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Modeling of layering growth virus epidemic and spread of harmful content on Poisson networks.

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ABSTRACT

Network security in information and telecommunication systems, reaction with harmful content in social networks are essential problems today. Virus attacks and distribution of unwanted contents efficiency depends on *the* attacked system structure. For this reason, the study of complex networks with degree of nodes distribution by Poisson distribution has great interest. This article is about modeling of layering growth virus epidemic and spread of harmful content on Poisson networks. This article is about modeling of layering virus infection growth process on heterogeneous Poisson networks. This paper contains probabilistic calculations of information risks in information and telecommunication systems with virus epidemic. This model can be used not only for epidemic analysis, but also for analyzing the spread of harmful content on networks.

Keywords: risk models, virus epidemics, complex networks, random networks, Poisson networks.

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INTRODUCTION

Many articles contain information about above mentioned problems [1-6, 24, 25], these papers are about counteraction in networks.

Quantity of layers depends on number of peaks N and the law of distribution peak's levels $P(k)$. In articles [7-15] analysable network class had fixed level of peaks. It is characteristic for rigidly organized networks of lattice type. The heterogeneous structure of communications is characteristic for Poisson networks. Hereof, $k_{\min}=1$ and $k_{\max}$ is calculated by function $H(x)$ from Fig. 1. Function $H(x)$ is a mapping from set $x\in[0,1]$ within a set $y\in\{0,1,2,...\}$, $H(x): x\to y$. As $1/N=P(k_{\max})$, $k_{\max}$ can be defined as function depending on $1/N$:

$$k_{\max}=H(1/N)=H(N).$$

For $\forall x\in X$, $\forall y\in Y$, $y=H(x)$ only when $x=\lambda^y e^{-\lambda}/y!$.

The function will be surjective, if $x\in[0,x_{\max}]$.

Analysing will be similar for multi-layer formalization on vulnerability (danger) level, but the exponent will be the function modeling infection spread.

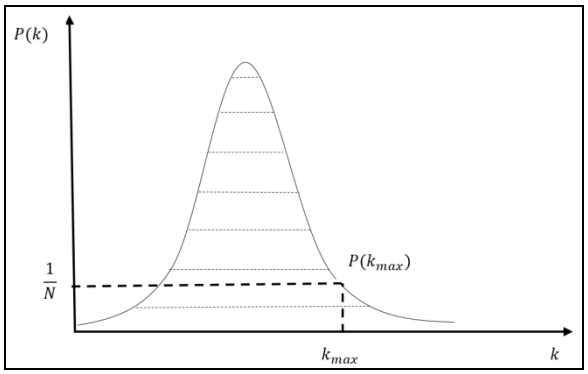

Fig.1. Calculating $k_{\max}$

Such multi-layer formalization gives opportunities for complex multilevel analyses of network in separate level infection context.

Thus, *the* situation for multy-layer formalization of a network on level peaks aspect will be following:

1. The attack from low layers on high layers is improbable $((k+1),...,k_{\max})$;
2. Natural attack on a layer $(k,...,k)$;
3. Attacks from high layers to the lower are easily feasible $((k-1),...,k_{\min})$.;
4. Attacks in all directions directly.

Infection probability will be defined as:

$$P_k=\alpha_k P(k)=\alpha_k e^{-\lambda}\lambda^k/k!.$$

The clustering coefficient for the non-uniform Poisson networks is calculated using the formula

$$K=\langle k\rangle/(n-1), \quad (1)$$

where *n* is number of nodes in the graph.

The clustering coefficient shows how strongly peaks are inclined to form groups (community), which are characterized by that the peaks entering into one group are connected among themselves much more densely, than all remaining graph.

Taking into account clustering coefficient(1):

$$P_k = \frac{\alpha_k K P(k)}{\beta_k} = \frac{K\alpha_k e^{-\lambda}\lambda^k}{\beta_k k!},$$

where *k* is clustering coefficient, β_k is correction coefficient. Level of layer danger depends on communities number directly, therefore two coefficients can be replaced:

$$P_k = \gamma_k K P(k) = \gamma_k K e^{-\lambda}\lambda^k / k!,$$

where $\gamma_k = \alpha_k / \beta_k$.

Thus all peaks on a network have different weight. The higher the layer is, the bigger weight peaks have. We will consider weight (peak value layerwise) under risk – analysis context and in considering damage assessment. For *k*- layer we have:

$$\delta_k \cong \beta / P(k). \qquad (2)$$

The summary peaks value of a network layerwise:

$$C = \sum_{k=1}^{M} \delta_k n_k, \qquad (3)$$

where $n_k = NP(k)$ is number of peaks in *k*-layer.

We will add in expression (3) δ_k from formula (2).

$$C = \sum_{k=1}^{M} \frac{\beta}{P(k)} NP(k) = = N\beta \sum_{k=1}^{M} \frac{1}{P(k)} (P(1) + P(2) + ... + P(M)) =$$
$$= MN\beta. \qquad (4)$$

We will express β from formula (4):

$$\beta = \frac{C}{MN} = \frac{C}{(H(N)-1)N},$$

where $(H(N)-1)N$ is n network potential.

Risk in the epidemiological simulation context is probability of that network separated nodes, layers of a network or all network will be damaged entirely. Therefore, we will calculate damage and risk to a network, proceeding from the selected scale: network node, layer of a network or whole network [11].

We will calculate damage from infectioned node in a Poisson non-uniform network:

$$U^k_{i\,t} = k\delta_k / S_t, \qquad (5)$$

where δ_k is weight of a node in k - layer of a Poisson network; S_t is number of no infection nodes in Poisson network. Further, we will add the formula (5) in expression (2), and we will get:

$$U_{i\ t}^{k} = k\beta / P(k) S_t , \qquad (6)$$

where $P(k)$ is Poisson distribution. Proceeding from the formula (6), the quantity of not infected nodes of a Poisson non-uniform network at timepoint t will be determined by the formula:

$$S_t = N_t - TI_t ,$$

where TI_t is total quantity of infected nodes (total infected). We will write the difference equation for finding total quantity of the infected nodes in a Poisson network. It will be calculated by the formula:

$$TI_t - TI_{t-1} - \ldots - 1 = 0 . \qquad (7)$$

Let $\mu_1, \mu_2 \ldots \mu_n$ *be* roots of characteristic equation:

$$Q(\mu) = \mu^t TI_t - \mu^{t-1} TI_{t-1} - \ldots - \mu TI_t = 0 . \qquad (8)$$

Then the common solvation will be as following:

$$TI_t = \sum_{i=0}^{t-1} I_i \sum_{m=1}^{i} \frac{\mu_m^{t+1}}{Q'(\mu)'} , \qquad (9)$$

where

$$Q'(\mu) = tTI_t \mu^{t-1} - (t-1) TI_{t-1} \mu^{t-2} - \ldots - TI_t .$$

Thus, having added expressions (7) and (8) in (9), and also having replaced by Poisson's formula of distribution, function of damage at timepoint to a node i of layer k taken form:

$$U_{i\ t}^{k} = \frac{kk!\beta}{e^{-\lambda}\lambda^k \left(N_t - \left(\sum_{i=0}^{t-1} I_i \sum_{m=1}^{i} \frac{\mu_m^{t+1}}{Q'(\mu)} \right) \right)} .$$

Further we will calculate risk for a network node. The probability of peak infection with an infection is constant on lattice networks with constant value k. In our case, when distribution of nodes levels is under Poisson law, the probability is not constant.

Therefore, we will express the probability of peak's infection by formula:

$$p_k = a_k P(k) ,$$

where a_k ***is*** the normalizing coefficient considering a level of infection danger to this layer.

The infection probability of peak in layer k is calculate by formula [9]:

$$P_k = p_k P(k) .$$

We can find infection risk at the time of the beginning of epidemic, considering the above-stated formulas:

$$Risk_0 = P_k \delta_k .$$

Therefore:

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$$Risk_0 = \alpha_k \beta P(k). \qquad (10)$$

Having added the distribution law of Poisson in the formula (10), we will get risk at a zero stage (the beginning of epidemic) of epidemic development proceeding on a spatial non-uniform network:

$$Risk_0 = \alpha_k \beta e^{-\lambda} \lambda^k / k!.$$

Connectivity matrixes of layers and micro fractals specifics of Poisson networks varieties

For epidemic simulation on a spatial Poisson network it is necessary to construct a matrix of layerwise intra network connectivity. Table 1 and 2 most precisely displays multi-layer feature of a spatial network.

TABLE.1. Matrix of layerwise connectivity

$K(k_{min}\|k_{min})$	…	$K(k_{min}\|k)$	…	$K(k_{min}\|k_{max})$
⋮	⋱	⋮	⋰	⋮
$K(k\|k_{min})$	…	$K(k\|k)$	…	$K(k\|k_{max})$
⋮	⋰	⋮	⋱	⋮
$K(k_{max}\|k_{max})$	…	$K(k_{max}\|k)$	…	$K(k_{max}\|k_{min})$

TABLE.2. A matrix of layerwise connectivity for Poisson network model

$K(1\|1)$	…	$K(1\|k)$	…	$K(1\|H(N))$
⋮	⋱	⋮	⋰	⋮
$K(k\|1)$	…	$K(k\|k)$	…	$K(k\|H(N))$
⋮	⋰	⋮	⋱	⋮
$K(H(N)\|1)$	…	$K(1\|k)$	…	$K(H(N)\|1)$

This matrix has number of properties. In particular, elements amount in each line is equal to number of these lines, i.e.:

$$\sum_{s=k_{min}}^{k_{max}} K(k \mid s) = k.$$

Besides, the matrix ||k|| is symmetric to K diagonals:

$$K(i \mid j) = K(j \mid i), \;\; i, j = k_{min}(1)k_{max}.$$

We will use this matrix in further calculations.

For a spatial network we have $M = \{k_{min}, ..., k_{max}\}$ layers, where

$$M = k_{max} - k_{min} = H(N) - 1.$$

The infected peak of level k has opportunity to interact with other layers by rules of matrix || K || - matrixes of layerwise intra network connectivity [5].

Then the probability of that there will be a contact with infected peak in layers (according to the polynomial law on the appropriate line of a matrix || K ||), will be equal to:

$$P\left[K(k\,|\,k_{\min})...K(k\,|\,k)...K(k\,|\,k_{\max})\right]=P\{k_1,...,k_M\}=\frac{M!}{k_1!...k_M!M^k},$$

where $k_s=K(s\,|\,k)$ at $s=k_{\min}(1)k_{\max}$, and $k_1,...,k_M$ are non-negative integers such that $k_1+...+k_M=k$.

For Poisson distribution, we will get:

$$P\left[K(k\,|\,1)...K(k\,|\,k)...K(k\,|\,H(N))\right]=\frac{(H(N)-1)!}{k_1!...k_M!(H(N)-1)^k}=\frac{(H(N))!}{k_1!...k_M!(H(N)-1)^k H(N)}.$$

From here it is obviously possible to define the expected quantity of the peaks which *were* caught in this s-layer (on the first step):

$$I_s[1]=[p_s k_s]=\left[\frac{\gamma_s K e^{-s}\lambda^s}{s!},k_s\right].$$

And damage size in s-layer:

$$u_s[1]=[p_s k_s]\delta_s=\left[\frac{\gamma_s K e^{-s}\lambda^s}{s!},k_s\right]\times\frac{\beta}{P(s)}=\left[\frac{\gamma_s K e^{-s}\lambda^s}{s!},k_s\right]\times\frac{(H(N)-1)N\times s!}{C\gamma_s K e^{-s}\lambda^s},$$

where $[p_s k_s]$ is the whole part of a mathematical expectations for quantity of infected (at contact with k-tops) s-layers. The damage on the first step of epidemic process will be calculated by:

$$u[1]=\sum_{S=k_{\min}}^{k_{\max}}[u_s].$$

Further we will define quantity of s-layer tops which were not infected from here:

$$s_s[1]=[(1-p_s)k_s].$$

Epidemic micro-models for layers of Poisson networks

We will consider infection spread within one network layer, using the scenario of network attack to an information and telecommunication network by network virus on the STL model. Infection spread begins with one layer k. In this model, virus infection within one level will be shown. The considered process can be sampled, as were in the previous works [3, 15-18]. Elements of an information and telecommunication network on the STL model can belong to one of following subsets:

1. Not infected knots in a timepoint $t(S_t)$ – a set of elements which weren't infectioned yet. As soon as the knot is attacked, it passes into group of the infected knots $S[t]$ – quantity of not caught elements in timepoint t of epidemiological process;
2. The infected knots at timepoint $t(L_t)$ are elements which are already infected from an infection source. $L[t]$ –infected elements quantity at timepoint t of epidemiological process;
3. Sick knots in a time point $t(T_t)$ – elements which are sick, but not infected. These knots act as sources of infection for other knots. $T[t]$ is quantity of sick elements at timepoint t of epidemiological process;

4. New knots in a time point $t(N_t)$ are elements which are new, just added for this network. $N[t]$ is quantity of new elements in a time point t of epidemiological process;
5. Died knots at timepoint $t(D_t)$ – elements which failed on development of the resource. $D[t]$ are dead elements number at timepoint t of epidemiological process.

We will describe development parameters of information epidemic as follows:

S_t - quantity of not infected knots at timepoint t.

L_t - quantity of the infected knots at timepoint t;

T_t - number of sick knots at timepoint t;

N_t - number of sick knots at timepoint t;

$D_{t/t+1}$ - number of dead knots from time point t to t +1;

$B_{t/t+1}$ - inflow of new knots in a network to a period with t to t +1; We will designate size as πN_t;

$L_{t/t+1}$ - quantity of the infected knots in a network; in period t to t +1; We will designate size as βT_t;

$DS_{t/t+1}$ - number of dead knots in group S in period t to t +1; we Will designate size as $\mu_1 S_t$;

$DT_{t/t+1}$ - number of dead knots in group L in a period with t to t +1; we will designate size as $\mu_2 L_t$;

$DT_{t/t+1}$ – number of dead knots in group T in a period with t to t +1; we will designate size as $\mu_3 T_t$;

$T_{t/t+1}$ – number of diseased in a period with t to t +1; we will designate size as δL_t;

$T_{t/t+1}$ – quantity of cured knots in a period with t to t +1; we will designate size as γT_t.

Therefore, the scheme of model will look as follows (Fig. 2).

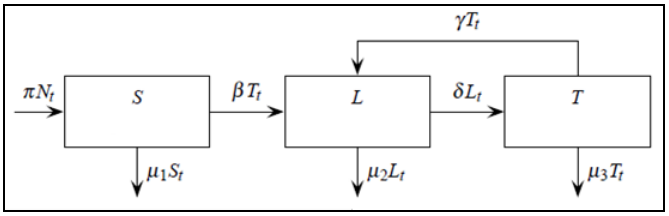

Fig. 2. The scheme of distribution epidemic on network knots model

We will work out the differential equations describing this model.

The quantity of knots which weren't infected in a time point of t +1 will be defined as:

$$S_{t+1} = S_t + B_{t/t+1} - DS_{t/t+1} - L_{t/t+1}.$$

The quantity of infected knots in a time point of t +1 will be defined as:

$$L_{t+1} = L_t + L_{t/t+1} + H_{t/t+1} - DL_{t/t+1} - T_{t/t+1}.$$

The number of patients at time point of t +1 will be calculated by :

$$T_{t/t+1} = T_t + T_{t/t+1} - DT_{t/t+1} - H_{t/t+1}.$$

The number of new knots in a time point of t +1 will be as following:

$$N_{t/t+1} = N_t + B_{t/t+1} - D_{t/t+1}.$$

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The number of dead knots in a time point of t +1 will be as following:

$$D_{t/t+1} = DT_{t/t+1} + DL_{t/t+1} + DS_{t/t+1}.$$

The system of differential equations describing the STL model of spreading infection within one level will look as follows:

$$\begin{cases} S_{t+1} = S_t + B_{t/t+1} - DS_{t/t+1} - L_{t/t+1}, \\ L_{t+1} = L_t + L_{t/t+1} - H_{t/t+1} - DL_{t/t+1} - T_{t/t+1}, \\ T_{t+1} = T_t + T_{t/t+1} - DT_{t/t+1} - H_{t/t+1}, \\ N_{t+1} = N_t + B_{t/t+1} - D_{t/t+1}, \\ D_{t/t+1} = DT_{t/t+1} + DL_{t/t+1} + DS_{t/t+1}. \end{cases}$$

Now we will construct a micro fractal for the STL model. For this purpose, being guided by the constructed schemes of virus epidemic distribution in a Poisson non-uniform network, we will construct a micro fractal for infection knots of a network STL model [10].

Further, being guided by the scheme of virus epidemic distribution in a Poisson non-uniform network, we will construct a micro fractal of knots infection model (figure 3). We will depict classes of network knots, and also transition conditions for knots from a class to a class in it.

We will allocate layer incubator: not infected, patients (latent infected) and infected knots.

Infection develops here, receiving one of several states (L or T). The dead knots are treated in a layer hospital.

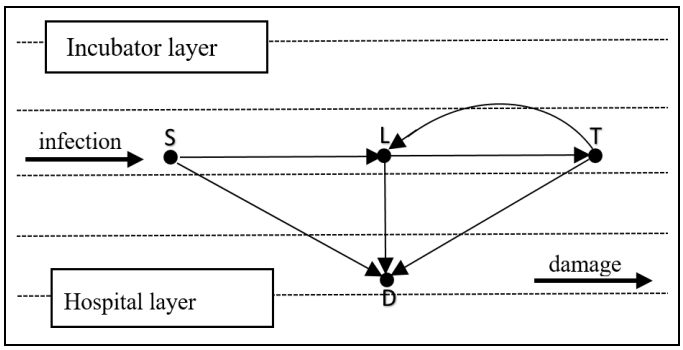

Fig. 3. A micro fractal of the epidemic process proceeding in a Poisson non-uniform network

We will remind that the micro fractal is constructed in a homogeneous environment, that is within the chosen s-layer of a network [16-23]. On Fig. 3, we see that the infected knot (in case it didn't pass into a condition of R – restored or D – disconnected) can become a source of secondary infection, and the infection passes to other layers of network.

We will consider probabilities of knots transition from one state into another (Table 3).

TABLE.3. Characteristics of sets of a micro fractal

Designation	Designation interpretation
$\|S(s)\|$	A power of set of not infected knots in s layer
$\|L(s)\|$	A power of set of infected knots in s layer
$\|T(s)\|$	A set power of sick knots in s layer

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$\|D(s)\|$	A set power of the failed knots in s layer
$\|I_{вх}\|$	A set power of the infected knots on an entrance
$\|I_{вых}\|$	A power of set of the infected knots at the exit

We will designate probabilities of transition as (Table 4):

TABLE.4. Probabilities of knots transition to various states

Designation	Designation interpretation
$P_{SL}(s)$	Probability of knot transition from condition S to L
$P_{SD}(s)$	Probability of knot transition from condition *L* to *I*
$P_{LT}(s)$	Probability of knot transition from condition *L* to *R*
$P_{LD}(s)$	Probability of knot transition from condition *L* to *D*
$P_{TL}(s)$	Probability of knot transition from condition *I* to *D*
$P_{TD}(s)$	Probability of knot transition from condition *I* to *R*
$P_I(s)$	Emergence probability of a secondary source

Thus, we can make the linear count of a micro fractal (Fig. 4) and show on it probabilities of knots transition from one state to another state [16]:

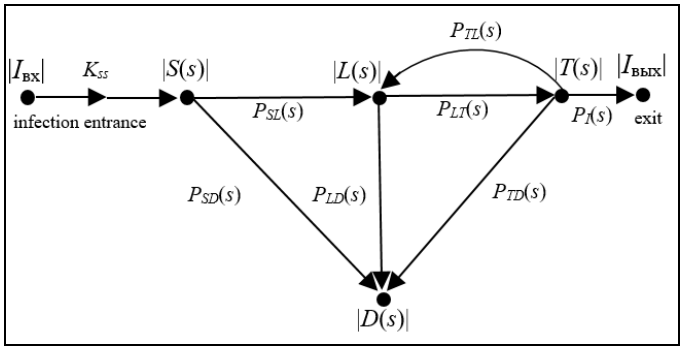

Fig. 4 – Linear count of a micro fractal

Considering all aforesaid, it is possible to work out the differential equations for each of sets. As a result it is necessary to calculate $|I_{вых}|$ – a set of secondary sources of power infection, that is knots which will transmit infection to other layers of network. In figure 4 K_{ss} is a share of not infected (susceptible) knots from layer s [16]. This size is calculated by formula:

$$K_{ss} = |S(s)| / n_s ,$$

where n_s is number of knots in layer s.

Thus, the equation for the set of not infected power knots will be following:

$$|S(s)| = |I_{вх}| K_{ss} .$$

The equation for finding uninfected knots set power is:

$$|L(s)| = |S(s)| P_{SL}(s) + |T(s)| P_{TL}(s) .$$

The equation for finding a set of infected knots power is:

$$|T(s)| = |L(s)| P_{LT}(s) .$$

The equation for finding a set of disconnected knots power has an appearance:

$|D(s)| = |I(s)|P_{TD}(s) + |L(s)|P_{LD}(s) + |S(s)|P_{SD}(s)$ According to Mason's formula, the probability of infection transmission from an entrance to an exit (p_s) will be equal *to*:

$$p_s = \frac{K_{ss}P}{1 - L_1 - L_2 - ... - L_n}, \qquad (11)$$

where P is work of branches transfer of a way from an entrance to an exit; L_1, L_2, L_n are the closed contours in the linear count.

From figure 4 we see that the way from an entrance to an exit represents work of branches count:

$$P = P_{SL}(s)P_{LT}(s)P_I(s). \qquad (12)$$

Further we will depict quantity of the closed contours in the column. As a result, we get one contour:

$$L_1 = P_{LT}(s)P_{TL}(s). \qquad (13)$$

Having substituted formulas (12) and (13) formula (11), we get:

$$p_s = \frac{|S(s)|P_{SL}(s)P_{LT}(s)P_I(s)}{n_s(1 - P_{LT}(s)P_{TL}(s))}.$$

Now we can find a set of secondry power sources of infection at the s-layer exit:

$$|I_{выхs}| = p_s K(s|k),$$

where $K(s|k)$ is a line of a connectivity matrix of s and k layers.

CONCLUSION

In this model, virus infection within one level will be shown. This article is about modeling of layering growth virus epidemic and spread of harmful content on Poisson networks. This article is about modeling of layering virus infection growth process on heterogeneous Poisson networks. This paper contains probabilistic calculations of information risks in information and telecommunication systems with virus epidemic. Their sharpness is largely dependent on the structural and functional features of the attacked network, and in this respect it is important to study attacks on networks with Poisson distribution.

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