Modeling of Disease Spreading on Trees

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Motivation

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$\rightarrow$ the motivation for the question

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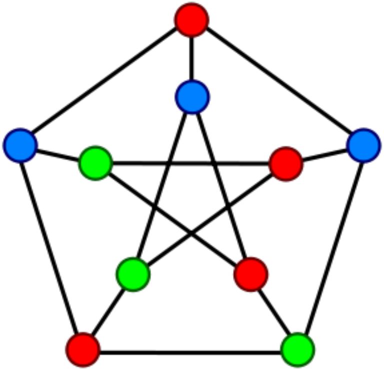

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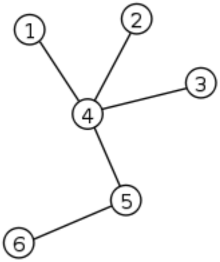

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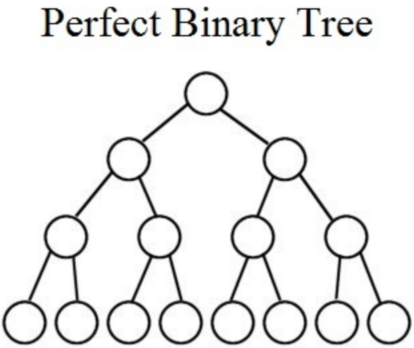
Perfect Binary Tree: A perfect binary tree is a binary tree with $2^N - 1$ vertices such that the last level is completely full.

Note that such a tree is unique, not including labeling or directed edges.

Perfect Binary Tree



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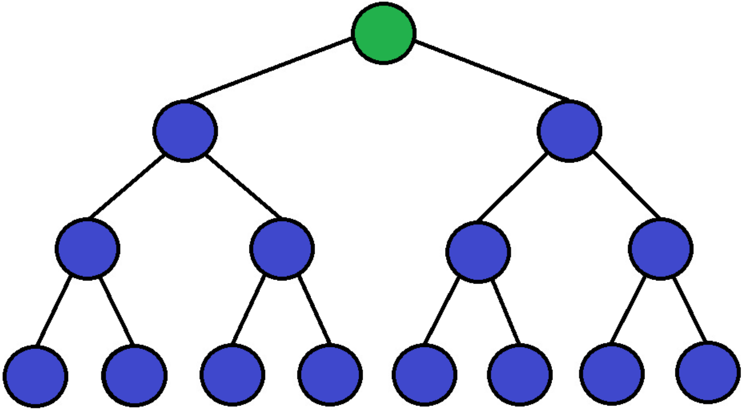
    - Each node has a chance to be infected at any given point
- Infection rate decreases with distance from node

An Example



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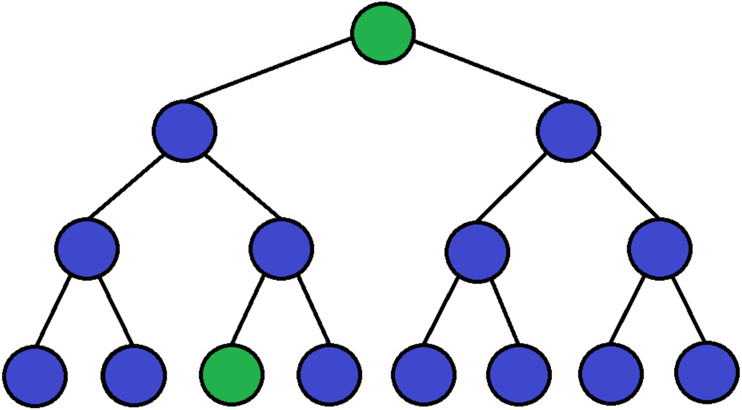

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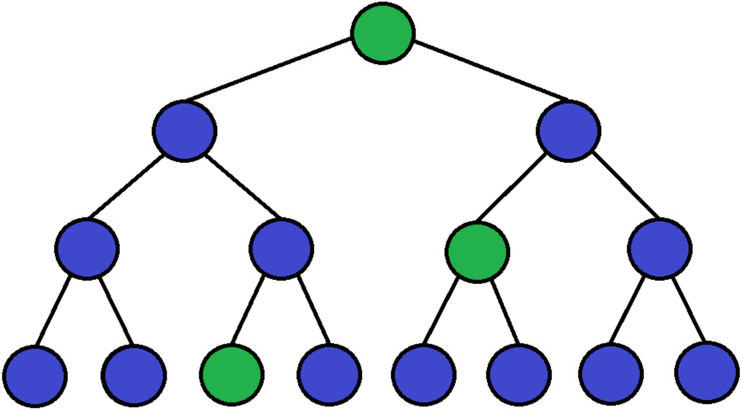

Questions

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2. How many infected nodes are there when this occurs?

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  - k is the difference in layers between the infecting/infected nodes

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Property

Probability: If $X_1, X_2, \ldots, X_n$, *are all exponential with rates* $r_1, r_2, \ldots, r_n$, *then the probability than* X_i *is the minimum of* $X_1, X_2, \ldots, X_n$ *is* $\frac{r_i}{r_1+r_2+\cdots+r_n}$.

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Properties can shorten simulation time

1. Pick a point that will infect, probability property

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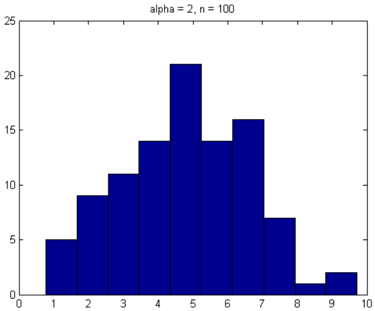
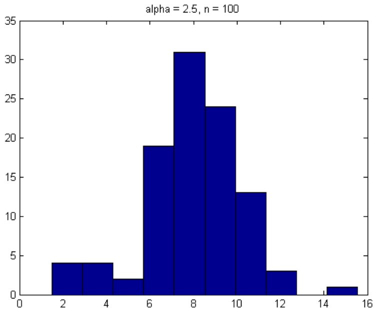
Properties can shorten simulation time

1. Pick a point that will infect, probability property
2. Pick point to be infected
3. Time generated from exp(sum of all infected node rates), minimum property

Results

The results seem to model a curve that is slightly skewed right





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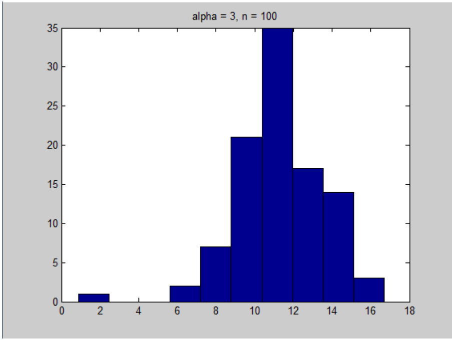

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If $1 < \alpha < 2$*, prediction is polynomial in n with degree* $\alpha - 1$

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If $\alpha \geq 2$, *prediction is linear in n*

Future Goals

Expand to different types of trees

Acknowledgments

Professor Partha Dey for mentoring me on this project
PRIMES and Tanya Khovanova for offering this opportunity