1. **INPUT**

   - Patterns of events $X = (x_{ij})_{1 \leq i \leq n}$, $1 \leq j \leq l$
   - Number of oncogenetic trees $K \geq 2$

2. **OUTPUT**

   - $K$-oncogenetic trees mixture model $\sum_{k=1}^{K} \alpha_k T_k$

3. **PROCEDURE**

   1. Guess initial responsibilities:
      (a) Run $(K-1)$-means clustering algorithm
      (b) Set responsibilities
         
         $$\gamma_{ik} = \begin{cases} 
         0.01, & \text{if } k = 0; \\
         0.99 \cdot \frac{3}{3 + (K - 2)}, & \text{if } x_i \text{ is in cluster } k - 1; \\
         0.99 \cdot \frac{1}{3 + (K - 2)}, & \text{else (the remaining } K - 2 \text{ clusters).}
         \end{cases}$$

   2. **M-like step.** Update model parameters:
      Set $N_k = \sum_{i=1}^{N} \gamma_{ij}$ for all $k = 1, \ldots, K$
      Let $T_1$ be a star with edge weights
         
         $$\beta = \frac{1}{lN_1} \sum_{j=1}^{l} \sum_{i=1}^{N} \gamma_{ij} x_{ij}$$

      For $k = 2, \ldots, K$:
      (a) For all pairs of events $(u, v)$, $1 \leq u, v \leq l$, estimate their joint probabilities
         
         $$p_k(u, v) = \frac{1}{N_k} \sum_{i=1}^{N} \gamma_{ik} x_{iu} x_{iv}.$$  

      (b) Compute the maximum weight branching $T_k$ from the complete digraph with weights $w$ derived from $p_k$.
      (c) Compute the mixture parameter $\alpha_k = \frac{N_k}{N}$.

3. **E-step.** Compute responsibilities:

   $$\gamma_{ik} = \frac{\alpha_k \Pr(x_i \mid T_k)}{\sum_{m=1}^{K} \alpha_m \Pr(x_i \mid T_m)}$$

4. Iterate steps 2 and 3 until convergence.