A Recurrent Neural Cascade-based Model for Continuous-Time Diffusion
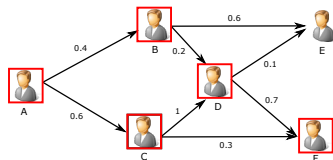
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Cascade-based models for diffusion

- Information *spreads* from users to users in the network, following independent transmission probabilities

Observed Diffusion Episode = {(A;1);(B;2);(C;2);(D;3);(F;4)}

The Continuous-Time Independent Cascade Model (CTIC) defines two parameters $k_{u,v}$ and $r_{u,v}$ per pair (u, v) of nodes in the network (Saito et al., 2011) :
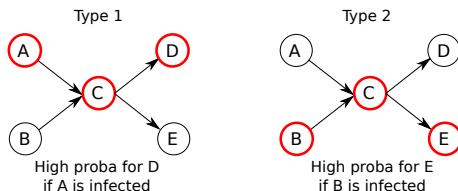
- $k_{u,v}$: probability that u succeeds in infecting v ;

- $r_{u,v}$: time-delay parameter from u to v

Likelihood of a set of episodes $\mathcal{D}$:

$$P(\mathcal{D}) = \prod_{D \in \mathcal{D}} \prod_{v \in U^D} P(v \text{ infected at time } t_v^D) \prod_{v \notin U^D} P(v \text{ not infected in } D)$$
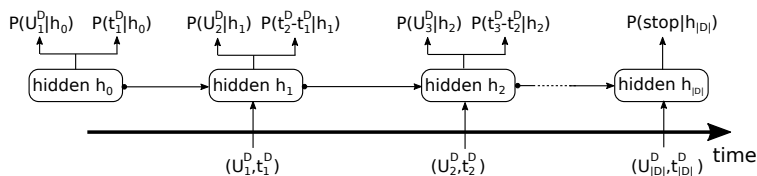
RNN models for diffusion

Markovian assumption does not hold in many situations :

Type 1

High proba for D
if A is infected

Type 2

High proba for E
if B is infected

$\Rightarrow$ Episode D as a sequence $((U_1^D, t_1^D), (U_2^D, t_2^D), ..., (U_{|D|}^D, t_{|D|}^D))$

- Recurrent Marked Temporal Point Processes (Du et al, 2016) :

$P(U_1^D|h_0)$ $P(t_1^D|h_0)$ $\quad P(U_2^D|h_1)$ $P(t_2^D-t_1^D|h_1)$ $\quad P(U_3^D|h_2)$ $P(t_3^D-t_2^D|h_2)$ $\quad P(stop|h_{|D|})$

hidden h_0 $\quad$ hidden h_1 $\quad$ hidden h_2 $\cdots\cdots$ hidden $h_{|D|}$

(U_1^D, t_1^D) $\qquad\qquad (U_2^D, t_2^D)$ $\qquad\qquad (U_{|D|}^D, t_{|D|}^D)$ time

- ... But diffusion is not a sequence !

RNN models for diffusion

Tree Dependencies

F does not depend on E
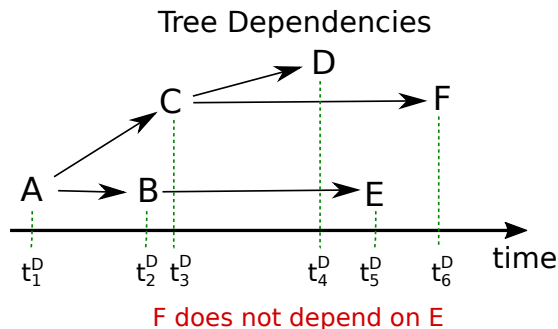
$\Rightarrow$ Cyan (Wang et al., 2017b) : RNN with attention to select previous states

$\Rightarrow$ DAN (Wang et al., 2018) : Similar to Cyan, but with a pooling mechanism rather than RNN

Hybrid Recurrent / Cascade-Based Model for Diffusion

$\Rightarrow$ Idea : Assign a continuous state $z_v^D \in \mathbb{R}^d$ to each infected node v, which depends on its infection path
- z_v^D then conditions distributions of subsequent infections from v

- P(u infects v)= $\sigma\left(< z_u^D, \omega_v^{(k)} >\right)$, with $\omega_v^{(k)} \in \mathbb{R}^d$ a continuous representation of v

- If u is the first node to infect v :
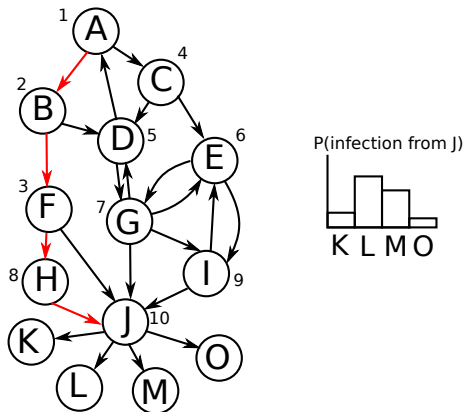
$$z_v^D = f_\phi(z_u^D, \omega_v^{(f)})$$

with :
- f_ϕ a GRU cell
- z_u^D the state of u for D (the memory)
- $\omega_v^{(f)} \in \mathbb{R}^d$ a static representation for v (the input)

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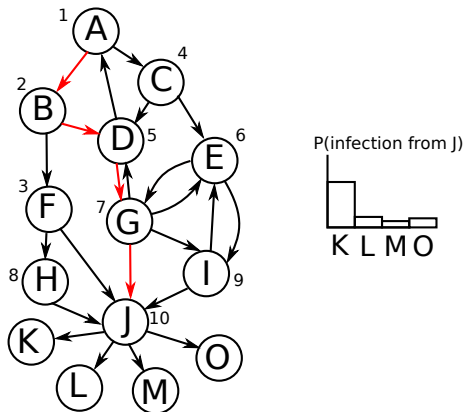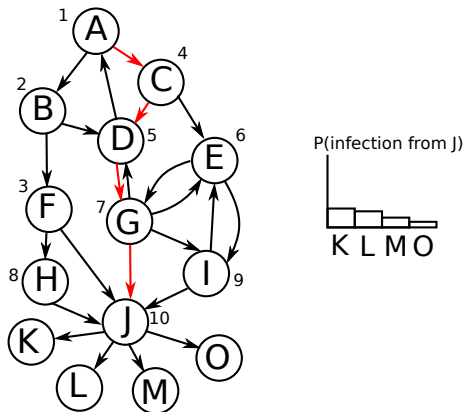 - z_v^D then conditions distributions of subsequent infections from v

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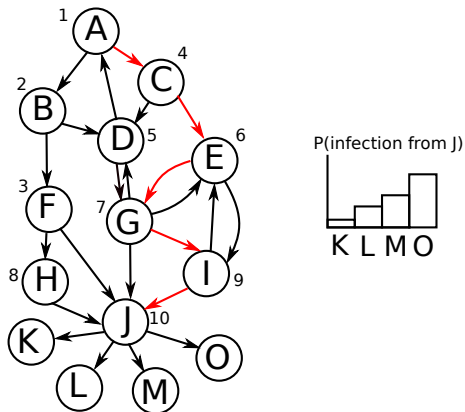# Hybrid Recurrent / Cascade-Based Model for Diffusion

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Inference on ancestors sequences I is required :

$$\log p(D) = \log \sum_{I \in \mathcal{I}^D} p(D, I)$$

Inference distribution : $q^D(I) = \prod_{i=1}^{|D|-1} p(I_i | D_{\leq i}, I_{<i}) \approx p(I|D)$

Score function estimator : $\nabla_\Theta \mathcal{L}(\mathcal{D}; \Theta) =$

$$\sum_{D \in \mathcal{D}} \mathbb{E}_{I \sim q^D} \left[\underbrace{\left(\log p^I(D) - b \right) \nabla_\Theta \log q^D(I)}_{\text{favors good paths}} + \underbrace{\nabla_\Theta \log p^I(D)}_{\substack{\text{increases likelihood} \\ \text{given the path}}} \right]$$