Analysis of an epidemic model on a network

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Abstract

We analyze a KermacK-Mckendrick model extended to a geographical network. This yields a system of coupled differential equations involving the graph Laplacian of the network. We study the influence of the different parameters and obtain a simple criterion for the onset of the epidemic. Finally, in order to curb the epidemic we examine different vaccination strategies and prove that it is most effective to vaccinate a node of highest degree.

1 Introduction

Many models of the propagation of an epidemic involve a network. This can be a contact network between species or a geographical network where the nodes correspond to locations and where the links are associated to communications between the nodes, see Murray’s book for some examples [1]. One of simplest dynamics of a disease is the Kermack-McKendrick system of equations [2] involving two populations of susceptible and infected individuals. Using this model together with a probability transition matrix [3] for the geographic coupling, Brockman and Helbling [4] performed a remarkable study of the propagation of well-known epidemics like SARS or H1N1 due to airline travel. They emphasized that the fluxes between the nodes govern the propagation of the epidemic. The authors were able to trace the origin of the disease.
An important fact outlined by Brockman and Helbling is that the epidemic front is controlled by the availability of susceptibles. If susceptibles are large enough, the front cannot be stopped. In fact, the Kermack-McKendrick equation can be reduced to a Fisher reaction-diffusion model by assuming that the sum of the populations of susceptible and infected is constant. Such a Fisher front with a quadratic non-linearity (monostable) cannot be stopped. On the contrary, we showed [5] that a bistable front (cubic non-linearity) can be pinned by the network if the geographic coupling is weak. For the Kermack-McKendrick model, reducing the number of susceptibles at a given location can be done through vaccination. In some cases, this is expensive and the whole network cannot be vaccinated. It is therefore important to address the question: what nodes are more useful to vaccinate to mitigate the epidemic?

In this article, we consider a model of a Kermack-McKendrick equation coupled to network through a graph Laplacian matrix [6]. This model is similar to the one of [4] if the transition matrix is symmetric. The graph Laplacian is symmetric and negative so that the eigenvalues are real and we can choose a basis of orthonormal eigenvectors on which to project the dynamics. Relying on this formalism, we introduce a criterion of epidemic and validate it by comparison to numerical experiments. Using this criterion, we define a vaccination policy of the network. We find that it is most useful to vaccinate the high degree nodes and that it is not efficient to vaccinate neighbors.

The article is organized as follows. In section 2, we introduce the model, discuss its main features and introduce the epidemic criterion. Numerical results illustrating the criterion are shown in section 3. Section 4 is devoted to the vaccination policy and we conclude in section 5.

2 The model and epidemic criterion

One of the main models to describe the time evolution of the outbreak of an epidemic is the Kermack-McKendrick model [2]

\[
\begin{align*}
S_t &= -\alpha SI, \\
I_t &= \alpha SI - \beta I \\
R_t &= \beta I
\end{align*}
\]

where the dynamics of transmission depends on the frequency and intensity of the interactions between (healthy) susceptible and infected individuals. The parameters $\alpha$ and $\beta$ are the infection rate and the recovery rate. Epidemic occurs if $\alpha S - \beta > 0$ [2].

We consider a geographic network of cities connected by roads or communications and obtain the model and introduce a geographical component so that $(S, I)$ become vectors and we drop $R$. This is similar to Murray’s model where he introduces spatial dispersion using a continuous Laplacian term [1]. Our
model of propagation on a network of \(n\) nodes is

\[
\begin{align*}
\dot{s} &= \varepsilon \Delta s - \alpha s, \\
\dot{i} &= \varepsilon \Delta i + \alpha s - \beta i.
\end{align*}
\]

(2)

Then \(s = (s_1, s_2, \ldots, s_n)^T\), \(i = (i_1, i_2, \ldots, i_n)^T\), \(\Delta\) is the graph Laplacian matrix \([6]\) and we denote by \(s_i\) the vector \((s_{i1}, s_{i2}, \ldots, s_{in})\)^T.

The graph Laplacian \(\Delta\) is the real symmetric negative-semi definite matrix, defined as

\[
\Delta_{kl} = w_{kl}, \quad \Delta_{kk} = -\sum_{l \neq k} w_{kl}.
\]

(3)

One can see it as a finite difference approximation of the continuous Laplacian \([7]\). It can also be written as

\[
\Delta = A - D
\]

where \(D\) is the diagonal matrix of the degrees (the number of links) and \(A\) is the adjacency matrix \(A_{kl} = w_{kl}\) \([6]\). The eigenvalues of \(\Delta\) are the \(n\) non positive real numbers ordered and denoted as follows:

\[
0 = -\omega_1^2 \geq -\omega_2^2 \geq \cdots \geq -\omega_n^2.
\]

(4)

The eigenvectors \(\{v^1, \ldots, v^n\}\) satisfy

\[
\Delta v^j = -\omega_j^2 v^j.
\]

(5)

and can be chosen to be orthonormal with respect to the scalar product in \(\mathbb{R}^n\), i.e. \(v^i \cdot v^j = \delta_{i,j}\) where \(\delta_{i,j}\) is the Kronecker symbol.

Brockmann and Helbing\([4]\) studied a similar model using a weighted graph for the propagation of worldwide epidemics. They modulated the reaction term by an activation function. Forgetting this function, their equations read

\[
\begin{align*}
\dot{s}_k &= \varepsilon \sum_{m \neq k} p_{mk} (s_m - s_k) - \alpha s_k j_k, \\
\dot{j}_k &= \varepsilon \sum_{m \neq k} p_{mk} (j_m - j_k) + \alpha s_k j_k - \beta j_k
\end{align*}
\]

(6)

where \(p_{mk}\) is the normalized flux between nodes \(m\) and \(k\) and \(j_k, s_k\) are the local fractions of infected and susceptibles at node \(k\). The matrix \(p_{mk}\) is a so-called transition matrix in probability \([3]\). If this matrix is symmetric, then it is a graph Laplacian\([6]\).

There are two main units of time in the system \([2]\), \(T_0 = 1/\varepsilon\) is a diffusion time and \(T_1 = 1/(\alpha s^* - \beta)\) is a reaction time for a given level of susceptibles \(s^*\). Interesting effects occur when \(T_0\) is close to \(T_1\). Scaling times by \(T_0\) we obtain our final system

\[
\begin{align*}
\dot{s} &= \Delta s - \alpha s, \\
\dot{i} &= \Delta i + \alpha s - \beta i.
\end{align*}
\]

(7)

The model \([7]\) is simple, yet very general. For example, \(\alpha\) can depend on the location \(k\) and also on time.
2.1 Well posedness and positivity

The model \( (7) \) has two equilibria \((s^*, i^*) = (\frac{\beta}{\alpha}, 0)\) and the origin \((s^*, i^*) = (0, 0)\).

The model is well posed in the sense that the solution remains bounded. We show this in the Appendix using standard techniques.

The biological domain of the system is
\[
\Omega = \{(s, i) : s \geq 0; i \geq 0\}.
\]

Let us show that \( \Omega \) is an invariant set for \( (7) \) so that the model makes sense in biology. Consider the different axes \( s = 0 \) and \( i = 0 \). First assume \( i = 0 \), then the equation \( (7) \) reduces to
\[
\dot{s} = \Delta s
\]
which conserves the positivity of \( s \). Similarly when \( s = 0 \), we get
\[
\dot{i} = \Delta i - \beta i
\]
and again the positivity of \( i \) is preserved.

2.2 Epidemic criterion

Here we extend the 1D epidemic criterion of Kermack-McKendrick \([2]\) to our graph model. Assuming the \( s \) vector to be constant, we can use the second equation of \( (7) \) and get
\[
\dot{i} = (\Delta - \beta)i + \alpha s i
\]
where the term \( s i \) means the product of a diagonal matrix \( \text{diag}(s_1, s_2, \ldots, s_n) \) by the vector \( i \).

Equation \( (8) \) describes the onset of the epidemic on the network. It can be written
\[
\dot{i} = Ai
\]
where \( A \) is the symmetric matrix
\[
A = \Delta - \beta Id_n + \alpha \text{diag}(s_1, s_2, \ldots, s_n).
\]

The eigenvalues of \( A \) \( \sigma_1, \ldots, \sigma_n \) are real. If one of them is positive, then the solution \( i(t) \) increases exponentially and the epidemic occurs. We can then write

**Epidemic criterion:** there is an onset of the epidemic if one eigenvalue \( \sigma_i \) of \( A \) is positive.

Because \( A \) is symmetric the eigenvalues of \( A \) remain in the same order as the ones of \( \Delta \). This is the interlacing property \([6]\). Then \( \sigma_1 \) will tend to 0 for \( \beta, \alpha \to 0 \).

Note also that since \( \|s\| \) decreases with time, the estimate given by the eigenvalues of \( A \) indicates the size of the epidemic i.e. \( \max \|i\| \).
Expanding $i$ on an orthonormal basis of eigenvectors $(v^i)$ of $\Delta$

$$i = \sum_{k=1}^{n} \gamma_k v^k,$$  \hspace{1cm} (10)

we get

$$\dot{\gamma}_k = (-\omega^2_k - \beta)\gamma_k + \alpha < s_i | v^k >.$$  \hspace{1cm} (11)

Assume that the susceptible population is constant on the network. Then $\text{diag}(s_1, s_2, \ldots, s_n) = s^* \text{Id}_n$ so that equation (13) reduces to

$$\dot{\gamma}_k = (-\omega^2_k - \beta + \alpha s^*)\gamma_k.$$  \hspace{1cm} (12)

The epidemic occurs if $-\beta + \alpha s^* > 0$ which is a simple generalization of the criterion in the scalar case.

A more interesting case is when the population of susceptibles is inhomogeneous. Then equation (13) becomes

$$\dot{\gamma}_k = (-\omega^2_k - \beta)\gamma_k + \alpha \sum_{l=1}^{n} \eta_l \left( \sum_{j=1}^{n} s_j v^l_j v^k_j \right).$$  \hspace{1cm} (13)

Then the eigenvectors and the geometry of the network play a role.

3 Numerical results

We illustrate the results given above on a 6 node network inspired from the geographical map of Mexico, see Fig. 1. A node represents a city and an edge is a communication link between two cities. For simplicity here we assume that the weights on all the branches are equal to 1.

![Graph of the six main cities in Mexico numbered from 1 to 6: Guadalajara, Zacatecas, Queretaro, Pachuca, Mexico City, Puebla. The links represent the main roads connecting these cities.](image)

The graph Laplacian is
\[
\Delta = \begin{bmatrix}
-3 & 1 & 1 & 0 & 1 & 0 \\
1 & -2 & 1 & 0 & 0 & 0 \\
1 & 1 & -4 & 1 & 1 & 0 \\
0 & 0 & 1 & -2 & 1 & 0 \\
1 & 0 & 1 & 1 & -4 & 1 \\
0 & 0 & 0 & 0 & 1 & -1
\end{bmatrix}
\]

The eigenvalues of this graph laplacian are

\[
0 \quad -0.885 \quad -1.70 \quad -3.25 \quad -4.86 \quad -5.31
\]

The corresponding eigenvectors are

\[
\begin{array}{cccccccc}
-0.4082 & -0.2410 & -0.2307 & -0.6432 & 0.5275 & 0.1735 \\
-0.4082 & -0.4011 & -0.5313 & 0.5802 & 0.0502 & -0.2261 \\
-0.4082 & -0.2061 & 0.0699 & -0.0844 & -0.6711 & 0.5731 \\
-0.4082 & -0.0975 & 0.7620 & 0.3323 & 0.3607 & 0.0525 \\
-0.4082 & 0.0975 & 0.1609 & -0.3323 & -0.3607 & -0.7466 \\
-0.4082 & 0.8483 & -0.2307 & 0.1474 & 0.0934 & 0.1735
\end{array}
\]

### 3.1 Effect of diffusion

First, we examine the effect of diffusion. For that consider solutions of (7) for two sets of parameters corresponding in the original system (2) to two different values of \( \epsilon \). Fig. 2 shows the solution \( i_k(t) \), \( k = 1, \ldots, 6 \) for \( \epsilon = 0.2 \) (left) and \( \epsilon = 1 \) (right).

![Figure 2: Time evolution \( i_k(t) \), \( k = 1, \ldots, 6 \) for \( \alpha = 25, \beta = 2.5 \) (\( \epsilon = 0.2 \)) on the left panel and \( \alpha = 5, \beta = 0.5 \) (\( \epsilon = 1 \)) on the right panel. The initial conditions are \( s = (0.75, 0.55, 0.6, 0.8, 0.05, 0.45)^T \), \( i = 0.1(1, 1, 1, 1, 1)^T \).](image)
One sees that the maxima of $i_k$ are well separated on the left for a small $\epsilon$. On the right, they are much closer and not as large. The diffusion over the network is stronger on the right so that the maximum of epidemic occurs at the same time. In the rest of the article, we consider the situation where the network plays an important role and choose $\epsilon = 1$.

### 3.2 The epidemic criterion

We now proceed to illustrate our epidemic criterion, i.e. the fact that to have an outbreak we need an eigenvalue of the matrix $A$ from (9) to be positive. For that, we select $\alpha = 10$ and $\alpha = 3$ for the same other parameters and initial conditions. The eigenvalues of $A$ are given in table 3.2.

| $\alpha$ | $\sigma_6$ | $\sigma_5$ | $\sigma_4$ | $\sigma_3$ | $\sigma_2$ | $\sigma_1$ |
|---------|-----------|-----------|-----------|-----------|-----------|-----------|
| 3       | -5.55     | -5.14     | -3.66     | -2.10     | -1.36     | -0.35     |
| 10      | -3.98     | -3.36     | -2.28     | -0.73     | -0.095    | 1.24      |

The time evolutions $i_k(t)$, $k = 1, \ldots, 6$ are shown in Fig. 3 where the left panel corresponds to $\alpha = 3$ and the right one to $\alpha = 10$. Clearly, there is no outbreak for $\alpha = 3$ while there is one for $\alpha = 10$.

![Figure 3: Time evolution $i_k(t)$, $k = 1, \ldots, 6$ for $\alpha = 3$ (left panel) and $\alpha = 10$ (right panel). The other parameter is $\beta = 1$ and the initial conditions are $s = (0.15, 0.25, 0.3, 0.18, 0.25, 0.15)^T$, $i = 0.1(1, 1, 1, 1, 1, 1)^T$](image)

### 4 Vaccination policy

From the amplitude equations (13), one can devise a strategy of vaccination. By this we mean choosing $s_j = 0$ at some well chosen indices $j$ so that the maximal
eigenvalue of \( A \) from the epidemic criterion is minimum. Table 1 shows the eigenvalues \( \sigma_1, \ldots, \sigma_n \) of \( A \) from (9) when vaccinating a node of the network, i.e. setting \( s_j = 0 \) at a specific node \( j \) and keeping the other nodes the same. We chose \( \alpha = 5.7 \) and \( s = (0.2, 0.2, 0.2, 0.2, 0.2)^T \).

We now vaccinate two cities in the network. The results are presented in table 2. We chose \( \alpha = 6.5 \).

The table shows that it is most effective to vaccinate nodes 1, 3 and 5. These nodes have the highest degree of the network.

Again the high degree nodes 1, 3 and 5 are the ones that reduce \( \sigma_1 \) the most and are therefore the most effective when applying vaccination. It is also not effective to vaccinate neighboring nodes.
4.1 A 15 node geographical graph

To confirm the results obtained in the previous section we consider the 15 node graph inspired from the north of France shown in Fig. 4. The three smallest eigenvalues in absolute value are

| $\omega_1^2$ | $\omega_2^2$ | $\omega_3^2$ |
|-------------|-------------|-------------|
| 0           | -0.3607     | -0.4644     |

The eigenvector $v^2$ corresponding to $\sigma_2$ is

$(-0.064, -0.62, -0.4, -0.05, -0.077, -0.063, -0.03, 0.22, 0.24, -0.046, 0.32, 0.3, 0.37, -0.046, -0.046)^T$

We follow the same procedure as above and vaccinate one city, keeping the others unchanged. The results are shown in Table 3.

![Graph of the fifteen main cities in the north of France numbered from 1 to 15: Le Havre, Abbeville, Amiens, Reims, Caen, Rouen, Paris, Le Mans, Orlon, Troyes, Angers, Tours, Bourges, Auxerre, Nevers.](image)
Table 3: Vaccinated node $i$ and associated eigenvalues of $A$

| $j$ | degree | $\sigma_3$     | $\sigma_2$     | $\sigma_1$     |
|-----|--------|----------------|----------------|----------------|
| 2   | 1      | $-7.62 \times 10^{-1}$ | $-3.80 \times 10^{-1}$ | $1.62 \times 10^{-2}$ |
| 13  | 1      | $-4.77 \times 10^{-1}$ | $-3.61 \times 10^{-1}$ | $1.11 \times 10^{-2}$ |
| 10  | 1      | $-4.35 \times 10^{-1}$ | $-3.22 \times 10^{-1}$ | $6.59 \times 10^{-3}$ |
| 3   | 2      | $-5.56 \times 10^{-1}$ | $-3.79 \times 10^{-1}$ | $4.66 \times 10^{-3}$ |
| 11  | 2      | $-4.75 \times 10^{-1}$ | $-3.64 \times 10^{-1}$ | $3.93 \times 10^{-3}$ |
| 5   | 2      | $-5.04 \times 10^{-1}$ | $-3.23 \times 10^{-1}$ | $2.63 \times 10^{-3}$ |
| 14  | 2      | $-4.38 \times 10^{-1}$ | $-3.22 \times 10^{-1}$ | $-3.60 \times 10^{-4}$ |
| 15  | 2      | $-4.38 \times 10^{-1}$ | $-3.22 \times 10^{-1}$ | $-3.60 \times 10^{-4}$ |
| 12  | 2      | $-4.81 \times 10^{-1}$ | $-3.66 \times 10^{-1}$ | $-9.37 \times 10^{-4}$ |
| 4   | 2      | $-4.65 \times 10^{-1}$ | $-3.22 \times 10^{-1}$ | $-2.33 \times 10^{-3}$ |
| 1   | 3      | $-4.90 \times 10^{-1}$ | $-3.23 \times 10^{-1}$ | $-4.44 \times 10^{-3}$ |
| 8   | 3      | $-4.51 \times 10^{-1}$ | $-3.57 \times 10^{-1}$ | $-7.29 \times 10^{-3}$ |
| 6   | 4      | $-4.92 \times 10^{-1}$ | $-3.23 \times 10^{-1}$ | $-7.31 \times 10^{-3}$ |
| 9   | 4      | $-4.61 \times 10^{-1}$ | $-3.61 \times 10^{-1}$ | $-7.47 \times 10^{-3}$ |
| 7   | 9      | $-4.33 \times 10^{-1}$ | $-3.22 \times 10^{-1}$ | $-2.09 \times 10^{-2}$ |

4.2 Discussion

The results shown in tables 1, 2 and 3 can be explained from the properties of the matrix $A$ and the graph Laplacian $\Delta$. The maximal eigenvalue $\sigma_1$ of $A$ verifies \cite{6}

$$\sigma_1 = \sup_{\|X\|=1} <X|AX>.$$  \hspace{1cm} (14)

We can find inequalities for $\sigma_1$ by choosing

$$X = (1, 0 \ldots 0)^T, \ X = (0, 1, 0 \ldots 0)^T, \ldots$$

Denoting $d_i$ the degree of node $i$, we get

$$\sigma_1 \geq -d_1 + \alpha s - \beta,$$  \hspace{1cm} (15)

$$\sigma_1 \geq -d_2 + \alpha s - \beta,$$  \hspace{1cm} (16)

$$\ldots$$  \hspace{1cm} (17)

$$\sigma_1 \geq -d_n + \alpha s - \beta,$$  \hspace{1cm} (18)

so that

$$\sigma_1 \geq -\min_k d_k + \alpha s - \beta.$$  \hspace{1cm} (19)

This relation shows that vaccinating a node that has not smallest degree does not change the estimate. Conversely, if there is a unique node of minimal degree and we vaccinate it, then the bound changes.

Using similar arguments, it can be shown that vaccinating two neighboring nodes, say 1 and 2 will be less effective than vaccinating two non neighboring nodes.
Now we look at what happens if we cut a link, which corresponds to condemning a road for example. Let $\Delta'$ be the Laplacian of the new graph obtained by deleting a link. Without loss of generality we can assume this link to be between vertices 1 and 2. Then $\Delta' = \Delta - M$ where

$$M = \begin{pmatrix} -1 & 1 & 0 & \ldots & 0 \\ 1 & -1 & 0 & \ldots & 0 \\ 0 & \ldots & \ldots & \ldots & 0 \end{pmatrix}$$

$M$ has all eigenvalues equal to 0 except one which has value $-2$. Applying the Courant-Weyl inequalities, see for example [6], we get the following result for the maximum eigenvalue of $\Delta'$

$$\sigma'_1 \leq \sigma_1.$$

Note that equality is possible: when $s$ is homogeneous, the maximum eigenvalue of $A$ will always be $-\beta + \alpha s$. In such a case, cutting a link is ineffective.

5 Conclusion

We analyzed a simple model of an epidemic on a network where the geographic term is a graph Laplacian. The symmetry of this matrix allows to choose an orthonormal basis of eigenvectors on which to project the dynamics. This provides a sound mathematical basis for the analysis.

We derived a simple epidemic criterion using the eigenvalues of a matrix $A$ [9] to predict the scale of the outbreak. Using it, we established a vaccination policy so as to reduce the magnitude of the epidemic. We proved that it is most effective to vaccinate the highest degree nodes, i.e. the nodes with most connections. We also proved that it is not effective to vaccinate neighboring nodes.

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6 Appendix : well-posedness of the model

To prove the well-posedness, we rewrite the system (7) as the following abstract differential equation:

\[
\begin{align*}
  x'(t) &= Ax(t) + f(x(t)) \\
  x(0) &= x_0 \in \mathbb{R}^n
\end{align*}
\]  

(20)

where \( x := \begin{pmatrix} s \\ i \end{pmatrix} \), \( A \) is the matrix given by

\[
A := \begin{pmatrix} \Delta & 0 \\ 0 & \Delta \end{pmatrix}
\]

and \( f : \mathbb{R}^n \times \mathbb{R}^n \to \mathbb{R}^{2n} \) defined by

\[
f(x) := \begin{pmatrix} -\alpha s_i \\ \alpha s_i - \beta_i \end{pmatrix}
\]

and \( x_0 := \begin{pmatrix} s_0 \\ i_0 \end{pmatrix} \).

It is clear that, the function \( f \) is \( L_f \)-lipschitzian with \( L_f \) depends only on \( \alpha \) and \( \beta \). Now, we formulate the well-posedness theorem, which is the main theorem of this section:

**Theorem 6.1** Given \( x_0 \in \mathbb{R}^n \). Then, the equation (20) has a unique solution satisfying the following formula:

\[
x(t) = e^{tA}x_0 + \int_0^t e^{(t-s)A}f(x(s))ds, \quad t \geq 0.
\]  

(21)
proof

Let \( x_0 \in \mathbb{R}^n \) and \( T > 0 \). Consider the mapping \( \Gamma : C \rightarrow C \) given by

\[
\Gamma u(t) = e^{tA}x_0 + \int_0^t e^{(t-s)A}f(u(s))ds
\]

where \( C := C([0,T],\mathbb{R}^n) \). Let us prove that \( \Gamma \) is a contraction. Indeed, let \( u, v \in C \), then

\[
\|\Gamma(u(t)) - \Gamma(v(t))\| \leq \int_0^t e^{(t-s)\|A\|} \|f(u(s)) - f(v(s))\|ds
\]

\[
\leq L_f \int_0^t e^{(t-s)\|A\|} \|u(s) - v(s)\|ds
\]

\[
\leq L_f e^{T\|A\|} \int_0^t \|u(s) - v(s)\|ds
\]

\[
\leq L_f e^{T\|A\|} t \|u - v\|_{\infty}.
\]

On the other hand

\[
\|\Gamma^2(u(t)) - \Gamma^2(v(t))\| = \|\Gamma(\Gamma(u(t))) - \Gamma(\Gamma(v(t)))\|
\]

\[
\leq L_f e^{T\|A\|} \int_0^t s \|\Gamma(u(s)) - \Gamma(v(s))\|ds
\]

\[
\leq \frac{(L_f e^{T\|A\|} t)^2}{2} \|u - v\|_{\infty}.
\]

Hence, by iterating for \( n \geq 1 \), we conclude that

\[
\|\Gamma^n(u(t)) - \Gamma^n(v(t))\| \leq \frac{(L_f e^{T\|A\|} T)^n}{n!} \|u - v\|_{\infty}.
\]

Now, for \( n \) large enough,

\[
\frac{(L_f e^{T\|A\|} T)^n}{n!} < 1.
\]

The mapping \( \Gamma^n \) is a contraction. Therefore, by using the iterating fixed point theorem \( \Gamma \) is also a contraction. Consequently, the system (13) has a unique solution which is given by (14). end proof