

Supply Chain Reconstruction

Aaron Schankler

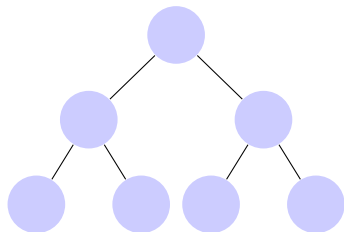
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The Problem

- The co-occurrence of cutting agents shows “a promising potential in an intelligence perspective for analysing the local distribution process of heroin” (Terrettaz-Zufferey et al.)
- We want to recover information about the structure of the supply chain, such as which seizures are more closely related.
- We want to use only information about the end product.
- To this end, we propose a new model.

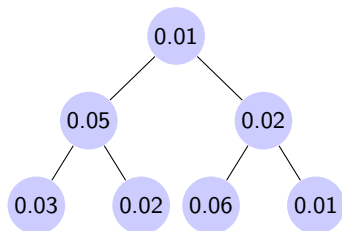
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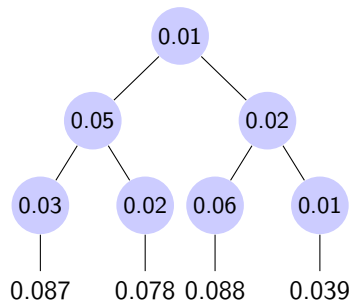
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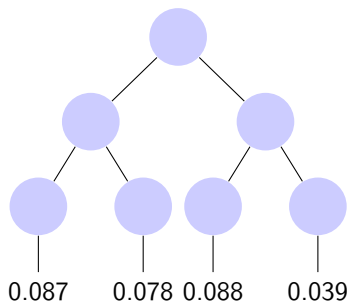
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- Each supplier adds cutting agents in a fixed proportion.

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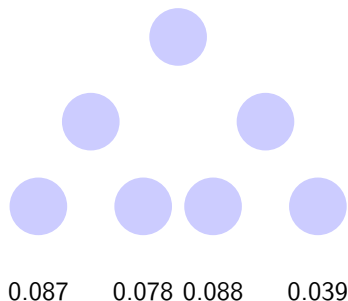
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- We know the total proportion of cutting agents at the lowest distribution level.
- We do *not* know the proportion of cutting agents added at any node.
- We do *not* know how each sample is related to the others.

Assumptions

- Each supplier uses at least one cutting agent.
- A supplier will always add cutting agents in the same way (no time dependency).
- We know the proportion of cutting agents present at *all* of the leaves.
- Our goal is to recover the position of the known nodes in the original tree.
 - This information will allow us to reconstruct sibling relationships.

Our Method

- We first guess a tree shape.
- Based on the shape of the tree:
 - We can create a set of expressions that correspond to the proportion of each cutting agent present at each leaf;
 - These expressions depend on parameters that correspond to the proportion of each agent added at each node.
- We guess an arrangement of leaves and based on this guess pair each leaf value with the corresponding expression.
- We attempt to solve the resulting system; a solvable system should correspond to a possible configuration of the supply chain.

Solving the Systems

- The systems are under-constrained and non-linear, and so cannot be solved explicitly.
- We search numerically for parameters that come close to a solution.
- Our method is a specialized version of a technique called simulated annealing.

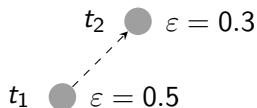
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$$t_1 \quad \bullet \quad \varepsilon = 0.5$$

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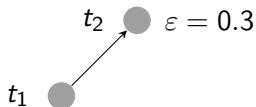
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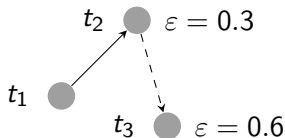
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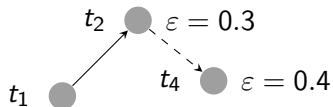
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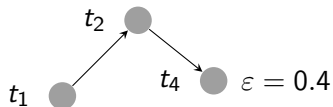
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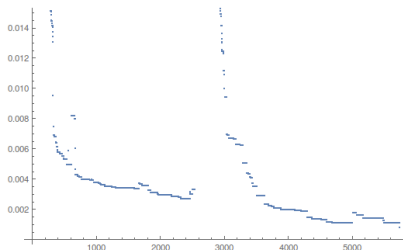
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Implementation and Testing

- We have not yet made use of data on drug supply chains
 - Instead, we pick random parameters for each node.
 - We can then calculate plausible values for leaves to test the program on.
- Our method only tells us when a solution is possible, not when it is impossible.
 - We reject if a configuration is taking 'too long' to solve.
 - It is more effective to do multiple trials with a lower rejection threshold.
 - Testing bad configurations is more expensive than testing good ones.
- When testing our method, we look for:
 - Whether it can solve a correct tree
 - Whether it rejects incorrect trees

Results

- The effectiveness is affected by the shape of the tree and the number of cutting agents considered.
- Increasing the depth of the tree makes the system less constrained.
- Increasing the number of children at each node does not make the system less constrained.
- Increasing the number of cutting agents makes the system more constrained.
 - There are many more parameters, so systems are harder to solve.
 - Considering more agents *significantly* increases differentiation.
- We can eliminate many incorrect configurations on small trees.

Conclusion

- We have developed a new model that takes into account more quantitative information about the supply chain.
- We show that for small cases, our model can be used to gain information about the supply chain.
- Work left to do:
 - Do tests on guessing the tree shape, not just the configuration of leaves
 - Improve the SA implementation to reliably solve more complex trees
 - Find other methods to reject configurations without resorting to SA
 - Look at empirical data to see if our model is plausible