The Spatial-temporal Dynamics of Chikungunya in Most

Affected Ecuadorian Provinces

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Abstract

Chikungunya (CHIK) appeared in the western hemisphere in 2013 and is rapidly spreading to South American countries such as Ecuador. In this study, we estimate the geographical distribution of transmission rates of CHIK for 12 majorly affected Ecuadorian provinces and evaluate how spatial heterogeneity and movement of individuals impact the dynamics of the disease. Using information from past CHIK outbreaks and human transportation patterns in Ecuador, we developed a 12 patch metapopulation network model that involves connectivity of nodes via specific routes. In addition to human mobility, the altitude of the different regions is considered because it is directly correlated with vector abundance. Our results aim to

illustrate the effect of altitude, human mobility, and population heterogeneity on the spatialtemporal transmission dynamics of CHIK in Ecuador. Since past records show regular CHIK outbreaks, this information will not only aid public health officials to focus control efforts to specific regions and prepare for future outbreaks, but also help in identifying regions where CHIK can be introduced and established.

1 Introduction

Chikungunya (CHIK) is a re-emerging vector-borne disease transmitted to humans primarily by the *Aedes aegypti* mosquitoes [17]. This specie is most common in tropical and subtropical regions and is the principal vector of diseases such as dengue, yellow fever, CHIK, and zika [21]. These mosquitoes are widely distributed in urban environments and bite primarily during the day [1]. Large quantities of *Aedes aegypti* can be found in objects such as tires, cans, flowerpots, plastic containers, bottles, and natural vessels which can hold water and foster their development [21]. The females of this species are the main carriers of the chikungunya virus (CHIKV) and can live up to 50 days in optimal conditions [26].

About 72%-97% of people infected with CHIKV display symptoms similar to dengue, a disease which is also spread by the *Aedes aegypti* mosquitoes. These symptoms include fever, rash, conjunctivitis, nausea, and vomiting [30]. CHIKV victims also suffer from severe polyarthralgia which can result in arthritis. This notable feature of the disease is highlighted in its name which means "that which contorts or bends up" [30, 9, 27]. Since there are currently no vaccines for CHIK, treatment methods for the disease are aimed at alleviating symptoms [15].

The first occurrence of CHIK was discovered in Tanzania in 1954 and resulted in outbreaks in various countries of Asia and Africa from the 1960s to the 1980s [29, 18]. Within the last decade, CHIK resurfaced and has since received national attention. A major outbreak of the disease occurred in Kenya in 2005 and spread to numerous islands in the Indian Ocean, notably the French island of La Reunion where over 266,000 people were infected [32]. From there, the virus made its way throughout most of Asia and is now being locally transmitted in Europe and the Americas [30, 15]. CHIK in South America was initially observed in French Guiana in December 2013 [22]. Since then, local transmission of the virus has been reported in the South American countries of Argentina, Bolivia, Brazil, Colombia, Ecuador, Guyana, Paraguay, Peru, Suriname, and Venezuela [22].

The earliest case of CHIK in Ecuador occurred in the Loja province on October 2014 and was imported from a woman who traveled to Colombia [25]. Since then, over 4,000 CHIK cases have been reported by Ecuador's Ministry of Public Health, most of which are concentrated in the coastal regions of Esmeraldas, Manabí, and Guayas [13]. The spread of CHIK in Ecuador poses a concern for many public health officials who are left with the task of controlling its spread. However, in order to control the spread, it is important for them to understand the nature of CHIK's geographical distribution.

In this study, a metapopulation model is used to describe the dynamics of CHIK in Ecuador. The model considers how human mobility and the altitude of twelve Ecuadorian provinces shape the CHIK epidemic in the country. Studies have shown that there is a negative correlation between the abundance of *Aedes aegypti* mosquitoes and elevation [11, 16, 19]. This change in vector population is a factor which we believe may effect CHIK outbreaks in regions of different altitudes. In addition to altitude, we investigate human mobility which is said to increase the transmission of infectious diseases [18, 4, 12, 20, 5, 6, 4]. Within our model, we consider the effect of human mobility by taking into account the land transportation connecting the twelve provinces that we are investigating.

2 Methods

Many research projects have explored the transmission of disease through metapopulation models [2, 5, 12, 20, 3]. In [20], authors use an 18,000 node metapaopulation model to study the effect of human and vector mobility on the CHIK epidemic in Reunion Island. Their study incorporates a stage structured SI model for the vector population and an SIR model for humans. After validating their model using data from the Reunion epidemic, authors found that human mobility was key in the spread of the epidemic. In another paper, mobile data and climate information are used to study the effect of human mobility and seasonal variability on the 2013 dengue outbreaks in Pakistan [31]. Numerous mathematical tools such as ordinary differential equations and time dependent parameters are used to create an epidemiological model that predicts the spread and timing of dengue outbreaks in the country. In [12], a 32 patch network is used to investigate reasons for the 2009 influenza outbreak in Mexico. Their work considers land transportation, public health measures, and social distancing and suggests that a combination of these factors shaped the course of the outbreak.

While the above studies highlight the importance of migration in shaping the spread of diseases, our model goes further to combine this factor with the geographical effect of altitude on a vector borne disease. Numerous papers such as [31] consider temperature and other seasonal variations in the development and survival of the vector population. However, we focus specifically on altitude since it effects vector abundance and hence transmission of CHIK [11, 16, 19]. The value in combining the two aspects of migration and altitude lies in the fact that both play vital roles in the spread of CHIK. The two factors do not work in isolation but together shape CHIK outbreaks and modeling their combined effect provides an additional layer of understanding for this epidemic.

The Ecuadorian provinces that we choose to explore correspond to regions reported by Ecuador's Ministry of Public Health in 2015 to have presence of the Aedes Aegypti vector as well as cases of CHIK [7]. The demographics of these provinces are shown in Table 1. The provinces mostly belong to the coastal and amazonian regions of Ecuador. Provinces such as Guayas, Manabí, El Oro, Santo Domingo, Esmeraldas, and Los Rios lie along the coast. These areas have a warm climate with a variation of temperature between 25 and 36 degrees Celsius . There is also a large influx of tourists to these regions during vacations and holidays because of their beautiful beaches [8]. Extensive road networks connect these provinces and have improved trade between different regions. Guayas, Manabí, El Oro, Esmeraldas and Los Ríos have immense commercial diversity and contain seaports and oil refineries [28].

In the amazonian region where there is great biodiversity of flora and fauna, annual temperatures range between 15 and 40 degrees Celsius [10]. The provinces of Sucumbios, Orellana, Pastaza, and Zamora Chinchipe are in this region and occupy an area of 120,000 square kilometers which accounts for 48% of Ecuadorian territory. Pichincha and Azuay provinces are found in the highlands which are notorious for their high altitudes. These regions are difficult to access because of their many mountains [8].

Ν	Province	Population	Altitude (meters)	Area (miles ²)
1	Guayas	2,794,156	21.25	6,617
2	Manabí	878,480	74.00	7,104
3	El Oro	437,289	20.60	2,312
4	Santo Domingo	348,331	535.00	1,614
5	Esmeraldas	233,064	17.40	5,750
6	Los Ríos	183,806	43.00	2,415
7	Sucumbíos	105,025	321.67	7,186
8	Orellana	71,703	267.50	8,020
9	Pastaza	43,292	926.00	11,398
10	Pichincha	38,170	360.50	3,666
11	Zamora Chinchipe	15,552	1,116.00	4,076
12	Azuay	10,643	1,575.00	3,334

Table 1: Demographics of 12 Ecuadorian Provinces

In order to understand the connectivity of different provinces, we used Google Maps. This interface allowed us not only to highlight major roadways connecting the provinces, but also allowed for the assessment of efficient pathways from one region to another based on travel time and geographical features (i.e. mountains and rainforests). With this information, we were able to create a network whose edges represent the flux of transportation to and from the various provinces. The network that we employ is shown in Figure 1.



Figure 1: **Transportation Network of Provinces.** The numbered circles in this map represent the twelve provinces with presence of CHIK vector and CHIKV cases. The provinces are numbered by population size with province 1 having the largest population and province 12 having the smallest population as shown in Table 1. As shown in the legend, the color of each province corresponds to its altitude. Finally, the edges in the network represent transportation flux between provinces.

From this network, a transportation matrix T was created. Each element $\alpha_{i,j}$ of the previous matrix represents the rate of transportation from province i to province j. In our model, we assume that this matrix is symmetric. This means that the proportion of people traveling out of each province is equal to the proportion of people traveling into each province. Hence we have $\alpha_{i,j} = \alpha_{j,i}$.

The values of α_{ij} that we use were estimated based on transportation information from the National Institute of Statistics and Census (INEC) in Quito-Ecuador [23]. This public database gave information on the number of buses leaving each province and the maximum number of people each bus can hold. From this, we calculated the maximum number of total individuals

leaving the provinces. However, there was no data on the destinations of the buses. Hence, we could not find accurate α_{ij} values. Instead, we assume that the people leaving each province travel only to the provinces they are connected to. With this, we calculated the proportion of people leaving each province and divided by the number of connections for that province. To attain α_{ij} , we took the average of the proportion of people leaving provinces *i* and *j*. The values of α_{ij} that we use are on Table 2 we estimate these by using information from the census as shown in Table 2.

$\alpha_{i,j}$	Value	$\alpha_{i,j}$	Value
$\alpha_{1,3}$	0.20	$\alpha_{4,6}$	0.04
$\alpha_{1,6}$	0.21	$\alpha_{4,5}$	0.03
$\alpha_{1,12}$	0.20	$\alpha_{4,10}$	0.10
$\alpha_{2,4}$	0.13	$\alpha_{7,10}$	0.10
$\alpha_{8,10}$	0.09	$\alpha_{9,10}$	0.09
$\alpha_{11,12}$	0.02		

Table 2: Values of Transportation: $\alpha_{i,j}$ represents the proportion of people traveling from province i to province j.

As mentioned earlier, altitude effects the abundance of vectors. Hence, we alter the initial population of *Aedes aegypti* mosquitoes in each province based on their altitude. Data presented in [19] is used to determine the quantity of vectors. This data, which is given in units of mosquitoes per km^2 , was converted to represent the number of mosquitoes per square mile. After plotting the data points and removing outliers, a best fit line constructed. Using the best fit, the number of mosquitoes per m^2 was estimated. This is multiplied by the area of the respective regions to approximate the total number of mosquitoes present in that region.

INCC Province	Total Buses	Proportion
GUAYAS	2,292.00	37.20%
MANABÍ	1,394.00	22.62%
EL ORO	190.00	3.08%
SANTO DOMINGO	179.00	2.90%
ESMERALDAS	223.00	3.62%
LOS RÍOS	318.00	5.16%
SUCUMBÍOS	142.00	2.30%
ORELLANA	77.00	1.25%
PASTAZA	48.00	0.78%
PICHINCHA	1,048.00	17.01%
ZAMORA CHINCHIPE	50.00	0.81%
AZUAY	201.00	3.26%
TOTAL	6,162.00	100.00%

Figure 2: Proportion of Buses in the 12 provinces. Instituto Nacional de Estadisticas y Censo de Ecuador

2.1 Mathematical Model

Within each province that we considered two populations are studied: a population of humans (H)and a population of mosquitoes (V). We assume that only humans travel in between provinces and that all vector populations move locally within each province. This assumption is made because the vector *Aedes aegypti* can only fly on average a range of 400 m. [24]. The human population in each province, *i*, is assumed to be constant and is modeled using an SEIAR model where S_{hi} is the susceptible human class in province *i*, E_{hi} the exposed, I_{hi} the symptomatic, A_{hi} the asymptomatic, and R_{hi} the recovered class. The vector population in province *i* is also considered to be constant and is described using an SI compartmental model with susceptible, S_{vi} , and infected, I_{vi} , classes. The epidemiological classes are shown in Table 3

The movement between different classes in each province is shown in Figure 3. This flowchart

	(0	0	$\alpha_{1,3}$	0	0	$\alpha_{1,6}$	0	0	0	0	0	$\alpha_{1,12}$
	0	0	0	$\alpha_{2,4}$	0	0	0	0	0	0	0	0
	$\alpha_{1,3}$	0	0	0	0	0	0	0	0	0	0	0
	0	$\alpha_{2,4}$	0	0	$\alpha_{4,5}$	$\alpha_{4,6}$	0	0	0	$\alpha_{4,10}$	0	0
	0	0	0	$\alpha_{4,5}$	0	0	0	0	0	0	0	0
т —	$\alpha_{1,6}$	0	0	$\alpha_{4,6}$	0	0	0	0	0	0	0	0
1 -	0	0	0	0	0	0	0	0	0	$\alpha_{7,10}$	0	0
	0	0	0	0	0	0	0	0	0	$\alpha_{8,10}$	0	0
	0	0	0	0	0	0	0	0	0	$\alpha_{9,10}$	0	0
	0	0	0	$\alpha_{4,10}$	0	0	$\alpha_{7,10}$	$\alpha_{8,10}$	$\alpha_{9,10}$	0	0	0
	0	0	0	0	0	0	0	0	0	0	0	$\alpha_{11,12}$
	$\backslash \alpha_{1,12}$	0	0	0	0	0	0	0	0	0	$\alpha_{11,12}$	0 /

Transportation Matrix. Each $\alpha_{i,j}$ represents the flux of transportation from province i to province j. We assume $\alpha_{i,j} = \alpha_{j,i}$.

corresponds to the system of ordinary differential equations 1.

State Variable	Description
S_{hi}	Susceptible Humans
E_{hi}	Exposed Humans
I_{hi}	Symptomatic Humans
A_{hi}	Asymptomatic Humans
R_{hi}	Recovered Humans
S_{vi}	Suseptible Vectors
I_{vi}	Infected Vectors

Table 3: Epidemiological Classes

$$\begin{aligned} \dot{S}_{hi} &= -b\beta_{vh} \frac{I_{vi}S_{hi}}{N_{hi}} + \sum_{j=1}^{12} \alpha_{jj}S_{hj} - \sum_{j=1}^{12} \alpha_{ij}S_{hi} \end{aligned} \tag{1} \\ \dot{E}_{hi} &= b\beta_{vh} \frac{I_{vi}S_{hi}}{N_{hi}} - \delta E_{hi} + \sum_{j=1}^{12} \alpha_{ji}E_{hj} - \sum_{j=1}^{12} \alpha_{ij}E_{hi} \end{aligned} \\ \dot{I}_{hi} &= \delta(1-\phi)E_{hi} - \gamma I_{hi} + \sum_{j=1}^{12} \alpha_{ji}I_{hj} - \sum_{j=1}^{12} \alpha_{ij}I_{hi} \end{aligned} \\ \dot{A}_{hi} &= \delta\phi E_{hi} - \gamma A_{hi} + \sum_{j=1}^{12} \alpha_{ji}A_{hj} - \sum_{j=1}^{12} \alpha_{ij}A_{hi} \end{aligned} \\ \dot{R}_{hi} &= \gamma (I_{hi} + A_{hi}) + \sum_{j=1}^{12} \alpha_{ji}R_{hj} - \sum_{j=1}^{12} \alpha_{ij}R_{hi} \end{aligned}$$

$$\dot{S}_{vi} &= -b\beta_{hv} \frac{(I_{hi} + A_{hi})S_{vi}}{N_{hi}} - \mu (S_{vi} - N_{vi}) \end{aligned}$$

$$\dot{I}_{vi} &= b\beta_{hv} \frac{(I_{hi} + A_{hi})S_{vi}}{N_{hi}} - \mu I_{vi} \end{aligned}$$

The susceptible humans, S_{hi} , within each province increases by transportation from susceptible individuals in other regions and decreases by movement of susceptible people out of the province. This influence of transportation, which is represented by the summations in the differential equations, is also true for other human classes that we study. Once a susceptible person gets infected with CHIKV through a mosquito bite, he or she enters an incubation phase of the



Figure 3: **Chikungunya Model Schematic.**: The solid lines in this flow chart represent movement between different state variables while the dotted lines signify interaction between the human and vector populations

virus which takes between 2 to 4 days [17]. The progression of susceptible people to the exposed class is given by the term $b\beta_{vh} \frac{I_{vi}S_{hi}}{N_{hi}}$ where b is the biting rate, and β_{vh} the infection probability of vectors to humans.

After exposure to the CHIKV, an individual may display symptoms unless he or she is asymptomatic. In either case, the individual is still a carrier of the virus and can infect susceptible mosquitoes. The transition from exposed humans to asymptomatic humans is represented by $\delta\phi E_{hi}$ with δ being the incubation rate and ϕ the proportion of exposed people that become asymptomatic. The proportion of individuals that become symptomatic is given by $(1 - \phi)$, where ϕ is in [0, 1]. Both symptomatic and asymptomatic people are assumed to recover from CHIK at a rate γ .

Mosquitoes in each province are born into the susceptible class with birth rate μ . This birth rate is equal to the death rate in the susceptible and infected classes. The mosquitoes becomes infected

with CHIK after feeding on an infected human (symptomatic or asymptomatic). The term that represents the force of infection is $b\beta_{hv} \frac{(I_{hi}+A_{hi})S_{vi}}{N_{hi}}$ where b is again the biting rate, and β_{hv} the transmission rate of the virus from human to mosquito. This is multiplied by the proportion to infected humans $\frac{(I_{hi}+A_{hi})}{N_{hi}}$ and susceptible vectors S_{vi} . A complete list of the parameters used in this model is shown in Table 4.

In the following sections, we provide mathematical and numerical simulations of our model. We start first by finding the disease free and endemic equilibrium and analyzing them for stability. Simulations are then used to first determine the effect of altitude and transportation on the spread of CHIK in two arbitrary provinces and then to the 12 Ecuadorian provinces in this study.

3 Analysis

3.1 Disease Free Equilibrium

The disease free equilibrium (DFE) point is the point where the disease is not present in the population. For that reason, in the model the following variables are: For each provinces $i \in$

Description	Value	Source
Infection probability, mosquito to hu-	0.24	[17]
man		
Infection probability human to	0.24	[17]
mosquito		
Proportion of exposed that become	0.15	[14]
asymptomatic		
Incubation period	35 [days]	[14]
Recovered time	8 [days]	[14]
Rate of people traveling from province	estimated	[23]
<i>i</i> to province <i>j</i>		
Life span of mosquito	14 [days]	[17]
Mosquito biting rate	$0.5 [day]^{-1}$	[17]
	DescriptionInfection probability, mosquito to humanmanInfection probability human tomosquitoProportion of exposed that becomeasymptomaticIncubation periodRate of people traveling from provincei to province jLife span of mosquitoMosquito biting rate	DescriptionValueInfection probability, mosquito to human 0.24 man 0.24 Infection probability human to 0.24 mosquito 0.15 Proportion of exposed that become 0.15 asymptomatic 35 [days]Incubation period 8 [days]Rate of people traveling from province $stimated$ i to province j 14 [days]Mosquito biting rate 0.5 [day] ⁻¹

Table 4: Model Parameters and Values

 $\{1, \cdots, 12\}$ with $i \neq j$:

$$E_{hi} = I_{hi} = A_{hi} = R_{hi} = I_{vi} = 0$$
(2)

With this, the system of equations (1) simplifies to:

$$\dot{S}_{hi} = N_{hi}$$

$$\dot{S}_{ni} = N_{ni}$$
(3)

Thus, the disease free equilibrium for each province *i* lies in the point $DFE = (N_{hi}, 0, 0, 0, 0, 0, N_{vi}, 0)$ To find conditions for stability, we calculate the Jacobian matrix for the previous system of equations, and evaluate it at the DFE in (3). The Jacobian matrix is:

$$J = \begin{pmatrix} -A & 0 & 0 & 0 & 0 & 0 & -b\beta_{vh} \\ 0 & -\delta - A & 0 & 0 & 0 & 0 & b\beta_{vh} \\ 0 & \delta(1 - \phi) & -\gamma - A & 0 & 0 & 0 \\ 0 & \gamma \phi & 0 & -\gamma - A & 0 & 0 & 0 \\ 0 & 0 & \gamma & \gamma & -A & 0 & 0 \\ 0 & 0 & -b\beta_{hv} & -b\beta_{hv} & 0 & -\mu & 0 \\ 0 & 0 & b\beta_{hv} & b\beta_{hv} & 0 & 0 & -\mu \end{pmatrix}$$

In this matrix, A is equal to $\sum_{j=1}^{12} \alpha_{ij}$. To determine stability we look at the trace and determinant of the Jacobian matrix. The trace of matrix J is given by:

$$trace(J) = -5A - \delta - 2\gamma < 0 \tag{4}$$

Since the trace is negative, it is necessary that the determinant be positive for stability to hold, that is:

$$det(J) = \mu A^{2}((A+\delta)(A+\gamma)\mu - b^{2}\delta\beta_{vh}\beta_{hv})(A+\gamma) > 0$$

$$(A+\delta)(A+\gamma)\mu - b^{2}\delta\beta_{vh}\beta_{hv} > 0$$

$$(A+\delta)(A+\gamma)\mu > b^{2}\delta\beta_{vh}\beta_{hv}$$
(5)

Notice that the following equation suggests stability when the fraction is less than one.

$$\frac{b^2 \delta \beta_{vh} \beta_{hv}}{(A+\delta)(A+\gamma)\mu} < 1.$$
(6)

3.2 Basic Reproduction Number

We compute the basic reproduction number R_0 of this model using the next generation matrix. We start by identifying the infectious and disease free classes. These classes correspond respectively to the vectors (X) and (Y).

$$X = \begin{vmatrix} E_{hi} \\ I_{hi} \\ A_{hi} \\ I_{vi} \end{vmatrix} \qquad Y = \begin{bmatrix} S_{hi} \\ R_{hi} \\ S_{vi} \end{bmatrix}$$
(7)

Now, we create the matrix (\tilde{F}) whose entries represent the gain terms of each infectious class. The partial derivative of this matrix with respect to each state variable is taken and evaluated at the DFE to attain:

The loss terms in the differential equations corresponding to the infectious classes is shown in matrix \tilde{V} .

$$\tilde{V} = \begin{bmatrix} \delta E_{hi} - B + \sum_{j=1}^{12} \alpha_{ij} E_{hi} \\ -\delta(1-\phi) E_{hi} + \gamma I_{hi} - C + \sum_{j=1}^{12} \alpha_{ij} I_{hi} \\ -\delta\phi E_{hi} + \gamma A_{hi} - D + \sum_{j=1}^{12} \alpha_{ij} A_{hi} \\ \mu I_{vi} \end{bmatrix}$$
(9)

where:

$$B = \sum_{j=1}^{12} \alpha_{ji} E_{hj}, \qquad C = \sum_{j=1}^{12} \alpha_{ji} I_{hj}, \qquad D = \sum_{j=1}^{12} \alpha_{ji} A_{hj}$$
(10)

The partial derivative of matrix \tilde{V} is taken and evaluated at the DFE :

$$V = \begin{bmatrix} \delta + \sum_{j=1}^{12} \alpha_{ij} & 0 & 0 & 0 \\ -\delta(1-\phi) & \gamma + \sum_{j=1}^{12} \alpha_{ij} & 0 & 0 \\ -\delta\phi & 0 & \gamma + \sum_{j=1}^{12} \alpha_{ij} & 0 \\ 0 & 0 & 0 & \mu \end{bmatrix}$$
(11)

In which case the inverse of (11) is given by:

$$V^{-1} = \begin{bmatrix} \frac{-1}{12} & 0 & 0 & 0\\ \delta + \sum_{j=1}^{12} \alpha_{ij} & & & \\ -\frac{-\delta(1-\phi)}{12} & \frac{-1}{12} & 0 & 0\\ \gamma + \sum_{j=1}^{12} \alpha_{ij} & \gamma + \sum_{j=1}^{12} \alpha_{ij} & & \\ -\frac{\delta\phi}{\gamma + \sum_{j=1}^{12} \alpha_{ij}\delta + \sum_{j=1}^{12} \alpha_{ij}} & 0 & \frac{-1}{\gamma + \sum_{j=1}^{12} \alpha_{ij}} & 0\\ \gamma + \sum_{j=1}^{12} \alpha_{ij}\delta + \sum_{j=1}^{12} \alpha_{ij} & \gamma + \sum_{j=1}^{12} \alpha_{ij} & 0\\ 0 & 0 & 0 & \frac{-1}{\mu} \end{bmatrix}.$$
(12)

Finally, the next generation matrix is constructed:

$$FV^{-1} = \begin{bmatrix} 0 & 0 & 0 & \frac{b\beta_{vh}}{\mu} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ M & \frac{b\beta_{vh}}{12} & \frac{b\beta_{vh}}{12} & 0 \\ \gamma + \sum_{j=1}^{12} \alpha_{ij} & \gamma + \sum_{j=1}^{12} \alpha_{ij} \end{bmatrix}$$

where:

$$M = \frac{b\beta_{hv}\delta(1-\phi)}{\left(\delta + \sum_{j=1}^{12} \alpha_{ij}\right) \left(\gamma + \sum_{j=1}^{12} \alpha_{ij}\right)} + \frac{b\beta_{hv}\delta(\phi)}{\left(\delta + \sum_{j=1}^{12} \alpha_{ij}\right) \left(\gamma + \sum_{j=1}^{12} \alpha_{ij}\right)}$$

Finally, we get the R_0 per province to be:

$$R_{0_{i}} = \sqrt{\frac{b^{2}\beta_{vh}\beta_{hv}\delta(1-\phi)}{(\mu)(\delta+\sum_{j=1}^{12}\alpha_{ij})(\gamma+\sum_{j=1}^{12}\alpha_{ij})} + \frac{b^{2}\beta_{vh}\beta_{hv}\delta(\phi)}{(\mu)(\delta+\sum_{j=1}^{12}\alpha_{ij})(\gamma+\sum_{j=1}^{12}\alpha_{ij})}}$$

The R_0 of the entire system is then bounded by:

$$\underset{i=1,2,..,12}{\min} R_0(i) \le R_0 \le \underset{i=1,2,..,12}{\max} R_0(i)$$

3.3 Endemic Equilibrium point

Now we consider the case where $I_{hi} \neq 0$ and $I_{vi} \neq 0$ to obtain the endemic equilibrium point. For the endemic equilibrium we focus on a special case involving only two patches which have no asymptomatic class. In other words we choose $\phi = 0$. The following system of equations corresponds to this scenario.

$$\begin{split} \dot{S}_{h1} &= -\frac{b\beta_{vh}I_{v1}S_{h1}}{N_{h1}} + \alpha_{21}S_{h2} - \alpha_{12}S_{h1} \\ \dot{S}_{h2} &= -\frac{b\beta_{vh}I_{v2}S_{h2}}{N_{h2}} + \alpha_{12}S_{h1} - \alpha_{21}S_{h2} \\ \dot{E}_{h1} &= \frac{b\beta_{vh}I_{v1}S_{h1}}{N_{h1}} - \delta E_{h1} + \alpha_{21}E_{h2} - \alpha_{12}E_{h1} \\ \dot{E}_{h2} &= \frac{b\beta_{vh}I_{v2}S_{h2}}{N_{h2}} - \delta E_{h2} + \alpha_{12}E_{h1} - \alpha_{21}E_{h2} \\ \dot{I}_{h1} &= \delta E_{h1} - \alpha_{12}I_{h1} - \gamma I_{h1} + \alpha_{21}I_{h2} \\ \dot{I}_{h2} &= \delta E_{h2} + \alpha_{12}I_{h1} - \alpha_{21}I_{h2} - \gamma I_{h2} \\ \dot{S}_{v1} &= -\frac{b\beta_{hv}I_{h2}S_{v2}}{N_{v2}} + \mu I_{v2} \\ \dot{S}_{v2} &= -\frac{b\beta_{hv}I_{h2}S_{v2}}{N_{v2}} + \mu I_{v2} \\ \dot{I}_{v1} &= \frac{b\beta_{hv}I_{h1}S_{v1}}{N_{v1}} - \mu I_{v1} \\ \dot{I}_{v2} &= \frac{b\beta_{hv}I_{h2}S_{v2}}{N_{v2}} - \mu I_{v2} \end{split}$$

Where the total individual and mosquito population are given by:

$$N_{h1} = S_{h1} + E_{h1} + I_{h1}$$

$$N_{h2} = S_{h2} + E_{h2} + I_{h2}$$

$$N_{v1} = S_{v1} + I_{v1}$$

$$N_{v2} = S_{v2} + I_{v2}$$
(14)

The endemic equilibrium point is found by setting to zero and solving the previous system equations. Here, we assume $\alpha_{12} = \alpha_{21}$. This simplifies the equations and gives the following solution:

$$E_{h1} = -\frac{\alpha_{21}\mu(N_{h1}N_{v1}S_{v2} - N_{h2}N_{v2}S_{v1})(\gamma + 2\alpha_{21})}{S_{v2}S_{v1}\beta_{hv}\beta_{vh}b^{2}\delta}$$

$$E_{h2} = \frac{\alpha_{21}\mu(N_{h1}N_{v1}S_{v2} - N_{h2}N_{v2}S_{v1})(\gamma + 2\alpha_{21})}{S_{v2}S_{v1}\beta_{hv}\beta_{vh}b^{2}\delta}$$

$$I_{h1} = -\frac{\alpha_{21}\mu(N_{h1}N_{v1}S_{v2} - N_{h2}N_{v2}S_{v1})}{\beta_{hv}\beta_{vh}S_{v1}S_{v2}b^{2}}$$

$$I_{h2} = \frac{\alpha_{21}\mu(N_{h1}N_{v1}S_{v2} - N_{h2}N_{v2}S_{v1})}{\beta_{hv}\beta_{vh}S_{v1}S_{v2}b^{2}}$$

$$I_{v1} = -\frac{\alpha_{21}(N_{h1}N_{v1}S_{v2} - N_{h2}N_{v2}S_{v1})}{b\beta_{vh}S_{v2}N_{v1}}$$

$$I_{v2} = \frac{\alpha_{21}(N_{h1}N_{v1}S_{v2} - N_{h2}N_{v2}S_{v1})}{b\beta_{vh}S_{v2}N_{v1}}$$

$$S_{h1} = \frac{(4\alpha_{21}^{2} + 2\alpha_{21}\delta + 2\alpha_{21}\gamma + \delta\gamma)N_{v1}N_{h1}\mu}{(b^{2}S_{v1}\beta_{vh}\beta_{hv}\delta)}$$

$$S_{h2} = \frac{(4\alpha_{21}^{2} + 2\alpha_{21}\delta + 2\alpha_{21}\gamma + \delta\gamma)\mu N_{h2}N_{v2}}{b^{2}\beta_{vh}\beta_{hv}\delta S_{v2}}$$

$$S_{v1} = S_{v1}$$

3.4 Stability for endemic equilibrium point

 $-\frac{b\beta_{vh}I_{v1}}{N_{h1}} - \alpha_{12}$ $-\frac{b\beta_{vh}S_{h1}}{N_{h1}}$ α_{21} $-\frac{b\beta_{vh}I_{v2}}{N_{h2}} - \alpha_{21}$ $\frac{b\beta_{vh}S_{h2}}{N_{h2}}$ α_{12} $\tfrac{b\beta_{vh}I_{v1}}{N_{h1}}$ $\frac{b\beta_{vh}S_{h1}}{N_{h1}}$ $-\delta - \alpha_{12}$ α_{21} $\frac{b\beta_{vh}I_{v2}}{N_{h2}}$ $\frac{b\beta_{vh}S_{h2}}{N_{h2}}$ $-\delta - \alpha_{21}$ α_{12} δ $-\alpha_{12} - \gamma$ α_{21} δ $-\alpha_{21} - \gamma$ α_{12} $-\frac{b\beta_{hv}S_{v1}}{N_{v1}}$ $\frac{b\beta_{hv}I_{h1}}{N}$ μ 0 $\frac{b\beta_{hv}S_{v2}}{N_{v2}}$ $\frac{b\beta_{hv}I_{h2}}{N_{v2}}$ μ $\tfrac{b\beta_{hv}S_{v1}}{N_{v1}}$ $\frac{b\beta_{hv}I_{h1}}{N_{v1}}$ $-\mu$ $\frac{b\beta_{hv}S_{v2}}{N_{v2}}$ $b\beta_{hv}I_{h2}$ μ

To analyze the stability of the equilibrium point, the first step is to find the Jacobian matrix:

This Jacobian matrix is evaluated at the endemic equilibrium point (EE) with the aim of finding the stability conditions for this point, where the terms are denoted by:

• $M_1 = \frac{\alpha_{12}(N_{h1}N_{v1}S_{v2}-N_{h2}N_{v2}S_{v1})}{S_{v2}N_{v1}N_{h1}}$

•
$$M_2 = -\frac{N_{v1}\mu(4\alpha_{12}^2 + 2\delta\alpha_{12} + 2\gamma\alpha_{12} + \delta\gamma)}{b\delta S_{v1}\beta_{hv}}$$

•
$$M_3 = -\frac{\alpha_{12}(N_{h1}N_{v1}S_{v2}-N_{h2}N_{v2}S_{v1})}{S_{v1}N_{v2}N_{h2}}$$

•
$$M_4 = -\frac{\mu N_{v2}(4\alpha_{12}^2 + 2\delta\alpha_{12} + 2\gamma\alpha_{12} + \delta\gamma)}{b\delta\beta_{hv}S_{v2}}$$

•
$$M_5 = -\frac{\alpha_{12}(N_{h1}N_{v1}S_{v2}-N_{h2}N_{v2}S_{v1})}{S_{v2}N_{v1}N_{h1}}$$

•
$$M_6 = \frac{N_{v1}\mu(4a_{12}^2 + 2\alpha_{12}\delta + 2\alpha_{12}\gamma + \delta\gamma)}{bS_{v1}\beta_{hv}\delta}$$

•
$$M_7 = \frac{\alpha_{12}(N_{h1}N_{v1}S_{v2}-N_{h2}N_{v2}S_{v1})}{S_{v1}N_{v2}N_{h2}}$$

•
$$M_8 = \frac{(4\alpha 12^2 + 2\alpha_{12}\delta + 2\alpha_{12}\gamma + \delta\gamma)\mu N_{v2}}{b\beta_{hv}\delta S_{v2}}$$

•
$$M_9 = -\frac{b\beta_{hv}S_{v1}}{N_{v1}}$$

•
$$M_{10} = \frac{\alpha_{12}\mu(N_{h1}N_{v1}S_{v2}-N_{h2}N_{v2}S_{v1})}{b\beta_{vh}S_{v1}S_{v2}N_{v1}}$$

•
$$M_{11} = -\frac{b\beta_{hv}S_{v2}}{N_{v2}}$$

•
$$M_{12} = -\frac{\alpha_{12}\mu(N_{h1}N_{v1}S_{v2}-N_{h2}N_{v2}S_{v1})}{b\beta_{vh}S_{v1}S_{v2}N_{v2}}$$

•
$$M_{13} = \frac{b\beta_{hv}S_{v1}}{N_{v1}}$$

•
$$M_{14} = -\frac{\alpha_{12}\mu(N_{h1}N_{v1}S_{v2}-N_{h2}N_{v2}S_{v1})}{b\beta_{vh}S_{v1}S_{v2}N_{v1}}$$

•
$$M_{15} = \frac{b\beta_{hv}S_{v2}}{N_{v2}}$$
 • $M_{16} = \frac{\alpha_{12}\mu(N_{h1}N_{v1}S_{v2}-N_{h2}N_{v2}S_{v1})}{b\beta_{vh}S_{v1}S_{v2}N_{v2}}$

And the matrix is:

$M_1 - \alpha_{21}$	α_{21}	0	0	0	0	0	0	M_2	0
α_{12}	$M_3 - \alpha_{21}$	0	0	0	0	0	0	0	M_4
M_5	0	$-\delta - \alpha_{12}$	α_{21}	0	0	0	0	M_6	0
0	M_7	α_{12}	$-\delta - \alpha_{21}$	0	0	0	0	0	M_8
0	0	δ	0	$-\alpha_{12} - \gamma$	α_{21}	0	0	0	0
0	0	0	δ	α_{12}	$-\alpha_{21} - \gamma$	0	0	0	0
0	0	0	0	M_9	0		0	μ	0
0	0	0	0	0	M_{11}	0	M_{12}	0	μ
0	0	0	0	M_{13}	0	M_{14}	0	$-\mu$	0
0	0	0	0	0	M_{15}	0	M_{16}	0	$-\mu$

To determine the conditions for stability, we look at the eigenvalues of the Jacobian evaluated at the EE point. The eigenvalues were not easily simplified. Hence, we took many realistic parameter values and calculated the eigenvalues of the Jacobian with these values. In all cases we got one eigenvalue with positive real part. For that reason we concluded the endemic point is unstable for any value of the parameters.

4 Results

This section is divided into four subsections. In the first three subsections we assess how transportation, altitude and the combination of these two factors effect CHIK dynamics in 2 provinces, province A and province B. In all cases, we start the epidemic with one infected individual in province A. This is because the simulations obtained when starting with one infected individual in province A had the same effect on peak size, peak time, final size, and duration of the epidemic as starting with one infected individual in province B. Although the numbers differed in each case, the general trend did not. Whenever these factors increased in the case where we start in province A, they also increased in the scenario starting with province B.

Following the two patch simulations, we consider CHIK dynamics in our 12 patch model based on the two factors that we expect affects the transmission of the CHIKV. We start with one infected individual in the Manabí province. This province was chosen because it was reported to have the most CHIK cases at the end of 2014. [7]

4.1 Effect of Transportation

4.1.1 **Provinces with Same Population Size**

Assume that province A and province B have the same population, namely the population size of Guayas province, 2,794,156 people. If we change the flux of transportation between the two provinces, we observe that a change in transportation does not significantly alter the dynamics in this system. Since this case is trivial, we do not include graphics for it.

4.1.2 **Provinces with Vastly Different Population Size**

We now consider two provinces with vastly different population size. Let province A have population size 2,794,156 (highest population) and province B have population 10,643 (smallest population). The effect of changing transportation flux between the two provinces can be seen in the following Figure 4 and Table 5. Decreasing α decreases peak time and duration for both provinces. This decrease in transportation increases the peak size and final size in province A and decreases the peak time in province B.



Figure 4: Transportation Effect in Provinces with Vastly Different Population Sizes: Province A has population size 2,794,156 and province B has population 10,643. In (a) $\alpha = 0.50$, (b) $\alpha = 0.25$, and (c) $\alpha = 0.10$.

Epidemiological	Province A	Province B	Province A	Province B	Province A	Province B
Variable	$\alpha =$	- 0.5	$\alpha =$	0.25	$\alpha =$	0.10
Peak Size	91,704	88,410	100,069	89,409	128,926	87,300
Peak Time	365	366	345	346	296	299
Final Size	2,399,000	8,981	2,420,000	8,564	2,471,000	7,251
Duration	350	350	320	320	300	300

Table 5: Effect of Changing Transportation in Provinces with Vastly Different PopulationSize: Province A has population size 2,794,156 and province B has population 10,643.

4.1.3 Provinces with Similar Population Size

When we consider two provinces with similar population sizes, province A and B with 233,063 and 183,806 people respectively, we observe that decreasing transportation increases peak size in province A and decreases it in province B. This change keeps peak time fairly constant and does not change duration. On the other hand, it results in an increase in final size for province A and a decrease in final size for province B. These observations can be seen in Table 6.

Epidemiological	Province A	Province B	Province A	Province B	Province A	Province B
Variable	$\alpha = 0.5$		$\alpha = 0.25$		$\alpha = 0.10$	
Peak Size	13,164	13,110	13,241	13,059	13,535	12,848
Peak Time	328	329	327	328	326	327
Final Size	199,900	157,300	200,600	156,700	203,500	154,000
Duration	370	370	370	370	370	370

Table 6: Effect of Changing Transportation in Provinces with Similar Population Size:Province A has population size 233,063 and province B has population 183,806.

4.2 Effect of Altitude

4.2.1 **Provinces with Same Population Size**

In this part, we consider two provinces with the same population. Let province A and B have size 10,643. The proportion of tansportation between the two provinces does not change. In all cases we let $\alpha = 0.1$ while varying altitude. Since an increase in altitude is said to decrease mosquito population, we assume that a low altitude region has 100% mosquitoes while the medium and high altitudes have 62% and 25% of mosquitoes respect the altitude.

Epidemiological	Province A	Province B	Province A	Province B	Province A	Province B
Variable						
Altitude	High	High	High	Low	High	Medium
Population	10,643	10,643	10,643	10,643	10,643	10,643
Peak Size	1	0	3,267	3,267	76	77
Peak Time	0	0	931	930	5,122	5,121
Final Size	1	0	600,000	3,000,000	200,000	700,000
Duration	200	days	1,100	days	8,000) days

Table 7: Effect of Changing Altitude with Same Population

By Table 7, we see that if two connected provinces with the same population both have high altitude, there will be no epidemic of CHIK. However when we have varying altitude, final size is higher in the lower altitude region. The total number of cases in connected provinces that have high-low altitudes is higher than that in connected provinces that have high-medium altitudes.

4.2.2 Provinces with Vastly Different Population size

We now chose provinces A and B to have population like Guayas and Azuay according the Figure

1.

Epidemiological	Province A	Province B	Province A	Province B	Province A	Province B
Variable						
Altitude	High	Medium	Low	High	Medium	High
Population	2,794,156	10,643	2,794,156	10,643	2,794,156	10,643
Peak Size	1	0	68,953	65,649	20,838	19,825
Peak Time	0	0	489	490	1,040	1,041
Final Size	3	0	2,000,000	1,813	2,000,000	2,005
Duration	200 days		1,150 days		8,000 days	

Table 8: Effect of Changing Altitude with Vastly Different Population

When looking at populations with vastly different sizes in Table 8, we see that if the bigger region has higher altitude, there is no CHIK epidemic. We also observed this case when province A has high altitude and province B has low altitude but do not include it on the table. However, if this region has either low or medium altitude, an epidemic ensues. In the case where province A is low altitude and province B is high altitude we get a larger peak size and smaller peak time than if province A were medium altitude and province B high altitude.

4.2.3 Provinces with Similar Population size

Let province A and B have population sizes corresponding to Esmeraldas (233, 064) and Los Ríos (183, 806) respectively.

When provinces of similar population are connected, we observe that there is no disease out-

Epidemiological	Province A	Province B	Province A	Province B	Province A	Province B
Variable						
Altitude	High	Medium	Low	High	Medium	High
Population	233,064	183, 806	233,064	183, 806	233,064	183, 806
Peak Size	1	0	3,916	3,787	245	238
Peak Time	0	0	778	779	2,963	2,964
Final Size	3	0	200,000	40,000	90,000	20,000
Duration	200 days		900 days		4,000 days	

Table 9: Effect of Changing Altitude with Similar Population

break when the larger province has high altitude. This is also the case when the larger province has high altitude and the smaller one has low altitude. in the other altitude combinations considered, an outbreak occurs.

4.3 Combined Effect of Altitude and Transportation

4.3.1 Provinces with Same Population size

After exploring the individual effects of transportation and altitude on two connected provinces, we simulate what would happen when considering both factors simultaneously. We first start by looking at two provinces with the same population size. We assume that one of these provinces, province A, has low altitude and that province B has high altitude. We alter transportation between the two provinces to obtain the following results.

Epidemiological	Province A	Province B	Province A	Province B	Province A	Province B
Variable	$\alpha = 0.5$		$\alpha = 0.25$		$\alpha = 0.10$	
Peak Size	148	147	154	149	180	159
Peak Time	682	683	667	667	614	611
Final Size	9,850	2,445	9,972	2,427	$1.1e^{4}$	2,341
Duration	1,000 days		1,000 days		775 days	

Table 10: Effect of Altitude (Low-High) and Changing Transportation: Province A and B have population size 10, 643. Province A has low altitude and province B low altitude.

In Table 10 we see that the province lower altitude has more cases of CHIK. In addition, decreasing transportation resulted in a decrease in peak time in both provinces. However, this same decrease in flux of transportation increased the final size and peak size of the epidemic in both provinces.

4.4 **Provinces with Vastly Different Population size**

The effects of altering altitude and transportation on provinces of vastly different populations is studied. Let province A have the same population size as Guayas which has 2,794,156 people, and let province B have the same population size as Azuay with population 10,643 people. Assume that A has low altitude and B with high altitude. We show the effect of changing transportation below.

Epidemiological	Province A	Province B	Province A	Province B	Province A	Province B
Variable	$\alpha = 0.5$		$\alpha = 0.25$		$\alpha = 0.10$	
Peak Size	200	196	217	202	286	221
Peak Time	505	504	484	483	424	427
Final Size	9,855	2,415	10,000	2,375	10,000	2,194
Duration	700	700	700	700	650	650

Table 11: Effect of Altitude (Low-High) and Changing Transportation with Vastly Different **Population Size**: Province A has population size 2, 794, 156 and low altitude. Province B has population 10, 643 and high altitude

Through Table 11 we see that decreasing transportation results in a decrease in peak time and increase in peak size. The final size for the low altitude region increased overall while the final size for the high altitude region increases from $\alpha = 0.5$ to 0.25 and decreases from $\alpha = 0.25$ to

0.1.

If province A were to have high altitude and province B low altitude, we observe that an epidemic does not occur regardless of changing transportation, as seen in Figure 5.



Figure 5: **Prevalence of Province A and B with Vastly Different Population Sizes.** Province A has population size 2,794,156 and high altitude. Province B has population 10,643 and low altitude.

In the case where province A has high altitude and province B has medium altitude. We observe results similar to the previous case where an epidemic does not occur regardless of a change in transportation. Switching the altitudes of province A and B (i.e. province A has medium altitude and province B has high altitude), we observe something different as shown in Table 12. An epidemic persists and a decrease in transportation increases peak size and decreases the peak time and duration for both provinces. However, it results in a decrease in final size for the high altitude province.

Epidemiological	Province A	Province B	Province A	Province B	Province A	Province B
Variable	$\alpha = 0.5$		$\alpha = 0.25$		$\alpha = 0.10$	
Peak Size	26,597	2,5631	31,808	28388	51,552	34,926
Peak Time	788	791	720	720	562	565
Final Size	2,000,000	2,398	2,000,000	2,344	2,000,000	2,071
Duration	800	800	700	700	600	600

Table 12: Effect of Altitude (Medium-High) and Changing Transportation with Vastly Different Population Size: Province A has population size 2,794,156 and medium altitude. Province B has population 10,643 and high altitude.

4.4.1 Provinces with Similar Population size

Assume that province A has population size 233,064 people as in Esmeraldas and that province

B has population size equal to that of Los Ríos which is 183,806 people. If province A has low

altitude and province B has high altitude we observe the following results.

Epidemiological	Province A	Province B	Province A	Province B	Province A	Province B
Variable	$\alpha = 0.5$		$\alpha = 0.25$		$\alpha = 0.10$	
Peak Size	5,096	4,969	5,543	5125	7,336	5,525
Peak Time	587	585	563	561	487	490
Final Size	200,000	40,000	200,000	40,000	300,000	40,000
Duration	600	600	600	600	600	600

Table 13: Effect of Altitude (Low-High) and Changing Transportation with Similar Population Size: Province A has population size 233,064 and low altitude. Province B has population 183,806 and high altitude.

In Table 13, we see that a decrease in transportation results in an increases in peak size and a decreases in peak time and duration for both provinces. However with a drastic reduction in

transportation, we see an increase in final size in the province with low altitude.

If province A were to have high altitude and province B low altitude, an outbreak does not

occur regardless of change in transportation. This is also true if A has high altitude and province

B medium altitude so we do not include these tables. However, when we switch the altitudes and allow province A to have medium altitude and province B to have high altitude we have the following results in Table 14 we see that a decrease in transportation results in an increase in final size for both provinces. It also results in a decrease in peak time and duration.

Epidemiological	Province A	Province B	Province A	Province B	Province A	Province B
Variable	$\alpha = 0.5$		$\alpha = 0.25$		$\alpha = 0.10$	
Peak Size	313	307	385	362	747	593
Peak Time	2,258	2,259	2,069	2,071	1,583	1,579
Final Size	60,000	19,000	66,000	20,000	90,000	23,000
Duration	3,200	3,200	2,900	2,900	2,000	2,000

Table 14: Effect of Altitude (Medium-High) and Changing Transportation with Similar Population Size: Province A has population size 233,064 and medium altitude. Province B has population 183,806 and high altitude.

4.5 Effect of considering Altitude in 12 provinces

After observing what happens in two arbitrary provinces, we extend our scope to the 12 Ecuadorian provinces with CHIK cases. We start by taking all $\alpha_{ij} = 0.08$ and compare this result to that of using the different transportation parameters that we calculated in Table 2. We then simulate what would occur if only the altitude of the regions was taken into account, keeping the same flux of transportation between all connected provinces. Finally, we compare our results of varying only transportation to varying transportation and altitude. Our simulations are shown below. In all of the simulations, we start with one infectious individual in the Manabí province.



Figure 6: **Prevalence of 12 Provinces- Same Transportation vs. Varying Transportation**: The blue line in each graph represents CHIK dynamics when making all $\alpha_{ij} = 0.08$ and the red line represents the dynamics when taking α values in 2



Figure 7: Difference in Final Size- Same Transportation Minus Varying Transportation :This histogram shows the difference between the final epidemiological size when all $\alpha_{ij} = 0.08$ and when taking α values in 2



Figure 8: Difference in Final Size- No Altitude Minus Altitude :This histogram shows the difference between the final epidemiological size when we do not consider altitude between regions and when we consider different altitude between regions as shown in 1. In both cases all $\alpha_{ij} = 0.1$.



Figure 9: Prevalence 12 Provinces- No Altitude vs. Altitude : The blue line in each graph represents CHIK dynamics when we do not considering different altitude between regions. The red line represents the dynamics when consider different altitude between regions as shown in 1. In both cases all $\alpha_{ij} = 0.1$.



Figure 10: **Difference in Final Size - Varying Transportation Alone minus Varying Altitude and Transportation**: This histogram shows the difference between the final epidemiological size when varying transportation alone versus varying atitude and transportation.



Figure 11: Prevalence of 12 Provinces- Varying Transportation Alone vs. Varying Altitude and Transportation: The top graph represents the prevalence of CHIK when varying only transportation between provinces as shown in 2. The bottom graph represents the combined effect of varying transportation and varying altitude between regions as seen in 1.



Figure 12: Differences in Prevalence- Varying Transportation Alone Minus Varying Altitude and Transportation: The blue lines show the prevalence of CHIK when varying only transportation between provinces as shown in 2. The red lines represents the combined effect of varying transportation and varying altitude between regions as seen in 1.

5 Conclusions

In order to understand the spacial-temporal dynamics of CHIK in 12 of Ecuador's most affected provinces, it was vital to first understand the spacial-temporal dynamics embedded in two provinces. Based on the results of the two patch system, we conclude that the factors of transportation, altitude, and region heterogeneity, especially with regards to varying population sizes, is essential to understanding the nature of CHIK outbreaks. This is because each factor shapes the epidemic dynamics of peak size, peak time, final epidemic size, and duration of the epidemic in different ways. For example, increasing transportation will decrease the total number of cases in regions of vastly different populations while increasing the peak time and duration of the epidemic. An increase in transportation may be beneficial for these regions for it lessens the total number of cases while providing time for control measures to be implemented. In another case, where two areas have similar but not identical population sizes, increasing transportation decreases the final size in the area with larger population and increases final size in the smaller region.

When altering only altitude between two provinces, we were able to visualize how geography effects the natural spread of CHIK. We saw that if regions with similar or identical population sizes and different altitudes are connected, altitude is usually a determining factor as to which region has a higher cumulative case of CHIK. This is almost always the region with lower altitude because of its abundance in mosquitoes. Some significant cases to consider are those that resulted in no CHIK outbreaks. This scenario happened most often when pairing a populous high altitude region with any other region. This result may be caused by a combination of varying population sizes and small number of vectors in the populous city.

Looking at the results from the previous section, we found that changing transportation in two provinces of the same population but different altitudes has the same effect on peak size, peak time, final size, and duration as altering transportation alone. We also see that decreasing transportation in provinces of different altitudes and populations varies widely in its effect on CHIK spread. However, when dealing with two cities of vastly different populations where the larger region has high altitude, an epidemic does not occur regardless of a change in transportation. This shows that the effect of altitude in these provinces supersedes that of transportation.

The above conclusions were true when looking at the 12 province simulations and helped explain the changes in CHIK dynamics in those patches. We noticed that varying the flux of transportation between provinces was more beneficial than keeping the flux constant for it decreases the final epidemiological size in most provinces. Varying only altitude between regions seems to drastically effect CHIK dynamics as seen in Figure 8. When varying both transportation flux and altitude among the 12 provinces another story is told in regards to the the peak size, duration, and final size of the epidemic in each region. This is a story which we believe may be more accurate than considering only the effect of transportation as many studies do.

The wide variation in results when considering spacial heterogeneity, connectivity, and altitude strongly supports the need to consider all three aspects in devising plans to combat CHIK in Ecuador. This information can help focus control efforts for this disease and can inform the creation of new risk maps based on transportation and altitude. Knowing scenarios where CHIK outbreaks are less likely to occur, based on this data, will allow efficient use of government money when funding control efforts. In addition, this information provides insight as to how the government can strategically utilize the transportation and geographical features specific to their region when dealing with CHIK. For example they may be able to temporarily limit the number of buses traveling between different regions as a sort of social distancing measure while they enforce vector control methods in high risk regions. They can even create different (or temporary) routes of transportation to get from one region to another to further the decline in CHIK cases.

While this study aimed at giving a fairly realistic analysis of the spread of CHIK in Ecuador, it has some limitations. The first of these is the lack of transportation information for the different provinces that we study. While we were able to approximate the proportion of people traveling out of each province through Ecuadorian transportation data, we could find no public information on what proportion of those people were going to the other provinces. Hence, our transportation parameters could not fully tell the story of CHIK spread in the 12 Ecuadorian provinces. There was also no substantial public data detailing CHIK cases in Ecuador which could validate our model. In our future work, we hope to attaining both transportation information and cases of CHIK in order to improve this model. We would also like to incorporate seasonality in the distribution of cases. Control measures such as pesticides and larvicides could also be included to see how effective they will be given the current state of CHIK in Ecuador.

Acknowledgements

We would like to thank the Mathematical and Theoretical Biology Institute (MTBI) co-Directors Dr. Carlos Castillo-Chavez, Dr. Anuj Mubayi, and Dr. Marlio Paredes for giving us the opportunity to participate in this research program. We would also like to thank Associate Director Sherry Woodley and Coordinator Ciera Duran for their efforts in planning and executing the day to day activities of MTBI. We also want to give special thanks to Dr. Mayteé Cruz-Aponte , Dr. Emmanuel J. Morales Butler, and Dr. Padmanabhan Seshaiyer for their help on this project. The research has been carried out at MTBI which is a Research Experience for Undergraduate (REU) summer program at the Simon A. Levin Mathematical, Computational and Modeling Sciences Center (SAL MCMSC) at Arizona State University (ASU). This project has been partially supported by grants from the National Science Foundation (DMS1263374), the Office of the President of ASU, and the Office of the Provost at ASU.

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