Input: a data set of n events, i.e., genomic alterations, and m samples packed in a data structure obtained from Algorithm 1.

Result: a *tree model* representing all the relations of selective advantage.

Pruning based on Suppes' criteria.

Let $G \leftarrow$ a complete directed graph over the vertices n.
forall *arcs* (a, b) *in* G **do**
    Compute a score $S(\cdot)$ for the nodes a and b based on Suppes' criteria.

    Verify Suppes' criteria, that is:
    if $S(a) \geq S(b)$ *and* $S(a) > 0$ **then**
        Keep (a, b) as edge. *I.e., select 'a' as "candidate parent".*
    else if $S(b) > S(a)$ *and* $S(b) > 0$ **then**
        Keep (b, a) as edge. *I.e., select 'b' as "candidate parent".*
end

Fit of the prima facie *directed acyclic graph to the best tree model.*

Let $\mathcal{T} \leftarrow$ the best tree model obtained by Edmonds' algorithm (see Edmonds(1967)).
Remove from $\mathcal{T}$ any connection where the candidate father does not have a minimum level of correlation with the child.

return *The resulting* tree *model* $\mathcal{T}$.