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EXPONENTIAL CONVERGENCE TO A QUASI-STATIONARY DISTRIBUTION WITH APPLICATIONS TO BIRTH AND DEATH PROCESSES

by

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Abstract

In this project we study the exponential convergence of Markov processes to quasi-stationary distributions (QSDs) with applications. Quasi-stationary distributions are useful when it comes to understanding the behavior of stochastic processes which appear to be persistent over a long time period before reaching extinction. A review of the concept of stationarity and ergodicity is given. Next quasi-stationarity is defined. A simple example that illustrates quasi-stationarity is considered- specifically the example of the finite state case. Finally, we choose a Corona Virus model, convert it to a birth and death process, then show that it converges to a particular QSD exponentially, we also choose the compartment of infected persons from the model and show that it is a branching process that also converges to a QSD over time.

Chapter 1

INTRODUCTION

Many models are used in stochastic analysis to study systems that change states many times per second. On rare occasions, the time scale of such steps is measured in hours or days. We are interested in the scenario where the time steps are measured in several hundreds, thousands or even a million times over periods extending to months, years and more. For us to understand how these systems work, we have to study their long time behaviour. These bring us to the concepts of stationarity, stationary distributions, limiting distributions and quasi-stationary distributions. We will discuss these concepts with regard to Markov processes, which are stochastic processes that exhibit the Markov property. The Markov property is also called the memoryless property in literature. It simply implies that the evolution of a process in the future depends only on the present state and does not depend on the past.

In this paragraph we introduce the notations used throughout this study. Let $\mathbb{Z}_+ = \{0, 1, 2, ...\}$ be the set of non-negative integers, $\mathbb{N}_+ = \{1, 2, ...\}$ be the set of positive integers and $\mathbb{R}_+ = [0, \infty)$ be the set of non-negative real numbers. Also, we let $\{X_t\}_{t\in\mathbb{Z}_+}$ denote a countable-state Markov chain with transition kernel P on a state space $(E, \mathcal{B}(E))$, where $\mathcal{B}(E)$ represents the σ-algebra. P_i and E_i denotes the probability and the expectation of the chain respectively, where $P^t(i, j) = P_i(X_t = j) = E_i(\mathbf{1}_{X_t} = j)$. The Markov chain is under the condition that its initial state $X_0 = i$ and $\mathbf{1}_A$ is the indicator function set of set A. We also consider a σ-finite measure on $\mathcal{B}(E)$ with the property

$$\{\pi(A)\} = \pi P(A) \triangleq \int \pi d(i) P(i, A), \;\; A \in \mathcal{B}(E), \tag{1.1}$$

which is called invariant.

1.1 Stationarity and Stationary Distributions

According to Kaspi et al in [11] a discrete-time stochastic process $\{X_t\}_{n\in\mathbb{N}}$ is stationary if for any time points $t_1, ..., t_n$ and any $m \geq 0$, the joint distribution of $(X_{t_1}, ..., X_{t_n})$ is the same as the joint distribution of $(X_{t_1+m}, ..., X_{t_n+m})$. Therefore 'stationarity' refers to 'stationary in time'. In particular, for a stationary process, the distribution of X_t is the same for all n. What makes

Markov chains peculiar is that we can often make them stationary. This leads us to the concept of stationary distributions. If a Markov chain is stationary, then we call the common distribution of all the X_t the *stationary distribution* of the Markov chain. The stationary distribution of the process X_t is a probability distribution that remains unchanged in the Markov chain as time progresses. It is often represented as a row vector π whose entries are probabilities that sum up to one, and given the transition matrix P, it satisfies

$$\pi = \pi P. \tag{1.2}$$

Looking at this equation, we can say, π is *invariant* by the matrix P [13]. Ergodic Markov chains have a unique stationary distribution. Absorbing Markov chains also have stationary distributions with non-zero elements only in the absorbing states.

Recalling some concepts of linear algebra, we notice that $\pi P = \pi$ is identical to the column vector equation $M\nu = \lambda\nu$ for eigenvalues and eigenvectors, with λ equals one. In fact by transposing the matrices,

$$(\pi P)^T = \pi^T \implies P^T \pi^T = \pi^T.$$

This means the transposed transition matrix P^T has eigenvectors with eigen-

value 1 that are stationary distributions expressed as column vectors. Hence if the eigenvectors of P^T are known, consequently so are the stationary distributions of the Markov chain with transition matrix P. This is because the stationary distribution is a left eigenvector (rather than the typical right eigenvector) of the transition matrix. If there are multiple eigenvectors related to an eigenvalue of 1, then each of such eigenvectors results in an associated stationary distributions. This, however, only occurs for a reducible Markov chain.

1.1.1 Relation to Limiting Distributions

The notion of limiting distributions attempts to describe the process $\{X_t\}_{t\in\mathbb{R}_+}$, it explains the behavior of the process after a long time. For the limiting distribution to exist, the following limit must exist for any state i and j

$$L_{i,j} = \lim_{n\to\infty} \mathbb{P}(X_t = j|X_0 = i). \tag{1.3}$$

Additionally, for any i, the following sum must be equal to 1,

$$\sum_{j\in E} \lim_{n\to\infty} \mathbb{P}(X_t = j|X_0 = i). \tag{1.4}$$

This makes certain that the numbers we get constitutes a probability distribution. When these two conditions are met, then the limiting distribution of

a Markov chain with $X_0 = i$ is the probability distribution given by equation (1.2). For any time-homogeneous Markov chain that is aperiodic and irreducible, $\lim_{n\to\infty} P^n$ converges to a matrix with all rows identical and equal to π. This is not the case with all stationary distributions though. Therefore not all stationary distributions are limiting distributions. However for time homogeneous Markov chains, any limiting distribution is a stationary distribution.

1.2 Quasi-Stationary Distributions

Getting to the core intention of this study, we now discuss the concept of quasi-stationary Markov processes. The works of Yaglom [22] as well as Darroch and Seneta [6] on Galton-Watson processes give us insight on quasi-stationary processes. We begin by defining a quasi-stationary distribution as given by Champagnat et al in [4]. Let $\{X_t\}_{t\in\mathbb{R}_+}$ be a discrete or continuous time homogeneous Markov process with state space $E \cup \{\partial\}$ which is absorbed at $\partial \notin E$, where $(E, \mathcal{B}(E))$ is a measurable space. A quasi-stationary distribution is a probability measure υ_{QSD} on E such that

$$\mathbb{P}_{\upsilon_{QSD}}(X_t \in A | t < \tau_\partial) = \upsilon_{QSD}(A),\ \forall t \in \mathbb{R}_+,\ A \in \mathcal{B}(E), \tag{1.5}$$

where $\tau_\partial = inf\{t \in \mathbb{R}_+, X_t = \partial\}$ is the absorption time of $\{X_t\}_{t\in\mathbb{R}_+}$. The

following is a necessary and sufficient condition for the probability measure υ_{QSD} on E to be a quasi-stationary distribution; there exists a probability measure μ on E such that

$$\upsilon_{QSD}(A) = \lim_{t\to\infty} \mathbb{P}_\mu(X_t \in A | t < \tau_\partial), \forall A \in \mathcal{B}(E). \tag{1.6}$$

Given a quasi-stationary distribution υ_{QSD}, there is a set of probability measures on μ such that (1.5) holds, it is called the *domain of attraction of* υ_{QSD}. This set is never empty since it contains at least υ_{QSD}, and may contain an infinitely many elements.When the limit in (1.6) exists for any $\mu = \partial_i$, $i \in E$, and does not depend on the initial position i, then υ_{QSD} is either called the *Yaglom limit* or the *minimal quasi-stationary distribution.*

Thus the minimal quasi-stationary distribution, if it exists, is the unique quasi-stationary distribution whose domain of attraction contains $\{\partial_i, i \in E\}$. It is well known that when υ_{QSD} is a quasi-stationary distribution, there exists $\lambda_0 \in \mathbb{R}_+$, such that for all $t \in \mathbb{R}_+$,

$$\mathbb{P}_{\upsilon_{QSD}}(t < \tau_\partial) = e^{-\lambda_0 t} \, and \, e^{\lambda_0 t} \upsilon_{QSD} P = \upsilon_{QSD}. \tag{1.7}$$

The absorption times and the absorption position are independent under $\mathbb{P}_{\upsilon_{QSD}}$. The independence of absorption times and absorption position leads to the concept of quasi-stationary distribution having a wide range of applications.

1.3 Ergodicity

Ergodicity is an important concept that we also have to review as we discuss the quasi-stationarity of Markov processes. There are several types of ergodicity, before we discuss them, we present a formal definition of ergodicity.Markov's theorem states that a Markov chain $\{X_t\}_{t\in\mathbb{Z}_+}$ is ergodic if there is a positive probability to pass from any state, say $i \in E$ to any other state, say $\cdot$, $P(i,\cdot) > 0$. In the subsection below we review some types of ergodicity.

1.3.1 Some Types of Ergodicity

Uniform Ergodicity

Uniform Ergodicity means that there exists positive constants $\rho < 1$ and $C < 1$ such that, for all $i \in E$,

$$\|e_i P(i,\cdot)^t - \pi(\cdot)\| \leq C\rho^n,\ t \in \mathbb{Z}_+, \tag{1.8}$$

where e_i is the probability measure concentrated at i.

Ordinary Ergodicity

The chain $\{X_t\}_{t\in\mathbb{Z}_+}$ is referred to as ordinary ergodic (or just ergodic) if for all $i, k \in E$,

$$P^t(i,k) \to \pi(k) \; as \; t \to \infty, \tag{1.9}$$

where the σ-finite measure π is the invariant limit distribution of the chain.

Geometric Ergodicity

If the t-step probability measures, P^t, converge in total variation norm to the stationary probability measure π at rate r^t (for some $r \geq 1$), that is

$$\lim_{t\to\infty} r^t \|P^t(i,k) - \pi(k)\| = 0, \text{ for } \pi \text{ almost everywhere,} \tag{1.10}$$

then according to [10] the Markov chain is said to be geometrically ergodic.

Sub-Geometric Ergodicity

In this case, the convergence in (1.10) happens at rate $r(t)$, which is slower, therefore we have

$$\lim_{t\to\infty} r(t) \|P^t(i,k) - \pi(k)\| = 0, \text{ for } \pi \text{ almost everywhere.} \tag{1.11}$$

When this convergence is true for suitably defined rates $r(t)$ which are slower than the geometric one, then the Markov chain is called sub-geometrically convergent.

1.3.2 Aims and Objectives

The objective of this study is to provide a sufficient theoretical framework that can help us study the time evolution and behavior of a death and death process. We then apply this to epidemiology. To achieve this we:

1. choose a deterministic Corona Virus (Covid-19) model.

2. convert it to a birth and death process.

3. show that it converges to a birth and death process.

This paper is organized as follows: Chapter 2 explores the necessary and sufficient condition for the uniform exponential convergence from various literature. Chapter 3 entails the main results. A deterministic model is chosen, converted to a stochastic model, then we show that it converges to a quasi-stationary distribution. In chapter 4 we simulate and discuss the behavior of our stochastic model as well as deterministic model. We also compare and contrast the two models. Finally, in the last chapter, we provide scientific conclusions with regard to the findings of this work.

Chapter 2

LITERATURE REVIEW

2.1 Necessary and Sufficient Condition for the Uniform Exponential Convergence to a Quasi-Stationary Distribution

Champagnat et al in [4] provided a necessary and sufficient condition on $\{X_t\}_{t\in\mathbb{Z}_+}$ for the existence of a probability measure υ on E and constants C, $\gamma > 0$ such that

$$\| \mathbb{P}_\mu(X_t \in A | t < \tau_\partial) - \upsilon_{QSD}(\cdot) \|_{TV} \leq Ce^{-\gamma t},\ \forall \mu \in \mathcal{B}(E)\, t \geq 0, \qquad (2.1)$$

where $\|\cdot\|_{TV}$ is the total variation norm. This immediately implies that $\upsilon_{QSD}(\cdot)$ is the unique quasi-stationary distribution of $\{X_t\}_{t\in\mathbb{Z}_+}$ and that (1.6) holds for any initial probability measure μ. The necessary and sufficient condition for (2.1) is given by the existence of a probability measure υ on E and of constants t_0, c_1,$c_2 > 0$ such that

$$\mathbb{P}_i(X_{t_0} \in \cdot | t_0 < \tau_\partial) \geq c_1 \upsilon(\cdot), \tag{2.2}$$

and

$$\mathbb{P}_\upsilon(t < \tau_\partial) \geq c_2 \mathbb{P}_i(t < \tau_\partial). \tag{2.3}$$

The preceding statement is the converse of the theorem given by [4]. The theorem is as follows:

Theorem 2.1.1 (see [4])**.** *Assume (2.2) and (2.3) then there exist a probability measure υ_{QSD} on E such that for any initial distribution $\mu \in \mathscr{M}_1(E)$*

$$\| \mathbb{P}_\mu(X_t \in \cdot | t < \tau_\partial) - \upsilon_{QSD}(\cdot) \|_{TV} \leq 2(1 - c_1 c_2)^{\lfloor t/t_0 \rfloor}, \tag{2.4}$$

where $\lfloor\cdot\rfloor$ is the integer part function and $\|\cdot\|_{TV}$ is the total variation norm. $\mathscr{M}_1(E)$ is the set of probability measures on E.

In this case, for all probability measures on μ_1 and μ_2 on E, and for all $t > 0$,

$$\|\mathbb{P}_{\mu_1}(X_t \in \cdot | t < \tau_\partial) - \mathbb{P}_{\mu_2}(X_t \in \cdot | t < \tau_\partial)\|_{TV} \leq \frac{2(1 - c_1 c_2)^{\lfloor t/t_0 \rfloor}}{c_2(\mu_1) \vee c_2(\mu_2)} \|\mu_1 - \mu_2\|_{TV}, \tag{2.5}$$

hence $c_2(\mu)$ is a positive constant that only depends on μ. The following consequences also follow from conditions (2.2) and (2.3):

Proposition 2.1.2 (see [5]). *Assume that condition (2.2) and (2.3) holds true. Then there exists a non-negative function η on $E \cup \{\partial\}$, positive on E and vanishing on ∂, defined by*

$$\eta(i) = \lim_{t \to \infty} \frac{\mathbb{P}_i(t < \tau_\partial)}{\mathbb{P}_{\nu_{QSD}}(t < \tau_\partial)} = \lim_{t \to +\infty} e^{\gamma_0 t} \mathbb{P}_i(t < \tau_\partial), \tag{2.6}$$

where the convergence holds for the uniform norm on $E \cup \{\partial\}$ and $\nu_{QSD}(\eta) = 1$. More precisely there exists a positive constant a_1 such that

$$|e^{\gamma_0 t} \mathbb{P}_i(t < \tau_\partial) - \eta(i)| \leq a_1 e^{\gamma_0 t} \mathbb{P}_i(t < \tau_\partial)(1 - c_1 c_2)^{t/t_0}. \tag{2.7}$$

Furthermore the function η is bounded, belongs to the domain of infinitesimal generator L of the semi-group $(P_t)_{t \geq 0}$ on $(\mathscr{B}_b(E \cup \{\partial\}), \|\cdot\|_\infty\})$ and

$$L\eta = -\lambda \eta.$$

In the irreducible case, exponential ergodicity is known to be related to a spectral gap property. These results imply a similar property under conditions (2.2) and (2.3) for the infinitesimal generator L of the semi-group on $(\mathscr{B}_b(E \cup \{\partial\}), \|\cdot\|_\infty\})$.

Proposition 2.1.3 ([5]). *Let condition (2.2) and (2.3) hold. If $f \in (\mathscr{B}_b(E \cup \{\partial\})$ is a right eigenfunction for L for an eigenvalue λ, then either*

1. *$\lambda = 0$ and f is constant,*

2. *$\lambda = -\lambda_0$ and $f = v_{QSD}(f)\eta$,*

3. *$\lambda \leq -\lambda_0 - \gamma, v_{QSD}(f) = 0$ and $f(\partial) = 0$.*

Finally we state an original result that has to do with a more refined speed of convergence of the conditional distribution of the process towards its quasi-stationary distribution.

Proposition 2.1.4. *Suppose that condition (2.2) and (2.3) holds. Then there exists a constant $C > 0$ such that,*

$$\|\mathbb{P}_\mu(X_t \in \cdot | t < \tau_\partial) - v_{QSD}(\cdot)\|_{TV} \leq C \left(1 - c_2 \frac{v(\eta)}{\|\eta\|_\infty}\right)^{t/t_0}. \tag{2.8}$$

The sketch of the proof for the sufficient condition is provided at the Appendix.

2.2 The finite state space case

The aim of this section is to give an application of Theorem (2.1.1) in a simple situation, recovering this classical result by [20] with additional explicit bounds on the rate of convergence. Let $\{X_t\}_{t\in\mathbb{Z}_+}$ be a discrete time Markov process on a finite space $E \cup \partial$, where $\partial \notin E$ is absorbing.

We say Z is irreducible and aperiodic if there exists $t_0 \in \mathbb{N}$ such that , for all i, $j \in E$, $\mathbb{P}_i(X_{t_0} = j) > 0$. There exist two positive constants such that the exponential convergence in (2.5) holds true, with γ being the second spectral gap of the transition matrix.

The following convergence result is not focused toward optimality, but rather aims at illustrating how to check conditions (2.2) and (2.3) in a simple case. We observe that, associated with proposition 2.1.3, it provides an explicit lower bound for the second spectral gap of the matrix P.

Proposition 2.2.1 ([20]). *Let $\{X_t\}_{t\in\mathbb{N}}$ be an irreducible and aperiodic Markov chain on a finite state space E with the transition matrix $(P_{i,j})_{i,j\in E}$. Let $t_0 \in \mathbb{N}$ be such that P^{t_0} has positive entries and set*

$$c_1 = \sum_{j\in E} \inf_{i\in E} \frac{P^{t_0}_{i,j}}{\sum_{k\in E} P^{t_0}_{i,k}} \text{ and } c_2 = \inf_{i,j\in E} \frac{P^{t_0}_{i,j}}{\sum_{k\in E} P^{t_0}_{i,k}}.$$

Then $\{X_t\}_{t\in\mathbb{N}}$ satisfies condition with the constants c_1, c_2 and t_0.

Since the aim of this section is to illustrate the application of Theorem (2.1.1), we detail the elementary proof of the above proposition.

Proof. We define the probability measure v on E by

$$v(\{j\}) = \inf_{i \in E} \frac{P_{i,j}^{t_0}}{c_1 \sum_{k \in E} P_{i,k}^{t_o}}, \forall j \in E.$$

We have for all $i, j \in E$,

$$\mathbb{P}_i(X_{t_0} | t_0 < \tau_\partial) = \frac{P_{i,j}^{t_0}}{\sum_{k \in E} P_{i,k}^{t_o}} \geq c_1 v(\{j\}),$$

which entails condition (2.2). Now, for all $i \in E$ and all $n \geq 2$,

$$\mathbb{P}_v(n < \tau_\partial) \geq v(\{i\}) \mathbb{P}_i(n < \tau_\partial) \geq c_2 \mathbb{P}_i(n < \tau_\partial),$$

which implies condition (2.3).

Chapter 3

MAIN RESULTS

The study of quasi-stationary distributions and their convergence has a myriad of applications [4]. Nevertheless, in this chapter we limit ourselves to their applications to birth and death processes. To achieve our goal we employ the SIQ epidemic model example formulated by Din et al in [7]. We note that the chosen model is a deterministic model which we convert to a stochastic model. We then show that the resulting model converges to a quasi-stationary distribution.

3.1 The SIQ Deterministic Model

As aforementioned Din et al [7] proposed a model in 2020 which investigates the dynamic behavior of the novel Corona Virus (Covid-19). It is a contagious disease which is mostly human-to-human transmitted. According to

[18], Covid-19 was declared a pandemic and has affected over 170 countries in the world. Din et al proposed a susceptible-infectious-quarantined deterministic model with fixed proportions. This model is adapted from SIR models introduced by Kermack and McKendrick and are described in [12]. The population N(t) at time t was divided into three groups: susceptible individuals S(t), infected individuals I(t) and quarantined individuals Q(t). The following assumptions were considered prior to formulating the model:

I. All parameters are non-negative.

II. The susceptible agents goes to the infection classes and there is a constant inflow into the susceptible population.

III. Initially infected or suspected people move to the quarantine class and confirmed cases from quarantine come back to the infected compartment.

With regard to the above assumptions, the dynamics of Covid-19 are in the form of three ordinary differential equations:

$$\begin{aligned}
\frac{d}{dt}S(t) &= \Lambda - \boldsymbol{\gamma} S(t)I(t) - d_0 S(t). \\
\frac{d}{dt}I(t) &= \boldsymbol{\gamma} S(t)I(t) - (d_0 + k + \eta)I(t) + \sigma Q(t). \\
\frac{d}{dt}Q(t) &= \eta I(t) - (d_0 + \mu + \sigma)Q(t).
\end{aligned} \tag{3.1}$$

The model parameters with initial conditions $S(0) = S_0 > 0$, $I(0) = I_0 \geq 0$ and $Q(0) = Q_0 \geq 0$ are explained as follows:

Λ : Recruitment rate.

γ : Disease transmission rate.

d_0 : Natural death rate.

η : Rate of getting quarantined.

μ : Disease-related death rate in quarantined individuals.

σ : Rate at which quarantined people are getting infected.

k : Disease-related death rate in the infected group.

Theorem 3.1.1. *The Model (3.1) in orthant $\mathbb{R}^3_+$ is invariant and its solution with initial conditions $S(0) = S_0, I(0) = I_0$ and $Q(0) = Q_0$ are positive and bounded. Furthermore if $T(0) \leq \frac{\Lambda}{d_0}$, then the problem as stated by Model (3.1) and the initial conditions is a well defined dynamical system whose region is given by:*

$$\Delta = \left\{ (S, I, Q) \in \mathbb{R}^3_+ : 0 < T \leq \frac{\Lambda}{d_0} \right\}, \tag{3.2}$$

which is biologically feasible. Moreover every solution in Δ remains in Δ for $t \geq 0$. The proof for this theorem has been presented by Din et al [7] in Section 3 of the article.

Remark. *The above theorem implies the well possedness of the proposed model.*

3.2 Formulation of the SIQ Stochastic Model

Stochastic models are necessitated by the fact that unlike deterministic models, the number of individuals is discrete and this explains real world situations better. The issue with deterministic models is that the number of individuals in a population is considered a continuous variable which is not really the case in a practical setting. Furthermore, with stochastic models we can explain such things as the probability of an outbreak, the final size distribution of an epidemic, the expected duration of an epidemic, and most importantly (as is our case here)- the quasi-stationary distribution of an epidemic.

Here, we consider a continuous time Markov Chain (CTMC) $X_t = (S_t, I_t)_{t\in\mathbb{R}_+}$ on state space $\mathbb{R}^2_+$. Accessible states from $X_t = (s, i)$ are $V_{(s,i)} = \{(s, i), (s+1, i), (s, i-1), (s-1, i), (s-1, i+1)\}$. X_t has an absorbing set corresponding to the disease free equilibrium state $E_0 = \{(s, i), s \geq 0, i = 0\}$.

We set $Q_{s,i} = \Lambda + \boldsymbol{\gamma} si + d_0 + (d_0 + k + \eta)i + \sigma(N - i - s)$.

$$P_{i,j} = \begin{cases} \Lambda & ;(k,j) = (s+1,i), s \geq 0, i \geq 0 \\ \gamma si & (k,j) = (s-1,i+1), s \geq 1, i \geq 0 \\ d_0 S & (k,j) = (s-1,i), s \geq 1, i \geq 0 \\ (d_0 + k + \eta)i & (k,j) = (s,i-1), s \geq 0, i \geq 1 \\ \sigma(N-i-s) & (k,j) = (s,i+1), s \geq 0, i \geq 0. \end{cases} \tag{3.3}$$

The transition probabilities of $X_t = (S_t, I_t)$ are defined by:

$$P_{(s,i),(k,j)} = \{P(X_{t+\delta T} = (k,j) | X_t = (s,i))\}.$$

We have $\forall s \geq 0$,

$$P_{(s,i),(k,j)} = \begin{cases} Q_{(s,i),(k,j)\delta t + o(\delta t 0)} & \text{if} \\ (k,j) \in \gamma(s,i) & \forall i > 0 \\ 1 - Q_{(s,i)}\delta t + o(\delta t) & \text{if} \\ (k,j) = (s,i) & i > 0 \\ P_{(s,o),(s,o)}(\delta t) = 1 & \forall i = 0. \end{cases} \tag{3.4}$$

The distribution if X_t is $P(s,i)(t) = 0$ if $s < 0$ or $i < 0$ and $P_{(s,i)}(t) = P\{X_t = (s,i)\}$ if $s \geq 0$, $i \geq 0$. Thus the marginal distributions are;

$$P\{I_t = i\} = \sum_{s\geq 0} P_{(s,i)}(t),$$

and

$$P\{S_t = s\} = \sum_{i\geq 0} P_{(s,i)}(t).$$

The Kolmogorov forward equation(from Equations (3.4)) are:

$$\begin{aligned}\frac{dP_{(s,i)}}{dt} &= \Delta[P_{(s-1,i)} - P_{(s,i)}] + \gamma[(s+i)(i-1)P_{(s+1,i+1)} - siP_{(s,i)}] \\ &+d_0[(s+1)P_{(s+1,i)} - sP_{(s,i)}] + (d_0 + k + \eta[(i+1)P_{(s,i+1)-iP_{(s,i)}}]) \\ &+\sigma[(N-s-i+1)]P_{(s,i-1)} - (N-s-i)P_{(s,i)}].\end{aligned} \tag{3.5}$$

The following results will lead us to note that for the stochastic approach, the number of infections will reach zero independent of the threshold R_0 almost surely. In other words, if $R_0 \leq 1$ then extinction occurs in finite mean time; and if $R_0 > 1$ the disease ultimately disappears in infinite mean time. We therefore notice that the parameter R_0, called the basic reproduction number, can give us important insight in epidemiology as stated in [1].

Theorem 3.2.1. *Let* $T_0 = \inf\{t \geq 0, I(t) = 0\}$ *with* $inf\phi = +\infty$. *Then for all* $i \in \mathbb{N}$, $\mathbb{P}_i[T_0 < +\infty] = 1$ *and* $\lim_{t\to+\infty} \mathbb{P}_i[I(t) = 0] = 1$.

Proof. This result is a consequence of lemma 5 in [17] and the properties of recurrent Markov chains with absorbing set of states that are non-empty. It reveals the absorbent characteristic of the Markov chain. □

Theorem 3.2.2. *Let* $T_0 = \inf\{t \geq 0, I(t) = 0\}$ *with* $inf\phi = +\infty$ *and* $(S_0^* = \frac{\Lambda}{d_0}, I_0^* = 0, Q_0^* = 0)$. *If* $R_0 \leq 1$, *then (1)* $E[T_0] < +\infty$ *and (2)* $\lim_{t\to+\infty}(\bar{S}(t), \bar{I}(t), \bar{Q}(t)) = (S_0^*, I_0^*, Q_0^*)$.

Proof. The first result is a consequent of the positive recurrence we get from lemma 5 in [17]. The second result follows from the absorbent nature of the Markov chain, and once in the absorbing state, the correlation of S(t) against I(t) is identically zero. As a result, the deterministic equations and the mathematical expectation equations have equal equilibrium points, asymptotically. □

Theorem 3.2.3. *Let* $T_0 = \inf\{t \geq 0, I(t) = 0\}$, $inf\phi = +\infty$ *and* $(S_e^* = \frac{\Lambda}{d_0 R_0}, I_e^* = \frac{d_0}{\gamma}(R_0 - 1), Q_e^* = \frac{d_0\eta}{b\gamma}(R_0 - 1))$. *If* $R_0 > 1$, *then (1)* $E[T_0] = +\infty$ *and (2)* $\lim_{t\to+\infty}(\bar{S}(t), \bar{I}(t), \bar{Q}(t)) = (S_e^*, I_e^*, Q_e^*)$.

Proof. Asymptotically, there are two equilibrium points, and essentially $\mathbb{E}(T) = \infty$ in the case $R > 1$, otherwise the two equilibrium points would be confused by the uniqueness of the stationary measure.This proves the first assertion. The second assertion proof is similar to that of the second assertion of Theorem 3.2.2. □

The instant of absorption takes place after a relatively long time, however before it happens the process passes through a quasi-stationary state. In order to comprehend this phenomenon, we study the long time behavior of this process conditioned on non-extinction.

It is well known that if the set of transient states is finite and irreducible then the quasi-stationary distribution exists. Contrarily, if this set is infinite then the existence of the quasi-stationary distribution is not guaranteed, also if it does exist, it is usually difficult to find it explicitly. Hence we naturally consider iterative methods or asymptotic solutions by diffusion processes for the quasi-stationary distribution.

Theorem 3.2.4. *Let* $(v_{QSD})_{(s,i)}$ *be the quasi-stationary distribution of the process* $(X_t)_{t\geq 1}$ *and* $(v_{QSD})_{(i)} = \sum_{s\geq 0}(v_{QSD})_{(s,i)}$ *the marginal distribution of the number* I^* *of the infected in a quasi-stationary system. If* $R_0 < 1$ *for all* $i \geq 1$*, then* $(V_{QSD})_{(i)} \approx (1 - R_0)R_0^{i-1}$.

Proof. For all $i, j \geq 1$ setting:

$$\begin{cases} P_i(i, j, \Delta t) = \mathbb{P}(I(t + \Delta t) = j | S(t) = s, I(t) = i). \\ P_x(i, j, t, \Delta t) = \mathbb{P}(I(t + \Delta t) = j | I(t) = i), \end{cases} \tag{3.6}$$

we have;

$$P_I(i, j, t, \Delta) = \sum_{s\geq 0} \mathbb{P}(S(t) = s) P_s(i, j, \Delta t), \tag{3.7}$$

and according to the process definition $(X_t)_{t>0}$,

$$P_s(i,j,\Delta t) = \begin{cases} \gamma si\Delta t + o(\Delta) & if \quad j = i+1 \\ (d_0+k+\eta)i & if \quad j = i-1 \\ 1-[\gamma si + (d_0+k+\eta)i]\Delta t + o(\Delta t) & if \quad j = 1, \end{cases} \tag{3.8}$$

we deduce that;

$$P_I(i,j,t,\Delta t) = \begin{cases} (d_0+k+n)i\Delta t + o(\Delta t) & if \quad j = i+1 \\ 1-[\gamma i\bar{S}(t) + (d_0+k+\eta)i]\Delta t + o(\Delta t) & if \quad j = i-1 \\ 1-[\gamma i\bar{S}(t) + (d_0+k+\eta)i]\Delta t + o(\Delta t) & if \quad j = i. \end{cases} \tag{3.9}$$

As in the case of disease free equilibrium, $\lim_{t\to+\infty} \bar{S}(t) = S_0^* = \frac{\Lambda}{d_0}$. We have (from equation (3.9));

$$P_I(i,j,t,\Delta t) = \begin{cases} \gamma iS_0^*\Delta t + o(\Delta t) & if \quad j = i+1 \\ (d_0+k+\eta)i\Delta t + o(\Delta t) & if \quad j = i-1 \\ 1-[\gamma iS_0^* + (d_0+k+\eta)i]\Delta t + o(\Delta t) & if \quad j = i, \end{cases} \tag{3.10}$$

thus asymptotically the process $I(t)$ is a linear birth-death process with infinitesimal generator:

$$q_{i,j} = \begin{cases} \lambda i \quad if \quad j = i+1 \\ \\ d_I i \quad if \quad j = i-1, \end{cases} \tag{3.11}$$

where $\lambda = \frac{\gamma\Lambda}{d_0}$ and $d_I = (d_0 + k + n)$. In this case, if $\lambda < d_I$, it is well known that there is a unique quasi-stationary for the process which follows the geometric law with parameter $1 - \frac{\lambda}{d_I} = 1 - R_0$. Hence if $R_0 < 1$ for all $i \geq 1$, we obtain;

$$(v_{QSD})_{(i)} \approx (1 - R_0)R_0^{i-1} \quad or \quad (v_{QSD})_{(i)} = \sum_{s\geq 0}(v_{QSD})_{(i,j)}. \tag{3.12}$$

□

Remark. *Under the condition $R_0 \leq 1$, the irreducible Markov chain $(X_t)_{t>0}$ is positive recurrent. Then a unique invariant probability π exists and*

$$\pi(s,i) = \frac{1}{\mathbb{E}_{(s,i)}(\tau_{s,i})},$$

where $\tau_{s,i} = \inf t > 0 | X_t = (s,i)$. thus the theorem simply states that for all $i \geq 1$, $\pi = \sum_{s\geq 0}\pi(s,i) \approx (1 - R_0)R_0^{i-1}$ if $R_0 < 1$.

3.3 Branching Process

From the previous section, we notice that the parameter R_0 plays an important role in epidemic modelling. We use it to understand the dynamics of an infection in both deterministic and stochastic models. According to [3] a suitable branching process can estimate the early stages of an epidemic. In such a case, giving birth implies infecting someone while death is implied by an actual death or recovery. In the same manner, R_0 corresponds to the mean.

We provide a brief review of branching processes. A branching process is a stochastic process which consists of random variables indexed by natural numbers. Initially, the intent of branching processes was to model a population in which each individual in generation n produces some random number of individuals in generation $n+1$. Suppose an organism has a random number of offspring, say 'j' before it dies. Let,

$$P(X_n = j) = p_j, \text{ for } j = 1, 2, ... \tag{3.13}$$

where $p_j \geq 0$ and $\sum_{j=0}^{\infty} p_j = 1$. X_n denotes the population size. We assume that all individuals reproduce independently of each other and the family sizes of each individual are independent and identically distributed. Then the process $\{X_n\}$, where X_n is the population size of the n^{th}-generation ,

is a Markov chain of a special structure called a branching process. The most important application in the theory of branching processes is finding the probability of ultimate extinction.

The Mean, the Variance and Extinction Probabilities

To determine the mean and variance of a branching process we let $\mu = \sum_{j=0}^{\infty} jp_j$ and $\sigma^2 = \sum_{j=0}^{\infty}(j-\mu)^2 p_j$ denote the mean number and variance of offspring of a single individual respectively. Then when $X_0 = 1$, that is, if there is initially only one individual, we have,

$$E(X_n) = \mu^n \text{ and } Var(X) = \begin{cases} \sigma^2\mu^n\left(\frac{\mu^n-1}{\mu-1}\right), & \mu \neq 1 \\ n\sigma^2, & \mu = 1. \end{cases} \tag{3.14}$$

For the long term expected generation size,

$$\lim_{n\to\infty} E(X_n) = \lim_{n\to\infty} \mu^n = \begin{cases} 0, & \text{if } \mu < 1 \\ 1, & \text{if } \mu = 1 \\ \infty, & \text{if } \mu > 1. \end{cases} \tag{3.15}$$

From the above we extricate three possible scenarios;

- For $\mu < 1$, the population dies out with an almost sure probability. This means that for any probability distribution ψ, $\exists n < \infty$ such that

$P_\psi(X_n = 0) = 1$, hence the expected extinction time is finite. This scenario is called subcritical.

- The second scenario is called critical. For this one $\mu = 1$. The population here dies out with probability one but this time around the expected extinction time is infinite.

- The final scenario is called supercritical. Here we have $\mu > 1$, and the population has a positive probability of survival, hence this leads us to having an infinite expected extinction time.

Remark. *For the branching process model, we do not have the p_j's which are used to calculate the expectation, therefore we will estimate μ with R_0. The population of infected person is always positive, therefore X_n takes values in $\mathbb{N}_+ = 1, 2, ...$ only.*

The results below (Theorem 3.3.1) shows us that the distribution that defines the infected persons does reach a quasi-stationary distribution for $\mu < 1$. The critical and supercritical scenarios do not have a quasi-stationary distribution.

According to the process definition, we consider a discrete time Markov chain (DTMC) $X_t = (I_t)_{t\in\mathbb{N}}$ defined on state space $\mathbb{N} = 0, 1, ...$ and with zero as an absorbing state.

Theorem 3.3.1. *Let V_{QSD_i} be the quasi-stationary distribution of the process $\{X_t\}_{t\geq 1}$. If $\mu < 1$, for all $i \geq 1$, then $V_{QSD_i} = (1-\mu)\mu^{i-1}$.*

The proof of the above theorem is similar to that of Theorem 3.2.4.

Chapter 4

SIMULATIONS AND DISCUSSIONS

In this chapter, we show forth the graphical representation of the simulations that help us verify our analytical results. These simulations were carried out using the Matlab software and the code used is provided in the Appendix section. Table 4.1 below shows the values and sources of the parameters used in the simulation. Some of the values where estimated whereas others where taken from available sources.

Parameter	Value	Source
Λ	0.03805333333	fitted
γ	0.0059334474	estimated
d_0	0.007121000000	[15]
η	0.144211141	estimated
μ	0.007121000000	[15]
σ	0.0052281	estimated
k	0.027864676	estimated

Table 4.1: Values and Sources of Parameters used in the Simulation.

According to figure 4.1, for a population of 3000 people, with time measured in monthly units, the ODE model suggests that the disease will become contained after about 30-40 months. Initially, almost the whole population was susceptible because Covid-19 is highly contagious and control measures were not yet established. Because of this the susceptible population dropped drastically while the infected persons population increased simultaneously in the same manner. The transmission rate was high hence elevating the reproduction number R_0.

The deterministic model assumes continuous time, hence the R_0 determines whether the disease will persist or not. If $R_0 > 1$ persistance often occurs, however for $R_0 < 1$ the disease free state is reached and infection is lost as time tends infinity.

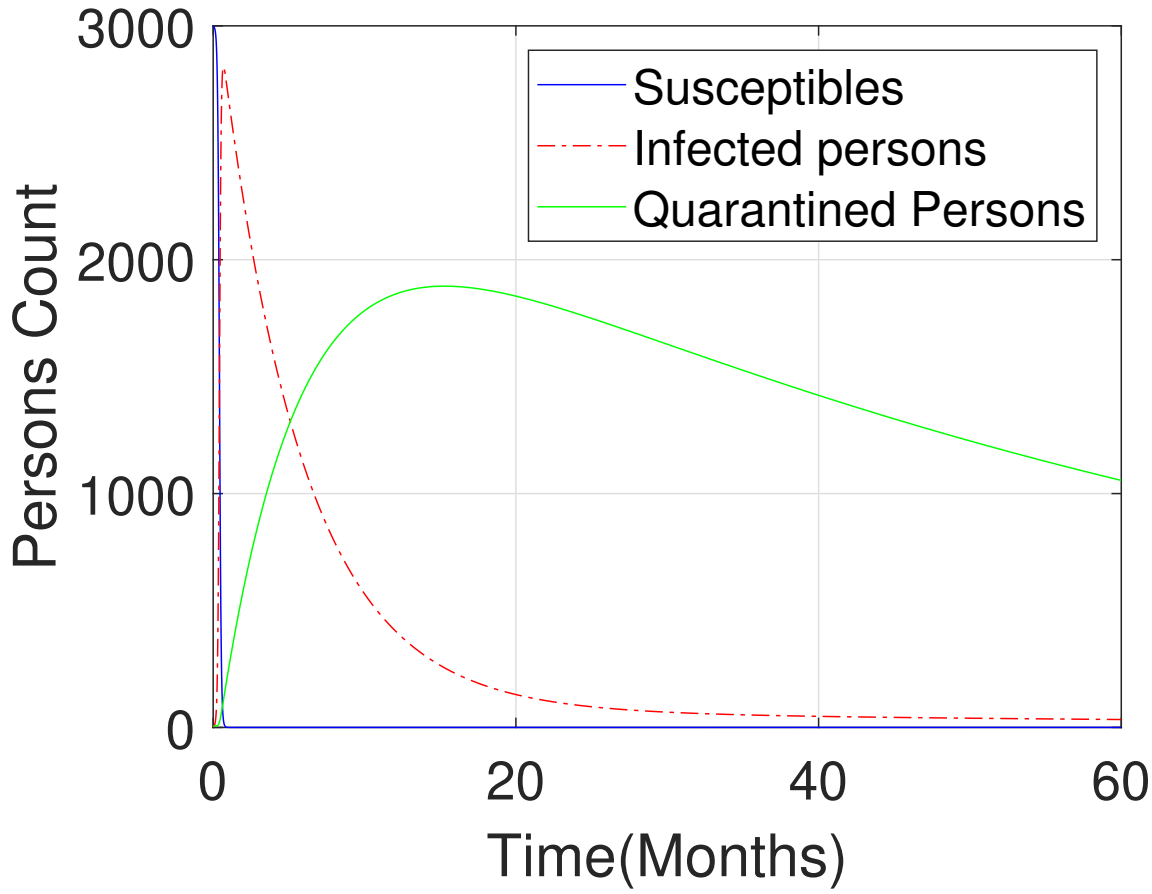

Figure 4.1: Deterministic Dynamics of Susceptible, Infected and Quarantined Persons Populations.

We notice that given similar initial conditions for a deterministic model, we observe the same results. As for the stochastic model we notice an element of randomness which better simulates the real world. Figure 4.2, for example, depicts the extinction behavior that we usually observe in life. The stochastic model also proved to be more appropriate for smaller populations(as observed by [19]), hence it worked well when we simulated with a starting population of three hundred. The results agrees with the findings of Allen and Burgin in [2] who conducted a study that analyzed ultimate disease extinction. They concluded that there exists a quasi-stationary probability distribution whose mean agrees with the deterministic endemic equilibrium for $R_0 \geq 1$. This is observed in Figure 4.2, both the populations of Susceptible and Infected persons reach a quasi-stationary state before being absorbed.

We used the Gillespie's algorithm to compute the sample paths of these processes. This algorithm is named after Daniel T. Gillespie's works in [8] and [9].

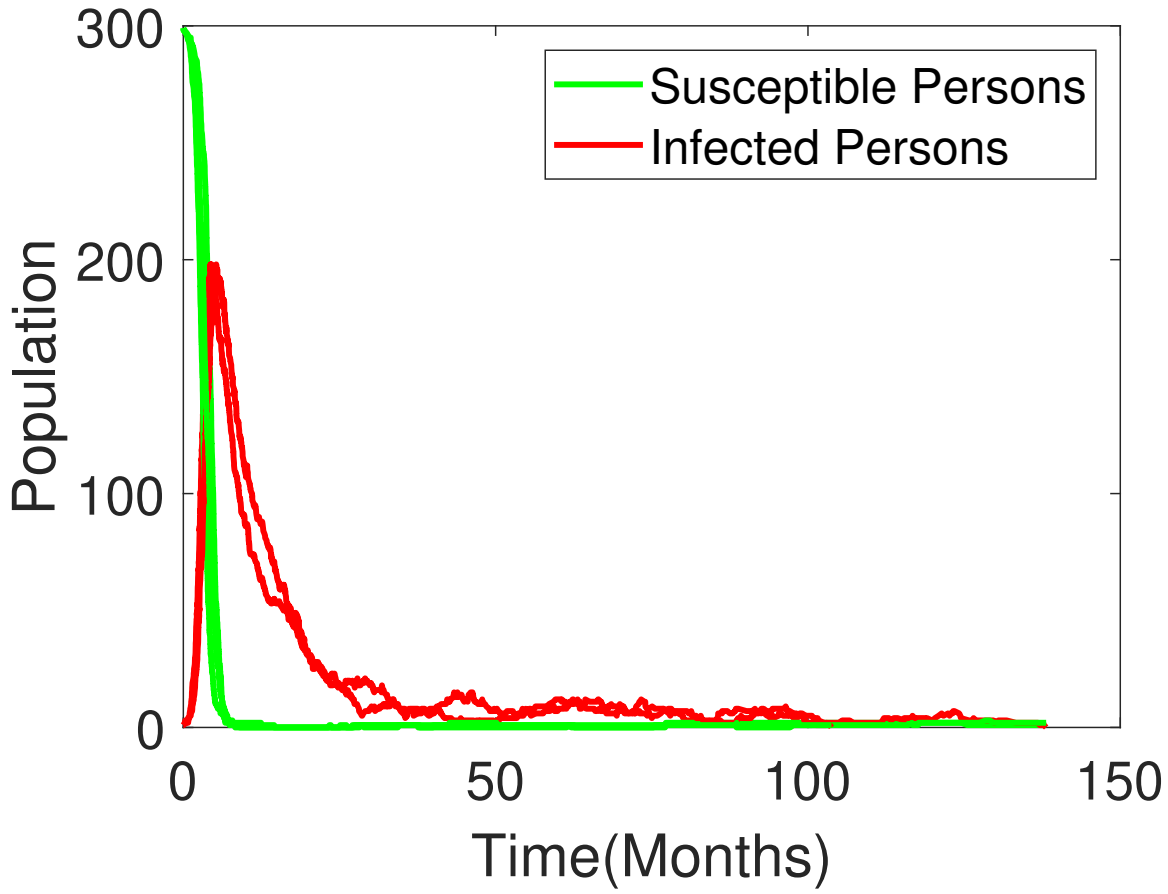

Figure 4.2: Stochastic Dynamics of Susceptible, Infected and Quarantined Persons Populations.

Chapter 5

CONCLUSIONS

The modelling theory in Statistics provides an adequate theoretical framework whenever we are faced with studying pandemics or epidemics. It allows us to understand the time evolution and behaviour of disease outbreaks. Consequently, we can come up with important predictions that are useful in managing diseases of interest. As observed by Din and Algehyne in [21] this includes determining how to effectively reduce rates of transmission, decreasing the probability of infection contact with infected persons and reducing the disease-death rate.

In this work we set out to show that the corona model of interest converges to a quasi-stationary distribution after a long time. We considered a model that analysed the susceptible and infected persons population. We also isolated the infected persons population which depicted a branching process

behavior. For both cases we showed that there is a convergence towards quasi-stationarity under certain behavior. For the former model we showed that if R_0 is less than one then the number of susceptible and infected persons will reduce to a certain point and fluctuate about it until it finally disappears. For the latter model we used R_0 to estimate the expected number of infections and proved that the number reduces to a certain point and depicts pseudo-stationarity before finally going extinct.

For future works, we intend to introduce the vaccinations compartment in the model. This is because according to [16] several vaccinations have been introduced and were reported to be non-endangering, easily assimilated and accepted by the body as well as able to trigger specific and necessary immune responses in participants. Therefore it is necessary to expand the model into a susceptible-vaccinated-infected and quarantined persons (SVIQ) model. The model in equation (5.1) below is improved by including the reduced probability of the supply. The supply is affected by the effectiveness of the vaccination. If the vaccination is effective then the number of susceptible persons decrease as people gain immunity hence becoming no longer endangered to infection.

$$\begin{aligned}
\frac{d}{dt}S(t) &= \Lambda(1-p) - \boldsymbol{\gamma} S(t)I(t) - d_0 S(t). \\
\frac{d}{dt}I(t) &= \boldsymbol{\gamma} S(t)I(t) - (d_0 + k + \eta)I(t) + \sigma Q(t). \\
\frac{d}{dt}Q(t) &= \eta I(t) - (d_0 + \mu + \sigma)Q(t).
\end{aligned} \tag{5.1}$$

We also plan to include stochastic differential equation models for better modelling and forecasts. This will offer a more competent platform for a prediction setup as they incorporate the random nature of this outbreaks better.

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APPENDIX

Sketch of the Proof for the Sufficient Condition

We want to sketch the proof of the direct implication: "Condition (2.2) and (2.3) $\implies$ Convergence", therefore we assume Z satisfies these conditions with $t_0 = 1$, the extension to any t_0 follows. So we define for all $0 \leq l \leq t \leq T$, the linear operator $K_{l,t}^T$ by,

$$K_{l,t}^T f(x) = \mathbb{E}_x(f(Z_t)|Z_l = x, t < \tau_\partial), \forall f \in \mathscr{B}(\mathscr{E})_b,$$

by the Markov property.

For any $T > 0$, the family $(K_{l,t}^T)_{0 \leq l \leq t \leq T}$ is a Markov (time-in-homogeneous) semi-group: we have, for all $0 \leq u \leq l \leq t \leq T$ and all $f \in \mathscr{B}(\mathscr{E})_b$,

$$K_{u,l}^T(K_{l,t}^T f)(x) = K_{u,t}^T f(x).$$

In essence this proof checks if the conservative semi-group satisfies a Doblin condition(See step 1): for all $T \geq 1$ and all $0 \leq t \leq T-1$, there exists a probability measure υ_{T-t} on E such that, for all measurable sets $A \subset E$ and all $x \in E$,

$$K_{t,t+1}^T(A) = \mathbb{P}_x(Z_1 \in A|T - t < \tau_\partial \geq c_1 c_2 \upsilon_{T-t}(A). \tag{5.2}$$

After proving this, we deduce (in a similar way to the classical time-uniform conservative case), a uniform mixing property for the conservative semi-groups K^T and then for the conditional distributions:

$$\|\mathbb{P}_{\mu_1}(Z_T \in \cdot | T < \tau_\partial) - \mathbb{P}_{\mu_2}(Z_T \in \cdot | T < \tau_\partial)\|_{TV} \leq 2(1 - c_1 c_2)^{\lfloor T \rfloor}, \ \forall \mu_1, \mu_2 \in \mathscr{M}. \tag{5.3}$$

This immediately implies that there is at most one quasi-stationary distribution and implies in particular that the sequence $\mathbb{P}_{\mu_1}(Z_T \in \cdot | T < \tau_\partial)_{T \geq 0}$ is a Cauchy sequence and hence that it converges to some probability υ_{QSD}(Recall that the set of probability measures endowed with the total variation norm is complete). By Meleard and Villemonais in [14], υ_{QSD} is a quasi-stationary distribution.

Step 1: Doblin condition

Let us show that, for all $t \geq 1$, there exists a probability measure v_t on E such that the Doblin Condition holds true.First one can check that condition (2.2) and Markov property imply that

$$\mathbb{P}_x(Z_1 \, and \, t < \tau_\partial) \geq c_1 v(\mathbf{1}_A(\cdot)\mathbb{P}_\cdot(T - 1 < \tau_\partial))\mathbb{P}_x(1 < \tau_\partial).$$

Dividing both sides by $\mathbb{P}_x(t < \tau)$, we deduce that

$$\mathbb{P}_x(Z_1 | t < \tau_\partial) \geq c_1 v(\mathbf{1}_A(\cdot)\mathbb{P}_\cdot(T - 1 < \tau_\partial)\frac{\mathbb{P}_x(1 < \tau_\partial)}{\mathbb{P}_x(t < \tau_\partial)}.$$

But, again using the Markov property ,we have,

$$\mathbb{P}_x(t < \tau_\partial) \leq \mathbb{P}_x(1 < \tau_\partial) \sup_{y \in E} \mathbb{P}_y(t-1 < \tau_\partial),$$

so that

$$\mathbb{P}_x(Z_1 \in E | \tau_\partial) \geq c_1 \frac{v(\mathbf{1}_A(\cdot)\mathbb{P}_\cdot(t-1 < \tau_\partial))}{\sup_{y \in E} \mathbb{P}_y(t-1 < \tau_\partial)}.$$

Now condition (2.3) implies that the non-negative measure

$$B \mapsto \frac{v(\mathbf{1}_A(\cdot)\mathbb{P}_\cdot(t-1 < \tau_\partial))}{\sup_{y \in E} \mathbb{P}_y(t-1 < \tau_\partial)},$$

has a total mass greater than c_2. Therefore the Doblin condition holds with the probability measure

$$v_t : B \mapsto \frac{v(\mathbf{1}_A(\cdot)\mathbb{P}_\cdot(t-1 < \tau_\partial))}{\mathbb{P}_v(t-1 < \tau_\partial)}.$$

Step 2: exponential contraction for the conditional distributions

Using the semi-group property of $(K^T_{l,t})_{l,t}$, we deduce that for any $x, y \in E$ and all $0 \leq t \leq T$,

$$\|\delta_x K^T_{0,t} - \delta_y R^T_{0,t}\|_{TV} \leq 2(1 - c_1 c_2)^{\lfloor t \rfloor}.$$

By definition of $K^T_{0,T}$, this inequality immediately implies that

$$\|\mathbb{P}_x(Z_t \in \cdot | T < \tau_\partial) - \mathbb{P}_y(X_t \in \cdot | T < \tau_\partial) \| \leq 2(1 - c_1 c_2)^{\lfloor T \rfloor}.$$

Since, in general,$\mathbb{P}_\mu(Z_T \in \cdot | t < T_\partial)$ is not linear in μ, it is not immediate that this equality extends to any pair of initial probability measures of μ_1, μ_2 on E.However, this is easily overcome by the following computations. Let μ_1 be a probability measure on E and $x \in E$. We have

$$\begin{aligned}
&\|\mathbb{P}_{\mu_1}(Z_T \in \cdot | T < \tau_\partial) - \mathbb{P}_x(Z_T \in T < \tau_\partial)\|_{TV} \\
&= \frac{1}{\mathbb{P}_{\mu_1}(T < \tau_\partial)} \|\mathbb{P}_{\mu_1}(Z_T \in \cdot) - \mathbb{P}_{\mu_1}(T < \tau_\partial)\mathbb{P}_x(Z_T \in \cdot | T < \tau_\partial)\|_{TV} \\
&\leq \frac{1}{\mathbb{P}_{\mu_1}(T < \tau_\partial)} \int_{y \in E} \|\mathbb{P}_y(Z_T \in \cdot) - \mathbb{P}_y(T < \tau_\partial)\mathbb{P}_x(Z_T \in \cdot | T < \tau_\partial)\|_{TV} d\mu_1(y) \\
&\leq \frac{1}{\mathbb{P}_{\mu_1}(T < \tau_\partial)} \int_{y \in E} \mathbb{P}_y(T < \tau_\partial) \|\mathbb{P}_y(Z_T \in \cdot | T < \tau_\partial) - \mathbb{P}_x(Z_T \in \cdot | T < \tau_\partial)\|_{TV} d\mu_1(y) \\
&\leq \frac{1}{\mathbb{P}_{\mu_1}(T < \tau_\partial)} \int_{y \in E} (T < \tau_\partial) 2(1 - c_1 c_2)^{\lfloor T \rfloor} d\mu_1(y) \\
&\leq 2(1 - c_1 c_2)^{\lfloor T \rfloor}.
\end{aligned}$$

The same computation, replacing δ_x by any probability measure, leads to (2.10). Using the fact that $\mathscr{M}_1(E)$ endowed with the total variation norm is a complete space, this easily leads to (2.4).

MATLAB CODE FOR SIMULATIONS

Code for the Deterministic Model

```
function dydt = siqfun(t,y,Lambda,gamma,d0,k,eta,sigma,mu,S_init,t_final)
%ODE45 equations for the SIQ model
dydt = zeros(3,1);
dydt(1) = Lambda-gamma*y(1)*y(2)-d0*y(1);
dydt(2) = gamma*y(1)*y(2)-(d0+k+eta)*y(2)+sigma*y(3);
dydt(3) = eta*y(2)-(d0+mu+sigma)*y(3);
```

```
%Here we make the deterministic run of the SIQ model odes from function
%siqfun
clear all
set(0,'DefaultAxesFontSize', 18);
set(gca,'fontsize',18);
Lambda=0.03805333333;
gamma=0.00594474;
d0=0.007121000000;
eta=0.144211141;
mu=0.007121000000;
sigma=0.0052281;
k=0.027864676;
N=1000;
S_init=3000;
t_final=60; % the time in days
tspan = [0 t_final];
y0 = [S_init 2 6];
[t,y] = ode45(@(t,y) siqfun(t,y,Lambda,gamma,d0,k,eta,sigma,mu,S_init,
    t_final), tspan, y0);
figure(1)
plot(t,y(:,1),'b-',t,y(:,2),'r-.'); grid on;
xlabel('Time'); ylabel('Persons Count');

hold on

plot(t,y(:,3),'g-'); grid on;
legend('Susceptibles','Infected persons','Quarantined Persons');
hold off
```

Code for the Stochastic Model

```
% SIQ Dynamic Model

% Three Sample Paths and the Deterministic Solution

clear

set(0,'DefaultAxesFontSize', 18);

set(gca,'fontsize',18);

Lambda=0.03805333333;

gamma=0.00594474;

d0=0.007121000000;

eta=0.144211141;

mu=0.007121000000;

sigma=0.0052281;

l=0.027864676;

N=300;%population

init=1;

time=150; % the time

sim=3;

 for k=1:sim

   clear t S I Q
```

```
t(1)=0;% the time at the beginning
 I(1)=init; %initial number of infected persons
 S(1)=N-init; %initial number of susceptible
    persons
 Q(1)=0; %initial number of quarantined persons
 j=1;
while I(j)>0 && t(j)<time
 a(j)=Lambda+gamma*S(j)*I(j)+d0*S(j)+(d0+l+eta)*I(
    j)+(d0+mu+sigma)*Q(j);
 a1(j)=Lambda/a(j);
 a2(j)=(Lambda+gamma*S(j)*I(j))/a(j);
 a3(j)=(Lambda+gamma*S(j)*I(j)+d0*S(j))/a(j);
 a4(j)=(Lambda+gamma*S(j)*I(j)+d0*S(j)+(d0+l)*I(j)
    )/a(j);
 a5(j)=(Lambda+gamma*S(j)*I(j)+d0*S(j)+(d0+l)*I(j)
    +eta*I(j))/a(j);
 a6(j)=(Lambda+gamma*S(j)*I(j)+d0*S(j)+(d0+l)*I(j)
    +eta*I(j)+sigma*Q(j))/a(j);
 a7(j)=(Lambda+gamma*S(j)*I(j)+d0*S(j)+(d0+l)*I(j)
    +eta*I(j)+sigma*Q(j)+(d0+mu)*Q(j))/a(j);
```

```
u1=rand; % uniform random number
u2=rand; % uniform random number
t(j+1)=t(j)-log(u1)./a(j);
 if u2 <= a1(j) % for Lambda prob. is btwn 0 and
    a1
 S(j+1)=S(j)+1;
 I(j+1)=I(j);
 Q(j+1)=Q(j);
 else if u2> a1(j) && u2 <= a2(j)% for the gamma*
    S(j)*I(j) probability
         S(j+1)=S(j)-1;
         I(j+1)=I(j)+1;
         Q(j+1)=Q(j)+1;
 else if u2> a2(j) && u2 <= a3(j) % for the d0*S(
    j) probability
          S(j+1)=S(j)-1;
          I(j+1)=I(j);
         Q(j+1)=Q(j);
 else if u2> a3(j) && u2 <= a4(j)% for the (d0+k)
    *I(j) probability
```

```
                S(j+1)=S(j);

                I(j+1)=I(j)-1;

                Q(j+1)=Q(j);
    else if u2> a4(j) && u2 <= a5(j) % for the eta*I
       (j) probability

                        S(j+1)=S(j);

                        I(j+1)=I(j)-1;

                        Q(j+1)=Q(j)+1;
    else if u2> a5(j) && u2 <= a6(j) % for the sigma
       *Q(j) probability

                        S(j+1)=S(j);

                        I(j+1)=I(j)+1;

                        Q(j+1)=Q(j)-1;
    else if u2> a6(j) && u2 <= a7(j) % for the (d0+
       mu)*Q(j) probability

                        S(j+1)=S(j);

                        I(j+1)=I(j);

                        Q(j+1)=Q(j)-1;
```

```
                        end
                    end
                end
            end
        end
    end
    j=j+1;
    a(j)=Lambda+gamma*S(j)*I(j)+d0*S(j)+(d0+k+eta)*I(
       j)+(d0+mu+sigma)*Q(j);
    a1(j)=Lambda/a(j);
    a2(j)=(Lambda+gamma*S(j)*I(j))/a(j);
    a3(j)=(Lambda+gamma*S(j)*I(j)+d0*S(j))/a(j);
    a4(j)=(Lambda+gamma*S(j)*I(j)+d0*S(j)+(d0+k)*I(j)
       )/a(j);
    a5(j)=(Lambda+gamma*S(j)*I(j)+d0*S(j)+(d0+k)*I(j)
       +eta*I(j))/a(j);
    a6(j)=(Lambda+gamma*S(j)*I(j)+d0*S(j)+(d0+k)*I(j)
       +eta*I(j)+sigma*Q(j))/a(j);
    a7(j)=(Lambda+gamma*S(j)*I(j)+d0*S(j)+(d0+k)*I(j)
       +eta*I(j)+sigma*Q(j)+(d0+mu)*Q(j))/a(j);
end
```

```
plot(t,I,'r-','LineWidth',2)

plot(t,S,'g-','LineWidth',2)

xlabel('Time'); ylabel('Population');

legend('Susceptible Persons','Infected Persons');

 hold on

 end
```