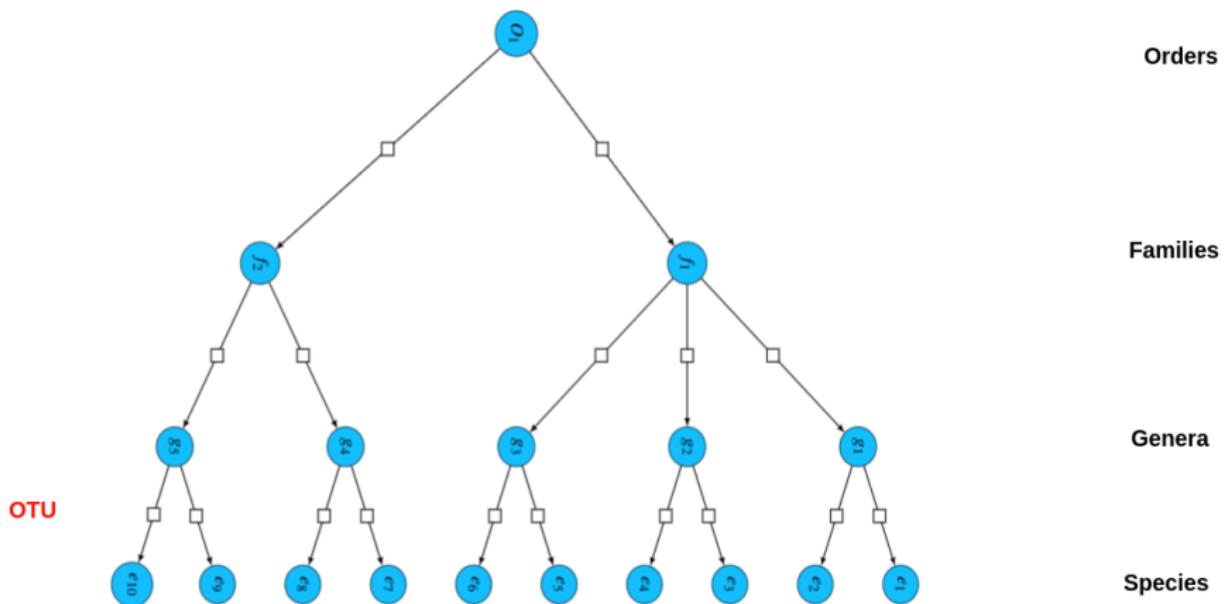
- 1458 trees from an experimental plot in French Guyana.

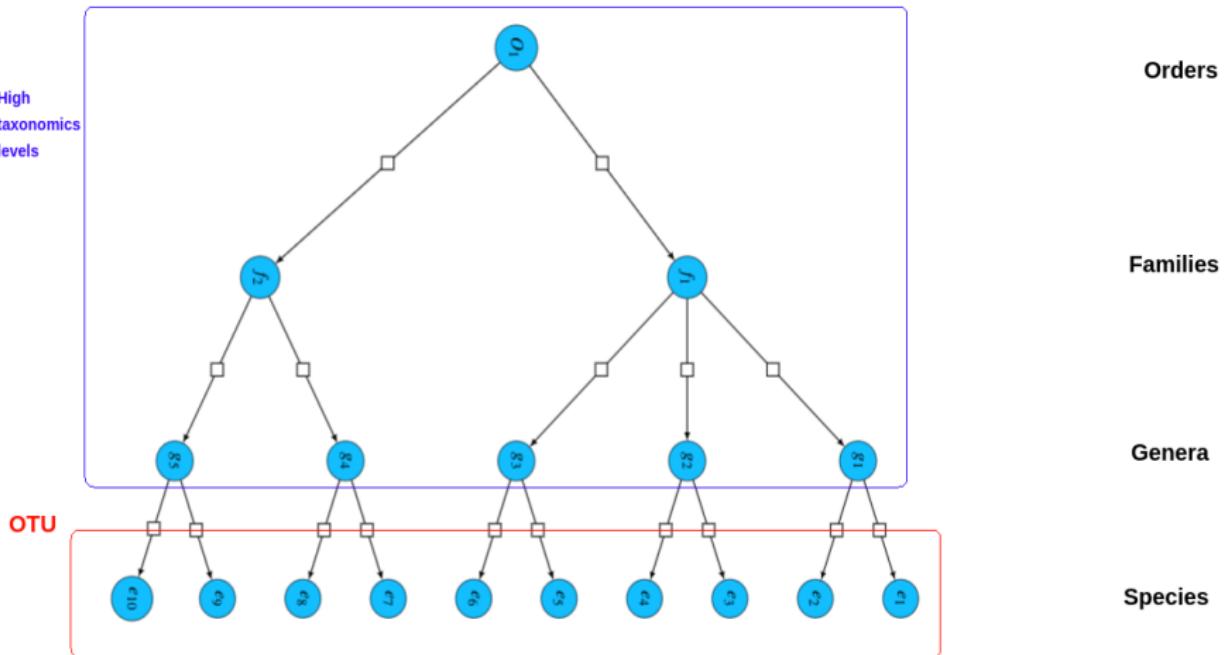


Order, family, genus and species of each individual.

DNA sequence of each individual.

AVCHB:00087:00584  
AGCTGAACTTAAAGGTCATCTTAAACATCAGTCGTGACAGAAGTTTACTCTGCTGAGATACTGCTGAAGCCCTGGTCTGTAATTGTTATGTCGATTTA  
AVCHB:00088:00849  
AGCTGAACTTAAAGGTCATCTTAAACATCAGTCGTGACAGAAGTTTACTCTGCTGAGATACTGCTGAAGCCCTGGTCTGTAATTGTTATGTCGATTTA  
AVCHB:00089:00813  
AGCTGAACTTAAAGGTCATCTTAAACATCAGTCGTGACAGAAGTTTACTCTGCTGAGATACTGCTGAAGCCCTGGTCTGTAATTGTTATGTCGATTTA  
AVCHB:00090:01986  
AGCTGAACTTAAAGGTCATCTTAAACATCAGTCGTGACAGAAGTTTACTCTGCTGAGATACTGCTGAAGCCCTGGTCTGTAATTGTTATGTCGATTTA  
AVCHB:00091:00855  
AGCTGAACTTAAAGGTCATCTTAAACATCAGTCGTGACAGAAGTTTACTCTGCTGAGATACTGCTGAAGCCCTGGTCTGTAATTGTTATGTCGATTTA  
AVCHB:00092:01130  
AGCTGAACTTAAAGGTCATCTTAAACATCAGTCGTGACAGAAGTTTACTCTGCTGAGATACTGCTGAAGCCCTGGTCTGTAATTGTTATGTCGATTTA  
AVCHB:00093:01192  
AGCTGAACTTAAAGGTCATCTTAAACATCAGTCGTGACAGAAGTTTACTCTGCTGAGATACTGCTGAAGCCCTGGTCTGTAATTGTTATGTCGATTTA  
AVCHB:00094:00848  
AGCTGAACTTAAAGGTCATCTTAAACATCAGTCGTGACAGAAGTTTACTCTGCTGAGATACTGCTGAAGCCCTGGTCTGTAATTGTTATGTCGATTTA  
AVCHB:00095:01235  
AGCTGAACTTAAAGGTCATCTTAAACATCAGTCGTGACAGAAGTTTACTCTGCTGAGATACTGCTGAAGCCCTGGTCTGTAATTGTTATGTCGATTTA  
AVCHB:00096:01912  
AGCTGAACTTAAAGGTCATCTTAAACATCAGTCGTGACAGAAGTTTACTCTGCTGAGATACTGCTGAAGCCCTGGTCTGTAATTGTTATGTCGATTTA  
AVCHB:00097:01162  
AGCTGAACTTAAAGGTCATCTTAAACATCAGTCGTGACAGAAGTTTACTCTGCTGAGATACTGCTGAAGCCCTGGTCTGTAATTGTTATGTCGATTTA  
AVCHB:00098:02048  
AGCTGAACTTAAAGGTCATCTTAAACATCAGTCGTGACAGAAGTTTACTCTGCTGAGATACTGCTGAAGCCCTGGTCTGTAATTGTTATGTCGATTTA  
AVCHB:00099:02676  
AGCTGAACTTAAAGGTCATCTTAAACATCAGTCGTGACAGAAGTTTACTCTGCTGAGATACTGCTGAAGCCCTGGTCTGTAATTGTTATGTCGATTTA  
AVCHB:00100:02287  
AGCTGAACTTAAAGGTCATCTTAAACATCAGTCGTGACAGAAGTTTACTCTGCTGAGATACTGCTGAAGCCCTGGTCTGTAATTGTTATGTCGATTTA  
AVCHB:00101:00411  
AGCTGAACTTAAAGGTCATCTTAAACATCAGTCGTGACAGAAGTTTACTCTGCTGAGATACTGCTGAAGCCCTGGTCTGTAATTGTTATGTCGATTTA  
AVCHB:00102:01539  
AGCTGAACTTAAAGGTCATCTTAAACATCAGTCGTGACAGAAGTTTACTCTGCTGAGATACTGCTGAAGCCCTGGTCTGTAATTGTTATGTCGATTTA  
AVCHB:00103:00917  
AGCTGAACTTAAAGGTCATCTTAAACATCAGTCGTGACAGAAGTTTACTCTGCTGAGATACTGCTGAAGCCCTGGTCTGTAATTGTTATGTCGATTTA  
AVCHB:00104:00893  
AGCTGAACTTAAAGGTCATCTTAAACATCAGTCGTGACAGAAGTTTACTCTGCTGAGATACTGCTGAAGCCCTGGTCTGTAATTGTTATGTCGATTTA  
AVCHB:00105:00881  
AGCTGAACTTAAAGGTCATCTTAAACATCAGTCGTGACAGAAGTTTACTCTGCTGAGATACTGCTGAAGCCCTGGTCTGTAATTGTTATGTCGATTTA  
AVCHB:00106:00881  
AGCTGAACTTAAAGGTCATCTTAAACATCAGTCGTGACAGAAGTTTACTCTGCTGAGATACTGCTGAAGCCCTGGTCTGTAATTGTTATGTCGATTTA  
AVCHB:00107:02398  
AGCTGAACTTAAAGGTCATCTTAAACATCAGTCGTGACAGAAGTTTACTCTGCTGAGATACTGCTGAAGCCCTGGTCTGTAATTGTTATGTCGATTTA  
AVCHB:00108:00917  
AGCTGAACTTAAAGGTCATCTTAAACATCAGTCGTGACAGAAGTTTACTCTGCTGAGATACTGCTGAAGCCCTGGTCTGTAATTGTTATGTCGATTTA  
AVCHB:00109:00893  
AGCTGAACTTAAAGGTCATCTTAAACATCAGTCGTGACAGAAGTTTACTCTGCTGAGATACTGCTGAAGCCCTGGTCTGTAATTGTTATGTCGATTTA  
AVCHB:00110:00893  
AGCTGAACTTAAAGGTCATCTTAAACATCAGTCGTGACAGAAGTTTACTCTGCTGAGATACTGCTGAAGCCCTGGTCTGTAATTGTTATGTCGATTTA





# General approach

## The three steps of the approach

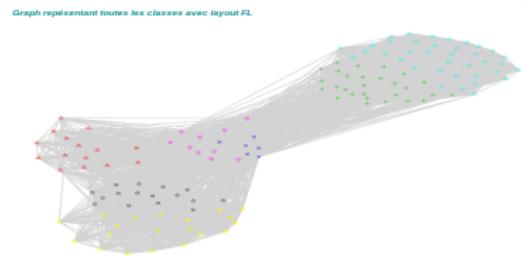
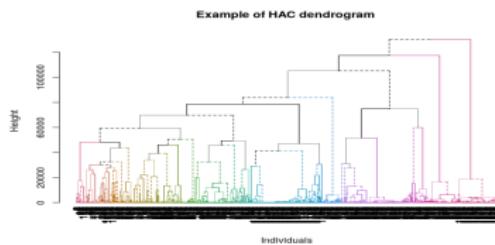
- **Step 1 :** Choice of sub-samples to study :
  - Our experiment: Selection

Taxonomic level	Sequences	Number of taxa	Minimal size
Species	313	55	5
Genera	845	36	10
Families	1349	30	10
Orders	1357	11	15

# General approach

## The three steps of the approach

- **Step 2 :** For each sub-sample, building partitions with three methods for each sub-sample and with Smith Waterman and kmer dissimilarities :
- **M<sub>1</sub> : Agglomerative Hierarchical Clustering (AHC)**
- **M<sub>2</sub> : Stochastic Block Model (SBM).**



# General approach

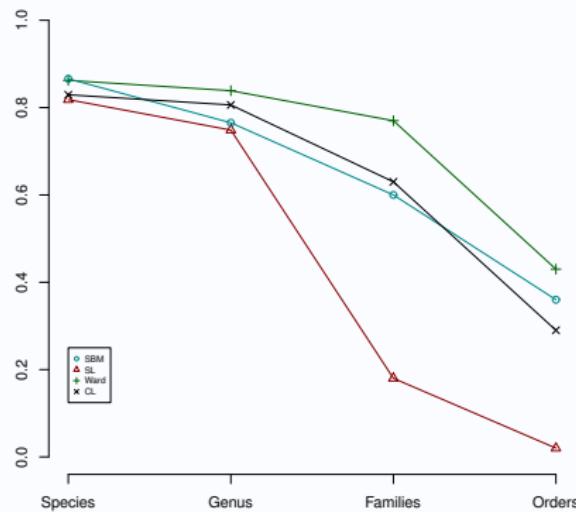
## The three steps of the approach

- **Step 3 :** Comparing the classifications two by two
  - Using visual tools
  - Using NMI to characterize the adequacy/independence

# Results as a function of taxonomic level

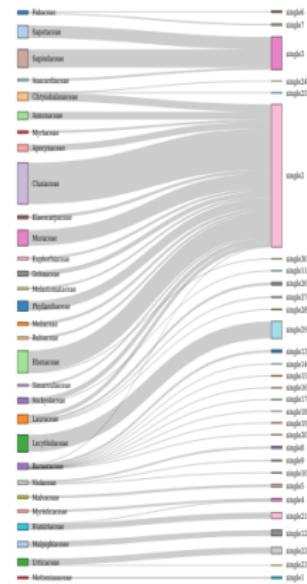
## Evolution of NMI index as a function of Taxonomic levels:

kmer based distances

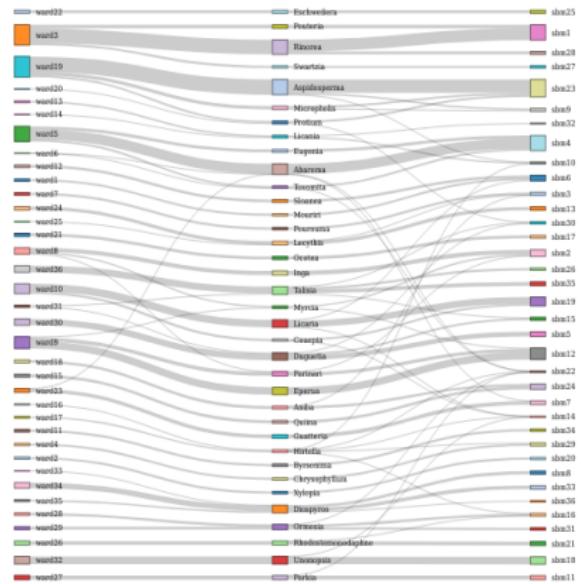


# Sankey plots for genera

## Botanics WRT SL

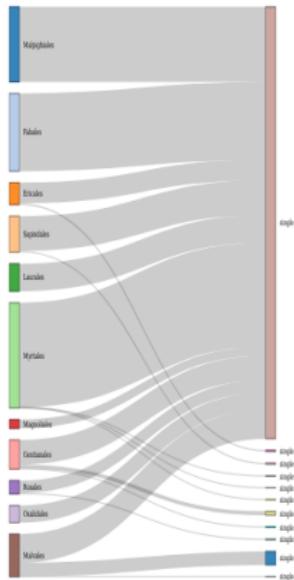


## Ward WRT Botanics WRT SBM

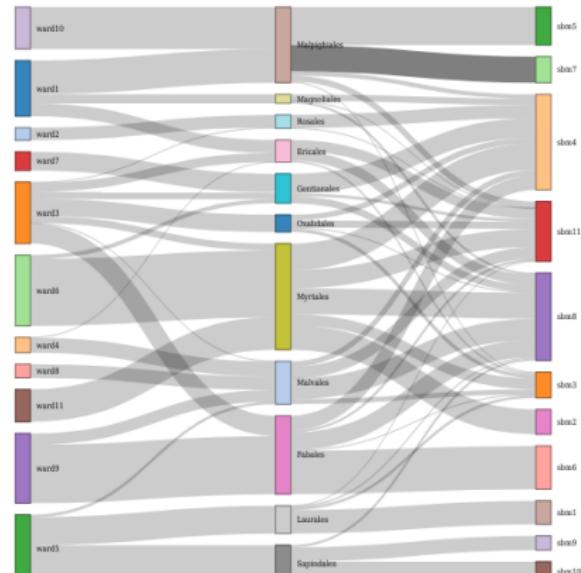


# Sankey plots for orders

Botanics WRT SL



Ward WRT Botanics WRT SBM



## In conclusion : Interest of SBM models

The main advantage between AHC and SBM :

- AHC produces community w.r.t. SBM produces classes (not necessary communities)
- Outputs of SBM are : Classes and  $\Lambda$ , distance matrix between classes.

Let's talk about  $\Lambda$  :

**Case 1 :**

$$\Lambda = \begin{pmatrix} 2 & 9 & 11 \\ 6 & 3 & 7 \\ 8 & 5 & 1 \end{pmatrix}$$

**There are 3 communities**  $\implies$  SBM  $\simeq$  CAH

# In conclusion : Interest of SBM models

## Case 2 :

$$\Lambda = \begin{pmatrix} 22 & 9 & 11 \\ 6 & 3 & 7 \\ 8 & 5 & 1 \end{pmatrix} \quad \Lambda = \begin{pmatrix} 2 & 9 & 11 \\ 6 & 23 & 7 \\ 8 & 5 & 1 \end{pmatrix} \quad \Lambda = \begin{pmatrix} 2 & 9 & 11 \\ 6 & 3 & 7 \\ 8 & 5 & 19 \end{pmatrix}$$

**There are 2 communities**  $\implies$  SBM (warning)  $\neq$  CAH

## Case 3 :

$$\Lambda = \begin{pmatrix} 22 & 9 & 11 \\ 6 & 23 & 7 \\ 8 & 5 & 19 \end{pmatrix}$$

**There are no communities**  $\implies$  SBM (warnings)  $\neq$  CAH

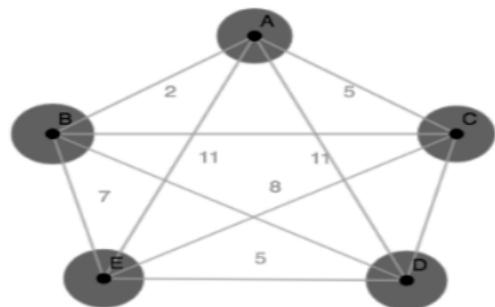
# SBM model

# Model intuition

Data set

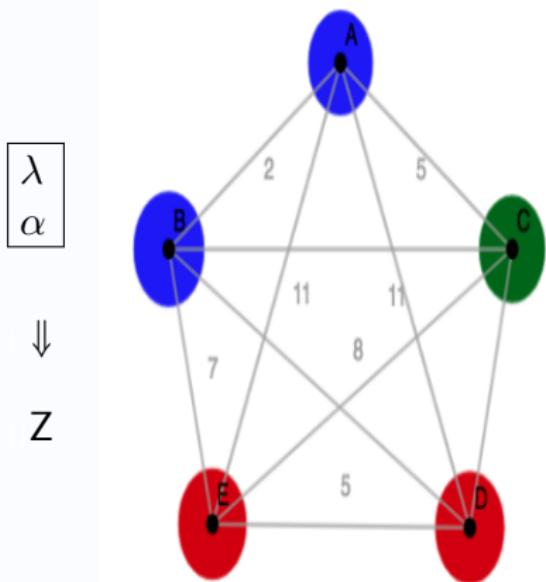
$$\begin{pmatrix} 0 & 2 & 5 & 11 & 11 \\ \vdots & 0 & \ddots & \ddots & 7 \\ \vdots & \vdots & \ddots & \ddots & 8 \\ \vdots & \ddots & \ddots & 0 & 5 \\ \vdots & \dots & \dots & \dots & 0 \end{pmatrix}$$

Representation as graph



# Model parameters

## Statistical model : SBM



## Clusters inference

Let  $q$  be the number of classes  
 $Z = (z_1, \dots, z_n)^T \in \mathbb{M}_{n,q}([0, 1])$



## Model Hypothesis

- $H_1$  Knowing  $Z$ , distances are independent.
- $H_2$  The latent variables  $z_{i,i=1,\dots,n}$  are iid in  $\{1, \dots, q\}$ .

# Parameters presentation

- $D_{i,j}|z_{i,b} = 1, z_{j,b'} = 1 \sim \text{Pois}(\lambda_{b,b'})$
- $\Lambda \in \mathbb{M}_{q,q}, \lambda_{b,b'}:$  The parameter of Poisson probability to have a distance  $d$  between a vertex of class  $b$  and a vertex of class  $b'$ .

$$\forall b, b' = 1, \dots, q, \lambda_{b,b'} = z_b^T \Lambda z_{b'}$$

$$\Lambda = \begin{pmatrix} 2 & 9 & 11 \\ 6 & 3 & 7 \\ 8 & 5 & 1 \end{pmatrix}$$

- $\alpha \in [0, 1]^q, \alpha_i:$  The probability to belong to class i.

# EM algorithm

$$Z = (z_1, \dots z_n)^T \in \mathbb{M}_{n,B}([0, 1])$$



- estimating  $Z$  needs to obtain  $\hat{\theta} = (\hat{\alpha}, \hat{\Lambda})$  we proceed by  
 $\hat{\theta}_{mv} = \text{argmax}(P(D|\theta))$
- The most natural way is the EM algorithm. Each iteration involves two steps :

- **E-step :** Compute :  $Q(\theta, \theta^t) = \mathbb{E}_Z[\log P_\theta(D|Z)|\theta^t, D]$
- **M-step :**  $\theta^{(t+1)} = \text{argmax}_\theta Q(\theta, \theta^t)$

! The main difficulty of the EM algorithm is to compute the marginals:  
It requires  $q^{n-1}$  sums.

# Estimation approach

There are two main classes of methods :

**Monte-Carlo methods** : characterize a distribution by randomly sampling values from the distribution.

- + Precision : Accurate
- Computation time : Slow

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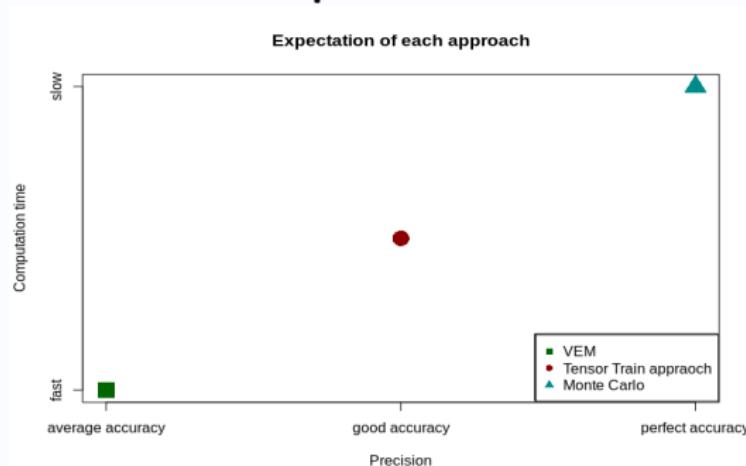
**Variational methods**: we assume the independence of the nodes knowing the graph to approximate marginal by mean field.

- Precision : Average accuracy
- + Computation time : Fast

# Estimation approach

- The ideal approach consists on having good to perfect accuracy and fast computation time

## Expectation :



How to get closer of this approach ?

# Tensor trains approximation for SBM estimation

# The idea

Let's  $\Psi$  express a graphical model,

$$\Psi[z_1, \dots, z_n] = \prod_{\ell=1,n} \psi_{A_\ell}(Z)$$

**Mean field**

$$\Psi : [1, q] \longrightarrow \mathbb{R}$$

$$z_1, \dots, z_n \longrightarrow \Psi[z_1, \dots, z_n]$$

**Tensor Train**

$$\Psi \in (\mathbb{R}^q)^{\otimes n}$$

$$\Psi[z_1, \dots, z_n] \in \mathbb{R}$$

# The idea

- **The mean field** which is approximation by products of scalar (rank =1).

Smartness

$$x_{ij} = a_i b_j$$

$$\sum_{i,j} x_{ij} = \sum_{i,j} a_i b_j = \left( \sum_i a_i \right) \left( \sum_j b_j \right)$$

$n^2$  products      1 product

- **Tensor Train** which is approximation by matrix products (rank >1).

Smartness

$$\sum_{i,j} \mathbf{a}_i \mathbf{b}_j = \left( \sum_i \mathbf{a}_i \right) \cdot \left( \sum_j \mathbf{b}_j \right)$$

$\underline{\mathbf{a}_i} | \mathbf{b}_j$

1 matrix product

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$$\underline{\mathbf{a}_i} | \mathbf{b}_i$$

1 matrix product

# The idea

## Tensor Train

- The tensor train format of the joint probability distribution :

$$\forall z_1, \dots, z_n, \Psi[z_1, \dots, z_n] = A_1[z_1] \cdot A_2[z_2] \dots A_{n-1}[z_{n-1}] \cdot A_n[z_n]$$

$$\Psi[z_1, \dots, z_n] = \_\_\_ \cdot \quad \square \dots \square \cdot |$$

$A_i[z_i]$  : The cores of  $\Psi$  (matrix)

- This format allows variable separation, suitable for marginals

# How ?

## How to compute $A_i[z_i]$ matrix ?

Novikov approach

- compute the TT-approximation of each factor
- then, it uses the Kronecker mixed-product property to compute the TT-approximation of  $\Psi$  from the TT approximation of each factor

# Improvement of this approach :

- The matrix  $A_i[z_i]$  are sizes  $O(q^n)$

A way to deal with this is to use the TT Format that allow us a storage

- + who requires much less memory space
- + who can be used for matrices
- + with efficient operations

# Computation of marginals

- Partition function :

$$\begin{aligned} W &= \sum_{z_1, \dots, z_n} A_1[z_1] \dots A_n[z_n] \\ &= \left( \sum_{z_1} A_1[z_1] \right), \dots, \left( \sum_{z_n} A_n[z_n] \right) \end{aligned}$$

Let's  $B_i = \sum_{z_i} A_i[z_i]$

$$W = B_1 \times \dots \times B_n$$

# Computation of marginals

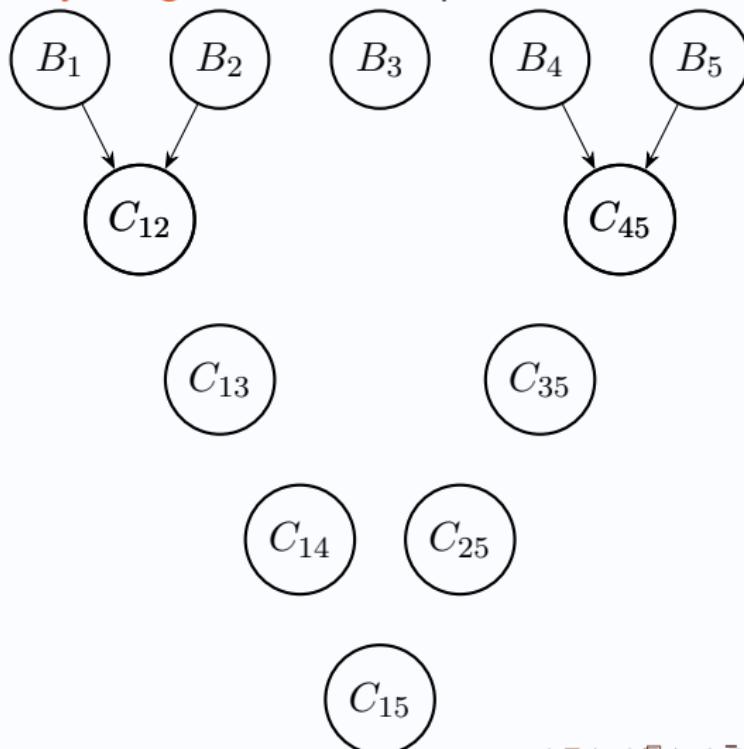
Let's  $B_i = \sum_{z_i} A_i[z_i]$

- **Binary marginals :**  $\forall i, j \in [1, n]^2, p_{i,j}(z_i, z_j)$

$$\underbrace{B_1 \times \dots \times B_{i-1}}_{\text{left}} A_i[z_i] \underbrace{B_{i+1} \times \dots \times B_{j-1}}_{\text{center}} A_j[z_j] \underbrace{B_{j+1} \times \dots \times B_n}_{\text{right}}$$

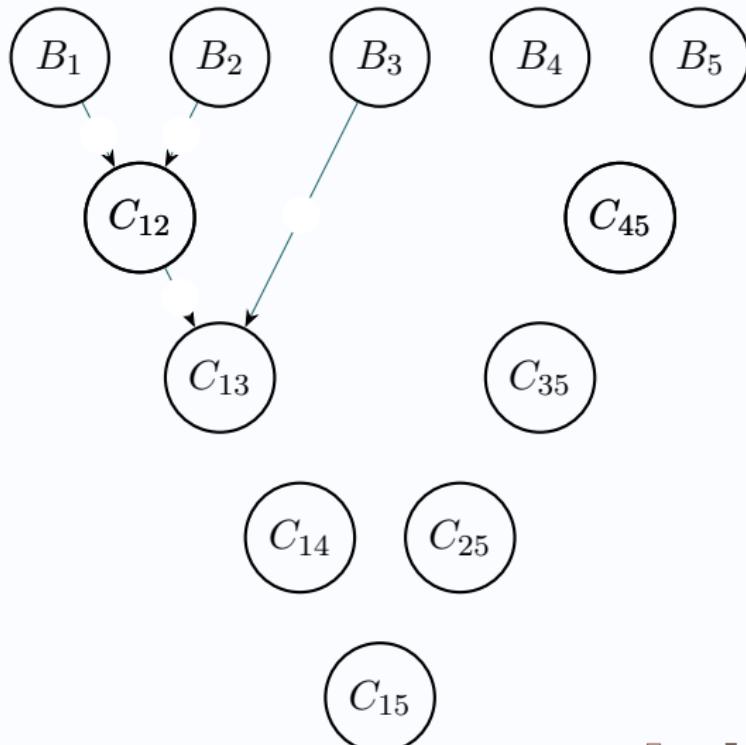
# Computation of marginals

- Unary and Binary marginals : First step :



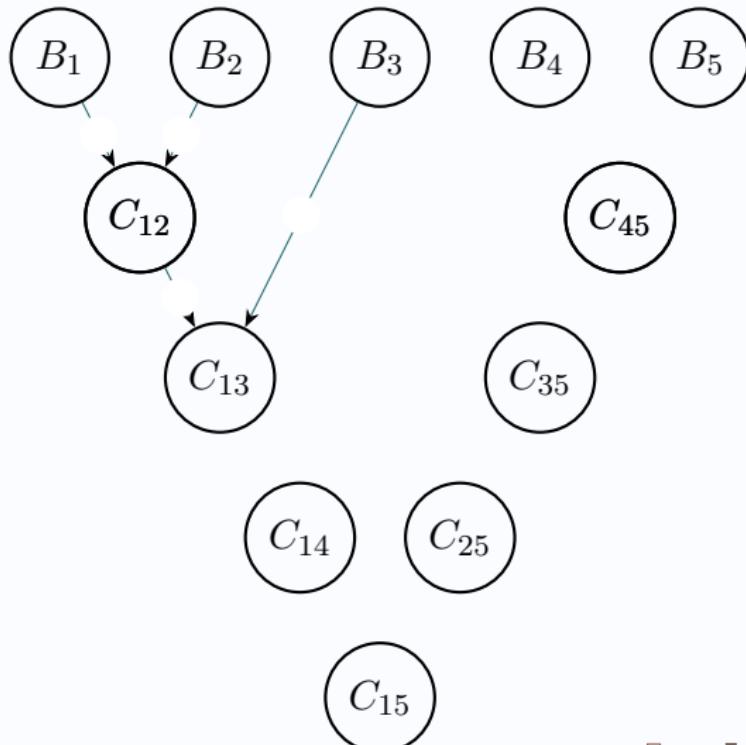
# Computation of marginals

- Unary and Binary marginals : Second step : Left side



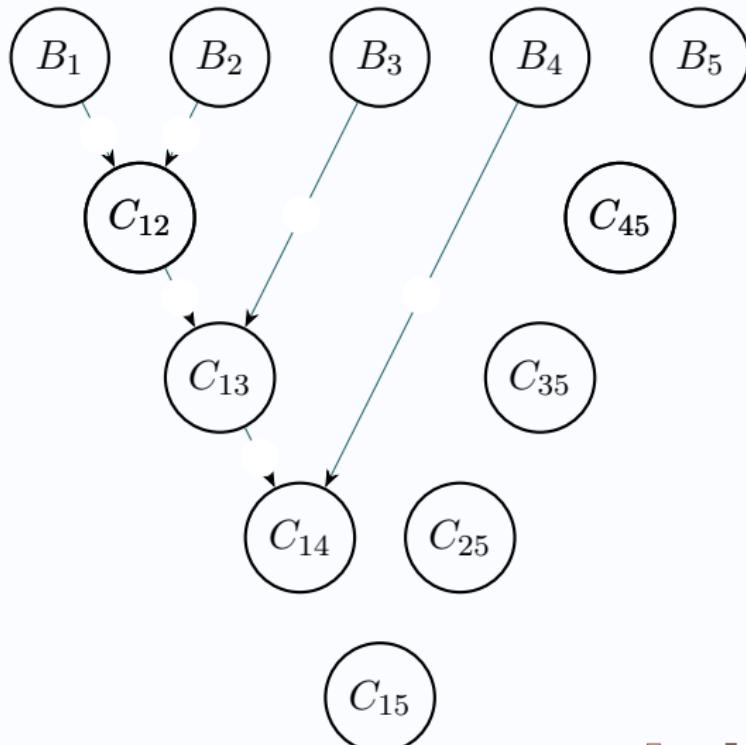
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- Unary and Binary marginals : Second step : Left side



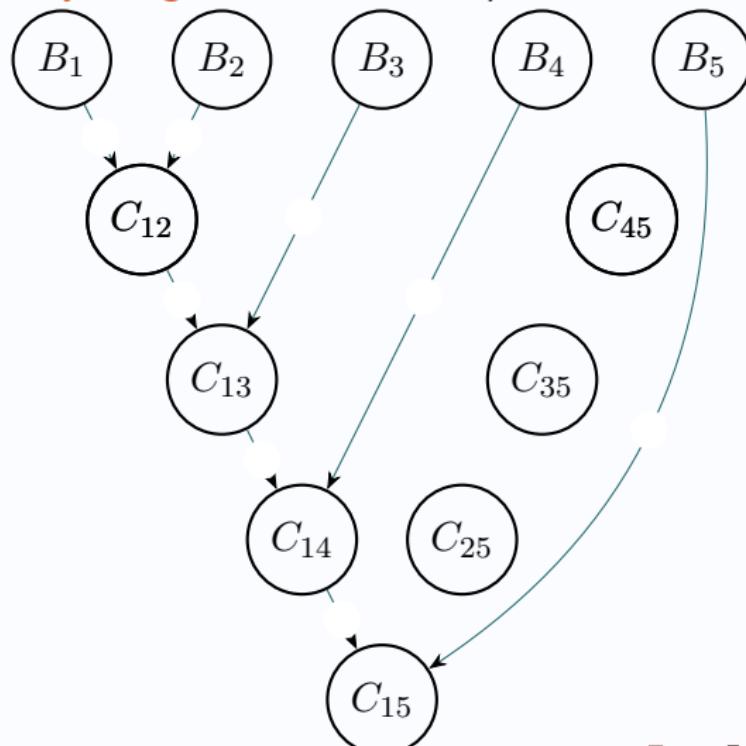
# Computation of marginals

- Unary and Binary marginals : Second step : Left side



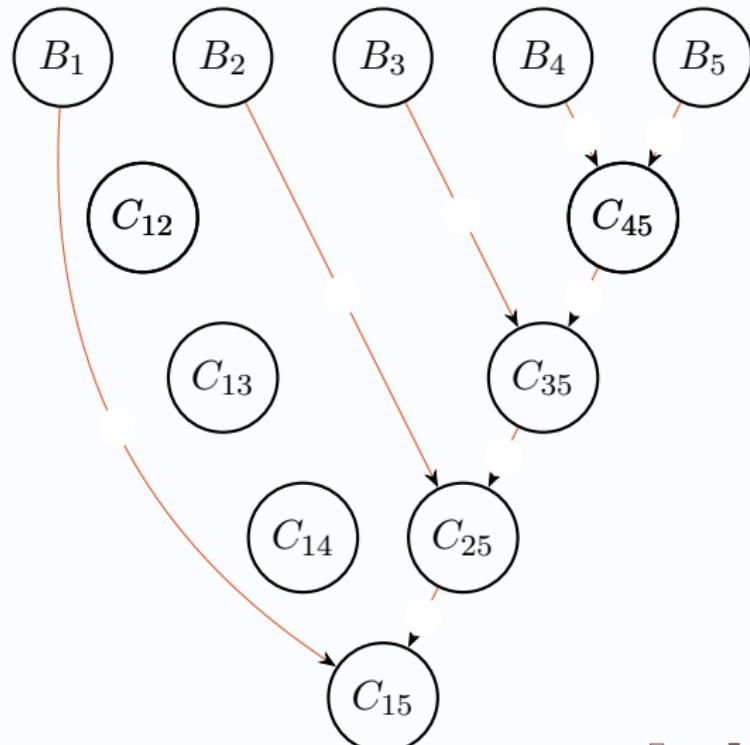
# Computation of marginals

- Unary and Binary marginals : Second step : Left side



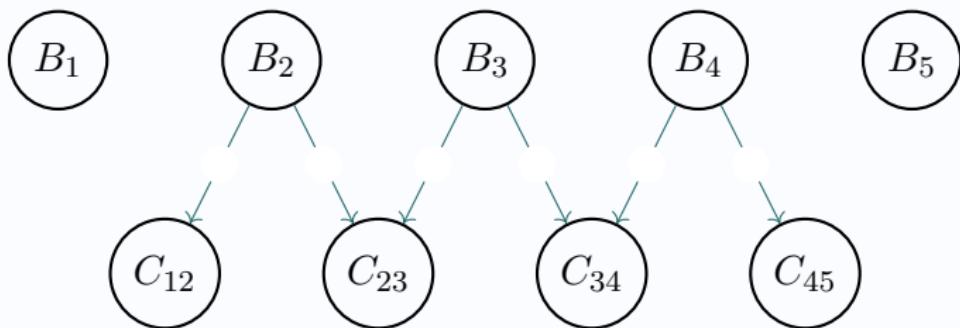
# Computation of marginals

- Unary and Binary marginals : Third step : Right side



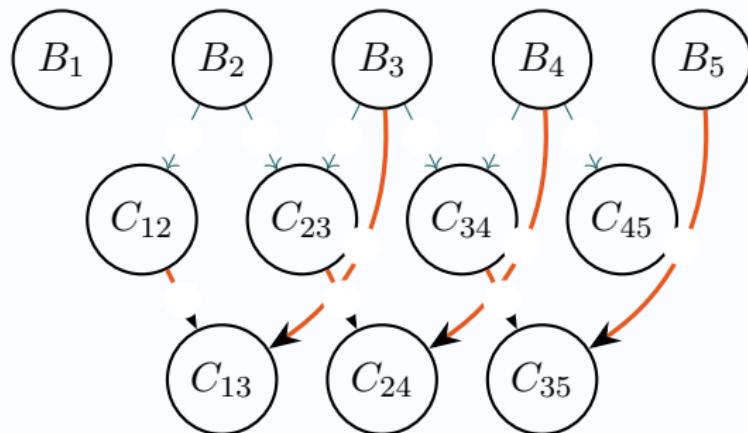
# Computation of marginals

- Binary marginals : Fourth step Centers



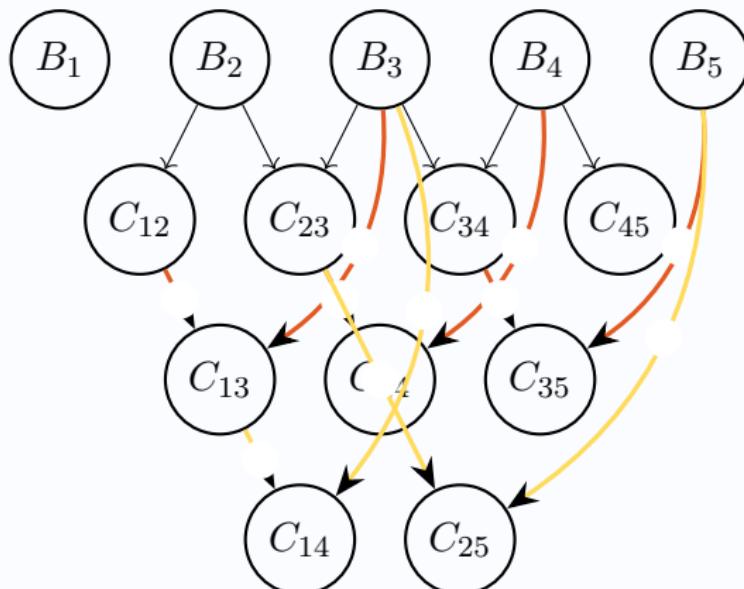
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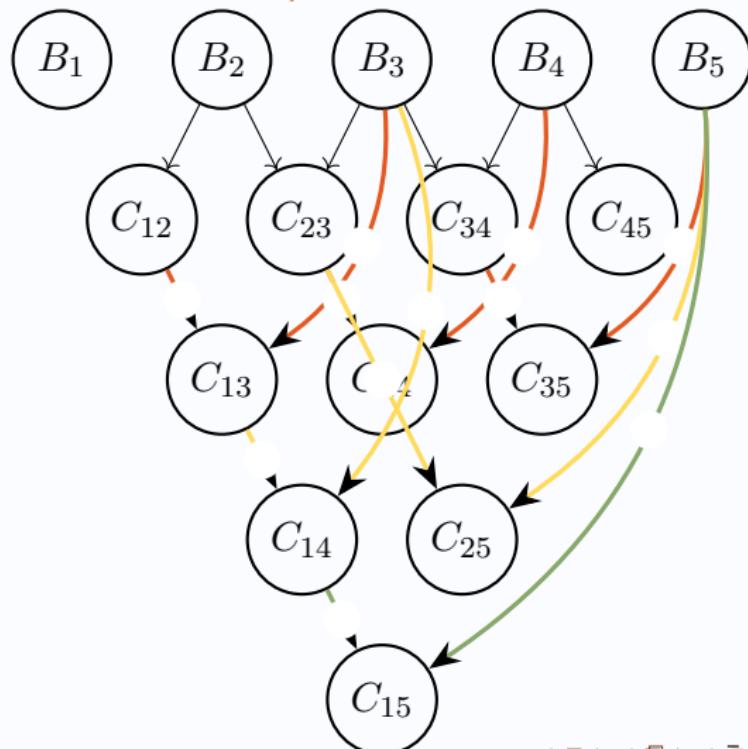
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# Computation of marginals

- Binary marginals : Fourth step Centers



# Conclusion and prospect

During this presentation, we showed that

- SBM models can be used for metabarcoding
- that we can potentially improve their accuracy thanks to a tensor based approach

# Conclusion and prospect

A legitimate question remains unanswered:

**How to scale up the SBM model to large datasets ?**

