EPIDEMIOLOGICAL MODELS APPLIED TO VIRUSES IN COMPUTER NETWORK

BY

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THESIS

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To the memory of my beloved family, my wife Rita,
my children's Redi and Bereket.

ABSTRACT

The computer viruses is a serious problem to individual and corporative computer systems, a lot of effort has been dedicated to study how to avoid their deleterious actions, trying to create anti-virus programs acting as vaccines in personal computers or in strategic network nodes. Another way to combat virus propagation is to establish preventive policies based on the whole operation of a system that can be modeled with population models, similar to those that are used in epidemiological studies.

This paper introduced the SAI_1I_2R model based on the epidemiological study.

The equilibrium points (virus-free and endemic), stability, basic reproduction numbers (R_0), quantitative and qualitative analysis are calculated and some numerical experiments are shown.

This model enabled us to understand better the dynamics nature of computer virus and the epidemiological models bring new hope for solving the computer virus problems.

NOMENCLATURE

S (t) = non-infected computers.

A (t) = non-infected computers equipped with anti-virus.

I_1 (t) = partially infected computer.

I_2 (t) = fully infected a computer entirely infected

R (t) = a computer recovered from the virus.

b = new computers

$\sim R$ = recovering rate of removed computer

SI_1 = infection rate of susceptible computers

¢ SA = conversion of non infected computer into antidotal

d_1 = death due to natural

d_2 = death rates due to virus

d_3 = death due to natural as well as the virus

¨ AI_1 = conversion of partially infected computer into antidotal

μI_1 = rates of transmissions from class I_1 to I_2

$d_1 + d_2$ = death rates due to natural and the virus

¥ I_2 = rates of transmission from I_2 to R

T = Total numbers of computers

INDEX WORD

Computer Networks, Pplane, Rungeu-Kutta 4th order, epidemiological model and Computer Virus

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CHAPTER 1

INTRODUCTION

1.1 Background of study

There are several computational techniques that look to biology for inspiration. Some common examples include networks, evolutionary algorithms, and immunological computation [1]. Many researchers have taken help of the biological system to understand the behavior of spread of malicious objects in a computer network and how to immune the computer system [2, 3, 4, 5, 6, 7, 9, 10, 12, 16, 17, 18, 19]. Based on the *Kermack and McKendrick*[1] SIR classical epidemic model [8,11,15], dynamical models for malicious objects propagation were proposed, providing estimations for temporal evolutions of infected nodes depending on network parameters considering topological aspects of the network [4, 5, 6, 13, 14, 18, 22] Mathematical modeling is an essential tool in studying a diverse range of such diseases to gain a better understanding of transmission mechanisms, and make predictions; determine and evaluate control strategies. Many authors have proposed various kinds of epidemic models to understand the mechanism of disease transmission. The basic elements for the description of infectious diseases have been considered by three epidemiological classes: S (t) that measures the susceptible portion of population, I (t) the infected, and R (t) the removed ones. Transmission of a disease is a dynamical process driven by the interaction between susceptible and infective. The model proposed in this paper is a modification of the original compartmental SIR model [21], including an antidotal compartment (A) representing nodes of the network equipped with fully effective anti-virus programs [20, 33].

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[1] Kermack and McKendrick described the simplest SIR model which computes the theoretical number of people infected with a contagious illness in a closed population over time.

Connections between the compartments represent operational parameters of the network (see Fig. 3).

1.2 The Scope of Study

The scopes of study are

- ✓ The computer virus study in windows operating system.
- ✓ The virus affects the computer not the files.
- ✓ The computer virus refers to as whole without the intention to tell the differences among them.

1.3 Objective

General objective

Analyze the computer virus using epidemiological models.

Specific objective

- To study the similarities between human and computer virus.
- To study the qualitative analysis of computer virus.

1.4 Thesis Outline

- ✓ In Chapter 1, the relation between Computer and Human virus , overview of computer virus, types of computer virus, how computer virus are spread, life-cycle of computer virus and Ant-virus discuses.
- ✓ In Chapter 2 to evaluate the literature that is relevant to the topic. Literature review includes types of epidemiology and basic SIR epidemiology model.
- ✓ In Chapter 3, in this chapter the formulation of the model, compartments analysis and assumption of a model will be presented.
- ✓ In Chapter 4, Qualitative analyses of equilibrium points and reproduction number model will be discussed.

- ✓ In Chapter 5, goes on to apply the model described in Chapter 4 numerical experiments and discussed the limitation of study.
- ✓ Finally looks in Chapter 6, at the conclusion one can make based on the analysis in Chapter 5, and details the directions that further research could take.

1.5 The relation between Human and Computer virus

1.5.1 Difference between computer and Human virus[24]

Biological Viruses (or Human Viruses) are Nanotechnology by Nature while computer viruses are infectious agent by made by humans. Most often the people think Biological viruses and Computer viruses as a same entity, although both cause infection and damage to their host (or target) and some of their features & characteristics are same but they are quite different from each other. Following table show some interesting main difference between Biological Virus and Computer Viruses.

Table 1 Difference between computer and Human virus

No	Difference	Human virus	Computer virus
1	Living and non-living	Are living (at least to some extent) biological entity who can reproduce itself	Are non – living at all they are manmade programmed code to perform specific functions
2	Components	Contain genetic material (in the form of RNA or DNA), covered by a Capsid[2] and sometime by a lipid Envelop[3]	Is not more than a few lines of code. It contains a script or code of programming language written in C, C^{++} or other assembly languages.

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[2] A capsid is the protein shell of a virus.

[3] The envelopes are typically derived from portions of the host cell membranes but include some viral glycoproteins.

3	Mechanism of action	Infect their host after they enter the host body and reach inside the cell where the virus uses the host genetic material (DNA or RNA) to replicate and expend their population.	Similarly infect computers when they enter and reach the registry (or the specific components/area for which they are programmed) where they cause the damage.
4	Host	Can infect all form of life including Human, Animals, Plants, Insects, Bacteria, Protozoa, Fungi, and other viruses	They are programmed, thus made impact on programs (software's), infect PCs, Servers, websites and software.
5	Usability	Some viruses have useful effects for the host	useful viruses do not exist

1.5.2 Similarities of Computer and Human virus[34]

Clearly defined the difference between a human virus and computer virus in above table the following table shows the similarities between Computer and Human virus.

Table 2 Similarities of Computer and Human virus

No	Human virus	Computer virus
1	Integrate in DNA	Attach to .exe or .com files
2	Spread to other hosts	Spread to other computers.
3	Infection of new host species	Infects new computers software
4	Can be treated to some extent with Antiviral drugs of Antivirus	Can be detect and remove with the help
5	Detected by virus signature	Detected by virus signature

6	Mutating the virus	Mutating the virus
7	Polymorphic virus	Polymorphic[4] virus
8	Immune system is costly for the organism	Anti-Virus software comes at price

1.6 Overview of computer viruses

1.6.1 History of computer virus

There are different types and kinds of computer viruses. However, there is much software released every day to detect and avoid these viruses. Although the wild spread of new and strong viruses, it still infects and spread only with user's permission.

There are endless arguments about the "first" virus. There were a number of malware attacks in the 1970s and some count these among the virus attacks. The description of the malware, however, would indicate these were worms and not viruses by general definition. Just to be complete, however, the questionable entries from the 1970s are included here with that Computer Knowledge considers virus history to start in 1981. And in year 1995 to 2000 the total number of computer virus are created. And in 2001 to 2010 them are increases up to 1221 number of newly create computer virus. The new computer virus are created from year 2005 to year 2010 are shown in table 3. [23]

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[4] The occurrence of more than one form

Table 3 Computer virus created from year 2005 to year 2010

Year	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec	Total
2004-2005	9	24	61	31	69	68	19	44	55	14	21	21	436
2005-2006	42	32	15	11	12	22	36	29	7	52	12	32	302
2006-2007	8	41	6	9	35	20	31	23	36	31	8	19	267
2007-2008	70	36	50	39	112	42	97	88	40	84	95	29	782
2008-2009	162	130	63	62	316	143	245	152	197	148	74	57	1749
2009-2010	79	140	116	67	107	128	110	97	64	77	179	57	1221

From 2010 up-to-date the computer viruses are spread widely and dynamically and more complex.

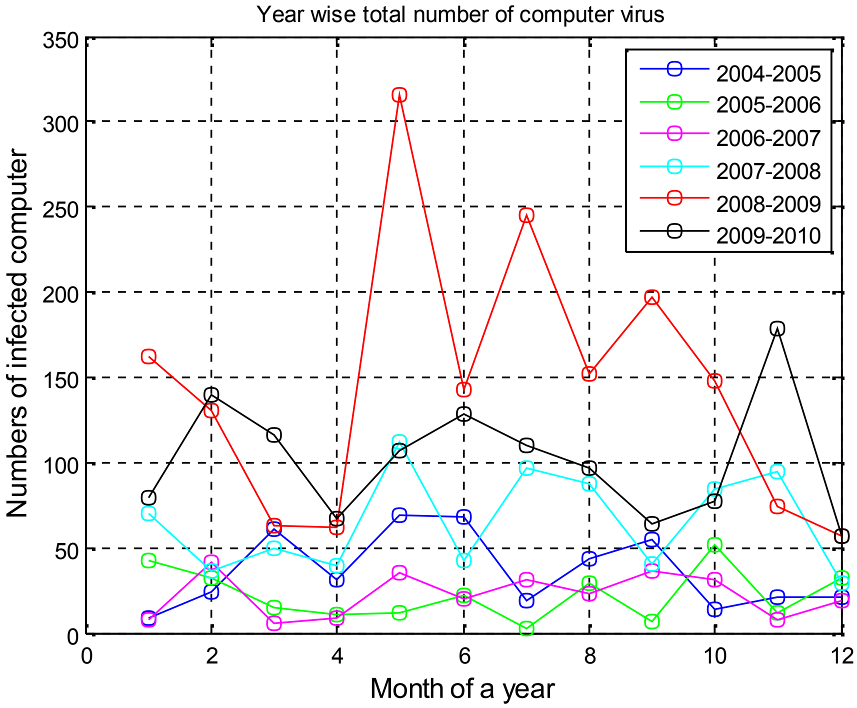

Fig. 1 Year wise total number of computer virus

Figure 1 shows that the computer virus is created much more and more in year's 2005 up to 2010.

1.6.2 What is a Computer Virus[5]?

Cohen [52] defines a computer ‘viruses ‘as a program that can infect other programs by modifying them to include a possibly evolved copy of it. A computer virus is designed to damage or disrupt the normal function of our computers, without the permission or knowledge of the user.

A computer virus must meet two criteria:

- It must execute itself. It will often place its own code in the path of execution of another program.
- It must replicate itself. For example, it may replace other executable files with a copy of the virus infected file. Viruses can infect desktop computers and network servers.

Some viruses are programmed to damage the computer by damaging programs, deleting files, or reformatting the hard disk. Others are not designed to do any damage, but simply to replicate themselves and make their presence known by presenting text, video, and audio messages. Even these benign viruses can create problems for the computer user. They typically take up computer memory used by legitimate programs. As a result, they often cause erratic behavior and can result in system crashes. In addition, many viruses are bug-ridden[6], and these bugs may lead to system crashes and data loss.

1.6.3 Types of computer viruses

Just like human viruses, computer viruses come in many forms and can affect your machine in different ways. They all operate differently and affect our computers and the information contained on them in different way. There are five recognized types of viruses:

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[5] There are several terms related to computer virus discussed in page 10, In this paper, the term “virus” is used to refer to them as whole without the intention to tell the differences among them.

[6] Infected

1.6.3.1 Boot sector viruses

Boot sector viruses infect the system area of a disk-that is, the boot record on floppy disks and hard disks. All floppy disks and hard disks (including disks containing only data) contain a small program in the boot record that is run when the computer starts up. Boot sector viruses attach themselves to this part of the disk and activate when the user attempts to start up from the infected disk. These viruses are always memory resident in nature. Most were written for DOS, but, all PCs, regardless of the operating system, are potential targets of this type of virus. All that is required to become infected is to attempt to start up your computer with an infected floppy disk thereafter, while the virus remains in memory, all floppy disks that are not write protected will become infected when the floppy disk is accessed.

1.6.3.2 Master boot record viruses

Master boot record viruses are memory resident viruses that infect disks in the same manner as boot sector viruses. The difference between these two virus types is where the viral code[7] is located. Master boot record infectors normally save a legitimate copy of the master boot record in an different location. Windows NT computers[8] that become infected by either boot sector viruses or master boot sector viruses will not boot. This is due to the difference in how the operating system accesses its boot information, as compared to Windows 95/98. If your Windows NT systems are formatted with FAT[9] partitions you can usually remove the virus by booting to DOS and using antivirus software. If the

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[7] A computer virus is a type of malicious software program ("malware") that, when executed, replicates itself by modifying other computer programs and inserting its own code. Infected computer programs can include, as well, data files, or the "boot" sector of the hard drive.

[8] Windows NT is a family of operating systems produced by Microsoft

[9] File Allocation Table

boot partition is NTFS[10], the system must be recovered by using the three Windows NT Setup disks

1.6.3.3 Multipartite viruses

Multipartite (also known as polypartite) viruses infect boot records and program files. If the boot area is cleaned, but the files are not, the boot area will be re-infected. The same holds true for cleaning infected files. If the virus is not removed from the boot area, any files that you have cleaned will be re-infected.

1.6.3.4 Macro viruses

These types of viruses infect data files. With the advent of Visual Basic in Microsoft's Office 97, a macro virus can be written that not only infects data files, but also can infect other files as well. Macro viruses infect Microsoft Office Word, Excel, PowerPoint and Access files. Newer strains are now turning up in other programs as well. All of these viruses use another program's internal programming language, which was created to allow users to automate certain tasks within that program. Because of the ease with which these viruses can be created, there are now thousands of them in circulation.

All viruses are operating in different ways and also affect our computers and the information contained on them in different ways. From the Table [Table: 4 Types of Computer Virus] gives further more information about it and also tell about, what it does, how a particular computer virus are affected with some example of commuter virus.

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[10] New Technology File System

Table 4: Types of computer viruses

Virus type	What It Does	How Affects Our PC	Example Of Virus
Resident Viruses	To live as a resident in the RAM memory	it interrupt all of the operations executed by the system	Randex,CMJ, Meve, and MrKlunky
Program or File Virus	Infects executables such as EXE, BIN, COM, SYS)	Destroys or alters Programs and data.	Sunday and Cascade
Boot sector Virus	Infects boot sectors on hard and floppy disks	Destroys or alters Programs and data	Disk Killer, Stone virus
Multipartite Virus	A hybrid of a program and boot sector virus	Destroys or alters Programs and data.	Invader, Flip, and Tequila
Macro Virus	Triggers on a command in Microsoft Office	Commonly affects Word & Excel	DMV, Nuclear, Word Concept
Stealth Virus	Uses various tactics to void detection.	Destroys or alters Programs and data	Frodo, Joshi, Whale
Polymorphic Virus	Uses encryption to foil detection, so that it appears differently in each infection.	Destroys or alters Programs and data.	Involuntary, Stimulate, Cascade, Phoenix, Evil, Proud, Virus 101

Email Virus	If the recipient opens the mail attachment, the word macro is activated then	spread only with the opening of the attachment in the mail	Melissa, ILOVEYOU, Love Bug
Spyware	It makes unnecessary alterations to your PC & changes your experience of it.	a computer system is causing it to slow down	7FaSSt, Elf Bowling
Trojan Horses	Programs that do things that are not described in their specifications	It allows other Computer users to take control of your PC over the internet	A2KM. Nitrogen , 91Cast, 8sec!Trojan
Worms	negative effects on your system, they are detected and eliminated by antivirus	It replicate themselves as standalone programs	Lovgate.F, Trile.C, Sobig.D, Mapson.
Directory Virus	It inserts a malicious code into a cluster and marks it as allocated in the FAT.	It prevents FAT Allocation from being allocated in the future	Spam Laws, DIR II virus

1.7. How computer viruses are spread?

Computer viruses are transmitted from computer to computer through the use of many techniques, both online and offline. There are numerous ways that computer viruses are spread from one computer to another. And a great deal of computer users lacks a clear understanding of how computer viruses are spread.

1.7.1 Email Attachments

Most computer users became familiar with the high occurrences of email attachments carrying viruses many years ago. Back in the early days of Microsoft Outlook Express, the email client would automatically open email attachments, with little user input. Now the email clients don't automatically open accompanying attachments and the mail preview option can be disabled. And since those changes were put into place, computer viruses spreading through email messages have decreased. They definitely haven't stopped, but they have decreased. Today users still receive infected attachments with messages, but most of the time they make a mistake and open the attachments because the message was supposedly sent from someone that they know and with a title that got them curious about what the attachment contained.

1.7.2 Computer Networks.

If your computer is connected to a home network or its part of a workgroup or domain, your computer could acquire a virus without you being at fault. Another person in your home or office employee at your job could unknowing download an infected file and then quickly spread it throughout your entire home or office network in a very short time, causing slowdowns, data corruption and possibly data loss. You should always have a reputable anti-virus installed and updated on any computer that you use. And if your computer is on an office network that is administered by professional Information Technology staff, you're probably covered. But keep in mind that no anti-virus utility can stop every computer virus. They might slow them down a bit, depending on the trojan or virus, but they still can't stop them all. And in a great deal of the situations that we come across out in the field, the installed anti-virus can't even manage to remove the infection once it's taken hold of a computer that was protected with the anti-virus utility to start with.

1.7.3 Infected Computer Software

There are countless games, productivity software packages, web browser add-ons, high definition video and high quality audio files available online for download. And a great deal of those is free. Unfortunately even though they may claim to be free, they may have strings attached. Many of those free programs include malicious files that were intentionally added to help pay for the work that was put into creating those applications and games. While other online software files are infected with trojans without the software creator's consent or approval. The best practice used to be to only download software from trusted sources but now many of the original trusted sources can no longer be trusted, because they're offering files for download that contain malicious files. One of the best practices to use when downloading files online is to carefully read the software use agreements. If they mention anything about containing advertising software that will monitor your online activities and then display advertisements based on those activities, then the software should be avoided.

1.7.4 Fake Programs/Trojans

Rogue[11] programs and security utilities are one of the most frequent ways that online users acquire computer viruses today. It's very irritating to download a program that you think will help keep your computer data safe, when in fact the fake anti-virus software that you download and install is actually exactly what

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[11] Fake anti-virus

you're trying to protect yourself against. You may come across rogue software advertisements on malicious websites and also on legitimate websites that participate in compromised ad networks. Unfortunately even some of the best and secure websites advertise rogue software programs displayed over ad networks. In most cases the advertisements are taken down quickly by the site administrators, if it's a legitimate site, while the flat out malicious websites may run the rogue advertisements continuously around the clock. And depending on the traffic that the websites receives during the time that the malicious software advertisements are being displayed, large amounts of site visitors may be infected. Depending on the exploits being utilized by the fake anti-virus utility advertisements, many of the visitors to those sites may acquire an infection even though they never actually clicked on the malicious advertisements, because the viruses were installed through the use of drive-by installation techniques.

1.7.4.5 Infected Websites/ Fake

Unsuspecting online users may become infected with computer viruses, trojans and also ransom ware from intentionally malicious websites and also websites that have been compromised. Depending on the currently installed operating system and also the installed software on a website visitor’s system, drive-by installations of malicious software can easily occur. While visiting a malicious website, without warning malicious programs can be installed on visitor’s computers without their consent or input. Microsoft Windows systems are the primary target of this type of attack. Other popular applications may also be the target of an attack, such as Sun Micro system’s Java, Microsoft Internet Explorer web browsers, the Adobe Reader and many other applications.

The best defense for this type of attack is to:

- Keep your operating system updated.
- Keep your applications updated with the latest updates.
- Install reputable Anti-virus, keep it updated and also perform weekly full system scans.
- Install a strong firewall with Windows process control to prevent malicious software from taking hold of your system. The built-in Windows firewall isn't enough to keep your system secure.
- Never click on security related advertisements, prompts for web browser updates, or prompts for the installation of video players needed to view online content. Only download your software from known sources. And always choose the "Custom Installation" options of applications so you can avoid the unwanted adware and other junk ware that may be included with free downloadable programs.

1.7.6 USB Flash Drives and Other External device

Sharing and transferring files on flash drives is a very common practice today. The little devices hold a lot of data, they're small, and also easy to transport. But unfortunately those external drives can easily be compromised and loaded with malicious files that will infect computers that the drives are connected to. Because of that vulnerability, Microsoft issued software patches that disabled the auto play feature of Windows Xp, Windows Vista, etc.

- Another area of concern involving malicious external devices involves smart phone chargers. Earlier this year three researchers at the Georgia Institute of Technology demonstrated how easily smart phones running the latest version of Apple IOS could be compromised by a malicious charger that installed malware on the smart phones in a matter of seconds once they were connected to the devices.

- Keep in mind that smart phones are just tablet personal computers that we can make telephone calls on. They're just as vulnerable to computer viruses as your desktop computer. New forms of malware are being discovered daily that compromise smart phones. So for additional protection, install a reputable mobile anti-virus program on your smart phone to help protect your device from external threats such as malicious programs and text messages.

1.8 Problems of computer virus

Many common computer problems are easy to fix but hard to diagnose. Once you figure out what is wrong with the computer, a solution is easy to find. Most of the time, it will either be a problem of viruses, malware, spyware or a computer running slow. [35]

There are some common problems occur due to the virus attacks which are given bellow.

- Computer speed or performance has slowed.
- The application on the computer does not work properly.
- You see unusual error messages.
- There is a double extension on an attachment files.
- New icons appear on the desktop that any one did not put there, or the icons are not associated with any recently installed programs.
- A program disappears from the computer even though you did not intentionally remove the program.

N.B: These are common signs of infection. However, these signs may also be caused by hardware or software problems that have nothing to do with a computer virus. Unless you run the Microsoft Malicious Software Removal Tool, and then you install industry-standard, up-to-date antivirus software on your computer, you cannot be certain whether a computer is infected with a computer virus or not. [30]

1.9 What is not a computer virus?

Because of the publicity that viruses have received, it is easy to blame any computer problem on a virus. The following are not likely to be caused by a virus or other malicious code:

- Hardware problems. There are no viruses that can physically damage computer hardware, such as chips, boards, and monitors.
- The computer beeps at startup with no screen display. This is usually caused by a hardware problem during the boot process. Consult your computer documentation for the meaning of the beep codes.
- You have two antivirus programs installed and one of them reports a virus. While this could be a virus, it can also be caused by one antivirus program detect the other program's signatures in memory.
- You are using Microsoft Word and Word warns you that a document contains a macro. This does not mean that the macro is a virus.
- You are not able to open a particular document. This is not necessarily an indication of a virus. Try opening another document or a backup of the document in question. If other documents open correctly, the document may be damaged.

- The label on a hard drive has changed. Every disk is allowed to have a label. You can assign a label to a disk by using the DOS Label command of from within Windows.

1.10 Life-cycle of computer virus

Computer viruses have a life cycle[12] that starts when they're created and ends when they're completely eradicated. The following figure describes life cycle of computer virus.[31]

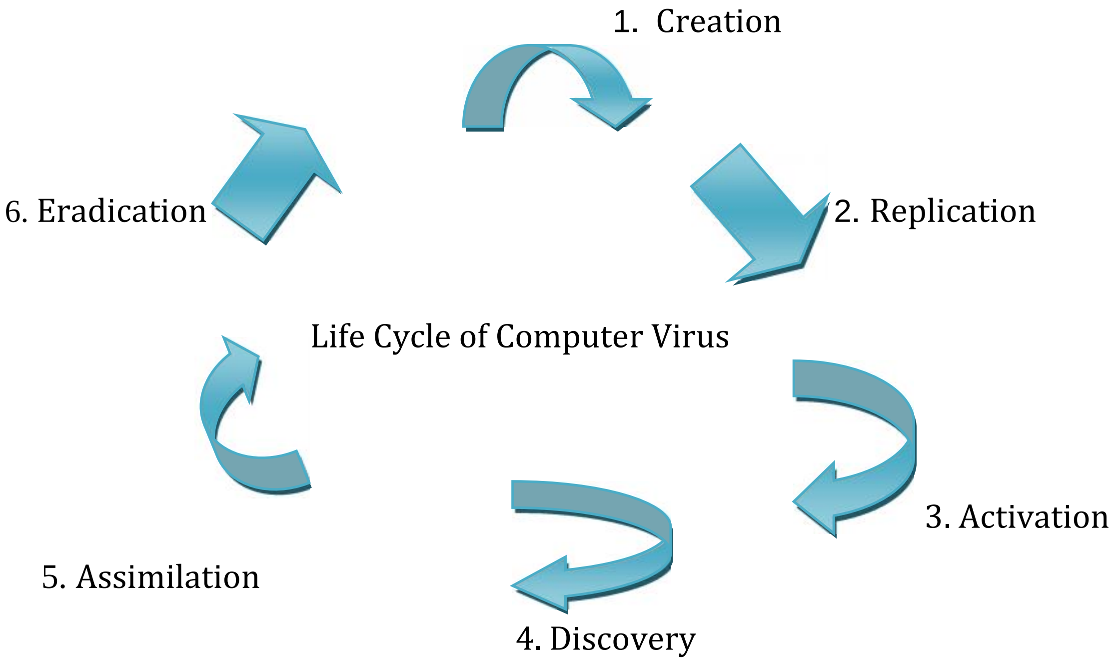

Fig. 2 Life Cycle of Computer Virus

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[12] Which refers to the stages of development of a computer virus

Stage 1 Creation

The Computer viruses are created by misguided individuals who wish to cause wide spread, random damage to computers.

Stage 2 Replication

Computer Viruses replicate by nature means it copies itself from one computer to anther computer.

Stage 3 Activation

Viruses that have damage routines will activate when certain Conditions are met. Viruses without damage routines don't activate, instead causing damage by stealing storage space.

Stage 4 Discoveries

This phase doesn't always come after activation, but it usually does discovery normally takes place at least a year before the virus might have become a threat to the computing community.

Stage 5 Assimilation

At this point, antivirus developers modify their software so that it can detect the new virus. This can take anywhere from one day to six months, depending on the developer and the virus type.

Stage 6 Eradication:

If enough users install up-to-date virus protection software, any virus can be wiped out. So far no viruses have disappeared completely, but some have long ceased to be a major threat. [31]

1.11 What is Anti-Virus?

Antivirus or anti-virus software (often abbreviated as AV), sometimes known as anti-malware software, is computer software used to prevent, detect and remove malicious software.[32] Anti-virus is a software program or set of programs that are designed to prevent, search for, detect, and remove software viruses, and other malicious software like worms, Trajan, adware, and more. These tools are critical for users to have installed and up-to-date because a computer without anti-virus software installed will be infected within minutes of connecting to the internet. There are several different companies that build and offer anti-virus software and what each offers can vary but all perform some basic functions:

- ✓ Scan specific files or directories for any malware or known malicious patterns.
- ✓ Allow you to schedule scan to automatically run for you.
- ✓ Allow you to initiate a scan of a specific file or of your computer, or of a CD or flash drive at any time.
- ✓ Always be sure you have the best, up-to-date security software installed to protect your computers, laptops, tablets and smart phones.

1.12 Conclusion

A computer virus is software intentionally written to copy itself without the computer owner's permission and then perform some other action on any system where it resides. Now a days, viruses are being written for almost every computing platform Anti-virus protection is, or should be, an integral part of any Information Systems operation, be it personal or professional. There are number of computer virus created and these computer viruses are affected in day today life. These viruses erase important data. Before finding the solution against the computer virus people must know the basic thing of computer virus like which are the type of computer virus are created now a days, working of computer virus, problem occurs from computer virus.

CHAPTER 2

LITERATURE REVIEW

Picking the right model for the job is a trade- off between simplicity, accuracy and generality. An inaccurate model is no good to anyone; we need a model that approximates what's going on in the real world. A complex model might be more accurate (in general), but it may be too complex to understand or parameterize. Finally, we need a model that is general enough that it can be adapted to suit our purposes. There are several computational techniques that look to biology for inspiration. Some common examples include networks, evolutionary algorithms, and immunological computation [1]. Many researchers have taken help of the biological system to understand the behavior of spread of malicious objects in a computer network and how to immune the computer system [2, 3, 4, 5, 6, 7, 9, 10, 12, 16, 17, 18, 19]. The action of malicious objects throughout a network can be studied by using epidemiological models for disease propagation [5, 6, 10, 12, 16, 18, 36]. Based on the *Kermack and McKendrick* SIR classical epidemic model [8, 11,15], dynamical models for malicious objects propagation were proposed, providing estimations for temporal evolutions of infected nodes depending on network parameters considering topological aspects of the network [4, 5, 6, 14, 18, 22, 37,].

This chapters' review the traditional of SIR model witch written different scholars because the kind of approach was applied to computer virus

2.1 Definition of Epidemiology

An epidemic[13] is the rapid spread of infectious disease to a large number of people in a given population within a short period of time, usually two weeks or less.

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[13] comes from two Greek word means epi "upon or above" and demos "people"

Epidemiology is the branch of medicine that deals with the incidence, distribution, and possible control of diseases and other factors relating to health.

2.2 Why Study Epidemic Models?

- ✓ To supplement statistical extrapolation.
- ✓ To learn more about the qualitative dynamics of a disease.
- ✓ To test hypotheses about, for example, prevention strategies, disease transmission, significant characteristics, etc.

2.3 What is a Mathematical Model?

Mathematical Model is a mathematical description of a scenario which improves understanding of the real-world. Mathematical models are used in the natural sciences (such as physics, biology, Earth science, meteorology) and engineering disciplines (such as computer science, artificial intelligence), as well as in the social sciences (such as economics psychology, sociology, political science). Physicists, engineers, statisticians, operations research analysts, and economists use mathematical models most extensively.

A model may help to explain a system and to study the effects of different components, and to make predictions about behavior.

2.4 Why do we use Epidemiological Modeling?

Many researchers have taken help of the biological system to understand the behavior of spread of malicious objects in a computer network and how to immune the computer system [26, 27, 28, 29, 38, 39, 40, 41, 42, 44, 48, 47, 50]. The action of malicious objects throughout a network can be studied by using epidemiological models for disease propagation [39, 40, 42, 44, 47, 48, and 53]. Based on the Kermack and McKendrick SIR classical epidemic model [43, 46, 54], dynamical models for malicious objects propagation were proposed, providing estimations for temporal evolutions of infected nodes depending on network parameters considering topological aspects of the network [38, 39, 42, 44, 45, 49, 55]. The kind of approach was applied to computer virus and modification of SIR models generated guides for infection prevention by using the concept of epidemiological threshold [39, 42, 44, 51].

The use of Epidemiology model is

- ✓ An Epidemiological model uses a microscopic description (The role of an infection individual) to predict the macroscopic behavior of disease spread through a population.
- ✓ An Epidemiological model is useful in comparing the effects of prevention or control procedures.

2.5 Types of Epidemic Model

✓ **Stochastic:** - its means being or having a random variable. This model depends on the chance variation in risk of exposure, disease and other illness dynamics.

✓ **Deterministic:** - when dealing with large populations, as in the case of tuberculosis, deterministic or compartment mathematical models are used. The transition rates from one class to another are mathematically expressed as derivatives, hence the model is formulated using differential equations. While building such model, it must be assumed that the population size in a compartment is differentiable with respect to time and that the epidemic process is deterministic.

2.6 Basic epidemiology model

The first mathematical model that could be used to describe an influenza epidemic was developed early in the 20th century by Kermack and McKendrick[14]. This model is known as the Susceptible-Infectious-Recovered (SIR) model. All ODE models of disease transmission are continuous-time compartment-level models.

The basic elements for the description of infectious diseases have been considered by three epidemiological classes:

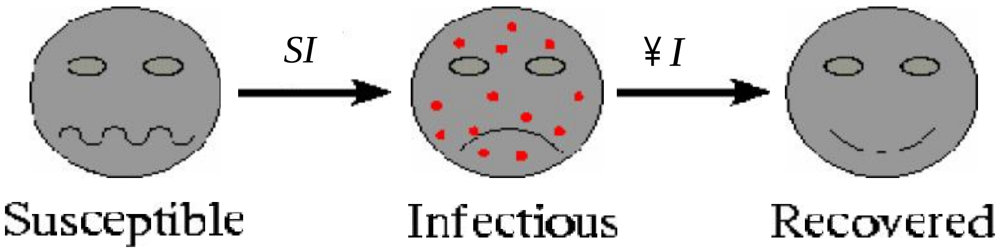

Fig. 3 Basic epidemiology model of SIR model

$$\frac{dS}{dt} = - \quad SI ---------- eq(1)$$

$$\frac{dI}{dt} = \quad SI - \text{¥} I --------- eq(2)$$

$$\frac{dR}{dt} = \text{¥} I ----------- eq(3)$$

A Susceptible-Infectious-Recovered (SIR) model is an epidemiological model that computes the theoretical number of people infected with a contagious illness in a closed population over time.

The basic elements for the description of infectious diseases have been considered by three epidemiological classes:

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[14] Kermack and McKendrick described the simplest SIR model which computes the theoretical number of people infected with a contagious illness in a closed population over time.

S(t): is used to represent the number of individuals not yet infected with the disease at time t, or those susceptible to the disease.

I(t): denotes the number of individuals who have been infected with the disease and are capable of spreading the disease to those in the susceptible category.

R(t): is the compartment used for those individuals who have been infected and then removed from the disease, either due to immunization or due to death.

Next chapter, focus on SAI_1I_2R model on computer virus which modify from the basic epidemiology model of SIR.

CHAPTER 3

METHODOLOGY

3.1 FORMULATION OF THE MODEL

The role of mathematical epidemiology is to model the establishment and spread of pathogens[15]. A predominant method of doing so is to use the notion of abstracting the population into compartments under certain assumptions, which represent their health status with respect to the pathogen in the system. One of the cornerstone works to achieve success in this method was done by Kermack and McKendrick[16] in the early 1900s. [45]

In a computer network to derive the model equation, the total number of nodes (N) is divided into five classes.

A. Susceptible nodes (S) non-infected computers.
B. Antidote node (A):- non-infected computers equipped with anti-virus.
C. Infectious nodes (I1):- partially infected computer.
D. Fully Infectious nodes (I2) :- a computer entirely infected
E. Recovered nodes (R):- a computer recovered from the virus.

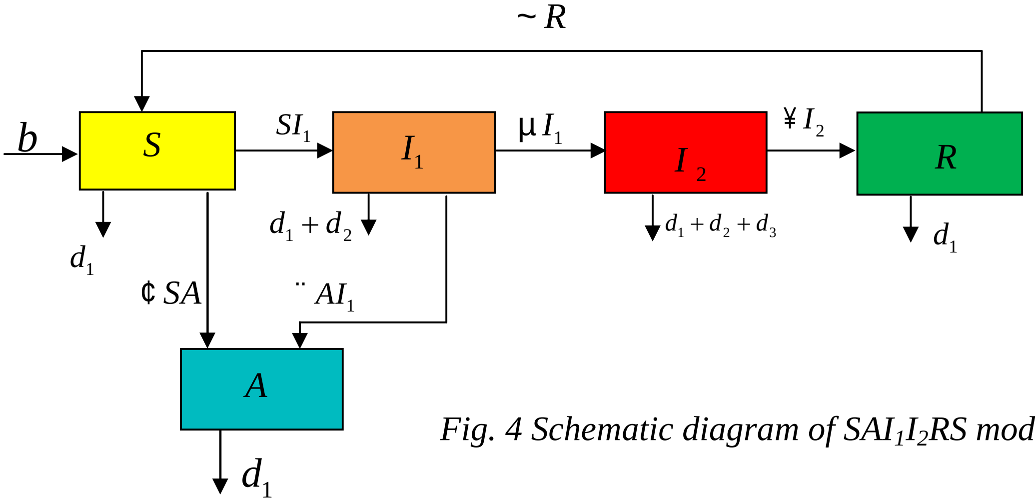

Fig. 4 Schematic diagram of SAI_1I_2RS model

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[15] Any disease-producing agent, especially a virus, bacterium, or other microorganism.

[16] Kermack and McKendrick described the simplest SIR model which computes the theoretical number of people infected with a contagious illness in a closed population over time.

3.2 Compartment Analysis

The method of compartment analysis translates the diagram into a system of linear differential equations and to show how to drive each equation from different compartments.

A compartment diagram consists of the following components.

Variable Names Each compartment is labeled with a variable

Arrows Each arrow is labeled with a inflow and outflow rate in parameter.

Input Rate an arrowhead pointing at compartment input rate.

Output Rate an arrowhead pointing away from compartment output rate.

The following diagram is a succinct way to summarize and document the various rates individually.

3.2.1 Susceptible compartment

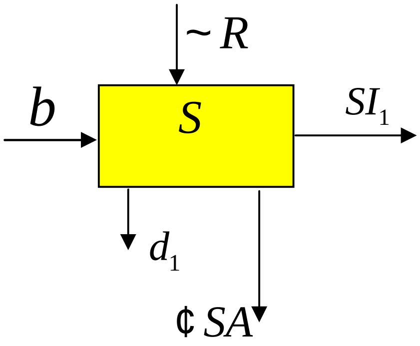

Fig. 5 Schematic diagram of susceptible class

b = new computers

$\sim R$ = recovering rate of removed computer

SI_1 = infection rate of susceptible computers

¢ SA = conversion of non infected computer into antidotal

d_1 = death due to natural

From Figure 5 we get the 1st ODE

$$\frac{dS}{dt} = b + \sim R - \quad SI_1 - \text{¢}\, SA - d_1 S \quad --------- eq(1)$$

3.2.2 Antidote compartment

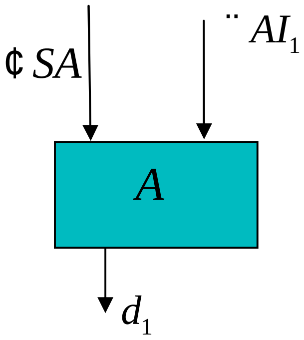

Fig. 6 Schematic diagram of Antidote class

$\text{¢}\, SA$ = conversion of non infected computer into antidotal
$\ddot{}\, AI_1$ = conversion of partially infected computer into antidotal
d_1 = death due to natural

From Figure 6 we get the 2nd ODE

$$\frac{dA}{dt} = \text{¢}\, SA + \ddot{}\, AI_1 - d_1 A \quad --------------- eq(2)$$

3.2.3 Partially infected nodes I$_1$ compartment

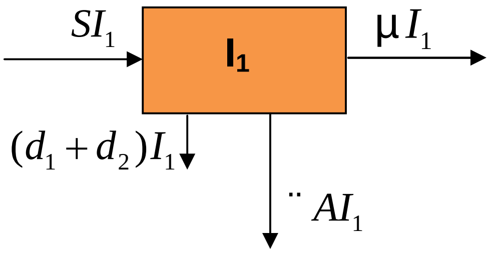

Fig. 7 Schematic diagram of partially infected class

SI_1 = infection rate of susceptible computers
$¨AI_1$ = conversion of partially Infected computer into antidotal
$μI_1$ = rates of transmissions from class I$_1$ to I$_2$
$(d_1+d_2)I_1$ = death rates due to natural and the virus

From Figure 7 we get the 3rd ODE

$$\boxed{\frac{dI_1}{dt} = (S - ¨A - μ - d_1 - d_2)I_1 ---------------eq(3)}$$

3.2.4 Fully infected nodes I$_2$ compartment

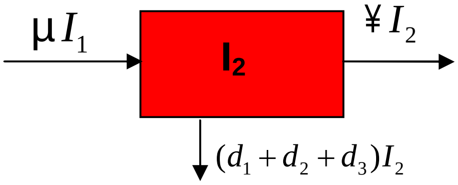

Fig. 8 Schematic diagram of fully infected class

$\yen I_2$ = rates of transmission from I_2 to R

μI_1 = rates of transmissions from class I_1 to I_2

$(d_1+d_2+d_3)I_2$ = death rates due to the reason of natural,
the virus and natural as well as the virus

From Figure 8 we get the 4th ODE

$$\boxed{\frac{dI_2}{dt} = \mu I_1 - (\yen + d_1 + d_2 + d_3)I_2 ------------ eq(4)}$$

3.2.5 Recovered compartment

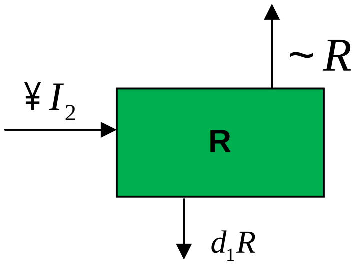

Fig. 9 Schematic diagram of Recovered class

$\yen I_2$ = rates of transmissions from class I_2 to R

$\sim R$ = recovering rate of removed computer

d_1 = death rate due to natural

From Figure 9 we get the 5th ODE

$$\boxed{\frac{dR}{dt} = \yen I_2 - \sim R - d_1R ------------------ eq(5)}$$

3.3 SAI$_1$I$_2$R model of equation

$$\frac{dS}{dt}=b+\text{~}R-\quad SI_1-\text{¢}SA-d_1S\quad ----------------eq(1)$$

$$\frac{dA}{dt}=\text{¢}SA+\text{¨}AI_1-d_1A------------------eq(2)$$

$$\frac{dI_1}{dt}=(\quad S-\text{¨}A-\text{µ}-d_1-d_2)I_1------------------eq(3)$$

$$\frac{dI_2}{dt}=\text{µ}I_1-(\text{¥}+d_1+d_2+d_3)I_2------------------eq(4)$$

$$\frac{dR}{dt}=\text{¥}I_2-\text{~}R-d_1R------------------------eq(5)$$

$$T=S+A+I_1+I_2+R------------------------eq(6)$$

3.4 Assumption

- The population is fixed.
- Any new node added into the network is susceptible.
- The parameters are assumed to be positive constants.
- The Antivirus fully effective.
- The computer virus affects the computer not the file.

Table 5: SAI_1I_2R model Notation

No	Parameters symbol	Definition
1	S	Non-infected computers
2	A	Non-infected computers equipped with anti-virus.
3	I_1	Partially infected computer.
4	I_2	Fully infected a computer entirely infected
5	R	A computer recovered from the virus.
6	b	New computers
7	SI_1	Infection rate of susceptible computers
8	$\sim R$	Recovering rate of removed computers
9	¢ SA	Conversion of non infected computer into antidotal
10	¨ AI_1	Conversion of partially infected computer into antidotal
11	µ I_1	Rates of transmissions from class I_1 to I_2
12	¥ I_2	Rates of transmission from I_2 to R
13	d_1	death rate due to natural
14	d_2	death rate due to virus
15	d_3	death rate due to natural as well as the virus
16	T	Total numbers of computers

CHAPTER 4

QUALITATIVE ANALYSES

4.1 Why do we study ODE's qualitatively?

There are basically three methods of studying ODE' namely analytical, numerical and Qualitative. The third approaches are a radical departure from the first and the second, because our expectation is not only on numbers and magnitude but on a 'long term' behavior of the differential system. To understand the equation always does not depend on the numerical or analytical solution alone we do have a lot of diagrams because figures are easily understood than equations. The qualitative behavior of a function is often simpler to visualize from a graph than from an explicit or implicit expression of the function.

The aim of qualitative solution predicting their long term behavior by observes the vector fields and relates them to equilibrium points and Eigen- values. This is very important for analysis and prediction [59].

In this chapter we discuses qualitative analysis of SAI_1I_2R model, evaluate the virus-free and Endemic equilibrium points and at the end of this chapter we have graphs drown in PPlean[17] (referee Appendix B)

4.2 Equilibrium Points:

A system at equilibrium does not change over time. A particular point of a variable is called an equilibrium point.

There are two types of equilibrium points.

4.2.1 Virus-free equilibrium points

4.2.2 Endemic equilibrium

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[17] A phase-plane diagram illustrates the state of one variable (vertical axis) versus the state of a second variable (horizontal axis). It shows the dynamics of the two computing values.

4.2.1 Virus-free equilibrium points

Virus-free equilibrium is a state corresponding to the absence of infected individuals (I_1, I_2 and R ≠0). Applying this condition to the equilibrium of the model represented by the five ODE's describe from eq.1 - eq.6 two points can be calculated:

$P_1^*= (S^*, A^*, I_1^*, I_2^*, R^*) = (0, T, 0, 0, 0)$

$P_2^*= (S^*, A^*, I_1^*, I_2^*, R^*) = (T, 0, 0, 0, 0)$

Linearization the ODE using Jacobin matrix

Definition of Jacobin Matrix:- Give n function $f_1(x_1,x_2,\dots, x_n)$, $f_2(x_1,x_2,\dots,x_n),\dots$, $f_n(x_1,x_2\dots, x_n)$ describing the n dynamics variables $x_1,x_2,\dots,x_n$, the Jacobin matrix J is defined as

$$J = \begin{bmatrix} \frac{\partial f_1}{\partial x_1} & \frac{\partial f_1}{\partial x_2} & \cdots & \frac{\partial f_1}{\partial x_n} \\ \frac{\partial f_2}{\partial x_1} & \frac{\partial f_2}{\partial x_2} & \cdots & \frac{\partial f_2}{\partial x_n} \\ \vdots & \vdots & \vdots & \vdots \\ . & . & . & . \\ \frac{\partial f_n}{\partial x_1} & \frac{\partial f_n}{\partial x_2} & \cdots & \frac{\partial f_n}{\partial x_n} \end{bmatrix}$$

Based on the Jacobin matrix evaluate the five ODE's

$$J(S,A,I_1,I_2,R) = \begin{bmatrix} \frac{\partial f_1}{S} & \frac{\partial f_1}{A} & \frac{\partial f_1}{I_1} & \frac{\partial f_1}{I_2} & \frac{\partial f_1}{R} \\ \frac{\partial f_2}{S} & \frac{\partial f_2}{A} & \frac{\partial f_2}{I_1} & \frac{\partial f_2}{I_2} & \frac{\partial f_2}{R} \\ \frac{\partial f_3}{S} & \frac{\partial f_3}{A} & \frac{\partial f_3}{I_1} & \frac{\partial f_3}{I_2} & \frac{\partial f_3}{R} \\ \frac{\partial f_4}{S} & \frac{\partial f_4}{A} & \frac{\partial f_4}{I_1} & \frac{\partial f_4}{I_2} & \frac{\partial f_4}{R} \\ \frac{\partial f_5}{S} & \frac{\partial f_5}{A} & \frac{\partial f_5}{I_1} & \frac{\partial f_5}{I_2} & \frac{\partial f_5}{R} \end{bmatrix} \begin{array}{l} \rightarrow \text{Sub. } \mathrm{f}_1 \text{ with eq.1 } (b + \alpha R - \beta \mathrm{SI}_1 - \delta \mathrm{S}A - d_1 S) \\ \rightarrow \text{Sub. } \mathrm{f}_2 \text{ with eq.2}(\text{¢} SA + \text{¨} AI_1 - d_1 A) \\ \rightarrow \text{Sub. } \mathrm{f}_3 \text{ with eq.3}((S - \text{¨} A - \mu - d_1 - d_2) I_1) \\ \rightarrow \text{Sub. } \mathrm{f}_4 \text{ with eq.4 } (\mu I_1 - (\text{¥} + d_1 + d_2 + d_3) I_2) \\ \rightarrow \text{Sub. } \mathrm{f}_5 \text{ with eq.5 } (\text{¥} I_2 - \sim R - d_1 R) \end{array}$$

Evaluate the stability at Point one (P_1^*)

We have 5*5 matrixes

$$J=(S,A,I_1,I_2,R)\begin{bmatrix} -\beta I_1-\delta A-d_1 & -\alpha S & -\beta S & 0 & \alpha \\ \delta A & (\delta S+\varphi I_1-d_1) & \varphi A & 0 & 0 \\ \beta I_1 & -\varphi I_1 & (\beta S-\varphi A-\omega-d_1-d_2) & 0 & 0 \\ 0 & 0 & \omega & -\gamma-d_1-d_2-d_3 & 0 \\ 0 & 0 & 0 & \gamma & -\alpha-d_1 \end{bmatrix}$$

Recall

P_1^* = (0, T, 0, 0, 0) that means A=T

Considering the equilibrium point P_1^*, the corresponding linear system around it has a Jacobean, J_{P1} given by:

$$J_{P1}=\begin{bmatrix} -¢T-d_1 & 0 & 0 & 0 & \sim \\ ¢T & -d_1 & ¨T & 0 & 0 \\ 0 & 0 & -¨T-µ-d_1-d_2 & 0 & 0 \\ 0 & 0 & µ & -¥-d_1-d_2-d_3 & 0 \\ 0 & 0 & 0 & ¥ & -\sim-d_1 \end{bmatrix}$$

To find the eigenvalues of J_{P1}

$$P(ª)=\det(J-ªI)=0$$

$$\Rightarrow \det\left(\begin{bmatrix} -\delta T-d_1 & 0 & 0 & 0 & \alpha \\ \delta T & -d_1 & \varphi T & 0 & 0 \\ 0 & 0 & -\varphi T-\omega-d_1-d_2 & 0 & 0 \\ 0 & 0 & \omega & -\gamma-d_1-d_2-d_3 & 0 \\ 0 & 0 & 0 & \gamma & -\alpha-d_1 \end{bmatrix}-\lambda\begin{bmatrix} 1 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 1 \end{bmatrix}\right)=0$$

$$\Rightarrow \det\begin{bmatrix} -\text{¢}T-d_1-\text{ª} & 0 & 0 & 0 & \sim \\ \text{¢}T & -d_1-\text{ª} & \text{¨}T & 0 & 0 \\ 0 & 0 & -\text{¨}T-\text{µ}-d_1-d_2-\text{ª} & 0 & 0 \\ 0 & 0 & \text{µ} & -\text{¥}-d_1-d_2-d_3-\text{ª} & 0 \\ 0 & 0 & 0 & \text{¥} & -\sim-d_1-\text{ª} \end{bmatrix}=0$$

$$\Rightarrow (-\text{¢}T-d_1-\text{ª})(-d_1-\text{ª})(-\text{¨}T-\text{µ}-d_1-d_2-\text{ª})(-\text{¥}-d_1-d_2-d_3-\text{ª})(-\sim-d_1-\text{ª})=0$$

$$P(\text{ª})=(-\text{¢}T-d_1-\text{ª})(-d_1-\text{ª})(-\text{¨}T-\text{µ}-d_1-d_2-\text{ª})(-\text{¥}-d_1-d_2-d_3-\text{ª})(-\sim-d_1-\text{ª})=0$$

Then we have five eigenvalues

$$\text{ª}_1=-\text{¢}T-d_1<0,$$
$$\text{ª}_2=-d_1<0,$$
$$\text{ª}_3=-\text{¨}T-\text{µ}-d_1-d_2<0,$$
$$\text{ª}_4=-\text{¥}-d_1-d_2-d_3<0,$$
$$\text{ª}_5=-\sim-d_1<0$$

For all parameter the eigenvalues are real and negative, implying $P_1^*$is asymptotically stable, this show that the stable equilibrium points.

Evaluate the stability at Point Two (P_2^*)

Considering the equilibrium point P_2*, (S=T) the corresponding linear system around it has a Jacobeans J_{p2} given by

$$J(S,A,I_1,I_2,R)=\begin{bmatrix} -\beta I_1-\delta A-d_1 & -\alpha S & -\beta S & 0 & \alpha \\ \delta A & (\delta S+\varphi I_1-d_1) & \varphi A & 0 & 0 \\ \beta I_1 & -\varphi I_1 & (\beta S-\varphi A-\omega-d_1-d_2) & 0 & 0 \\ 0 & 0 & \omega & -\gamma-d_1-d_2-d_3 & 0 \\ 0 & 0 & 0 & \gamma & -\alpha-d_1 \end{bmatrix}$$

After substitute S = T and the value of A, I_1, I_2, R = 0 we can get the following 5*5 matrix

$$J_{P2} = \begin{bmatrix} -d_1 & -\sim T & - \ T & 0 & \sim \\ 0 & ¢T - d_1 & 0 & 0 & 0 \\ 0 & 0 & T - µ - d_1 - d_2 & 0 & 0 \\ 0 & 0 & µ & -¥ - d_1 - d_2 - d_3 & 0 \\ 0 & 0 & 0 & ¥ & -\sim - d_1 \end{bmatrix}$$

To find the eigenvalues of J_{P2}

$$P(ª) = \det(J - ª I) = 0$$

$$\Rightarrow \det \begin{bmatrix} -d_1 - ª & -\sim T & - \ T & 0 & \sim \\ 0 & ¢T - d_1 - ª & 0 & 0 & 0 \\ 0 & 0 & T - µ - d_1 - d_2 - ª & 0 & 0 \\ 0 & 0 & µ & -¥ - d_1 - d_2 - d_3 - ª & 0 \\ 0 & 0 & 0 & ¥ & -\sim - d_1 - ª \end{bmatrix} = 0$$

$$P(ª) = (-d_1 - ª)(¢T - d_1 - ª)(\ \ T - µ - d_1 - d_2 - ª)(-¥ - d_1 - d_2 - d_3 - ª)(-\sim - d_1 - ª) = 0$$

Then we have five eigenvalues of J_{P2}

$$ª_1 = -d_1 < 0,$$
$$ª_2 = ¢T - d_1 < 0 \ iff \ ¢T < d_1,$$
$$ª_3 = \ \ T - µ - d_1 - d_2 < 0 \ iff \ \ \ T < µ + d_1 + d_2,$$
$$ª_4 = -¥ - d_1 - d_2 - d_3 < 0,$$
$$ª_5 = -\sim - d_1 < 0$$

Consequently, for all possible parameter values, there are two real and positive eigenvalue, implying that P_2^* is unstable.

The stability analysis performed above indicates that this model presents two virus-free equilibrium points, one asymptotically stable and the other unstable. As the linear approximation method is local, it is not made sure whether any initial condition drives the network to the asymptotically stable virus-free equilibrium. Therefore, the existence of endemic equilibrium must be studied.

4.2.2 Endemic equilibrium

Endemic equilibrium points are characterized by the existence of infected nodes in the network (I_1, $I_2 \neq 0$) and, as a consequence of Eq. (1-5), $R \neq 0$.

To find the endemic equilibrium first put all variables interims of parameters.

Recall equation (1 – 5)

From equation 5

$$\boxed{I_2 = \frac{R(\sim + d_1)}{\text{¥}} \text{-------------} eq(7)}$$

From equation (2)

$$A = 0 \ or \ \text{¢}S + \text{¨}\, I_1 - d_1 = 0$$

$$\boxed{I_1 = \frac{d_1 - \text{¢}S}{\text{¨}} \text{--------------------} eq(8)}$$

From equation (3)

$$I_1 = 0 \ or \quad S - \text{¨}\, A - \mu - d_1 - d_2 = 0 \qquad S = \mu + d_1 + d_2 \ \ Since \ \ A = 0 \ \ from \ eq(2)$$

$$\boxed{S^* = \frac{\mu + d_1 + d_2}{} \text{-------------} eq(9)}$$

From equation (1)

$$I_1 = 0 \; or \quad S - \text{¨} A - \mu - d_1 - d_2 = 0$$

$$b + \sim R - d_1 S = 0 \quad Since\ from\ eq(2)\, A = 0\ \ from\ \ eq(3)\, I_1 = 0$$

$$R = \frac{d_1 S - b}{\sim}$$

$$R = \frac{d_1(\frac{\mu + d_1 + d_2}{}) - b}{\sim} \qquad by\ sub.\, eq(9)$$

$$\boxed{R^* = \frac{d_1(\mu + d_1 + d_2) - \ \ b}{\sim} \text{ ---------- } eq(10)}$$

Substitute eq.(7) in to eq.(8)

$$I_2 = \frac{R(\sim + d_1)}{\text{¥}}$$

$$I_2 = \frac{d_1(\mu + d_1 + d_2) - \ \ b}{\sim}(\frac{(\sim + d_1)}{\text{¥}})$$

$$\boxed{I_2{*} = \frac{(d_1(\mu + d_1 + d_2) - \ \ b)(\sim + d_1)}{\sim\text{¥}} \text{----------} eq.(11)}$$

Substitute eq. (8) in to eq. (9)

$$I_1 = \frac{d_1 - \text{¢} S}{\text{..}}$$

$$I_1 = \frac{d_1 - \text{¢}(\frac{\mu + d_1 + d_2}{})}{\text{..}}$$

$$\boxed{I_1^* = \frac{d_1 \quad - \text{¢}\,(\mu + d_1 + d_2)}{\text{..}} \text{ ------------ } eq.(12)}$$

Substitute the value of R*, I₁*, I₂* and S* in to eq.(1)

$$b + \sim R - \quad SI_1 - \text{¢}SA - d_1S = 0$$

$$\Rightarrow b + \sim\left(\frac{d_1(\mu + d_1 + d_2) - \quad b}{\sim}\right) - \left(\frac{d_1 \quad - \text{¢}(\mu + d_1 + d_2)}{..}\right)*$$

$$\left(\frac{\mu + d_1 + d_2}{}\right) - d_1\left(\frac{\mu + d_1 + d_2}{}\right) - \text{¢}\left(\frac{\mu + d_1 + d_2}{}\right)A = 0$$

$$\Rightarrow \frac{b + d_1(\mu + d_1 + d_2) - \quad b}{} - \frac{(d_1 \quad - \text{¢}(\mu + d_1 + d_2)(\mu + d_1 + d_2))}{..} -$$

$$d_1\left(\frac{\mu + d_1 + d_2}{}\right) - \text{¢}\left(\frac{\mu + d_1 + d_2}{}\right)A = 0$$

$$\Rightarrow - \frac{(d_1 \quad - \text{¢}(\mu + d_1 + d_2))(\mu + d_1 + d_2)}{..} - \text{¢}A\left(\frac{\mu + d_1 + d_2}{}\right) = 0$$

$$A = \frac{-(d_1 \quad - \text{¢}(\mu + d_1 + d_2)(\mu + d_1 + d_2)}{..}\left(\frac{}{(\text{¢})(\mu + d_1 + d_2)}\right)$$

$$\boxed{A^* = \frac{\delta(\omega + d_1 + d_2) - d_1\beta}{\beta} --------------- eq.(15)}$$

Finally get the endemic points of $P_3^*=(S^*, A^*, I_1^*, I_2^*, R^*)$

$$S^* = \frac{\mu + d_1 + d_2}{\quad} ------------------ eq(9)$$

$$R^* = \frac{d_1(\mu + d_1 + d_2) - \quad b}{\sim} ---------- eq(10)$$

$$I_2^* = \frac{(d_1(\mu + d_1 + d_2) - \quad b)(\sim + d_1)}{\sim \text{¥}} ------ eq.(11)$$

$$I_1^* = \frac{d_1 \quad - \text{¢}\,(\mu + d_1 + d_2)}{..} ------------- eq.(12)$$

$$A^* = \frac{\delta(\omega + d_1 + d_2) - d_1\beta}{\beta} ---------------- eq.(15)$$

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$$J_{P3}(S,A,I_1,I_2,R) = \begin{bmatrix} -\beta I_1 - \delta A - d_1 & -\alpha S & -\beta S & 0 & \alpha \\ \delta A & (\delta S + \varphi I_1 - d_1) & \varphi A & 0 & 0 \\ \beta I_1 & -\varphi I_1 & (\beta S - \varphi A - \omega - d_1 - d_2) & 0 & 0 \\ 0 & 0 & \omega & -\gamma - d_1 - d_2 - d_3 & 0 \\ 0 & 0 & 0 & \gamma & -\alpha - d_1 \end{bmatrix}$$

Substitute the endemic points $J_{P3}(S^*, A^*, I_1^*, I_2^*, S)$ in to $J\ (S, A, I_1, I_2, R)$

$$J_{P3}(S^*,A^*,I_1^*,I_2^*,R^*) = \begin{bmatrix} -\beta I_1^* - \delta A^* - d_1 & -\alpha S^* & -\beta S^* & 0 & \alpha \\ \delta A^* & (\delta S^* + \varphi I_1^* - d_1) & \varphi A^* & 0 & 0 \\ \beta I_1^* & -\varphi I_1^* & (\beta S^* - \varphi A^* - \omega - d_1 - d_2) & 0 & 0 \\ 0 & 0 & \omega & -\gamma - d_1 - d_2 - d_3 & 0 \\ 0 & 0 & 0 & \gamma & -\alpha - d_1 \end{bmatrix}$$

$$J_{P3}=\begin{bmatrix} -d_1 & \frac{-\delta(\omega+d_1+d_2)}{\beta} & -(\omega+d_1+d_2) & 0 & \alpha \\ \frac{\delta(\omega+d_1+d_2)-d_1\beta}{\varphi} & 0 & (\omega+d_1+d_2)-\frac{d_1\beta}{\delta} & 0 & 0 \\ \frac{d_1\beta-\delta(\omega+d_1+d_2)}{\varphi} & \frac{\delta(\omega+d_1+d_2)-d_1\beta}{\beta} & \frac{d_1\beta}{\delta}-(\omega+d_1+d_2) & 0 & 0 \\ 0 & 0 & \omega & -(\gamma+d_1+d_2+d_3) & 0 \\ 0 & 0 & 0 & \gamma & -(\alpha+d_1) \end{bmatrix}$$

$$Let \quad c=\text{¢}(\mu+d_1+d_2)-d_1$$

$$e=\delta(\omega+d_1+d_2)$$

$$f=\mu+d_1+d_2$$

$$h=(\mu+d_1+d_2)-\frac{d_1}{\text{¢}}$$

$$g=(\gamma+d_1+d_2+d_3)$$

$$J=\begin{bmatrix} -d_1 & \frac{-e}{} & -f & 0 & \sim \\ \frac{c}{\text{..}} & 0 & h & 0 & 0 \\ \frac{-c}{\text{..}} & \frac{c}{} & -h & 0 & 0 \\ 0 & 0 & \mu & -g & 0 \\ 0 & 0 & 0 & \text{¥} & -(\sim+d_1) \end{bmatrix}$$

To find the eigenvalues of J_{P3}

$$P(\text{ª})=\det(J-\text{ª}I)=0$$

$$\Rightarrow \det\begin{bmatrix} -d_1 - \text{a} & \frac{-e}{} & -f & 0 & \sim \\ \frac{c}{..} & -\text{a} & h & 0 & 0 \\ \frac{-c}{..} & \frac{c}{} & -h - \text{a} & 0 & 0 \\ 0 & 0 & \mu & -g - \text{a} & 0 \\ 0 & 0 & 0 & \text{¥} & -(\sim + d_1) - \text{a} \end{bmatrix} = 0$$

Finally we get the following characteristic equation

$$P(\lambda) = a_5 \text{a}^5 + a_4 \text{a}^4 + a_3 \text{a}^3 +_2 \text{a}^2 + a_1 \text{a}^1 + + a_0$$

Where

$$a_5 = 1$$

$$a_4 = (d_1 + h) + g(\sim + d_1)$$

$$a_3 = [((d_1 + h)^2 (g + (\sim + d_1)) + g(\sim + d_1) + \frac{ce}{..} - \frac{cf}{..} - \text{¥}]$$

$$a_2 = [(d_1 h(g + (\sim + d_1) + \frac{ce}{..}(\sim + d_1)(h + g) +$$

$$fc^2 - (\frac{ech}{..} + cf(g + (\sim + d_1)) + ((\sim + d_1) + (d_1 + g)))]$$

$$a_1 = [d_1 hg(\sim + d_1) + (hg + (\sim + d_1))(h + g)\frac{ce}{..} + (gf + f(\sim + d_1))\frac{c^2}{..\,2} -$$

$$(((\sim + d_1)((d_1 + g) + d_1 g) + \frac{ech}{..}(g + (\sim + d_1)) + \frac{cfg(\sim + d_1)}{..})]$$

$$a_0 = \frac{cehg}{..}(\sim + d_1) - chd_1 g(\sim + d_1) - (\mu\text{¥}\sim - fg(\sim + d_1))\frac{c^2}{..\,2} - \frac{gech}{..}(\sim + d_1)$$

By Routh-Hurwitz Criterion (Referee Appendix C), the following condition must be true if the system become stable unless unstable.

$$Condition\ 1 \quad a_4a_3 > a_5a_2,$$

$$Condition\ 2 \quad a_2(a_4a_3 - a_5a_2) > a_4(a_4a_1 - a_5a_0)\ ,$$

$$Condition\ 3 \quad (a_4(a_2a_3 + a_5a_0) - (a_2{}^2a_3 + a_4{}^2a_1))(a_4{}^2a_1 - a_5a_0a_4) >$$
$$(a_0(a_4a_3 - a_5a_2)(a_4a_3 - a_5a_2)(a_4a_3 - a_5a_2),$$

$$Condition\ 4 \quad a_4 > 0$$

4.3 Next-generation matrix

In epidemiology, the next-generation matrix is a method used to derive the basic reproduction number, for a compartmental model of the spread of diseases To calculate the basic reproduction number by using a next-generation matrix. (Referee Appendix A)

4.4 Calculate basic reproduction number (R_0)

Let

F be the rate of appearance of new infections in compartment
V^- be the transfer of individual out of compartment *i* .
V^+ be the transfer of individual into compartment *i*
Where $V = V^- - V^+$
$\text{°} =$ the largest eigenvalue

$$R_o = \text{°}(F_J V_J{}^{-1})$$

$$\frac{dI_1}{dt} = SI_1 - (\text{¨}A + \mu + d_1 + d_2)I_1$$

$$\frac{dI_2}{dt} = \mu I_1 - (\text{¥} + d_1 + d_2 + d_3)I_2$$

$$F = \begin{bmatrix} SI_1 \\ 0 \end{bmatrix}, \quad V^- = \begin{bmatrix} (\text{¨}A + \mu + d_1 + d_2)I_1 \\ (\text{¥} + d_1 + d_2 + d_3)I_2 \end{bmatrix}, \quad V^+ = \begin{bmatrix} 0 \\ \mu I_1 \end{bmatrix}$$

$$V = V^- - V^+ = \begin{bmatrix} (\text{¨}A + \mu + d_1 + d_2)I_1 \\ (\text{¥} + d_1 + d_2 + d_3)I_2 - \mu I_1 \end{bmatrix}$$

Differentiate both F and V with respect to I1 and I2

$$F_J = \begin{bmatrix} & 0 \\ 0 & 0 \end{bmatrix}, \quad V_J = \begin{bmatrix} (\text{¨}A + \mu + d_1 + d_2) & 0 \\ -\mu & \text{¥} + d_1 + d_2 + d_3 \end{bmatrix}$$

$$V_J^{-1} = \frac{1}{\det(V_J)} \begin{bmatrix} \text{¥} + d_1 + d_2 + d_3 & 0 \\ \mu & (\text{¨} + \mu + d_1 + d_2) \end{bmatrix}$$

$$V_J^{-1} = \frac{1}{(\text{¥} + d_1 + d_2 + d_3)(\text{¨} + \mu + d_1 + d_2)} \begin{bmatrix} \text{¥} + d_1 + d_2 + d_3 & 0 \\ \mu & (\text{¨} + \mu + d_1 + d_2) \end{bmatrix}$$

$$F_J V_J^{-1} = \frac{1}{(\text{¥} + d_1 + d_2 + d_3)(\text{¨} + \mu + d_1 + d_2)} \begin{bmatrix} & 0 \\ 0 & 0 \end{bmatrix} * \begin{bmatrix} \text{¥} + d_1 + d_2 + d_3 & 0 \\ \mu & (\text{¨} + \mu + d_1 + d_2) \end{bmatrix}$$

$$= \frac{1}{(\text{¥} + d_1 + d_2 + d_3)(\text{¨} + \mu + d_1 + d_2)} \begin{bmatrix} (\text{¥} + d_1 + d_2 + d_3) & 0 \\ 0 & 0 \end{bmatrix}$$

Find the eigenvalue of a matrix

$$\Rightarrow \det\left(\begin{bmatrix} (\text{¥} + d_1 + d_2 + d_3) - \text{ª} & 0 \\ 0 & -\text{ª} \end{bmatrix}\right) = 0$$

$$(\text{¥} + d_1 + d_2 + d_3) = \text{ª} \quad or \; \text{ª} = 0$$

$$\text{°} = (\text{¥} + d_1 + d_2 + d_3)$$

$$\mathrm{R_o} = \text{°}(\mathrm{F_J V_J^{-1}}) = \frac{(\text{¥} + d_1 + d_2 + d_3)}{(\text{¥} + d_1 + d_2 + d_3)(\text{¨} + \mu + d_1 + d_2)}$$

$$\mathrm{R_o} = \frac{}{(\text{¨} + \mu + d_1 + d_2)}$$

Basic reproduction number (R_0) the average number of secondary infections that occurs when one infective is introduced into a completely non infected computes.

If $R_0 < 1$, then

Virus-free and endemic equilibrium are stable, the virus dies out.

If $R_0 > 1$, then

Virus-free and endemic equilibrium are unstable, the virus spreads.

4.5 Represented the SAI_1I_2R model in Phase Plane

Pplane (phase plane) and Dfield (direction field) are software program for the interactive analysis of ordinary differential equation (ODE). Pplane is used for system of differential equation of the form x’=f(t,x), y’=g(x,y) while Dfield is used on first order differential equation of the form x’=f(x.) .

As Pplane includes all function available in Dfield, a discussion of Pplane will be sufficient. (Referee Appendix B)

Rewrite the five equations in to coupled equations.

We have $T= S+A+I_1+I_2+R$ which implies $R=T- S+A+I_1+I_2+R$ and

$$T = S + A + I_1 + I_2 + R$$
$$I_1 = T - (S + A + I_2 + R)$$

Recall equations (1-5)

$$\begin{aligned} I_1 &= T - (S + A + I_2 + R) \\ &= T - (b - \quad SI_1 + \sim R - \text{¢}SA - d_1S + \text{¢}SA + \text{¨}AI_1 - d_1A + \\ &\quad SI_1 - \text{¨}AI_1 - (\mu + d_1 + d_2)I_1 + \\ &\mu I_1 - (\text{¥} + d_1 + d_2 + d_3)I_2 + \text{¥}I_2 - \sim R - d_1R) \end{aligned}$$

$$I_1 = \frac{T(1+d_1) - b + (d_2 + d_3)I_2}{(1 - d_1 - \quad S + \text{¨}A + \mu)} ------- eq(16)$$

$$\begin{aligned} I_2 &= T - (S + A + I_1 + R) \\ &= T - (b - \quad SI_1 + \sim R - \text{¢}SA - d_1S + \text{¢}SA + \\ &\text{¨}AI_1 - d_1A + \quad SI_1 - \text{¨}AI_1 - (\mu + d_1 + d_2 + d_3)I_1 + \\ &\text{¥}I_2 - (\sim + d_1)R) \end{aligned}$$

$$I_2 = \frac{T(1+d_1) - b + (\mu + d_2)I_1}{(1 - d_1 + \text{¥})} ----- eq(17)$$

Substitute eq. (17) into eq. (16)

$$I_1 = \frac{T(1+d_1)-b}{(1-d_1- \quad S+\text{¨}A+\mu)} + \frac{(d_2+d_3)}{(1-d_1- \quad S+\text{¨}A+\mu)} * \frac{T(1+d_1)-b+(\mu+d_2)I_1}{(1-d_1+\text{¥})}$$

$$Let\ k = (1-d_1- \quad S+\text{¨}A+\mu)$$

$$c = (1-d_1+\text{¥})$$

$$I_1' = \frac{c(T(1+d_1)-b)+(d_2+d_3)(T(1+d_1)-b)}{kc(d_2+d_3)(\mu+d_2)} --------eq.(18)$$

Substitute eq. (16) into eq. (17)

$$I_2' = \frac{T(1+d_1)\text{-}b+(\mu+d_2)I_1'}{(1\text{-}d_1+\text{¥})}$$

$$I_2' = \left(\frac{T(1+d_1)-b}{(1-d_1+\text{¥})} + \frac{(\mu+d_2)}{(1-d_1+\text{¥})}\right)\left(\frac{c(T(1+d_1)-b)+(d_2+d_3)(T(1+d_1)-b)}{kc(d_2+d_3)(\mu+d_2)}\right)$$

$$I_2' = \frac{T(1+d_1)-b}{c} + \frac{(\mu+d_2)(T(1+d_1)-b)(c+(d_2+d_3))}{c(kc(d_2+d_3)(\mu+d_2))} --------eq.19$$

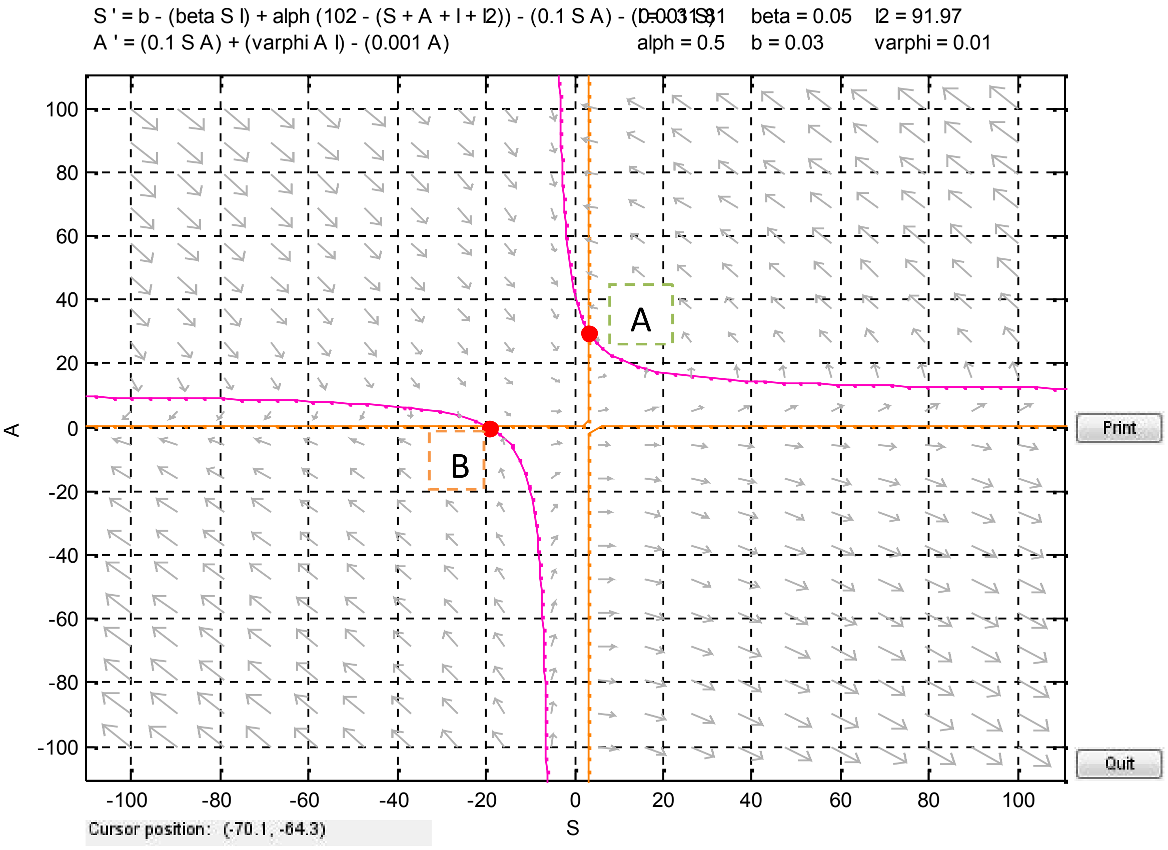
Finally we have got the following coupled equations

$$\left.\begin{aligned} \frac{dS}{dt} &= b- \quad SI_1+\sim(T-(S+A+I_1+I_2))-\text{¢}SA-d_1S \\ \frac{dA}{dt} &= \text{¢}SA+\text{¨}AI_1-d_1A \end{aligned}\right\} --------eq.(20)$$

Table 6: Parameters values for the model

Symbol	Description	Values
S_o	Initial number non- infected computer	*87*
A_o	Initial number Antidote computer	*1*
I_{1o}	Initial number of partially infected computer	*9*
I_{2o}	Initial number of fully infected computer	*5*
R_o	Initial value of Recovered computer	*0*
b	The rate of new computers to the new work	*0.03*
	Infection rate	*0.05*
~	Recovering rate	*0.5*
¢	Conversion rate of non-infected computer	*0.1*
¨	Conversion rate of partially infected computer	*0.01*
¥	Rate transmission from I_2 to R	*0.003*
µ	Rate transmission from I_1 to I_2	*0.3*
d_1	Death rate due to natural	*0.001*
d_2	Death rate due to virus	*0.03*
d_3	Death rate due to natural as well as the virus	*0.003*
T	Total numbers of computers	*120*

Based on the table 6 information the following figures can plot in PPlane8 and we can easily know the behaviors of a system.



S ' = b - (beta S I) + alph (102 - (S + A + I + I2)) - (0.1 S A) - (0.001 S)
A ' = (0.1 S A) + (varphi A I) - (0.001 A)

alph = 0.5
beta = 0.05
b = 0.03
I2 = 91.97
varphi = 0.01

Fig. 10 Direction field and phase representation of SAI_1I_2R model

From the equilibrium point data which in PPlane8 we can get the following information by easily observe, figure 8 show that the system has two equilibrium points the first equilibrium points “**A**” (3.191, 29.8213),

The Jacobian is $\begin{pmatrix} -1.8926 & -0.8191 \\ 2.9821 & 0 \end{pmatrix}$

The egenvalues and eigenvectors are

$$-0.94831+1.2438i \qquad (0.28107-0.36944i, \qquad -0.88573)$$

$$-0.94631-1.2438i \qquad (0.28107+0.36944i, \qquad -0.88573)$$

Therefore, the eigenvalue are negative and the vector filed goes into equilibrium points that impale there is spiral sink which means stable.

The second equilibrium point “**B**” is (-19.229, 0)

The Jacobian is $\begin{pmatrix} 1.0895 & 1.4229 \\ 0 & -2.242 \end{pmatrix}$

The eigenvalues and eigenvectors are

$1.0895 \quad (1, 0)$

$-2.242 \quad (-0.39278, \quad 0.91963)$

The eigenvalues which is real and different sign, there is a saddle point thus this is unstable.

When we linearization figure 10, point **“A”** we will see such figure and information

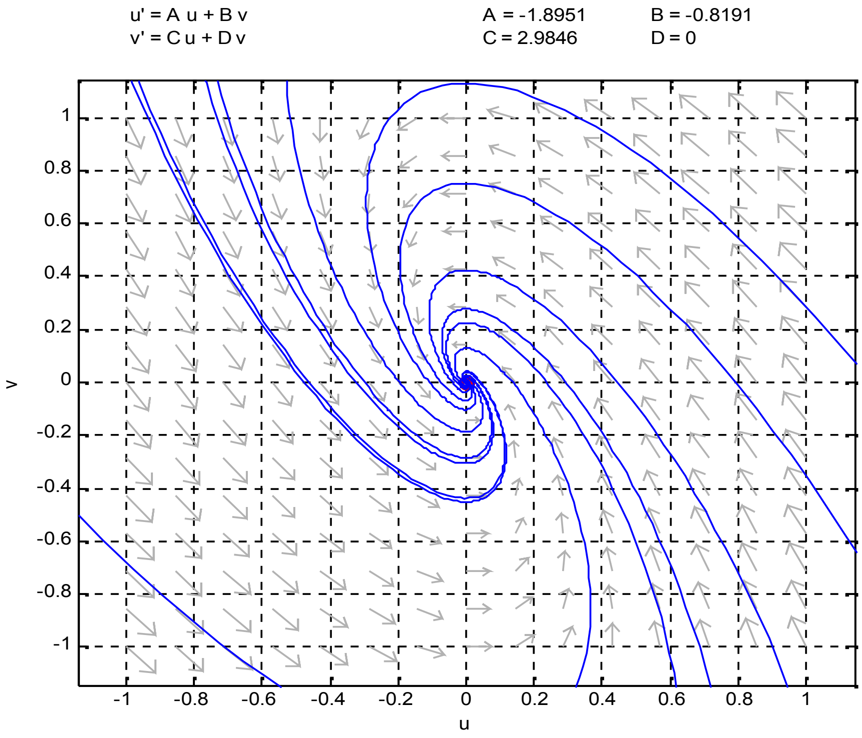


*Fig. 11 Display the linearization of point “**A**”*

Figure 11 show that the linearization points “A” from Equilibrium point data window we get such information

- There is a spiral sink
- The Jacobian matrix
- The eigenvalues

Linearization figure 10 point “B”

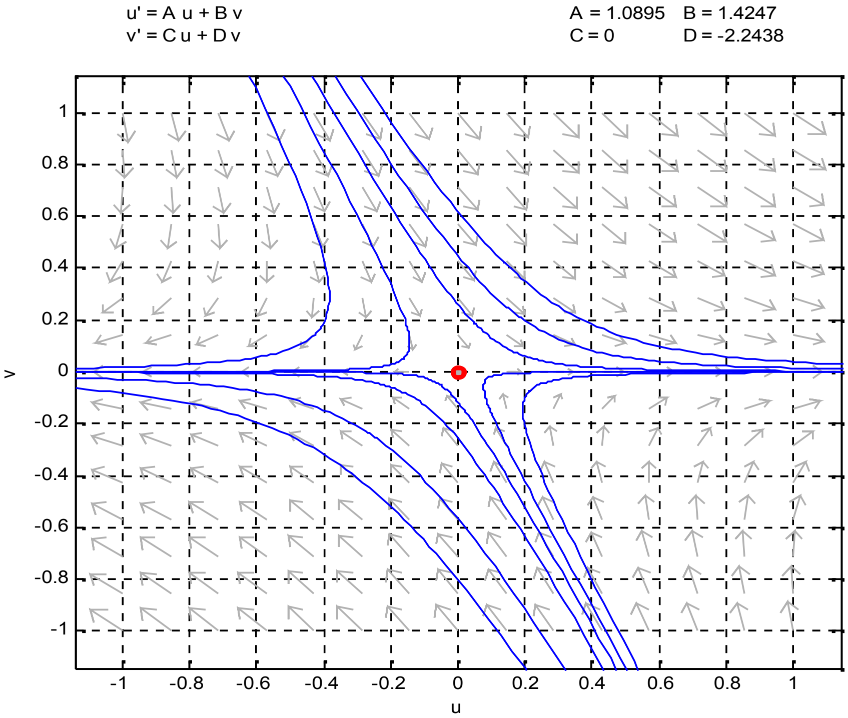


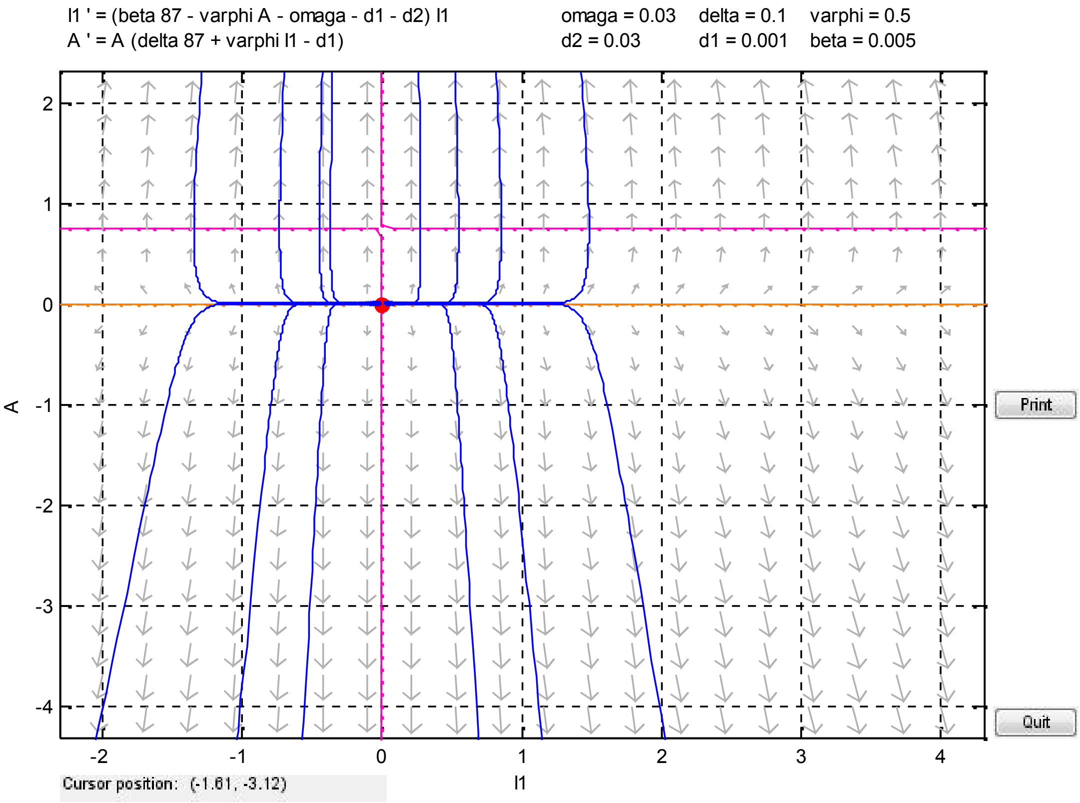
Fig. 12 Display the linearization of point B

Figure 11 show that the linearization points “**B”** from Equilibrium point data window we get the following information

There is a Saddle point

- Theer is a Saddle point
- The Jacobian matrix
- The eigenvalues

Partially infected with Antidote compartments



I1 ' = (beta 87 - varphi A - omaga - d1 - d2) I1
A ' = A (delta 87 + varphi I1 - d1)

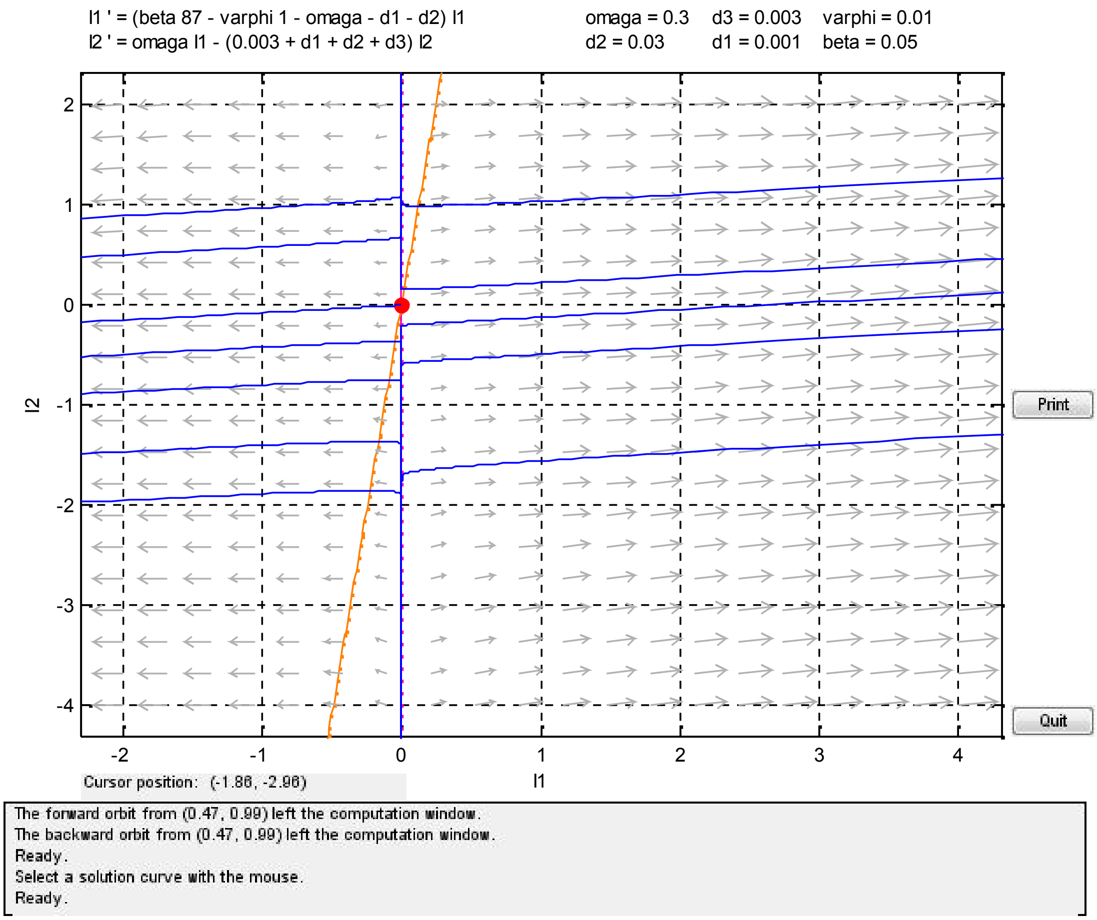
omaga = 0.03
delta = 0.1
varphi = 0.5
d2 = 0.03
d1 = 0.001
beta = 0.005

Cursor position: (-1.61, -3.12)

Fig. 13 the phase representation of A vs I_1 compartment

Figure: 13 shows that there is a nodal source at equilibrium point of (0, 0) and the eigenvalues are (0.374, 8.699) because the two distinct real eigenvalues, same sign and positive this implies unstable. The vector field show that the arrow goes out from equilibrium points.

I_1 with I_2



I1 ' = (beta 87 - varphi 1 - omaga - d1 - d2) I1
I2 ' = omaga I1 - (0.003 + d1 + d2 + d3) I2

omaga = 0.3   d3 = 0.003   varphi = 0.01
d2 = 0.03   d1 = 0.001   beta = 0.05

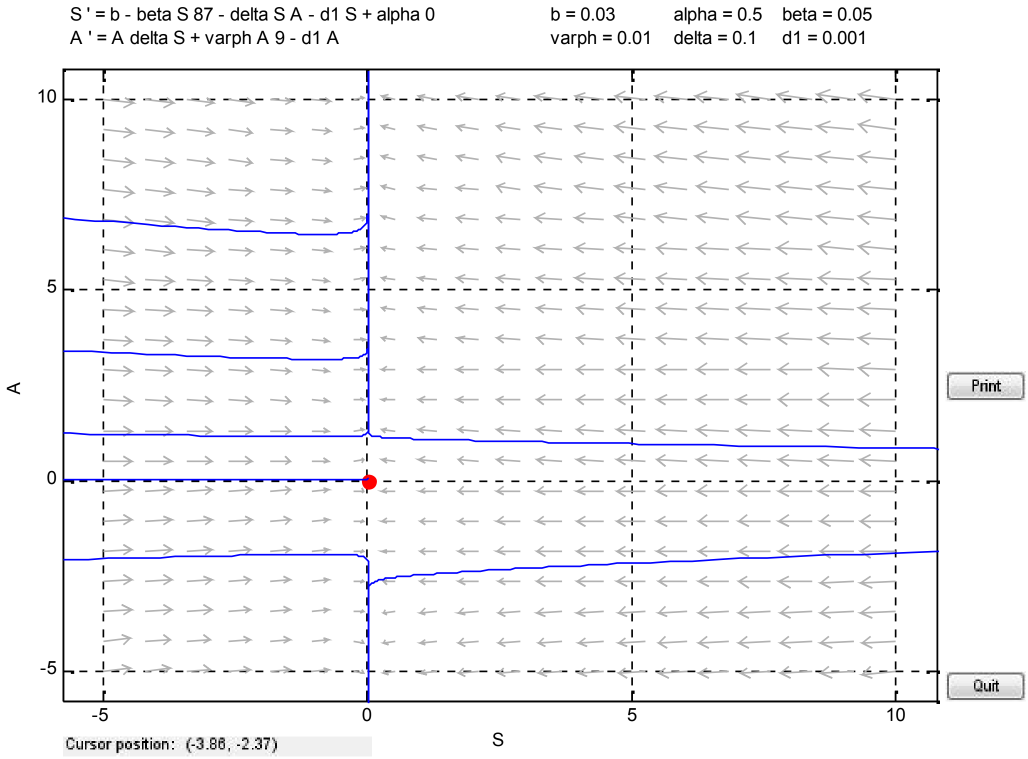
Cursor position: (-1.86, -2.96)

```
The forward orbit from (0.47, 0.99) left the computation window.
The backward orbit from (0.47, 0.99) left the computation window.
Ready.
Select a solution curve with the mouse.
Ready.
```

Fig. 14 The phase representation of I_1 & I_2 compartment

Figure 14: There is a saddle point at (0, 0) eigenvalues are (-0.374, 4.009) because the two distinct real eigenvalues, have opposite signs this tells as the system is always unstable.

Non- infected and Antidote compartment



S ' = b - beta S 87 - delta S A - d1 S + alpha 0
A ' = A delta S + varph A 9 - d1 A

b = 0.03
varph = 0.01
alpha = 0.5
delta = 0.1
beta = 0.05
d1 = 0.001

Cursor position: (-3.86, -2.37)

Fig. 15 The phase representation of S vs A compartment

The above figures 15 there is a saddle point at (0.006898, 0) the eigenvalue are -4.351 and 0.089689 that means the system is unstable.

CHAPTER 5

RESULT AND DISCUTION

5.1 Numerical Experiments

There are many different schemes for solving ODEs numerically. Many of the more advanced techniques are more complex to derive, analyze, or program but all schemes are based on the ideas we have introduced. One of the standard workhorses for solving ODEs is the called the Runge-Kutta method. In this chapter, some numerical experiments are conducted by using MATLAB with Runge-Kutta 4th order method with two different conditions being considered absence and presence of Antidote computer in a network All the simulation are with a normalized total numbers of computer T=102.

The effect of Antidote in each compartment

Non Infected Compartment (*S*):

Table 7: Initial values of S and A compartments

Representation	*Values*	*Color*	
		S without A	*S with A*
S	*87*	*Blue*	*Green*
A	*1*		

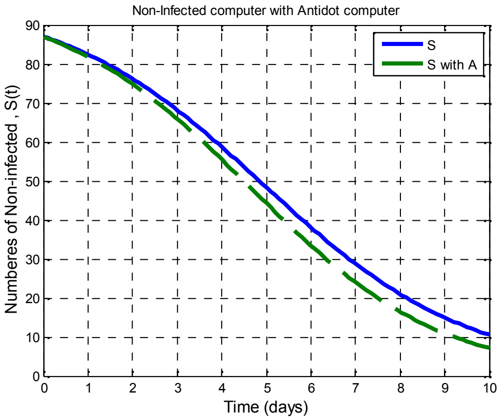


Fig. 16(a) the effects of A in S compartment delta=0.05

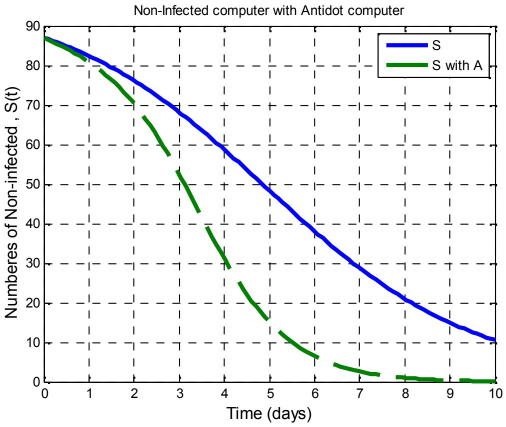


Fig. 16(b) the effects of A in S compartment delta=0.1

Figure 16(a) and (b) show that the effects of having fully effective Antivirus compartment in a network. If the rate of conversion non-infected computers (δ) is greater the virus free from network.

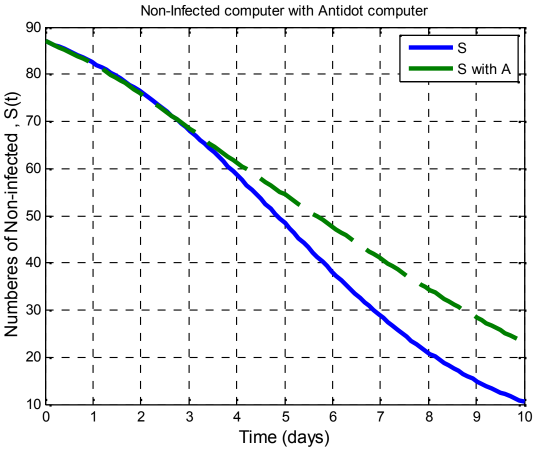


Fig. 16(c) the effects of A in S compartment delta=0.03 and beta=0.05

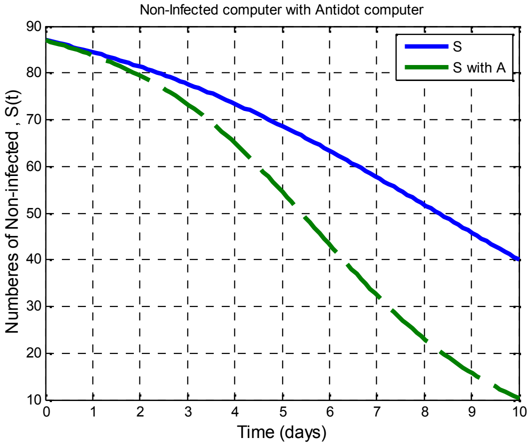


Fig. 16(d) the effects of A in S compartment delta=0.05 and beta=0.03

Figure 16(c) and (d) also show that the effects of Infection rate (β) and conversion rate of non-infected computers (δ) in the network.

Partially Infected Compartment (I_1):

Table 8: Initial values of I_1 and A compartments

Representation	*Values*	*Color*	
		I_1 without A	*I_1 with A*
I_1	*9*	*Blue*	*Green*
A	*1*		

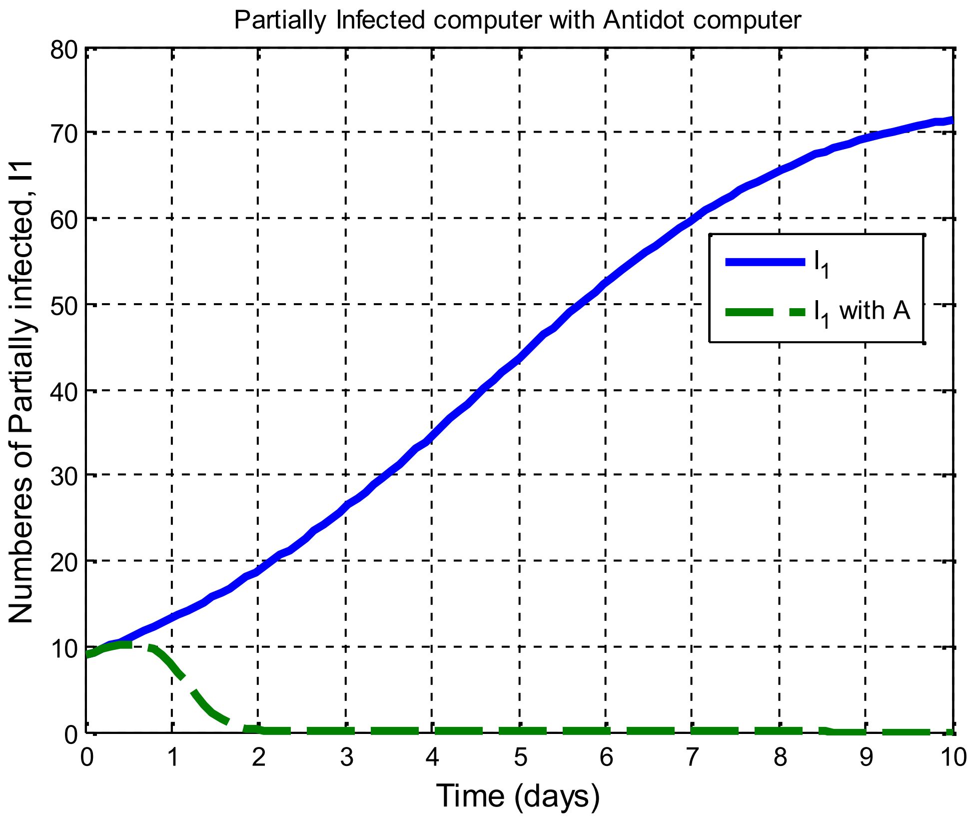


Fig. 17 The effect of Antidote computer in I_1 compartment

The conversion rate of partially infected computers (φ) is greater than the infection rate of non-infected compartment.

Fully Infected Compartment (I_2):

Table 9: Initial values of I_2 and A compartments

Representation	Values	Color	
		I_2 without *A*	I_2 with *A*
I_2	*5*	*Blue*	*Green*
A	*1*		

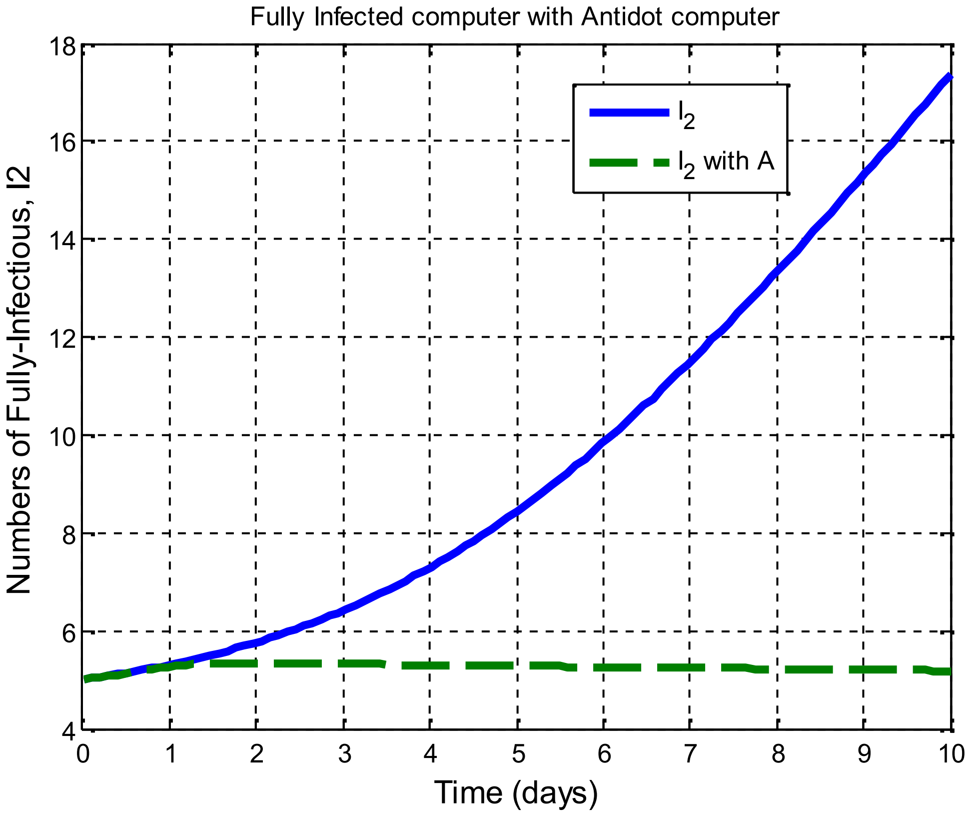


Fig. 18 the effect of Antidote compartment in I_2 compartment

The Antidote compartment also affect fully infected compartment because the partially infected compartment is treated and the rate of transmission rate from I_1 to I_2 is less.

Recovered Compartment (R):

Table 10: Initial values of R and A compartments

Representation	*Values*	*Color*	
		R without A	*R with A*
R	*0*	*Blue*	*Green*
A	*1*		

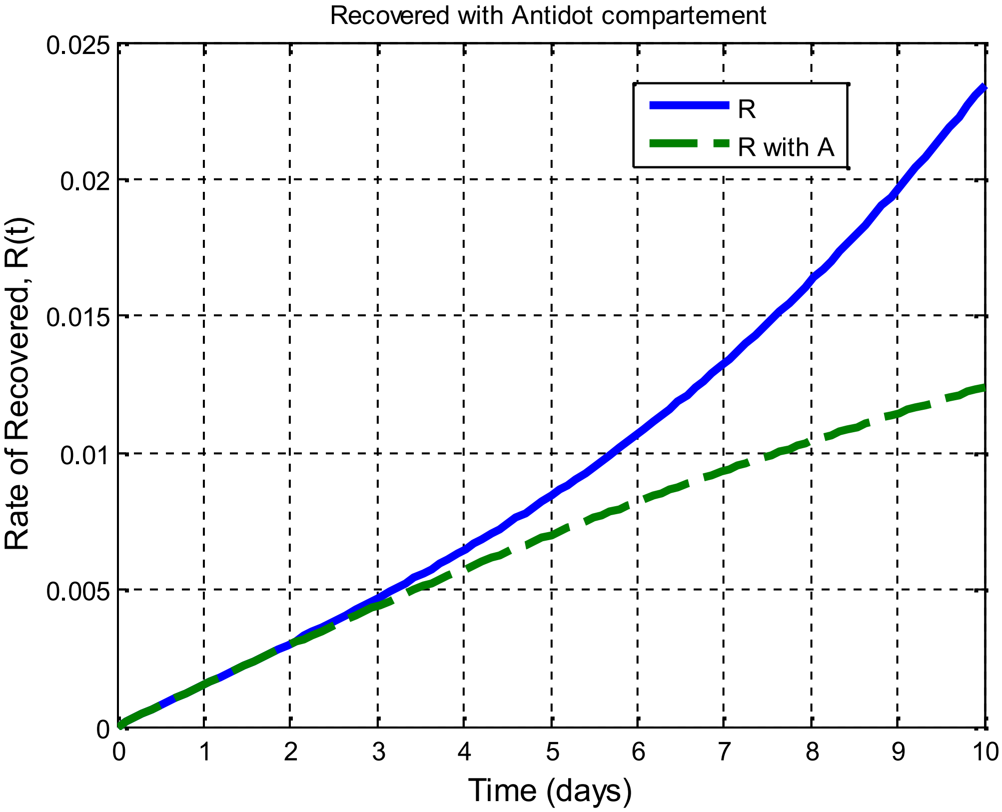


Fig. 19 The effect of Antidote compartment in R compartment

The recovery compartment is less because the virus treated in other compartments

5.2 Limitation

Every epidemiological tool has limitations. Unlike other methods the SAI_1I_2R epidemiological model has the following limitations,

- ✓ Anti-virus, the current models assumed that the anti-virus is fully effective that means clear all viruses. In the real world this assumption is not hold true because there is different types of computer virus and conditions
- ✓ The network Topology, different network architecture has to own impact in spread of computer virus.

CHAPTER 6

CONCLUSION AND FUTURE WORK

6.1 Conclusion

People who wish to solve problems associated with the spread of computer virus in many different approaches to their solution. It is common assumption that solves the virus simply scanning the computer without unlicensed antivirus, this assumption create a problem with this in mind; this has explored the methodology associated with epidemiology. Particularly, it has focused on the mathematical model used by epidemiologists to model the spread of epidemics.

In this paper, introduce a new model (SAI_1I_2R) to study the spread of computer virus in network. This model enabled us to understand better the dynamics nature of computer virus.

6.2 Future work

There are still a lot of works need to done towards a more complex and realistic epidemiological model that hope fully can solve these mysteries around the propagation of computer viruses.

As a future extension of this work the model these countermeasures in order to assess their value in protecting the Internet infrastructure and evaluate the spread of virus in files.

Reference

xNz=mK=hK=e~°«£°I=mK=aK= t §aa§~«±I=dK=eK=d ³¬±¡¦I=~¬¢=dK=_K=i~«-¬²I=?^¬=~°²§¤§¡§~ª==

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b´-ª³²§-¬~°·=`-«®³²~²§-¬I=´-ªK=SI=¬-K=PI=®®K=ORO=J=OUMI=OMMOK=

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=fbbb=p®£¡²°³«I=´-ªK=PMI=¬-K=RI=®®K=OMJOSI=NVVPK=

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xNNz= t K= l K=h£°«~¡©=~¬¢=^K=dK= j ¡h£¬¢°§¡©I=?`-¬²°§ ³²§-¬±=-¤=«~²¦£«~²§¡~ª=²¦£-°·=²-=£®§¢£«§ ¡±I=ffJq¦£=®°- ª£«=-¤=£¬¢£«§¡§²·?I=m°-¡££¢§¬¥±=-¤=²¦£=o-·~ª=p-¡§£²·=-¤=i-¬¢-¬I=p£°§£±=^I=

´-ªK=NQNI=®®K=VQ=JNOOI=NVPPK=

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xNPz= j K=gK=h£££ª§¬¥=~¬¢=hK=qK=aK=b~«£±I=?k£²µ-°©±I=~¬¢=£®§¢£«§¡=«-¢£ª±?I=g-³°¬~ª=-¤=²¦£=

o-·~ª=p-¡§£²·=f¬²£°¤~¡£I=´-ªK=OI=¬-K=QI=®®K=OVR=J=PMTI=OMMRK=

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¢£²£¡²§-¬=-¤=§¬²£°¬£²=µ-°«±?I=IEEE/ACM Transactions on Networking, vol. 13, no. 5, pp. 961-974, 2005.

xNRz= t K= l K=h£°«~¡©=~¬¢=^K=dK= j ¡h£¬¢°§¡©I=?`-¬²°§ ³²§-¬±=-¤=«~²¦£«~²§¡~ª=²¦£-°·=²-=

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®®K=TMM=J=TONI=NVOTK=

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xNTz=gK= l K=h£®¦~°²I=?^=_§-ª-¥§¡~ªª·=§¬±®§°£¢=«« ³¬£=±·±²£«=¤-°=¡-«®³²£°±I?=m°-¡££¢§¬¥±=-¤=f¬ ²£°¬~²§-¬~ª=g-§¬²=`-¬¤£°£¬¡£=-¬=^°²§í¡§~ª=f¬²£ªª§¥£¬¡£I=®®K=NPT=J=NQRI=NVVRK=

xNUz=_K=hK= j§±¦°~=~¬¢=aK=hK=p~§¬§I="SEIRS epidemic model with delay for transmission of malicious objects in computer network", Applied Mathematics, and Computation, vol. 188, no. 2, pp. 1476 - 1482, OMMTK

xNVz=gK= l K=h£®¦~°²=~¬¢=pK=o= t ¦§²£I=?j£~±³°§¬¥I=~¬¢=«-¢£ª§¬¥=¡-«®³²£°=´§°³±=®°£´~ª£¬¡£?I= fbbb=`-«®³²£°=p£¡³°§²·=p·«®-±§³«=-¬=o£±£~°¡¦=§¬=p£¡³°§²·I=~¬¢=m°§´~¡·I®®K=O=JNRI=NVVPK=

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xOPz=q¦£= t §ª¢=i§±²= l °¥~¬§¸~²§-¬=f¬²£°¬~²§-¬~ªl=µµµK µ§ª¢ª§±²K-°¥=

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=k£²µ-°©K=OMMOK=¦²²®WLLµµµK¬£µ±¤~¡²-°K¡-«L®£ºªL®°§¬²£°LNSQMTL=

xRUz=gK= I K=h£®¦~º²=~¬¢=pK=oK= t ¦§²£K=Ña§°£¡²£¢Jd°~®¦=b®§¢£«§-ª-¥§¡~ª=«-¢£ª±=-¤=`-«®³²£°=s§°

³±£±ÒI=f¬=m°-¡££¢§¬¥±=-¤=²¦£=NVVN=fbbb=`-«®³²£°=p-¡§£²·=p·«®-±§³«=-¬=o£±£~°¡¦=§¬==

p£¡³°§²·=~¬¢=m°§´~¡·K=I~©ª~¬¢I=`~ª§¤-°¬§~K=®®K=PQP=J=PRVINVVNK==

xRVz=m°-¤£±±-°K=I©£·=I©£·=I±£ª-©~=I¬·£¨£©µ£I=i£¡²³°£=¬-²£=~ -³²=n³~ª§²~²§´£=p-ª³²§-¬I==

f¬=^¢¢§±=^ ~ ~=r¬§´£°±§²·=`-«®³²~²§¬~ª=p¡§£¬¡£=m°-¥°~«=I=OMNTK===

xSMz=i§¬~Kq~·±££°KvK=~¬¢=f±~~¡K?=q¦£=o-³²¦Je³°µ§²¸=¡°§²£°§-¬=~¬¢=~®®ª§¡~²§-¬=²-²¦£=±²~ §ª§²·=-¤==

²¦£=´§°~ª=¤££=±²~¢·=±²~²£?I=_§-«~²¦£«~²§¡I=OMMRK=

APENDEX A

Calculate the R_0 in Next generation

In epidemiology, the next-generation matrix is a method used to derive the basic reproduction number, for a compartmental model of the spread of infectious diseases.

To calculate the next generation R_o

Let

F_i be the rate of appearance of new infections in compartment *i*

V^- be the transfer of individual out of compartment *i* by all other means

V^+ be the transfer of individual into compartment *i* by all other means

$^{\circ} =$ the largest eigenvalue

Where $V = V^- - V^+$

R_o is the largest eigenvalue in a magnitude of the matrix

$R_o = {}^{\circ}(F_J V_J^{-1})$

From SAI_1I_2R model (eq.3 and 4)

$$\frac{dI_1}{dt} = SI_1 - (\text{¨}A + \mu + d_1 + d_2)I_1$$

$$\frac{dI_2}{dt} = \mu I_1 - (\text{¥} + d_1 + d_2 + d_3)I_2$$

$$F = \begin{bmatrix} SI_1 \\ 0 \end{bmatrix}, \quad V^- = \begin{bmatrix} (\text{¨}A + \mu + d_1 + d_2)I_1 \\ (\text{¥} + d_1 + d_2 + d_3)I_2 \end{bmatrix}, \quad V^+ = \begin{bmatrix} 0 \\ \mu I_1 \end{bmatrix}$$

$$V = V^- - V^+$$
$$= \begin{bmatrix} (\text{¨}A + \mu + d_1 + d_2)I_1 \\ (\text{¥} + d_1 + d_2 + d_3)I_2 - \mu I_1 \end{bmatrix}$$

Differentiate both F and V with respect to I_1 and I_2

$$F = \begin{bmatrix} & 0 \\ 0 & 0 \end{bmatrix}, \quad V = \begin{bmatrix} (\text{¨}A + \mu + d_1 + d_2) & 0 \\ -\mu & \text{¥} + d_1 + d_2 + d_3 \end{bmatrix}$$

$$V=\begin{bmatrix}(\text{¨}+\mu+d_1+d_2) & 0\\ -\mu & \text{¥}+d_1+d_2+d_3\end{bmatrix}$$

$$V^{-1}=\frac{1}{\det(V)}\begin{bmatrix}\text{¥}+d_1+d_2+d_3 & 0\\ \mu & (\text{¨}+\mu+d_1+d_2)\end{bmatrix}$$

$$\mathrm{V}^{-1}=\frac{1}{(\gamma+\mathrm{d}_1+\mathrm{d}_2+\mathrm{d}_3)(\varphi+\omega+\mathrm{d}_1+\mathrm{d}_2)}\begin{bmatrix}\gamma+\mathrm{d}_1+\mathrm{d}_2+\mathrm{d}_3 & 0\\ \omega & (\varphi+\omega+\mathrm{d}_1+\mathrm{d}_2)\end{bmatrix}$$

$$\mathrm{FV}^{-1}=\frac{1}{(\gamma+\mathrm{d}_1+\mathrm{d}_2+\mathrm{d}_3)(\varphi+\omega+\mathrm{d}_1+\mathrm{d}_2)}\begin{bmatrix}\beta & 0\\ 0 & 0\end{bmatrix}*\begin{bmatrix}\gamma+\mathrm{d}_1+\mathrm{d}_2+\mathrm{d}_3 & 0\\ \omega & (\varphi+\omega+\mathrm{d}_1+\mathrm{d}_2)\end{bmatrix}$$

$$\Rightarrow\frac{1}{(\text{¥}+d_1+d_2+d_3)(\text{¨}+\mu+d_1+d_2)}\begin{bmatrix}(\text{¥}+d_1+d_2+d_3) & 0\\ 0 & 0\end{bmatrix}$$

$$\Rightarrow\frac{(\text{¥}+d_1+d_2+d_3)}{(\text{¥}+d_1+d_2+d_3)(\text{¨}+\mu+d_1+d_2)}$$

$$R_o=\frac{}{(\text{¨}+\mu+d_1+d_2)}$$

APENDEX B

Dfield and Pplane in MATLAB

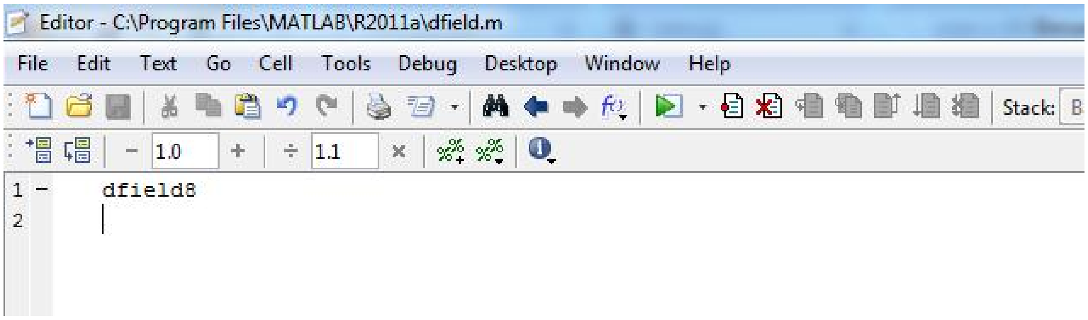
Phase plane and Direction field

Pplane (phase plane) and Dfield (direction field) are software's program for the interactive analysis of ordinary differential equation (ODE).

Dfield

Then we can download dfield8.m and Pplan8.m from the web address *http://math.rice.edu/~dfield/*

Start MATLAB and set the working directory to be the folder into which we download the program to start dfield8 simply type dfield8 in the MATLAB command window



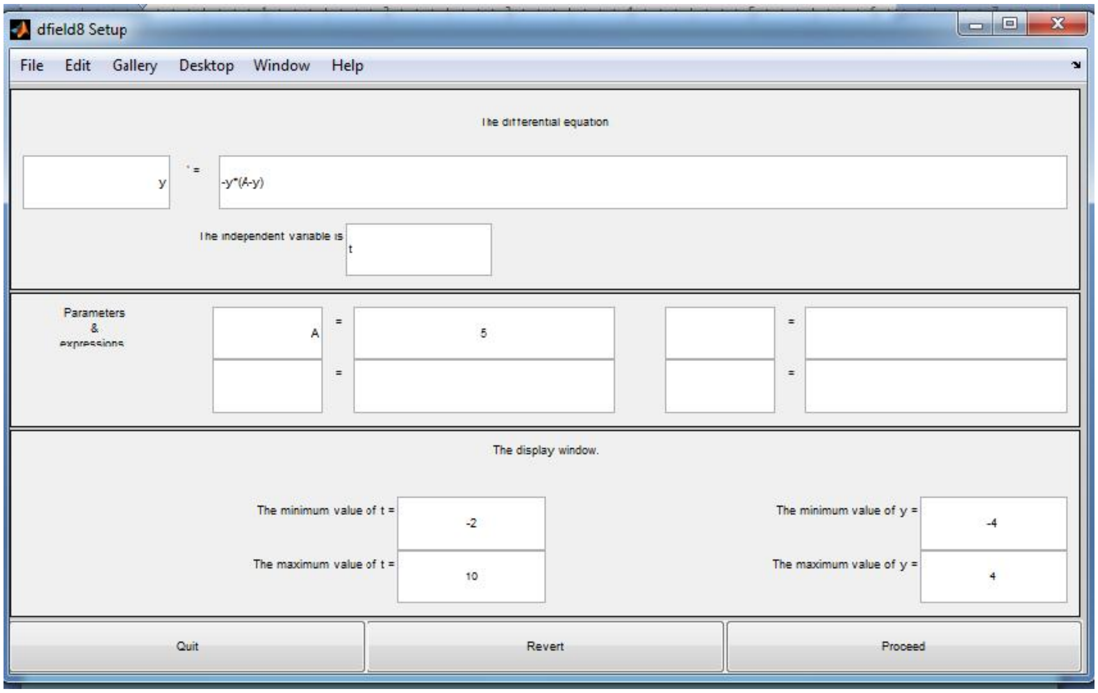
```
dfield8
```

Figure B-1 MATLAB command window

When Dfield starts it display the default setup window with one of the examples (available under gallery) already loaded. Edit the equation in Setup windows to look like figure B-2 and press Proceed.

For example

x'=y(A-y) , A=5



y ' = -y*(A-y)

The independent variable is t

A = 5

The minimum value of t = -2

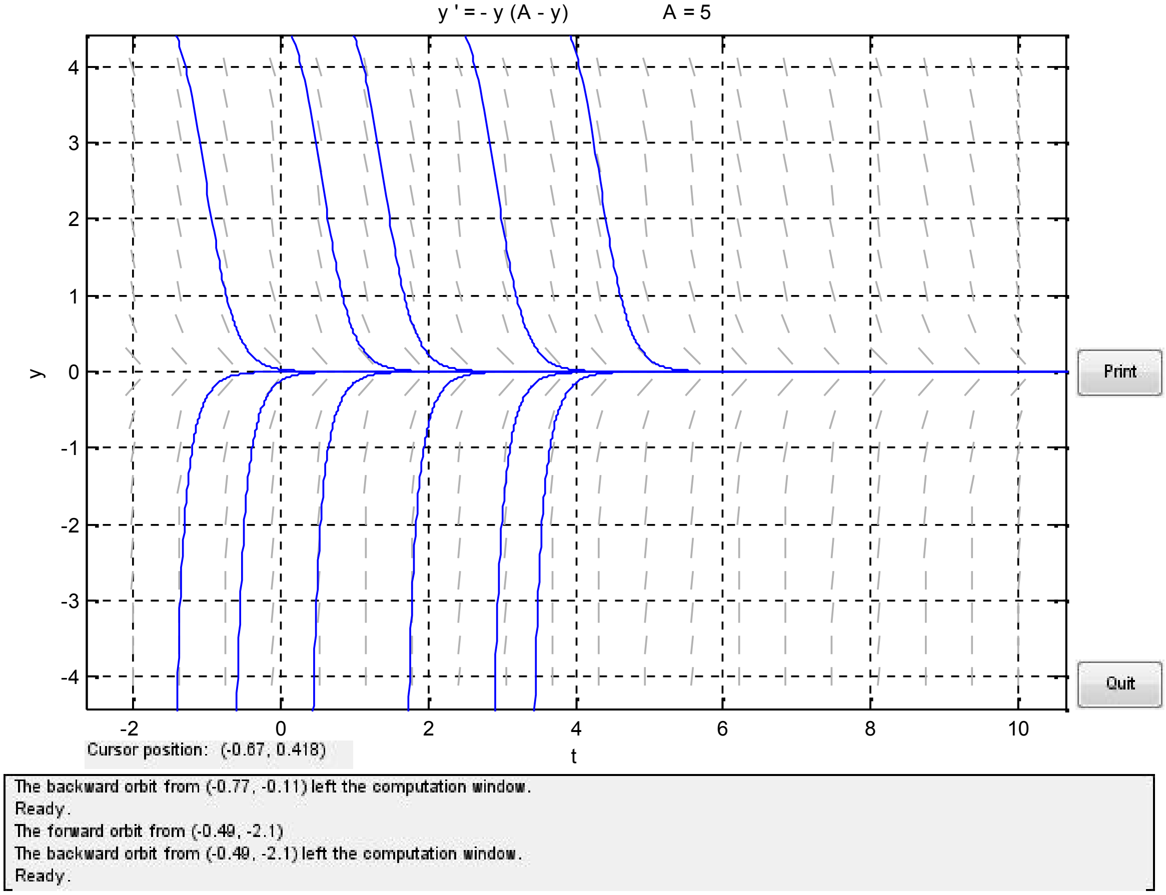
The maximum value of t = 10

The minimum value of y = -4

The maximum value of y = 4

Figure B-2 Setup window of Dfield

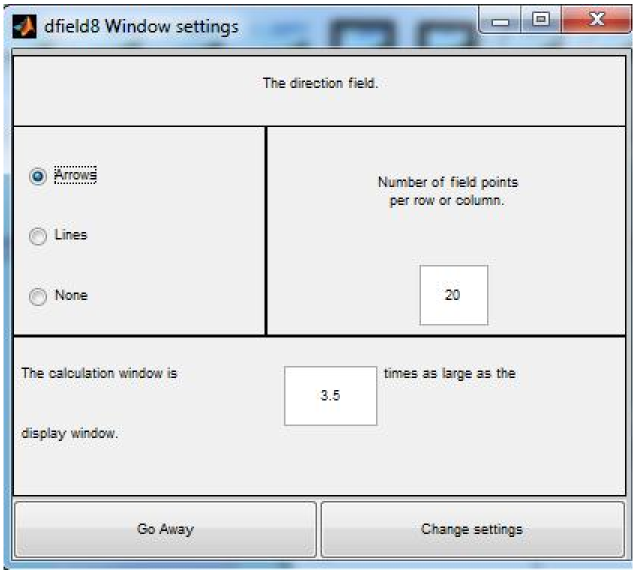
The Display window, Figure B-2 will appear. The line segments represent the slop of the straight line tangent to the integral curves (solution) of the differential equation. The collection of these line segments is the direction field of the differential equation for the range of *y* and *t* values chosen in the setup window.



```
The backward orbit from (-0.77, -0.11) left the computation window.
Ready.
The forward orbit from (-0.49, -2.1)
The backward orbit from (-0.49, -2.1) left the computation window.
Ready.
```

Figure B-3 Display window

To fill up the display window with more line segments (to better see the direction field) in the form of arrow go to *Option* → *Window Setting* and edit the pop-up window change Settings and observe the changes in the Display window (Figure B-4).



The direction field.

● Arrows
○ Lines
○ None

Number of field points per row or column. 20

The calculation window is 3.5 times as large as the display window.

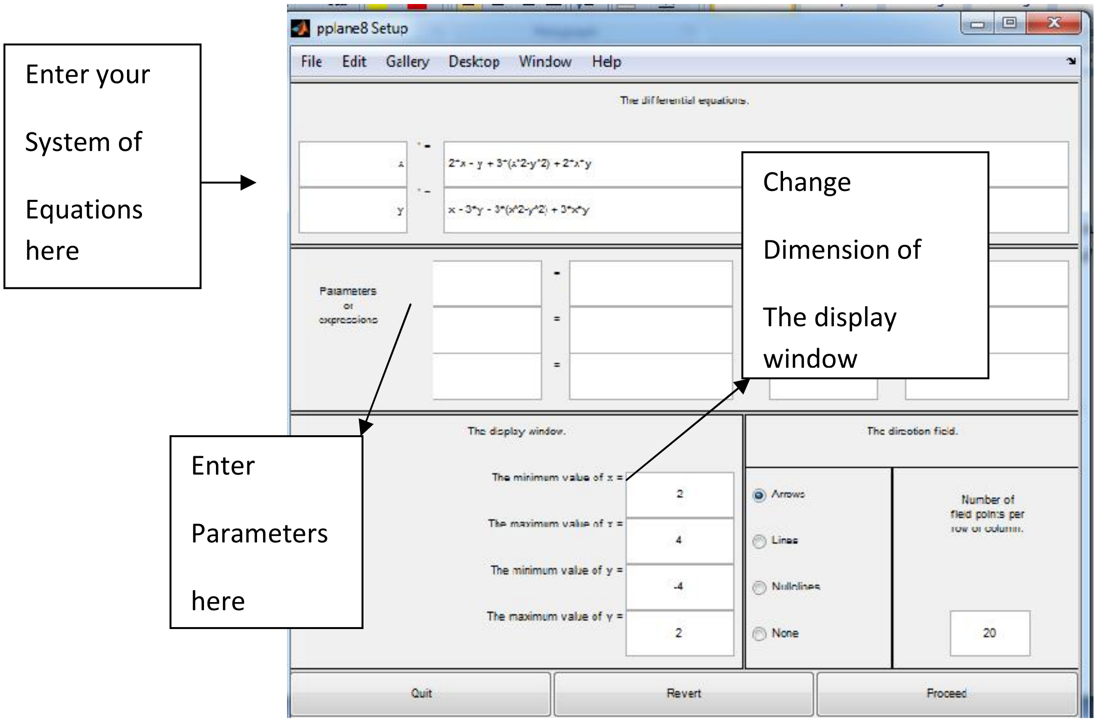
Figure B-4 Display window

Caution: if you quit Dfield and then restart it in the same matlab session you will likely encounter error/etc. So, if you quit Dfield and want to restart it, issue a close all and and then a clear all in the command window. Then restart Dfield.

PPlane

In the same way do in Dfield first Download the script Pplane8.m and open Matlab and change your working folder to the folder in which you save pplane8.m next type “pplane8” in Matlab the Set up window will pop-up in which you enter differential equations in the plane and any parameters that appear in these equations.

When Pplane8 starts it display the default setup window with the example which is already loaded.



x ' = 2*x - y + 3*(x^2-y^2) + 2*x*y

y ' = x - 3*y - 3*(x^2-y^2) + 3*x*y

The minimum value of x = 2

The maximum value of x = 4

The minimum value of y = -4

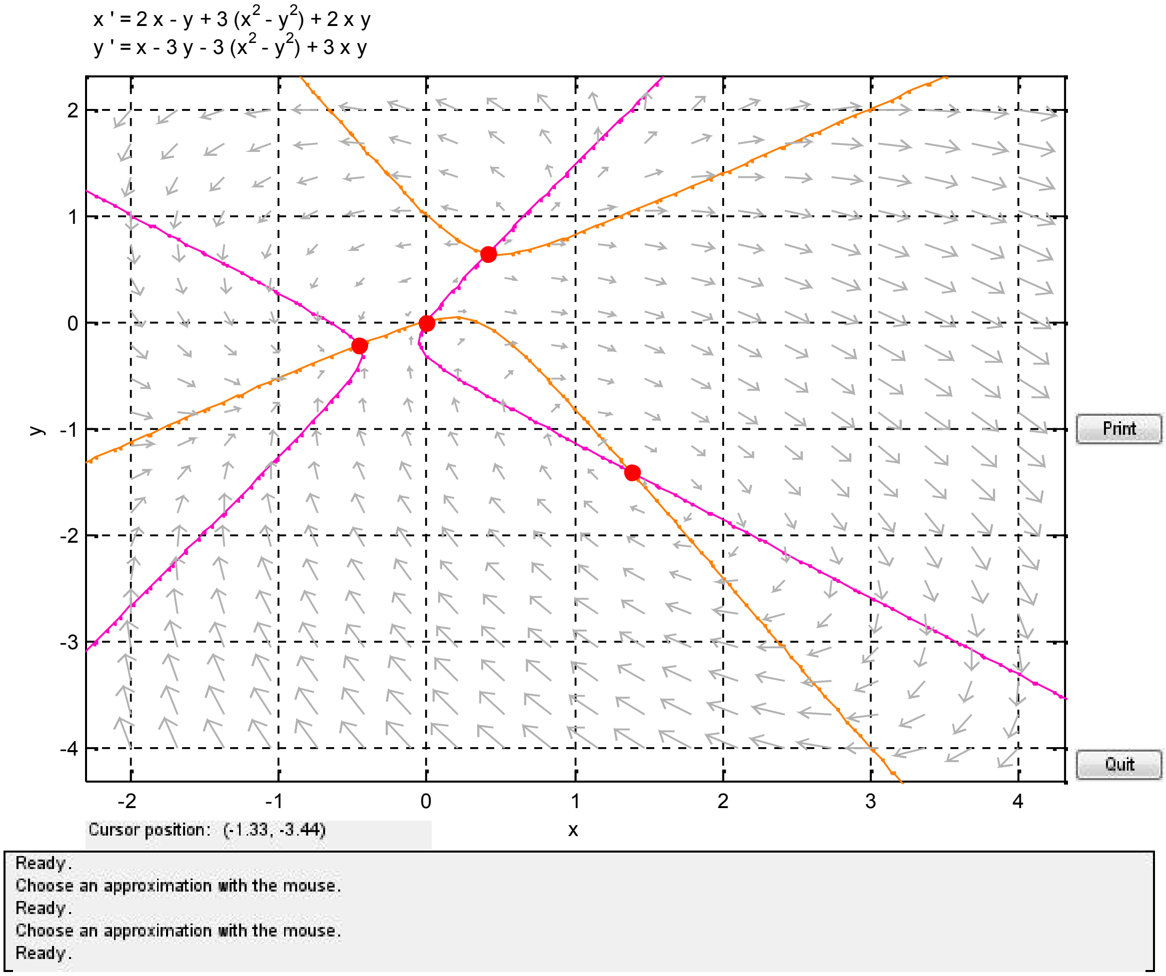
The maximum value of y = 2

● Arrows

Number of field points per row or column. 20

Figure B-5 Default pplane8 Display window

After click the proceed button we get Pplane8 Display window in this window click in *Solution* then show nullclines then after in *solution* tape click *Find an equilibrium point* finally get figure.(figure B-7)The intersection point of all the nullclines is call equilibrium points or fixed point of the system and after by click one of the equilibrium then Pplane8 Equilibrium point data window appear next we can observe the jacobian , eigenvalue and eignvectors.



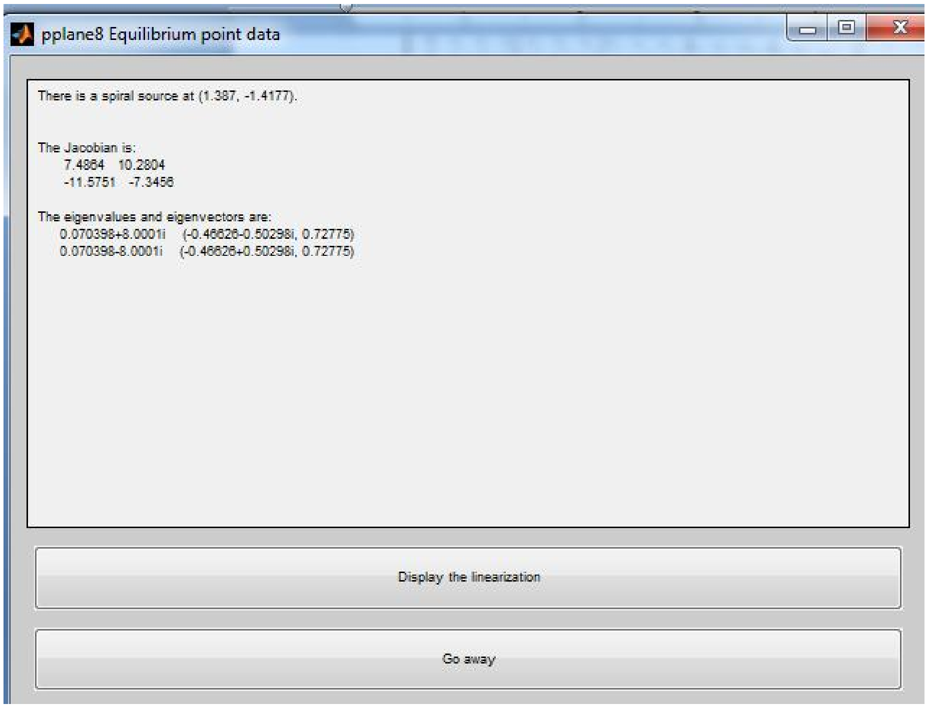
$x' = 2x - y + 3(x^2 - y^2) + 2xy$

$y' = x - 3y - 3(x^2 - y^2) + 3xy$

Cursor position: (-1.33, -3.44)

```
Ready.
Choose an approximation with the mouse.
Ready.
Choose an approximation with the mouse.
Ready.
```

Figure B-6 the figures show the equilibrium points.



```
There is a spiral source at (1.387, -1.4177).


The Jacobian is:
      7.4864    10.2804
     -11.5751    -7.3456

The eigenvalues and eigenvectors are:
     0.070398+8.0001i    (-0.46626-0.50298i, 0.72775)
     0.070398-8.0001i    (-0.46626+0.50298i, 0.72775)
```

Figure B-7 equilibrium point data window

Table 7: Various initial values of S and A compartments

Appendix C

Routh-Hurwitz Stability Criterion

The Routh-Hurwitz criterion is a method for determining whether a linear system is stable or not by examining the locations of the roots of the characteristic equation of the system. In fact, the method determines only if there are roots that lie outside of the left half plane; it does not actually compute the roots. Consider the characteristic equation

$$\mathrm{P}(\lambda) = a_5 \mathrm{a}^5 + a_4 \mathrm{a}^4 + a_3 \mathrm{a}^3 +_2 \mathrm{a}^2 + a_1 \mathrm{a}^1 + + a_0$$

To determine whether this system is stable or not, check the following conditions

1. Two necessary but not sufficient condition that all the roots have negative real parts are
   a. All the polynomial coefficients must have the same sign.
   b. All the polynomial coefficients must be nonzero
2. If condition 1 is satisfied then compute the Routh-Hurwiz arrayxSMz
3. The necessary condition that all roots have negative real parts is that all the elements of the first column of the array have the same sign. The number of changes of sign equals the number of roots with positive real parts.
4. Special Case 1: The first element of a row is zero, but some other elements in that row are nonzero. In this case, simply replace the zero elements by "Є", complete the table development, and then interpret the results assuming that “Є" is a small number of the same sign as the element above it. The results must be interpreted in the limit as Є → 0.
5. Special Case 2: All the elements of a particular row are zero. In this case, some of the roots of the polynomial are located symmetrically about the origin of the s-plane, e.g., a pair of purely imaginary roots. The zero row will always occur in a row associated with an odd power of s. The row just above the zero rows holds the coefficients of the auxiliary polynomial. The

roots of the auxiliary polynomial are the symmetrically placed roots. Be careful to remember that the coefficients in the array skip powers of s from one coefficient to the next.

$$\begin{array}{c|ccc}
\lambda^5 & a_5 & a_3 & a_1 \\
\lambda^4 & a_4 & a_2 & a_0 \\
\lambda^3 & b_1 & b_2 & \\
\lambda^2 & c_1 & c_2 & \\
\lambda^1 & d_1 & & \\
\lambda^0 & a_0 & &
\end{array}$$

Compute using the following pattern

$$b_1 = \frac{-1}{a_4}\begin{vmatrix} a_5 & a_3 \\ a_4 & a_2 \end{vmatrix} \qquad b_3 = \frac{-1}{b_1}\begin{vmatrix} a_4 & a_2 \\ b_1 & b_2 \end{vmatrix} \qquad c_2 = \frac{-1}{b_1}\begin{vmatrix} a_4 & a_0 \\ b_1 & b_3 \end{vmatrix}$$

$$b_1 = \frac{-1}{a_4}\begin{vmatrix} a_5 & a_1 \\ a_4 & a_0 \end{vmatrix} \qquad c_1 = \frac{-1}{a_4}\begin{vmatrix} a_5 & a_1 \\ a_4 & a_0 \end{vmatrix} \qquad d_1 = \frac{-1}{c_1}\begin{vmatrix} b_1 & b_2 \\ c_1 & c_2 \end{vmatrix}$$

$$b_1 = \frac{a_4a_3 - a_5a_2}{a_4}, \quad b_2 = \frac{a_4a_1 - a_5a_0}{a_4}, \quad d_1 = \frac{c_1b_2 - b_1c_2}{c_1},$$

$$c_1 = \frac{b_1a_2 - a_4b_2}{b_1}, \quad c_2 = \frac{b_1a_0 - a_4b_3}{b_1}, \quad b_3 = \frac{a_4(0) - a_5(0)}{a_4}$$

$$c_1 = \frac{a_2\left(\frac{a_4a_3 - a_5a_2}{a_4}\right) - a_4\left(\frac{a_4a_1 - a_5a_0}{a_4}\right)}{\left(\frac{a_4a_3 - a_5a_2}{a_4}\right)}$$

$$c_1 = \frac{\dfrac{a_2(a_4a_3 - a_5a_2) - a_4(a_4a_1 - a_5a_0)}{a_4}}{\dfrac{a_4a_3 - a_5a_2}{a_4}}$$

$$c_1 = \frac{a_2(a_4a_3 - a_5a_2) - a_4(a_4a_1 - a_5a_0)}{a_4a_3 - a_5a_2}$$

$$d_1 = \frac{c_1b_2 - b_1c_2}{c_1}$$

$$d_1 = (\frac{a_2(a_4a_3 - a_5a_2) - a_4(a_4a_1 - a_5a_0)}{a_4a_3 - a_5a_2})(\frac{a_4a_1 - a_5a_0}{a_4})$$

$$-(\frac{a_4a_3 - a_5a_2}{a_4})(\frac{a_4a_3 - a_5a_2}{a_4})a_0 - a_4(0))$$

$$d_1 = \frac{(a_2(a_4a_3 - a_5a_2) - a_4(a_4a_1 - a_5a_0)}{a_4a_3 - a_3a_2}(\frac{a_4a_1 - a_5a_0}{a_4})$$

$$-(\frac{a_4a_3 - a_5a_2}{a_4})(\frac{a_4a_3 - a_5a_2}{a_4})a_0$$

$$d_1 = \frac{((a_2(a_4a_3 - a_5a_2) - a_4(a_4a_1 - a_5a_0))(a_4a_1 - a_5a_0)}{a_4(a_4a_3 - a_5a_2)}$$

$$-\frac{(a_4a_3 - a_5a_2)(a_4a_3 - a_5a_2)a_0}{{a_4}^2}$$

$$d_1 = \frac{1}{a_4}\frac{((a_2(a_4a_3 - a_5a_2) - a_4(a_4a_1 - a_5a_0))(a_4a_1 - a_5a_0)}{(a_4a_3 - a_5a_2)}$$

$$-\frac{(a_4a_3 - a_5a_2)(a_4a_3 - a_5a_2)a_0}{a_4}$$

$$d_1 = \frac{1}{a_4}((a_2(a_4a_3 - a_5a_2) - a_4(a_4a_1 - a_5a_0))(a_4a_1 - a_5a_0)a_4 -$$

$$\frac{(a_4a_3 - a_5a_2)(a_4a_3 - a_5a_2)a_0(a_4a_3 - a_5a_2)}{a_4(a_4a_3 - a_5a_2)}$$

$$d_1 = \frac{1}{a_4}((a_2(a_4a_3 - a_5a_2) - a_4(a_4a_1 - a_5a_0))(a_4a_1 - a_5a_0)a_4 -$$

$$\frac{a_0(a_4a_3 - a_5a_2)(a_4a_3 - a_5a_2)(a_4a_3 - a_5a_2)}{a_4(a_4a_3 - a_5a_2)})$$

$$d_1 = \frac{1}{a_4^{\,2}}((a_4(a_2a_3 + a_5a_0) - (a_2^{\,2}a_5 + a_4^{\,2}a_1))(a_4^{\,2}a_1 - a_5a_0a_4) -$$

$$\frac{((a_0(a_4a_3 - a_5a_2)(a_4a_3 - a_5a_2)(a_4a_3 - a_5a_2))}{a_4a_3 - a_5a_2}$$

Finally we have general formula for

$$d_1 = \frac{1}{a_4^{\,2}}((a_4(a_2a_3 + a_5a_0) - (a_2^{\,2}a_5 + a_4^{\,2}a_1))(a_4^{\,2}a_1 - a_5a_0a_4) -$$

$$\frac{((a_0(a_4a_3 - a_5a_2)(a_4a_3 - a_5a_2)(a_4a_3 - a_5a_2))}{a_4a_3 - a_5a_2}$$

$$c_1 = \frac{a_2(a_4a_3 - a_5a_2) - a_4(a_4a_1 - a_5a_0)}{a_4a_3 - a_5a_2}$$

$$a_5 = 1$$

$$a_4 = (d_1 + b) + g(\sim + d_1)$$

$$b_1 = \frac{a_4a_3 - a_5a_2}{a_4}$$

$$a_0 = \frac{cehg}{\cdot\cdot}(\sim + d_1) - chd_1 g(\sim + d_1) - (\text{µ¥}\sim - fg(\sim + d_1))\frac{c^2}{\cdot\cdot\,2} - \frac{gech}{\cdot\cdot}(\sim + d_1)$$

By Routh-Hurwitz Criterion the following condition must be true if the system become stable unless unstable.

$Condition\ 1 \quad a_4 a_3 > a_5 a_2,$

$Condition\ 2 \quad a_2(a_4 a_3 - a_5 a_2) > a_4(a_4 a_1 - a_5 a_0)\ ,$

$Condition\ 3 \quad (a_4(a_2 a_3 + a_5 a_0) - (a_2{}^2 a_3 + a_4{}^2 a_1))(a_4{}^2 a_1 - a_5 a_0 a_4) >$
$(a_0(a_4 a_3 - a_5 a_2)(a_4 a_3 - a_5 a_2)(a_4 a_3 - a_5 a_2),$

$Condition\ 4 \quad a_4 > 0$