Random Walking with a Purpose

Trenton W. Ford CSE 60742

Graph Kernel: Random Walk Pseudocode

A Random Walk:

Given a graph G(V, E) where V is a set of vertices, and E is a set of edges. 1. Select an arbitrary starting node *u* in *G*. 2. (Randomly) select a neighbor of u, say v. 3. Move across the edge (u, v), let u < -v and repeat steps 2 and 3... or stop.

Complexity: It depends on the purpose(stopping criteria) of the walk.

• For practically all scenarios: $\Omega(RW) = \Omega(|V|+|E|)$ for basic traversal



Random Walk Applications

- Modeling diffusion (Brownian, epidemics, mosquitos, etc.)
- Sampling from large networks (embeddings, grammars, etc.)
- Fun games (Conway's Game of Life... others?)

Data Set Considerations

Changes in epidemic transmission behaviors rely on many network properties:

Recovery Time, Epidemic Infectiousness, Average Node Degree, Clustering Propensity, and many more.



Data Sets: Real-world Networks

Advantages:

Results are more meaningful

Disadvantages:

Scaling via subsetting real-world datasets is hard



Potential Datasets

Dataset	Approximate Order	Approximate Siz
DOT Railway Data	196K	250
SNAP Airport Data	456	71
KNB Shipping Data	3700	15





Data Sets: Synthetic Networks

Advantages:

Scaling is easy and repeatable.

Disadvantages:

The networks may not accurately represent a real-world scenario

Source:

Temporal Graph Generation Based on a Distribution of Temporal Motifs



- 1. At t_0 each room contains a person, and one person is infectious and if in contact with a susceptible person will infect them with probability p.
- 2. Between each time step, each person has a probability λ to move from one room to another, with a uniform probability between the rooms they have access to.
- 3.Each infectious person has a μ probability of recovering at each time step after their initial infection.











1. Transportation networks can be converted to planar networks by duplicating confounding nodes and edges.

2. Fáry's theorem says that any planar network can be represented via a grid layout

3. Simple Grid Model is extensible, but becomes a less intuitive abstraction.

Simplified Grid Random Walk Language: Boost Graph Library

Basic Structures:

```
struct VertexProperties
   struct step_data{};
    step_data current_step;
    step_data future_step;
   uint row = 0;
   uint col = 0;
    static boost::random::mt19937 rng;
    static boost::random::uniform_real_distribution<double> gen;
    static constexpr float p = 0.5; // Infection Probability
    static constexpr float lamb = 0.5; // Movement Probability
    static constexpr float mu = 0.25; // Recovery Probability
    VertexProperties(){}
    VertexProperties(uint r, uint c, uint pop){}
    void infect(){}
    void recover(){}
    void update(){}
    void set_current_values(pop , ipop , spop){}
    void adjust_future_values(pop = 0, ipop = 0, spop = 0){}
    void advance_timestep(){}
```

#include <boost/graph/grid_graph.hpp> typedef grid_graph<2> GraphType;



for (uint i = 0; i < DIMENSIONS; ++i)</pre> for (uint j = 0; j < DIMENSIONS; ++j)</pre> Vertex v = Traits::vertex_descriptor {{i, j}} vertex_data = get(dataMap, v);(out_verts in boost::adj(vertex_data)) do a thing using vertex_data put(dataMap, v, vertex_data)







Simplified Grid Random Walk **Complexity:**



convergenceRate is based on the graph structure distribution of p, λ , and μ , and has yet to be thoroughly analyzed, but appears that

 $O(convergenceRate^{-1}) < O(n^2)$

Runtime Analysis:

System already distributing simple operations.

Process Name	% CPU ~	CF
Terminal	135.6	







Random Walking + Dynamic Weights: Parallel Implementation Refactor for parallelism using Parallel Boost Change graph type from grid for greater flexibility Work on graph partitioning strategy for different distributions Analyze hyper-parameter sensitivity (p, λ, μ)

Questions?

Let I_i be the set of infective vertices at time t_i . Let $New_I_i = I_i - I_{i-1}$

Define:
$$IR_i(u) = \frac{ipop_i(u)}{pop_i(u)}$$

 $Transfer_i(u, v) = \text{contact between } u \text{ an}$
between time t_{i-1} and

Let $T_i(u, v)$ = transition count from *u* to *v* at time t_i . $T_i(u, v) = Transfer_i(u, v) \times IR_{i-1}(u)$

This can be defined in many ways.



Factors not being considered:

- 1. Random Spread
- 2. Disease Carriers
- 3. Non-Random Distribution of Carriers
- 4. Population Shift
- 5. Inanimate Disease Vectors



$$I_0 = \{\}$$
$$IR_0(v \in V) = \frac{ipop_i(v)}{pop_i(v)} = \frac{0}{pop(v)}$$

At time t₀ there are no infective vertices. But they are all susceptible.



 $I_{1} = \{D\}$ $New_{I_{1}} = I_{1} - I_{0} = \{D\}$ $IR_{1}(D) = 1/100 = .01$

$T_2(D, A) = Transfer_2(D, A) \times IR_1(D) = 1$ $T_2(D, B) = Transfer_2(D, B) \times IR_1(D) = .2$

 $T_i(u, v) = Transfer_i(u, v) \times IR_{i-1}(u)$



 $I_2 = \{D, A\}$ $New_{I_2} = I_2 - I_1 = \{A\}$ What is the probability that vertex A was infected via vertex D $Transfer_2(B, A) = 20 \ people$ $Transfer_2(C, A) = 50$ people $Transfer_2(D, A) = 100 \ people$ $T_2(B,A) = Transfer_2(B,A) \times IR_1(B) = 0$ $T_2(C,A) = Transfer_2(C,A) \times IR_1(C) = 0$ $T_2(D,A) = Transfer_2(D,A) \times IR_1(D) = 1$ $likelihood(A < -D | A \in New_{I_2}) \propto$



 $I_{3} = \{D, A, B\}$ $New_{I_{3}} = I_{3} - I_{2} = \{B\}$ Through which vertex is B more likely to be infected?

 $Transfer_3(A, B) = 100 \ people$ $Transfer_3(D, B) = 100 \ people$

 $T_3(A, B) = Transfer_3(A, B) \times IR_2(A) = 0$ $T_3(D, B) = Transfer_3(D, B) \times IR_2(D) = 0$

 $likelihood(A < -D | A \in New_I_2) \propto$

