

# Algorithms for Computational Viral Extension Direct & Inverse Problems

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## Abstract

The computational viral extension direct and inverse problems are problems of long-standing interest in mathematics, epidemic and natural disaster studies. We designed and developed a set of algorithms for the construction of the closure of the arbitrary chaotic set that can efficiently be used in evaluations of the propagations autooscillatory waves. The algorithms presented in this paper are readily applicable to applications in the management of epidemics, disaster handling, political propaganda issues, and the study of marketing (and others). The first author of this paper has successfully applied these algorithms to Chernobyl Zone, forest fire in Siberia, cholera epidemic in Odessa (Ukraine) and Astrakhan (Russia), and anthrax in Altai (Russia).

## 1. Introduction

Let the set  $B$  be the infection's zone or the disaster zone. We will consider the general direct algorithm for viral extension and disaster advances (GVE) which is given by the closer of the set  $B \subseteq A$  for the chaotic  $H = (A, \Omega)$ ,  $\Omega \subseteq 2^A$ . Let  $t$  be an iteration number of GVE;  $B$  is the infection zone. The GVE takes the extension  $B$  to  $\sim(B)$

$$B \subseteq C_1 \subseteq \dots \subseteq C_i \subseteq \dots \subseteq C_t = \sim(B) \subseteq A, \quad (1)$$

where  $C_i$  is the part closer of  $B$ . Cycles  $\chi_k$  are elements of  $\Omega$ . Let  $\chi_t$  be given by  $C_{t+1} \supseteq \chi_t \not\subseteq C_{t+1}$ . Then  $\chi_t$  is interpreted as the infection source. The inverse algorithm for computational viral extension and disaster advances (IVE) is given by the coordinates of the infection sources  $\{\chi_t\}$ ,  $t = [1, n]$ ,  $n = \mu(\Omega)$ .

A more detailed description can be found in references [1] – [4].

Let the groundset  $A \subset \mathbb{Z} \times \mathbb{Z}$ . See references [1] – [4]. The direct algorithm of single-center infection on  $\mathbb{Z} \times \mathbb{Z}$  with the ramified boundary of the ground-set  $A \subset \mathbb{Z} \times \mathbb{Z}$  can be found in references [1] – [4]. The inverse algorithm for computational viral extension (IVE) of single-center infection on  $\mathbb{Z} \times \mathbb{Z}$  with the ramified boundary of the ground-set can be found in references [1] – [5].

## 2. Chaotics and others

We begin with some definitions.

A Combinatorial Configuration  $K$  is an ordered pair

$$K = (A, B), B \subseteq 2^A$$

where  $A$  is a nonempty set.  $A$  is called the groundset of  $K$ , and elements of  $A$  are called the points of  $K$ . The elements of  $B$  are called the configurations of  $K$ .

Let  $\mathfrak{S} = (A, C)$ ,  $C \subseteq 2^A$  be combinatorial configurations. Combinatorial  $c$ .  $\mathfrak{S}$  is called a *chaotic* if

(H)  $c_1, c_2 \in B$  &  $c_1 \subseteq c_2 \Rightarrow c_1 = c_2$ .

Let  $\mathfrak{S} = (A, C)$  be a chaotic. A set  $\sim(B)_{\mathfrak{S}} \subseteq A$  is called a *closure* of a subset  $B \subseteq A$  if the following conditions hold:

1)  $B \subseteq \sim(B)_{\mathfrak{S}}$ ,

2)  $b \in \sim(B)_{\mathfrak{S}} \setminus B \Leftrightarrow$  there exists two f-sequences  $\{\alpha(i)\}$ ,  $\{\tau(i)\}$ , where  $\alpha(i) \in A$ ,  $\tau(i) \in C$ ,

$\alpha(i) \neq \alpha(k)$ ,  $\alpha(n) = b$ ,  $\tau(i) \neq \tau(k)$  such that  $\alpha(i) \in \tau(i) \subseteq B \cup \left(\bigcup_1^i \alpha(j)\right)$ , where

$1 \leq i < k \leq n$ ,  $j = [1, i]$ ,  $i = [1, n]$ .

By  $\sim(B)_{\mathfrak{S}}$  denote a *closer* of a subset  $B \subseteq A$  in  $\mathfrak{S}$ .  $\sim(B)_i_{\mathfrak{S}} = B \cup \left(\bigcup_1^i \alpha(j)\right)$  is

called a *part closer* of subset  $B \subseteq A$  in  $\mathfrak{S}$ . A subset  $D \subseteq A$  is called a *flat* if  $\sim(D)_{\mathfrak{S}} = D$ . A minimal flat is called an *atom*. A flat  $P \subseteq A$ ,  $\mu(P) = 1$  is called a *loop*.

$\mathbb{Z} \times \mathbb{Z}$  is called *square lattice* over  $\mathbb{Z}$ , where  $\mathbb{Z}$  is a ring of integer numbers. The ground-set  $A \subseteq \mathbb{Z} \times \mathbb{Z}$ . Now consider a graph  $\Gamma = (V, E)$ , where the vertex-set  $V = A$  and edge-set  $E = \{e \in B: e \in \{(i, j) \in V: (i-1, j), (i, j-1), (i+1, j), (i, j+1)\}\}$ . The *inverse function* on a graph  $\Gamma$ , can be written in the form

$$\aleph(\Gamma) = \sum_{\pi} \prod_{(i, j) \in E} \theta^{\pi_i \pi_j} \quad (4)$$

where  $\pi_i \pi_j$  is either 1 or  $-1$ ,  $\theta = e^I$ , here  $I$  is a number of iterations.

Let  $W$  be the infection's network on square lattice  $Q^2$  with ground-set  $A \subseteq \mathbb{Z} \times \mathbb{Z}$ . Suppose that there is a supply of virus' fluid (vf) at the origin and that each edge of  $Q^2$  allows fluid to pass along it with probability  $p$ , independently for each edge. Let  $P_i(p)$  is the probability that vf spreads to at least  $i$  vertices. Thus

$$p^W = \lim_{i \rightarrow \infty} P_i(p) \quad (5)$$

is called a *critical probability* of  $W$ .

**Theorem 1.** [See 5]. The critical probability that vf spreads to at least vertices on the square lattice  $W$  is between 0.51 and 0.68.

### 3. General Direct Algorithm (Algorithm 1)

Let  $A$  be a ground-set of a chaotic  $H = (A, \Omega)$ ,  $\Omega \subseteq 2^A$ . Elements of  $A$  are persons, animals, insects (potential infected objects). The cycles of  $\Omega$  are infecting sources for vireos. The subset  $B \subseteq A$  is a *infected zone*. A triple

$$\mathfrak{S} = (A, \Omega, B) \quad (6)$$

is called a *beginning infect front* (BIF). By definition of  $\sim(B)_{\mathfrak{S}}$ , put

## Algorithm 1

```

give Om – Commentary 1
find:
nom - Commentary 2;
A - Commentary 3;
nA - Commentary 4;
T = Om (Commentary 5);
nmax = min(nom,nA) - (Commentary 6
);
for kom =1:nom - Commentary 7;
  find:
  AmOm = A\Om(kom) - Commentary 8;
  nAmOm - Commentary 9;
  for knAmOm=1:nAmOm - Commentary 10;
    find:
    b = AmOm(knAmOm) - Commentary 11;
    for n=1:nmax - Commentary 12;
      find:
      ap – Commentary 13;
      omp – Commentary 14;
      for ia=(in rows of the data ap) – Commentary 15;
        find:
        a – the sequence a:
          Commentary 16;
        if a(n)=b – Commentary 17;
          for iom=1: ( in rows of the data ap omp) –
            Commentary 18;
            find:
            ntau - Commentary 19;
            ClipYes = True - Commentary 20;
            for i=1:n – Commentary 21;
              if a(i)∉Om(ntau(i)),
                ClipYes = False -
                break - go out from circuit “for i”;
              else - a(i)∈τ(i) - Commentary 22;
                find B=Om(kom)∪(∪a(j)):
                B = Om(kom) – Commentary 23;
                for j=1:i,
                  B = B∪a(j);
                end % B = Om(kom)∪(∪a(j))
                if Om(ntau(i))∉B
                  ClipYes = False -
                  break – go out from circuit “for i”;
                end
              end
            end
          end
        if ClipYes=True -
          T(kom) = T(kom)∪a – Commentary 24;
          break; go out from circuit „for iom“
        end
      end
    end
  end
end

```

end  
 end  
 end  
 end  
 end

Using Algorithm 1 we obtain the chaotic  $H_1 = (A, \Omega_1)$ ,  $\Omega_1 = \Omega_0 \cup \Omega_1^N$ , where  $\Omega_0 = \Omega / \{-(B)_{\mathfrak{S}}\}$  and  $\Omega_1^N$  is the set of new infect cycles. Further, let us algorithm 1 to the infected front  $\mathfrak{S}_1 = (A, \Omega_1, -(B)_{\mathfrak{S}})$ . If

$$\mathfrak{S} = \mathfrak{S}_1, \tag{7}$$

then algorithm 1 is stopped. (7) is the criterion of halting for the algorithm 1.

**Example 1.** (See [4], [6]) Figure 1 (Wasily Kandinsky Picture) is the adequately model of the algorithm 1 and viral extensions.



Figure 1

#### 4. General Direct Algorithm on $\mathbb{Z} \times \mathbb{Z}$ (Algorithm 2)

Let  $A \subset \mathbb{Z} \times \mathbb{Z}$  be a finite ground-set of a chaotic  $H = (A, \Omega)$ ,  $\Omega \subseteq 2^A$ . Let the subset  $B \subseteq A$  be a beginning infected zone with a boundary  $L$ ;  $L$  is a cycle curve without an intersection.  $L$  is called a *boundary zone*  $B$ .  $\mathfrak{S} = (A, \Omega, B)$  is a beginning of infect front. Further, we can apply Algorithm 1.

Suppose  $S(A) \supseteq A$  is a minimal sphere with the center  $O_A = (i_0, j_0) \in B$ ,

$$\pi: A \longrightarrow \{+1, -1\}, \tag{9}$$

the function that takes each two cells  $k = (i_k, j_k)$  and  $m = (i_m, j_m)$  to

- 1)  $\pi(k, m) = +1$ , if  $|i_m - i_0| > |i_k - i_0|$  or  $|j_m - j_0| > |j_k - j_0|$ ;
- 2)  $\pi(k, m) = -1$  on the other case.

$S(A)$  is called a *restriction sphere*.

**Theorem 2.** [See 5]. Let a finite ground-set  $A \subseteq \mathbb{Z} \times \mathbb{Z}$  be a restriction sphere  $S(A)$ ; it is a finite ground-set  $A$  and  $\Gamma = (V, E)$  is a finite graph, where the vertex-set  $V = A$  and edge-set  $E = \{e \in B: e \in \{\forall (i, j) \in V: (i-1, j), (i, j-1), (i+1, j), (i, j+1)\}\}$ ,  $\aleph(\Gamma)$  is the inverse function (4) for Algorithm 1 on a graph  $\Gamma$ . Then we have

$$\aleph(\Gamma) = \sum_{\pi} \theta^{\mu(E_{\pi}^+) - \mu(E_{\pi}^-)}, \quad (10)$$

where  $E_{\pi}^+$  to be the set of edges  $(d, r)$  of  $\Gamma$  such that  $\pi_d \pi_r = 1$  and  $E_{\pi}^-$  be the remaining edges of  $\Gamma$ , here  $\pi_d \pi_r = 1$  if the diedge  $(d, r)$  is “ $i \bullet \rightarrow j$ ”,  $\theta = e^I$ , here  $I$  is a number that is used to iterate Algorithm 1 and  $\pi$  is function (9).

**Corollary 2.1.** [See 5]. Suppose  $N^0$  is an iteration number used in Algorithm 1 on graph  $K$ ; then  $N^0 \leq \mu(\aleph(\Gamma))$ .

**Corollary 2.2.** Algorithm 1 on  $\mathbb{Z} \times \mathbb{Z}$  has significant computability complexity.

## 5. Direct Algorithm of single-center infection on $\mathbb{Z} \times \mathbb{Z}$ (Algorithm 3)

Suppose conditions of theorem 2 are satisfied. The subset  $B \subseteq A$  is a beginning infected zone with the boundary zone  $L$ . Let  $L \subseteq B$  and the subset  $A^{\heartsuit} \subseteq A/B \subseteq \mathbb{Z} \times \mathbb{Z}$  are *infection-screened cells*. Infection screened cells are denoted by the symbol “ $\heartsuit$ ”, see fig.2. The boundary zone  $B$  contains an *infection center*  $O_A \in B$ . Any cell  $c \in B$  is called *active* if  $\{c\} \cap L \neq \emptyset$ ; the active cells are *starting points* of Algorithm 3. The cells

$$c_{ij} = \{(i \pm 0; 1, j \pm 0; 1) \neq (i, j)\} \in A$$

are called *neighbouring cells* of cell  $(i, j) \in A$ . Any cell  $c \in A / (B \cup A^{\heartsuit})$  is called a *freedom cell (f-cell)*. For any cells  $c_1 = (i, j), c_2 = (k, l) \in A$  there exists a *distance*  $d(c_1, c_2) = \sqrt{(i-k)^2 + (j-l)^2}$ .

### Algorithm 3

(RI) We get  $L_1 = L$ .

(Z) An active cell  $m \in L$  is said to be *initial* if  $d(m, O_A) \xrightarrow{L} \min$ . Let  $C_m = \{m_1, m_2, m_3\}$  be the f-cells, where  $\mu(m_i \cap m) = 2$ , and  $m^*$  be the cell of  $C_m$  such that  $m^*$  have the maximal number  $n(m^*)$  of neighbouring active cells.  $m^*$  stand of the active cell.  $L_1 := L_1 / \{m\} \cup \{m^*\}$ . If  $m^*$  does not exist, then  $L_1 := L_1$ .

The rule (Z) is repeated  $\mu(L) - 1$  times in the clock-wise direction.

If  $L_1 \neq L$ , then  $L = L_1$ , we add to  $A^\heartsuit$  the new f-cell and go to (RI). Finally, if  $L_1 = L$ , then Algorithm 3 is stopped.

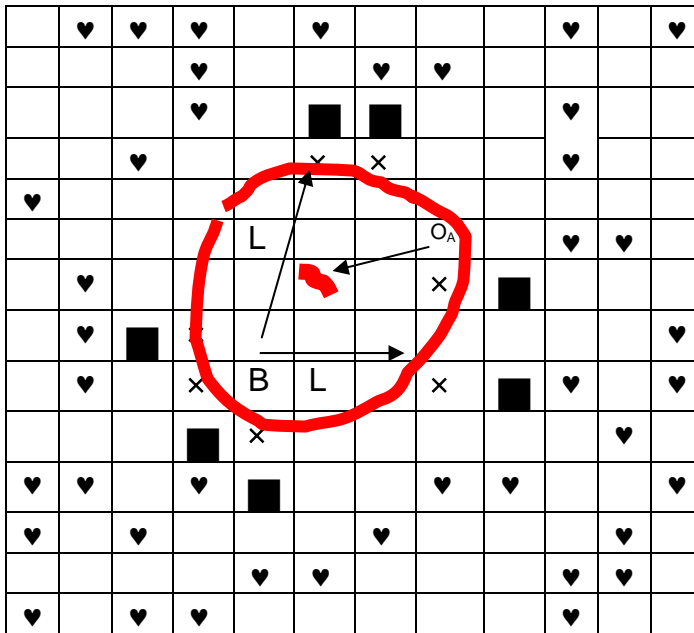


Figure 2

**Example 2.** In Fig.2 the new active cells are marked using the sign “■”, the active cells are marked with sign “x”, and the f-cells are shown as “♥”.

**Theorem 3.** [See 5]. Algorithm 3 has the computation complexity  $O(n^2)$ , where  $n = \mu(L)$ .

**Corollary 3.1.** Algorithm 3 is an effective solution for real problems of computational viral extension.

**Corollary 3.2.** Let  $B = O_A = L$ ; then  $P = \frac{n_a}{n_f} \approx 0.57$ , where  $n_a$  is the number of the new active cells and  $n_f$  is the number of the f-cells. Applying Algorithm 3 to the computational experiments we obtain  $n_a$  and  $n_f$ .

**Hypothesis.** The number  $P$  is a critical probability [see (5)] of single-center infection on  $\mathbb{Z} \times \mathbb{Z}$ .

## 6. Inverse Algorithm of Single-Center Infection on $\mathbb{Z} \times \mathbb{Z}$

Suppose conditions of § 5 is satisfied. Let  $B = O_A = L$  for an initial infection. Furthermore,  $B^* \subseteq A$  is an infected zone before starting the inverse algorithm.  $H \subseteq A / B^*$  is fixed subset of f-cells.

**Theorem 4.** Let  $A \subseteq \mathbb{Z} \times \mathbb{Z}$  be the finite ground-set,  $S(A)$  is a restriction sphere, and  $\pi$  is function (9). Further, let  $\Gamma = (V, E)$  be a finite graph, where the vertex-set  $V = A$  and edge-set  $E = \{e \in B: e \in \{\forall (i,j) \in V: (i-1,j), (i,j-1), (i+1,j), (i,j+1)\}\}$ ,  $\aleph(\Gamma)$  is the inverse function (4) for Algorithm 3 on a graph  $\Gamma$ . Then we have

$$\aleph(\Gamma) = (\theta + \theta^{-1}) \times \aleph(\Gamma \ominus \{e\}) - \theta^{-1} \times \aleph(\Gamma \div \{e\}), \quad (12)$$

where  $\Gamma \ominus \{e\}$  is the graph obtained by deleting an edge  $e$  from  $\Gamma$ ,  $\Gamma \div \{e\}$  is the graph obtained by deleting an edge  $e$  and then identifying its end points,  $\theta = e^I$ , here  $I$  is the number of iterations used in Algorithm 3.

**Theorem 5.**

$$I^* \leq (\mu(A) - \mu(H))^2,$$

where  $I^*$  is the number of iterations in Algorithm 4.  $H$  is the subset.

Our main result is the following.

**Theorem 6.** There exists an algorithm (Algorithms 4) for finding solutions for the inverse problems for computational viral extension.

The proof of theorems 4-6 can be found in references [2]-[7] and Algorithm 4 is shown in reference [1].

**Corollary 6.1.** Using Algorithm 4, we get the coordinates:

$$O_A = (i_0, j_0), \quad (11)$$

where  $O_A$  is an infection center.

**Remark 1.** coordinates (11) are readily usable by antiterrorist organizations.

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