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## Modeling the spread of a wheat pathogen in the United States of America

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# Modeling the spread of a wheat pathogen in the United States of America

## Abstract

Stem rust of wheat (*Puccinia graminis tritici*) is certainly not a new fungal pathogen; however, in 1999 a new variety of the disease (which became known as Ug99) was discovered in eastern Africa. This new strain of wheat rust has become epidemic in this area of the world and has now spread to parts of Asia and the Middle East, resulting in significant crop loss. Moreover, Ug99 has shown an ability to overcome resistance genes bred into wheat cultivars intended to fend off stem rust. In this paper, we explore techniques to model the path of a hypothetical outbreak of a Ug99-variety stem rust in the United States of America and its effect on wheat production through a discrete deterministic model run via computer simulation. The model explores an adapted SEIR model for a single region and then extends it to consider the interactions between multiple regions. The effects of distance and wind patterns are accounted for. Finally, a brief sensitivity analysis of the parameters used in the model is performed.

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A WHEAT PATHOGEN IN THE  
UNITED STATES OF AMERICA

By  
Patrick T. Davis  
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with Honors in Mathematics

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## Abstract

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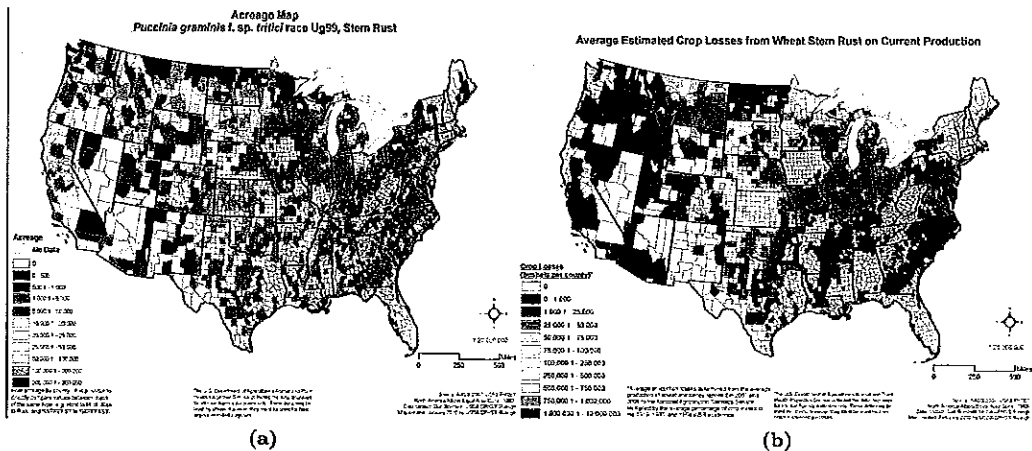
## 1 Introduction

There are many diseases that have ravaged crops since humans first started cultivating plants as a source of sustenance. Some of the oldest and most devastating of these diseases come from the rust family, the worst of which being *Puccinia graminis*, commonly known as stem rust. Stem rust results from a specific family of fungal spores and can affect a number of different cereal plants; however, it primarily attacks barley and wheat through the species known as *Puccinia graminis tritici* [5, p 4]. Stem rust of wheat has been chronicled throughout much of history, and many scientists today argue that the disease would have affected the crop fields of ancient societies similar to modern day fields, meaning that farmers would have seen around 15% drop in yield as a result of infection [7, p 1, 121].

As stem rust is not a new disease, a number of methods to control it have been implemented across the world in order to curtail crop loss. These methods of control can be broken down into three general types: chemical controls, cultural controls, and biological controls. Chemical control of wheat rust is mostly limited to fungicide application and has worked effectively in short-term situations where fields are well-managed and well-funded (since the high cost of fungicide can act as a deterrent) [8, pp 244-245]. Cultural controls fall into one of two main categories: eradication of barberry or development of stem rust-resistant variations of wheat. *Berberis vulgaris* (the common barberry bush) is the alternate host for *Puccinia graminis* and must be present for the disease to complete sexual reproduction (although need not be present for the fungus to spread) [9, p 16]. In the past, ridding an area of barberry has been an effective tactic to mitigate the disease at a local scale over multiple growing seasons. Moreover, the development of stem rust resistant variations of wheat (known as cultivars) which involves breeding diverse resistance genes into high-yielding wheat plants has proven to completely alleviate epidemics in the past [10, p 289]. Finally, biological controls involve the use of organic treatments (as opposed to fungicides)

and can produce results similar to chemical controls if properly executed - although biological controls are typically associated with higher costs than chemical controls.

In 1999, a new variation of wheat stem rust was discovered in eastern Africa (specifically in the countries of Uganda, Kenya, and Ethiopia) [2]. The new variety, known as Ug99, is devastating to crop yield and seems to be unaffected by the resistance genes currently present in the varieties of wheat harvested around the world, including most U.S. wheat [4, p 637]. Although the possibility of Ug99 spreading to the U.S. from the area currently infected by natural means is slim, the concern is not negligible when considered with the potential destruction the fungus could have on U.S. wheat production [5, pp 9-10]. Consequentially, the rise of Ug99 has spurred a large amount of funding for research, mostly focused on developing a Ug99-resistant strain of wheat [5, pgs 2-3]. New research on stem rust is imperative because much of the literature written on the topic is from antiquated sources. Stem rust in the United States and Canada has been relatively tame because of the barberry eradication program of the 1920s. In fact, the last severe stem rust epidemic ended in 1974 [7, pp 119-120]. However, the current problem is compounded by the ever-developing nature of the fungus; new varieties of Ug99 arise as quickly as botanical geneticists can breed resistance to the previous strain [5, p 5].



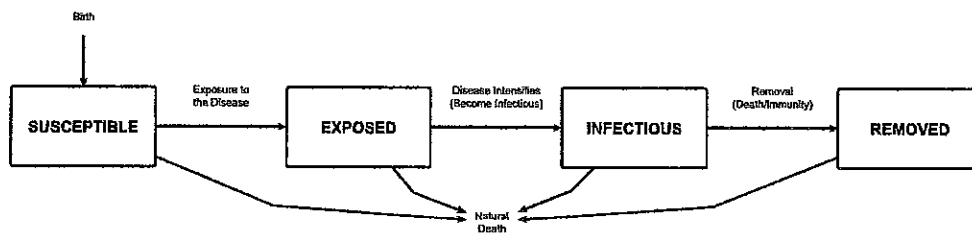
The National Agricultural Statistical Services (NASS) department of the United States Department of Agriculture (USDA) has performed some research regarding potential loss in the United States should a Ug99-type stem rust emerge as part of the National Plant Disease Recovery System (NPDRS) [5]. In fact, it has even published a recovery plan to suggest what might be done in the event such an occurrence takes place [5]. Figure 1 displays two of the risk maps that the NASS has produced as part of the recovery plan. As detailed in the report, the maps come from the application of previous statistics on current wheat production levels [5, p 11-12]. Thus, the work that has been published as part of the USDA research falls short of actually modeling the spread of the disease using conventional epidemiological practices. This type of modeling will be important to developing prescriptive measures should a Ug99-type stem rust reach the United States.

A number of previous studies have been concerned with the spread of airborne fungal pathogens, including the generalized work of van den Bosch et al. [11] modeling spread using a canopy structure and the more specific results of Cowger et al. [1] concerning the velocity of wheat stripe rust. This paper will further this type of work by exploring techniques for modeling the path of a hypothetical outbreak of a Ug99-type fungal pathogen in the United States and its effect on wheat production through a discrete deterministic model run via computer simulation. We start by explaining a general SEIR epidemiological model and build a technique applicable to stem rust from that basis. The end result is an adapted SEIR model for wheat rust in a single region. We then extend it to consider the interactions between multiple regions. Spores for stem rust are mostly spread via wind vectors and can travel up to thousands of miles, which has the result of one region infecting another [5, p 9]. Thus, the effects of distance and wind patterns are accounted for in the model set-up for multiple regions.



## 1.1 The General SEIR Model

In general, most models for epidemiological work are compartmental models. With this method, the population is partitioned into different compartments based on criteria relating to the disease being studied [12]. The conventional models are useful for tracking disease numbers in a relatively homogeneous population; and the model structure easily lends itself to adaptation for specific diseases. An SEIR model is a specific form of compartmental model that divides the population into four classes (which give rise to the model's name) [12].



**Figure 2:** General SEIR Model Dynamics for a Single Region.

Figure 2 illustrates the dynamics between classes in a standard SEIR model. Individuals start in the Susceptible ( $S$ ) compartment. These are members of the population who are yet to be affected by the disease. Changes in this class occur in one of three fashions. First, if the population is not assumed to be constant, then new members are added to this compartment via a specified birth rate ( $b$ ). In a standard SEIR model, this is the only compartment for which new members can be added to the population - although this might not be the case for an inherited disease. Secondly, if we continue to assume a non-constant population, then we can also allow for deaths not related to the disease (which will be referred to as a “natural death”). Individuals who undergo a natural death are removed from the Susceptible class at a given mortality rate ( $\mu$ ). It should be noted that natural deaths may occur in any compartment, although the rate from each class is usually assumed to be the same. Finally, members of the Susceptible class can move to the Exposed compartment ( $E$ )

after exposure to the disease. The rate at which this happens is known as the disease transmission rate ( $\alpha$ ).

Once a disease has successfully infected an individual and they are now capable of spreading the disease, he or she moves from the Exposed compartment to the Infectious ( $I$ ) compartment. In a standard SEIR model, this happens via an infection maturation rate ( $\beta$ ). Finally, after a disease has run its course, members of the population transition from the Infectious class to the Removed ( $R$ ) class. This transition is usually a result of an individual dying from the disease or as a result of an individual gaining immunity to the disease. In either case, the population members who have undergone this process have been removed from the dynamics of the disease.

The system can be described using the following set of differential equations, where the letters  $S(t)$ ,  $E(t)$ ,  $I(t)$ , and  $R(t)$  represent the number of individuals in those compartments and  $N(t) = S(t) + E(t) + I(t) + R(t)$  for any given time:

$$\frac{dS}{dt} = bN(t) - \mu S(t) - \alpha \frac{I(t)}{N(t)} S(t) \quad (1a)$$

$$\frac{dE}{dt} = \alpha \frac{I(t)}{N(t)} S(t) - (\beta + \mu) E(t) \quad (1b)$$

$$\frac{dI}{dt} = \beta E(t) - (\gamma + \mu) I(t) \quad (1c)$$

$$\frac{dR}{dt} = \gamma I(t) - \mu R(t) \quad (1d)$$

These equations track the changes for each compartment in continuous time. Many models will assume that the birth rate is equal to the natural death rate for the whole population. In these cases, the lifespan of the disease is considerably shorter than the average lifespan of the organisms being infected and the effects of birth and death are negligible, dropping a number of terms from the differential equations [12]. This assumption was made when generating the graph seen in Figure 3, which shows one realization of a general SEIR model. It is worth noting that the simulation was allowed to run until the disease had peaked and then left the population (marked by the flattening out as time increases).

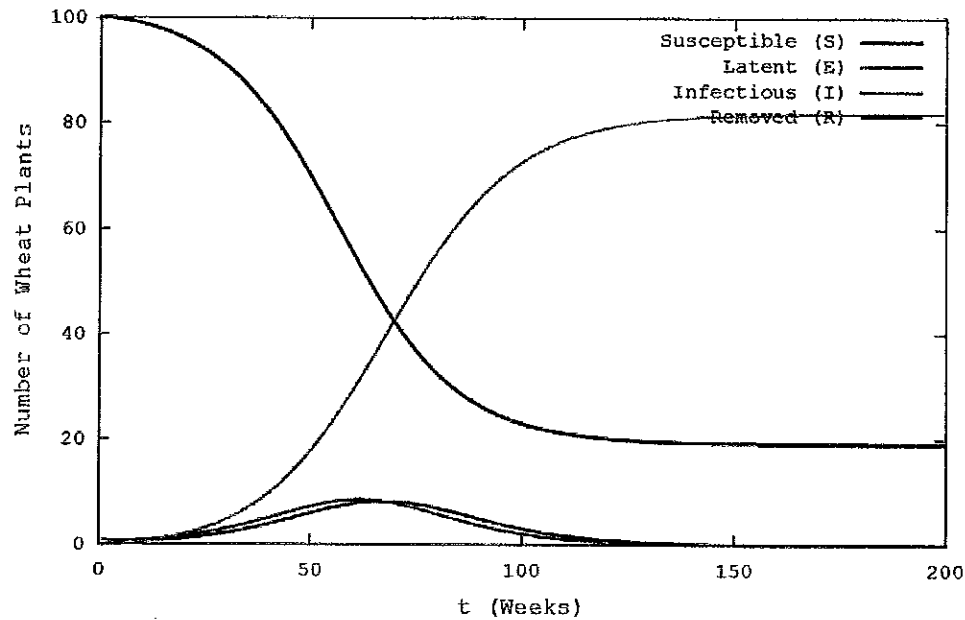


Figure 3: Standard SEIR Model Population Breakdown for a Single Region.

There are different patterns that result from running an SEIR model with various parameters. Probably the most interesting is when the dynamics reach some steady-state within the population. In the case of Figure 3, the number of individuals infected peaks and then decreases, lagging just behind the curve representing the Exposed class. One will note that the disease removed a large portion of the population, which is not replaced because the birth rate was assumed to be negligible. This is a steady state where the disease has left the population which is a result of the removal rate being significantly greater than the disease transmission rate. By changing the parameters and allowing for a non-constant population, it would be possible to determine a steady state where the disease has become endemic (meaning that  $I > 0$  for all  $t > 0$ ), although this is less of a concern when modeling plant epidemiology.

## 2 The Adapted SEIR Model for a Fungal Wheat Pathogen

### 2.1 A Single Region

In order to determine the spread of a wheat pathogen in the entire United States, one must first develop techniques to determine what happens when a single region of wheat crop is infected with the disease. Once this is considered, the situation can be expanded in order to characterize what might happen in successively larger areas. The model used in this paper to track the number of wheat plants affected by stem rust is an SEIR model adapted from the standard model described above.

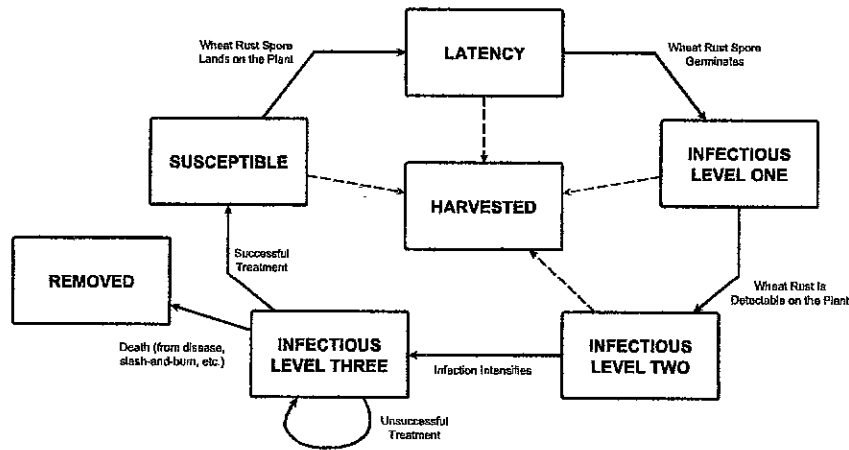


Figure 4: Wheat Rust Dynamics For a Single Region.

The initial task for a single region is to translate from how the disease progresses in nature to a structured layout with specified differential equations, similar to those found in the general SEIR model. Figure 4 diagrams the development of wheat rust in a single patch of farmland. As can be seen in the figure, the Susceptible ( $S$ ) compartment has been left unchanged from the typical SEIR model; however, nearly everything else has been altered. The first change was a subtle shift in meaning of the Exposed ( $E$ ) class. Here, we have changed the compartment from simply being exposed to the disease to reflect that the wheat plant in question has actually had a wheat rust spore land on it. Then in a sense, the disease has become latent on

the plant. This is really the start of the wheat rust cycle, since the disease has a germination period before it successfully infects the plant and starts producing additional fungal spores. After this has happened, the plant moves through three separate divisions of the Infectious ( $I$ ) compartment: 1) infected but undetectable; 2) infected and detectable (but still at an early stage of the disease); and 3) infected at a severe level (and assumably detected).

Since an individual spore produces a limited number of rust spots on a plant, it is possible for an infected plant to go unnoticed by the farmer for a relatively long length of time. That being said, a threshold where detection is possible must exist. When that threshold is passed, the plant moves from the first Infectious compartment ( $I_1$ ) to the second ( $I_2$ ). After additional time has passed, the infection intensifies until it has been detected on the plant, moving to the third Infectious class ( $I_3$ ). It should be noted that while each level of the Infectious compartment is capable of spreading wheat rust, a higher level of infection translates into a higher probability of infecting other plants. This is a result of additional rust spots on the plant, each of which is capable of producing a sizable number of spores.

Once a plant has progressed to the highest level of infection, there are three possible occurrences. When the crop is treated for rust (through fungicides, etc.) and that treatment is successful, it will move from the  $I_3$  class into the Susceptible category. It is also possible that treatment is unsuccessful, in which the plant remains in the  $I_3$  compartment. Thirdly, the plant may die and be moved into the Removed ( $R$ ) class. In the model, there are no direct stipulations as to how the death occurs (other than it is not considered to be a natural death). This means that the death could have been a direct result of the disease, or it could also be an effect of a drastic treatment method such as slash-and-burn. This model does not account for post-disease immunity because such a concept is not applicable to wheat plants, as they do not have immune systems.

Finally, we also allow for a “pseudo-compartment” that reflects the harvested

population at the end of the crop season. The Harvested compartment contains all of the wheat that has been collected for consumption from the region at hand. We will assume that the entire Susceptible and Latent populations are harvested; however, we will only allow for a percentage of the  $I_1$  and  $I_2$  to be moved into this section. For a discrete model, this corresponds to allowing a specified number of time steps to occur and then moving wheat from each harvestable compartment into the Harvested class.

As with the standard SEIR model, these biological processes translate into a set of differential equations that can be used to model the system dynamics:

$$\frac{dS}{dt} = -\alpha S(t) [\rho_1 I_1(t) + \rho_2 I_2(t) + \rho_3 I_3(t)] + \gamma_1 I_3(t) \quad (2a)$$

$$\frac{dE}{dt} = \alpha S(t) [\rho_1 I_1(t) + \rho_2 I_2(t) + \rho_3 I_3(t)] - \beta_1 E(t) \quad (2b)$$

$$\frac{dI_1}{dt} = \beta_1 E(t) - \beta_2 I_1(t) \quad (2c)$$

$$\frac{dI_2}{dt} = \beta_2 I_1(t) - \beta_3 I_2(t) \quad (2d)$$

$$\frac{dI_3}{dt} = \beta_3 I_2(t) - \gamma_1 I_3(t) - \gamma_2 * I_3(t) \quad (2e)$$

$$\frac{dR}{dt} = \gamma_2 I_3(t) \quad (2f)$$

Descriptions for all of the parameters in the equations can be found in Table 1. The parameter values were chosen based on the biological processes of wheat rust and in order to generate an appropriate number in the Harvested class.  $\beta_1 = 0.5$  was chosen to reflect the standard two week period required for the rust spots on a newly infected plant to start producing additional spores [5, p 7]. Note that these equations assume a constant population. This makes sense because wheat is planted only at the start of a growing period, and the percentage of wheat that dies after it has already made it to the age at which wheat rust can infect the plant is negligible. By allowing  $\gamma_1 \neq 0$ , we give our model the flexibility to include farmers' efforts to combat wheat rust once it affects their crops. Moreover, the effect of wind and other

climatic conditions that may influence the spread of the disease in a single enclosure are assumed to be factored into the parameters; and we will not specifically account for these phenomena through additional terms in the single region case.

Parameter	Value	Label	Description
$\alpha$	0.006	SE	disease transmission rate
$\beta_1$	0.50	EI1	infection maturation rate
$\beta_2$	0.27	I1I2	infection detection rate
$\beta_3$	0.80	I1I3	infection development rate
$\gamma_1$	0.05	I3S	successful treatment rate
$\gamma_2$	0.20	I3R	death rate (from wheat rust and related events)
$\rho_1$	0.10	I1	potency level for $I_1$ infected plants
$\rho_2$	0.60	I2	potency level for $I_2$ infected plants
$\rho_3$	1.00	I3	potency level for $I_3$ infected plants

**Table 1:** The Parameter Set. Alterations made to these parameter values are explicitly mentioned where they occur.

The programming software Octave was used to code the system, run the simulations, and then produce graphs [3]. The specific code is presented in the Appendices. In accordance with this, there are three main sources of error in our model:

1. **Parameter value estimations.** Very little real data exists to guide our choice of parameter values.
2. **Deterministic.** Our model does not incorporate randomness.
3. **Discrete time.** We solve the differential equations using a simple Euler method with a 1-week time step.

The first source of error is clearly the most important, making the other two acceptable simplifications. The slight inaccuracies they cause are overwhelmed by the problem of parameter estimation. Thus, even though the simulations are discrete and deterministic, this in no way diminishes their validity.

In order to explore the dynamics of the model, we present a specific realization of the output. Since no outside influence is considered, we start our model with 1% of plants in the region in the Latent class. The length of the growing season is assumed to be 38 weeks, which is a reasonable average for the entire United States [7]. Figure

5 is the resulting compartment levels from a total population of wheat plants (100%) in a single enclosure. The parameters have been set at the values reported in Table 1. As can be seen in the graph, the total crop yield at the end of the season is just over 64%. This is not a completely unrealistic value, although better estimation of the parameters will allow for a more accurate single region model.

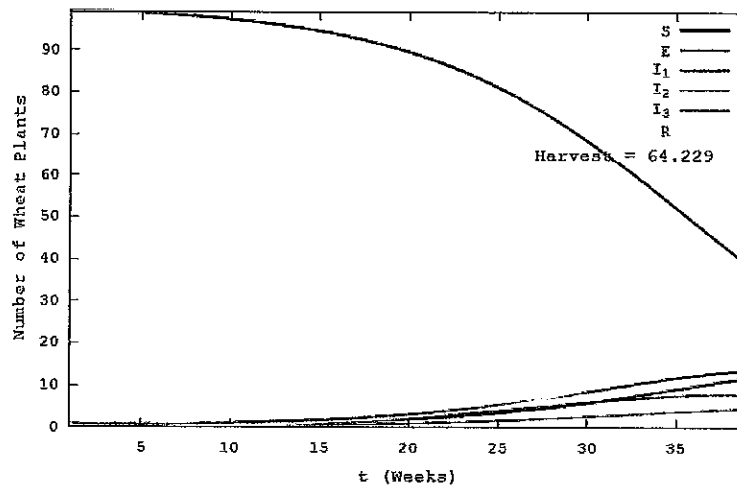


Figure 5: Single Region Population Breakdown.

## 2.2 Multiple Regions

Now that a system for a single region has been constructed, we are able to expand upon this in order to accurately model the spread of a wheat pathogen in multiple subregions. By breaking up the United States into smaller and smaller sections, each of which can be modeled using the method described above, we will be able to more accurately model the disease's geographical spread through time and then determine wheat production levels for a single growing season. In this section, we also allow for cross-infectivity between areas as a result of movement of spores across regional boundaries. Cross-infections happen at a specified rate, which we will refer to as an interaction strength.

In order to consider how two patches might influence each other, we first need to



define the geometrical layout of the model as it corresponds to the geographical layout in real life. In this system, we will refer to each individual subregion as a node. Each of these nodes are then linked to each other via a certain interaction coefficient. This is similar to the mathematical concept known as a directed graph (i.e. as a system of objects called vertices connected by specific links referred to as edges). The primary advantage of this is that the model is not limited to a lattice structure. Instead, it can be adapted to model wheat rust in any geographical area having either regular or irregular interior boundaries.

There are two specific concerns for determining the interaction coefficient between two nodes. The first (and probably the most obvious) is distance. Simply put, the greater the distance between two subregions, the less likely they are to have any sort of influence on each other. For any two fixed subregions, we will use the following formula to determine this portion of the interaction coefficient:

$$C_{distance} = \frac{1}{(1 + \frac{distance}{K})^2}$$

This equation is ideal for modeling this aspect because it is relatively simple and decreases the interaction strength as the two subregions get further apart. Moreover, the parameter  $K$  is capable of acting as a scaling factor, which will allow flexibility when determining a reasonable magnitude for the distance coefficient.

The second effect that must be accounted for is the dominant wind patterns. Wind is the primary dispersal mechanism for wheat rust spores or any similar fungal pathogen. The effect of the wind depends on two aspects. The first is the wind direction, and the second is the angle created by the location of the two nodes in question. As a result of this, it should be noted that the wind effect between two separate nodes is not symmetrical. In fact, it is possible that one node cross-infects another without being affected by the second node at all. We will use the following

function to calculate the effect of wind dispersal between two nodes:

$$C_{wind} = \frac{\cos(\theta_{node\ locations} - \theta_{wind\ direction})}{2} + \frac{1}{2}$$

This function corresponds to a zero effect should the node in question be directly upwind from the infected node and a full effect when the node is downwind. For any angle in between, the wind coefficient will be a fraction of the full effect. Future work might include using a von Mises distribution for wind interaction strength. Once these two influences have been determined, we can calculate the interaction strength from node  $j$  to node  $i$ :

$$C_{i,j} = C_{distance} \times C_{wind}$$

Allowing for cross-infections means that now there exists the possibility that a wheat plant may move to the Latent compartment as a result of infectious wheat in another subregion. In turn, this mandates a change in the portions of the first and second differential equations seen in the single region model that determine movement between the Susceptible and Latent classes. Thus, for subregion  $i$ , we have the following equations:

$$\frac{dS_i}{dt} = -\alpha_i S_i(t) \sum_{\forall j} C_{i,j} [\rho_{1,j} I_{1,j}(t) + \rho_{2,j} I_{2,j}(t) + \rho_{3,j} I_{3,j}(t)] + \gamma_{1,i} I_{3,i}(t) \quad (3a)$$

$$\frac{dE_i}{dt} = \alpha_i S_i(t) \sum_{\forall j} C_{i,j} [\rho_{1,j} I_{1,j}(t) + \rho_{2,j} I_{2,j}(t) + \rho_{3,j} I_{3,j}(t)] - \beta_{1,i} E_i(t) \quad (3b)$$

$$\frac{dI_{1,i}}{dt} = \beta_{1,i} E_i(t) - \beta_{2,i} I_{1,i}(t) \quad (3c)$$

$$\frac{dI_{2,i}}{dt} = \beta_{2,i} I_{1,i}(t) - \beta_{3,i} I_{2,i}(t) \quad (3d)$$

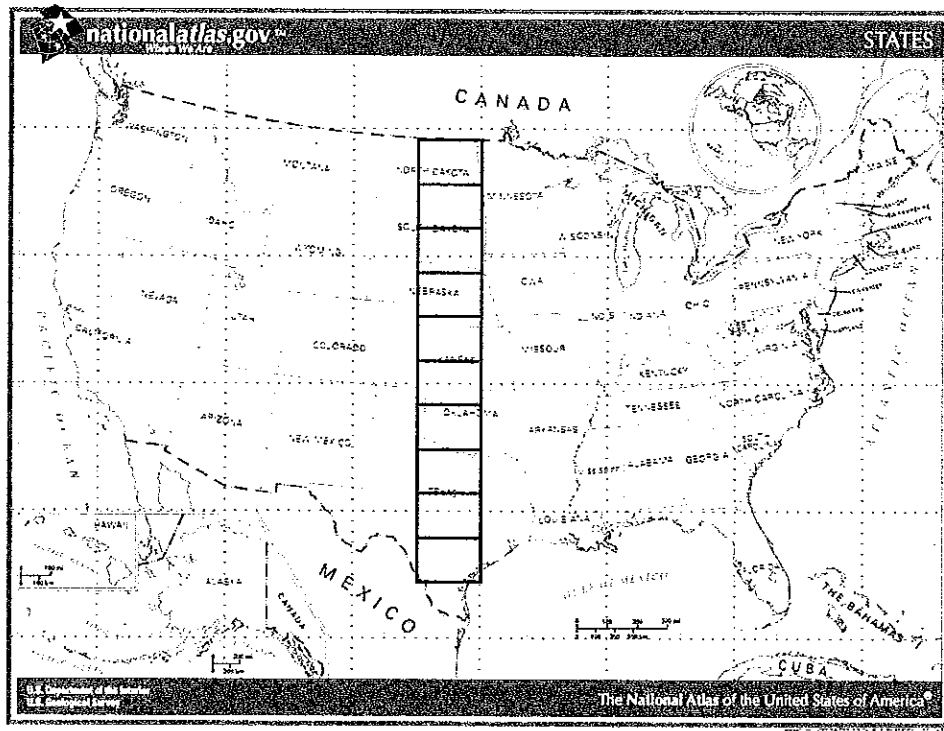
$$\frac{dI_{3,i}}{dt} = \beta_{3,i} I_{2,i}(t) - \gamma_{1,i} I_{3,i}(t) - \gamma_{2,i} I_{3,i}(t) \quad (3e)$$

$$\frac{dR_i}{dt} = \gamma_{2,i} I_{3,i}(t) \quad (3f)$$

Note that  $j$  indexes all of the subregions within the model set-up, including  $i$  itself.

To illustrate how this model works, we explore a specific set-up inspired by the

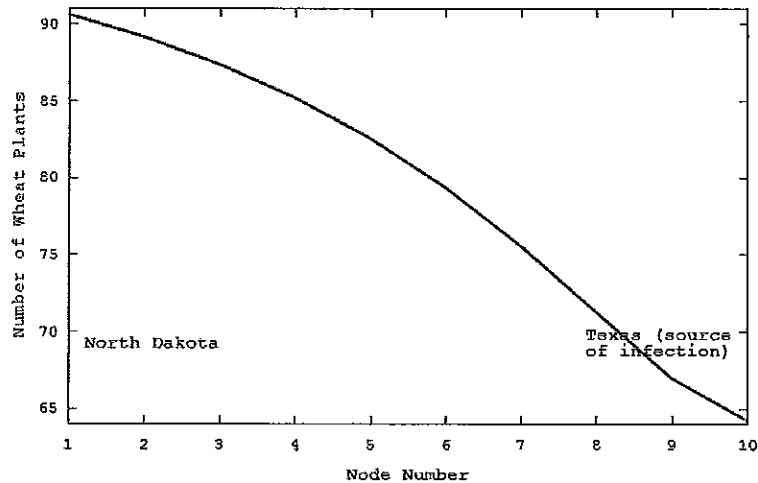
“Puccinia pathway” seen in Figure 6 [5, pg 8]. This pathway is a strip of land that runs from the southern United States all the way to the Canadian border and is the likely dispersal path for a Ug99-type rust in the United States. Our set-up will assume a strip of ten homogeneous regions, each identical to the example explored with the single region model for easy comparison. We will also assume that the dominant wind direction for each subregion is north; and that the distances are simply in units corresponding to the node number. The source of infection will be node 10 (which corresponds to southern Texas in Figure 6). Here, we will start with 1% of plants in the Latent compartment (as in the single region example earlier). We will also use  $K = 1$  as the value of our distance scaling parameter. Both of these settings are easily changed if needed.



**Figure 6:** Conceptual Illustration of a Strip Model for the US, inspired by the “Puccinia pathway” [6].

After running the simulation, we recorded the amount of wheat harvest in each

node and graphed the results in Figure 7. From the graph, one can see that the source of the infection fared the worst in terms of harvestable wheat crop. It should also be noted that the harvest in this region directly matches the value found in the single region case because no downwind infection is permitted. As one moves northward along the strip from node 10, the amount of wheat harvested increases. This would be expected since the rust has had less time to develop in these regions.



**Figure 7:** The Percentage of Wheat Plants Harvested in a Strip, with a dominant northern wind pattern.

### 2.3 Model Comparison

For comparison, the wheat rust dynamics were also simulated using a general SEIR model that did not include all of the possibilities diagrammed in Figure 4. Instead, we only considered the four standard compartments. The parameter values were not altered so that a direct comparison could be made, and the  $I_3$  compartment was considered to be the sole Infectious class. Figure 8 shows the population breakdown in this case, which is highly similar to the general SEIR model. Note that in this situation, we harvest a significantly less amount than in our adapted model. The figure of only around 24% yield is unrealistic; wheat rust does not affect the crop that severely.

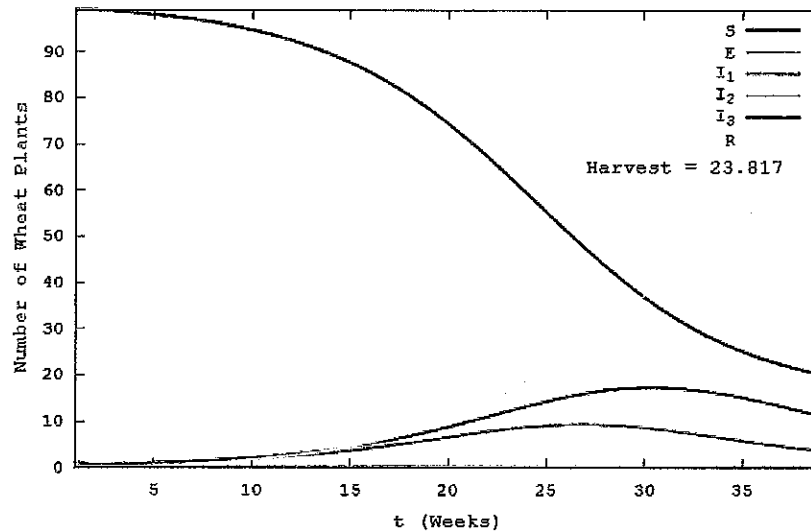


Figure 8: Single Region Population Breakdown, using a standard SEIR model.

Figure 9 shows the harvest amounts for a standard SEIR model for a strip of ten subregions, laid out as examined above. The source of the infection (node 10) behaves exactly as the single region case; however, we can see in the graph that the amount of harvested wheat sharply decreases immediately outside of the infected node, and then slightly increases as we move left on the graph. This is likely a result of the potency parameters in cross-infectivity and the amount of time that the disease is allowed to develop for in each subregion. The subregions within close proximity of the source of infection will have almost the entire growing season to develop wheat rust and will also be continuously bombarded by fungal spores from node 10. This combination effect explains the shape of the curve; however, this does not make sense in a model, as it does not approximate reality. The source of the infection should not have the highest harvest. Thus, we can conclude that the adapted SEIR model performs better for modeling wheat rust.

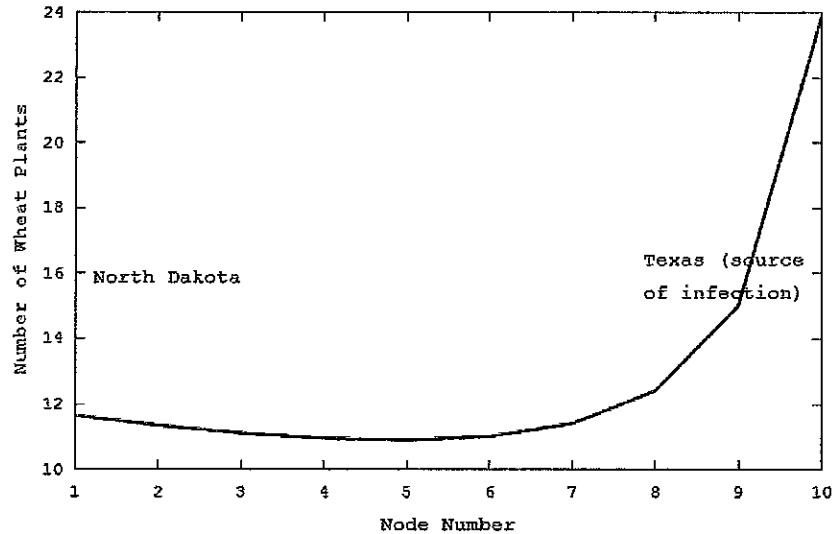
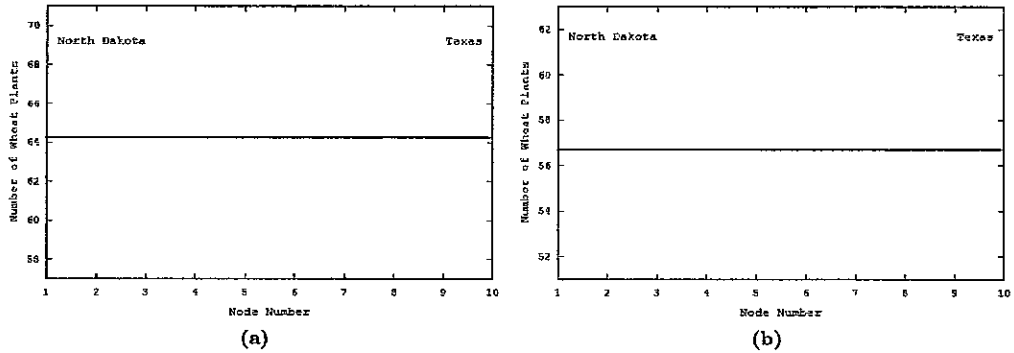


Figure 9: Percentage of Wheat Plants Harvested in a Strip, using a general SEIR model.

## 2.4 Parameter Analysis

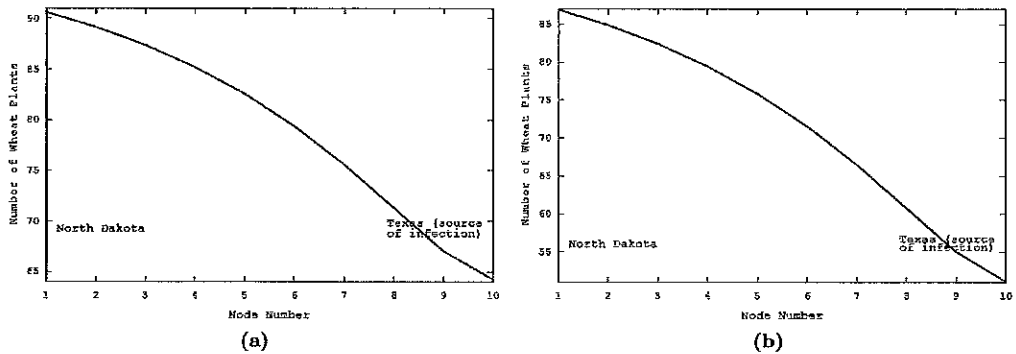
To further test the model dynamics, we performed a series of investigations involving the parameters. The first was a simulation allowing for no cross-infectivity at all. For this case, we assumed that each subregion contained 1% Latent plants, rather than just node 10. The results can be seen in Figure 10. As expected, we determined harvest amounts for each node equal to the yield in the single region model. For comparison's sake, we also simulated the multiple region model with total cross-infectivity. Each subregion was capable of infecting the others at a 1% level. The resulting graph for this is also shown in Figure 10. It is important to note that the harvest figures from this method of cross-infection were noticeably lower than in the simulation omitting cross-infection, which is compatible with the understanding that if each subregion can infect all the others, then we should see an increased level of affected plants. Here, this is clearly the case.

We also explored what would happen if no treatment to the infected crops was performed. In this situation,  $\gamma_1 = 0$ . The results are graphed in Figure 11. The curve has approximately the same shape as the standard case where treatment is



**Figure 10:** The Percentage of Wheat Plants Harvested in a Strip, with no cross-infectivity and with total cross infectivity. (Note the different scales for the y-axis in each graph.)

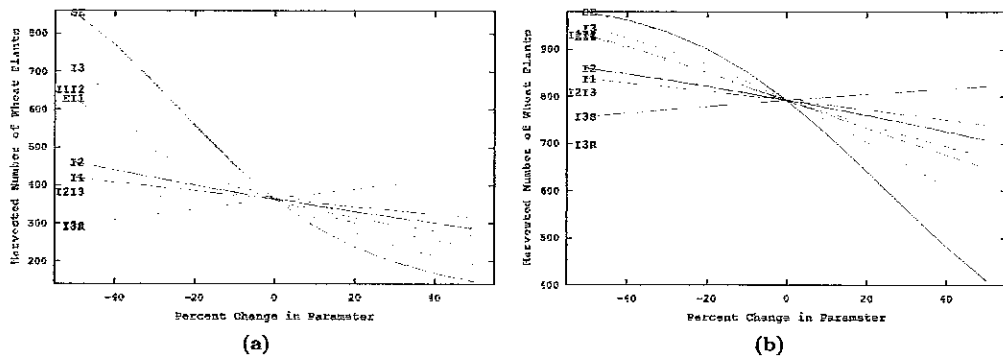
allowed; however, here we have a vertical shift downward. This is easily attributed to the fact that removing the possibility of treatment increases the number of wheat plants moving into the Removed compartment, which happens as a result of increased accumulation in  $I_3$ . Furthermore, the removal of treatment procedures prevents plants in  $I_3$  from being cured of wheat rust and reentering the cycle as a susceptible.



**Figure 11:** The Percentage of Wheat Plants Harvested in a Strip, with no treatment permitted ( $\gamma_1 = 0.00$ ). On the left, the default case (Figure 7) is displayed for easy comparison. (Note the different scales for the y-axis in each graph.)

The next procedure performed for the analysis was a comprehensive investigation of how the parameters in Table 1 affect the model output. The multiple region model was run with incremental changes in a single parameter value, and the resulting harvest value across all ten nodes was plotted against the percent change in the

parameter. Note that since we are looking at all ten nodes at once, there is a total of 1,000% wheat plants for all of the regions combined. Once again, either all nodes were initially infected at the 1% level or only node 10 was infected. Figure 12 details the effects seen. From the graph, it is clear that the SE parameter ( $\alpha$ ) which corresponds to the disease transmission rate has the greatest effect on the percentage of plants harvested, as evidenced by the spread of its curve. In fact, for the case where all the nodes exhibit an initial infection, a 20% increase in its value causes about a 50% drop in harvest, and a 20% decrease in the value causes over a 100% increase.

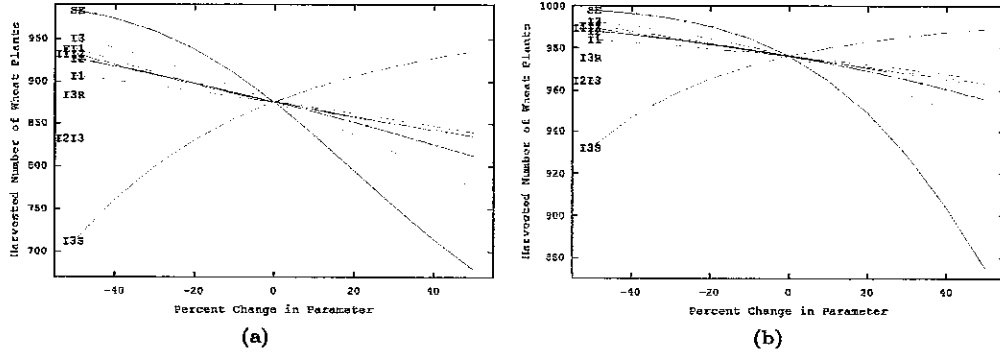


**Figure 12:** A Parameter Analysis of the Model, based on percentage changes in each of the parameter values. On the left, each region is infected the same; whereas the right graph, only node 10 has an initial infection.

Another interesting thing to note is that the I3S ( $\gamma_1$ ) curve is relatively flat compared to many of the other parameters, indicating that the rate at which effective treatment occurs is a relatively insensitive parameter in the model. This is slightly deceptive, however, because the code changes the parameters based on a percentage. Since in the default case  $\gamma_1 = 0.05$ , the actual change in the parameter value is relatively small. From a second comprehensive parameter analysis that was run after letting  $\gamma_1 = 0.50$  (shown in Figure 13), we can see that the curve for I3S has the second largest spread. This suggests that the rate at which wheat moves from the  $I_3$  class to the  $S$  compartment is more sensitive than previously implied. In terms of the model application, this is good news because it suggests that treatment of the crop



is a worthwhile enterprise to battle wheat rust.



**Figure 13:** A Parameter Analysis of the Model, based on percentage changes in each of the parameter values. As in Figure 12, the left graph shows where each region had the same initial infection; however, the right graph starts with an initial infection only in node 10.  $\gamma_1 = 0.50$ .

After the parameter analysis for the subregion dynamics was performed, we considered the parameter within the distance interaction coefficients ( $K$ ). This parameter is important in determining how easily wheat rust spreads over a given set of subregions. As explained above, the equation itself is designed to decrease the interaction strength as the distance between nodes increases; however, the extent of that decrease is controlled by  $K$ . Since  $K$  is in the denominator of a term in the distance function denominator, we expect that as the value of  $K$  increases, the value of the whole function should increase. This would lead us to expect a higher and higher level of cross-infectivity for larger and larger values of the distance parameter.

Figures 14 and 15 are the result of running the model numerous times and using a different value for  $K$  in each simulation. As indicated on the graphs,  $K$  ranged in value from 0.10 to 6.00, using a 0.10 step size. For both graphs, it is important to note that the harvest level in node 10 is identical to the default simulations run in the model section (as would be expected). Figure 14 is the resulting graph when each of the ten nodes is initially infected with 1% Latent wheat plants. Here, we are able to see that as  $K$  increases, we see more cross-infection, as we conjectured. Figure 15 results from only node 10 having an initial infection of wheat rust. As expected, we

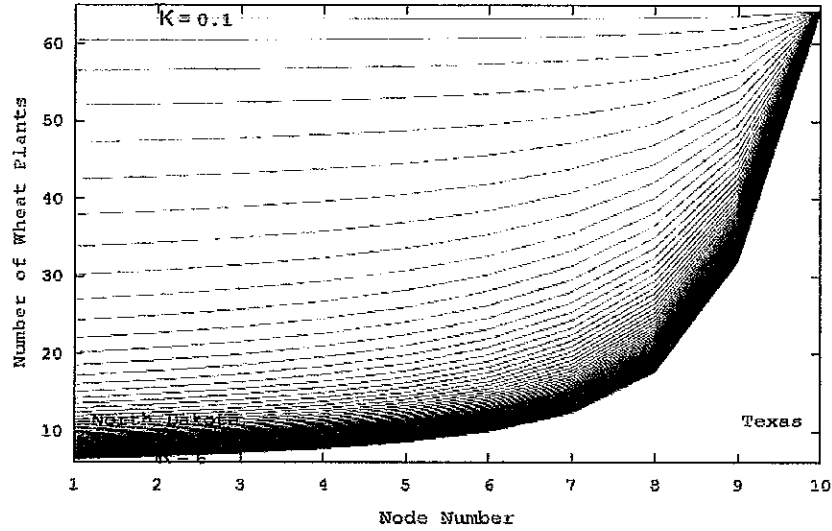


Figure 14: Analysis of Distance Parameter ( $K$ ). Each region is infected the same.

notice a similar pattern in this graph; however, the top set of curves actually have an increase in harvest. This is because for these simulations, the distance parameter took values  $0.10 \leq K \leq 0.90$ , which actually served to decrease the level of cross-infectivity. We did not see that in Figure 14 because each node started off with some degree of infection, which was enough to overcome the effect of a small  $K$ .

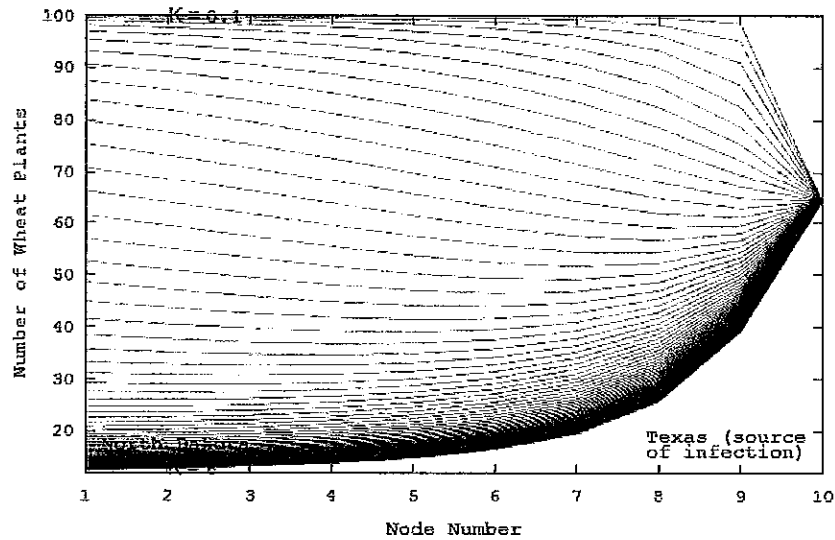


Figure 15: Analysis of Distance Parameter ( $K$ ). Initially, only node 10 is infected.

### 3 Discussion and Future Expansions

Ultimately, the model presented in this paper is very much in line with epidemiological models that are traditionally used to track disease numbers and provides a solid base technique to further explore the possibilities of a Ug99-type wheat pathogen in the United States. The adapted compartmental approach is key in devising an accurate mathematical correspondence to the biological mechanisms which control the disease development. This way, each compartment can be given its own set of parameters that will better simulate the real world, which is important when considering natural variation within sections of the population. Moreover, we have successfully created a model that uses a node structure to track the disease in specified areas. This design frees the model to be adapted to fit any conceivable geographical layout, while still maintaining the flexibility of having different parameters for each subregion. This model also accounts for cross-infections between subregions through functions that measure the influence of both distance and dominant wind patterns.

That being said, there are number of things that could be done in order to improve the model. First and foremost, fine tuning the interaction coefficients for both wind and distance will facilitate more accurate modeling of the cross-infectivity between nodes. Moreover, the work presented here falls short of actually applying the model to the United States. Incorporating geographical data, along with wheat production levels and dominate climate patterns will allow one to model the spread of wheat rust as it moves through the United States in a single growing season. This would also need to include staggering the timing for each subregion because wheat is not planted at the same time in every location across the country. Moreover, moving from a weekly tracking period to a daily tracking period might also be considered. This will come with the cost of additional computations; however, it will undoubtedly be a more detailed representation of what is actually going on in the system.

Furthermore, the current model is only able to track wheat rust numbers over a

single growing season. Accounting for the disease path over multiple years will require expanding the model to include a year-by-year memory of where wheat rust was and thus where it might originate from in the following growing cycle. This tactic will be a highly useful tool when determining the appropriate course of action to prevent the spread of a Ug99-type wheat rust. Finally, we might consider adding a stochastic component to the model in order to account for the randomness of real life. Using statistical techniques will result in a more realistic and natural model for the spread of wheat rust. It is likely that the best course of action to model the spread of wheat rust is a combination of any and all of the above considerations. Starting with basic models and working towards more complex systems will offer a deeper understanding of how wheat rust would hypothetically spread across the United States. The work presented here is without a doubt a step in the right direction and will be imperative to future studies of wheat rust epidemiology as Ug99 and its variations continue to threaten the world's wheat crop.

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Each Appendix contains the Octave code for one portion of the model for multiple regions. Changes made to the values in `multiregionSEIR.m` (Appendix A) will result in the single region case. Also, note that this code was used to generate everything; however, in order to generate specific graphs, some physical changes must be made to the code at times.

## A Octave Code: `multiregionSEIR.m`

```
% this is the driving m-file that invokes all of the other m-files
in order to run the model

clear all
close all

% SET UP THE REGION

% these are the values to change in order to change the "resolution"
total_rows=10;
total_columns=1;
num_nodes=total_rows*total_columns;

% SET UP THE INITIAL CONDITIONS

breakdown=zeros(1,num_nodes,6); % breakdown(time, node index,
[1:Susceptible, 2:Latent, 3:Infected1, 4:Infected2,
5:Infected3, 6:Removed])

if( 0 ) % change this to a 1 to infect just one region, or
a 0 for everything infected.
% Infect only one region
experimenttype="Just one region infected initially";
experiment=1;
infected_node=num_nodes; % the last node is picked as the initially
infected node. This is changeable (in fact, it would probably
be good to make this a separate function...)
breakdown(1,:,1) = 100;
breakdown(1,infected_node,2)=1;
breakdown(1,infected_node,1)=99;
else
% infect every region equally
experimenttype="Every region infected initially";
```

```

experiment=0;
breakdown(1,:,1) = 100;
breakdown(1,:,2)=1;
breakdown(1,:,1)=99;
end

% SET UP THE PARAMETERS FOR THE SUBREGIONS

P=zeros(num_nodes,9); % P(node index, [1=SE, 2=EI1, 3=I1I2, 4=I2I3,
5=I3S, 6=ILR, 7=I1, 8=I2, 9=I3])
labels={'SE','EI1','I1I2','I2I3','I3S','I3R','I1','I2','I3'};
parameter=zeros(9);

for i=1:num_nodes
parameter=multiregionSEIRparameter(i);
for n=1:9
P(i,n)=parameter(n);
end
end

% SET UP THE INTERACTION COEFFICIENTS FOR THE SUBREGIONS

A=zeros(num_nodes,num_nodes); % this is the matrix that will store
the interaction coefficients [A(from_node,to_node)]
from_node=1;
to_node=1;

for from_node=1:num_nodes
for to_node=1:num_nodes
interaction = multiregionSEIRinteraction(from_node,
to_node,total_columns);
A(from_node,to_node)=interaction;
end
end

% RUN THE SEIR DYNAMICS FOR ALL THE SUBREGIONS, CHANGE THE VALUES,
AND LOOP IT OVER DESIRED TIME

for tstep=2:39
for nodenum=1:num_nodes
%nodenum
delta=multiregionSEIRDynamics(P,tstep,breakdown,A,nodenum);
for i=1:6
breakdown(tstep,nodenum,i)=breakdown((tstep-1),nodenum,i)+delta(i);
end
end
end

```



```

end

% DETERMINE THE WHEAT HARVESTED IN EACH REGION

inf3_harvested=0/3; % the percentage of wheat in I3
that can be harvested

harvest = zeros(num_nodes,1);
t=tstep;
for i=1:num_nodes
harvest(i)=breakdown(t,i,1)+breakdown(t,i,2)+breakdown(t,i,3)+
breakdown(t,i,4)+inf3_harvested*breakdown(t,i,5);
end

%harvest=breakdown(tstep,1,1)+breakdown(tstep,1,2)+
inf_harvested*breakdown(tstep,1,3);

% GRAPH THE RESULTS

if (total_columns==1 && total_rows==1)
figure;
plot(breakdown,'LineWidth',2)
%title('General SEIR Model','FontSize',14)
xlabel('t (Weeks)','FontSize',11,'FontName','Courier')
ylabel('Number of Wheat Plants','FontSize',11,'FontName','Courier')
text(27,65,['Harvest = ',num2str(harvest)],'FontSize',11,
'FontName','Courier')
legend('S','E','I_1','I_2','I_3','R');
end

if (total_columns>1 || total_rows>1)
figure;
plot(harvest,'LineWidth',2);
%title('Amount of Wheat Harvested','FontSize',14)
xlabel('Node Number','FontSize',11,'FontName','Courier')
ylabel('Number of Wheat Plants','FontSize',11,'FontName','Courier')
xleft=0.12*num_nodes;
xright=0.98*num_nodes;
y=min(harvest)+5;
yup=y+0.5;
ydown=y-0.5;
text(xleft,y,['North Dakota'],'FontSize',11,'FontName','Courier')
horizontalalignment = 'right';
if(experiment==1)
text(xright,yup,['Texas (source)'],'FontSize',11,'FontName',
'Courier','horizontalalignment',horizontalalignment)

```

```
text(xright,ydown,['of infection'],'FontSize',11,'FontName',
'Courier','horizontalalignment',horizontalalignment)
else
text(xright,y,['Texas'],'FontSize',11,'FontName','Courier',
'horizontalalignment',horizontalalignment)
end
% text(xright,yup,['Texas (source)'],'FontSize',11,'FontName',
'Courier','horizontalalignment',horizontalalignment)
% text(xright,ydown,['of infection'],'FontSize',11,'FontName',
'Courier','horizontalalignment',horizontalalignment)
end
```

## B Octave Code: multiregionSEIRparameter.m

```
function parameter=multiregionSEIRparameter(i)

% this is the m-file that will run the code that determines
the parameters for each of the subregions

parameter=zeros(9);

% everything below is changeable. Right now, it's assigning
the same parameters to all of the subregions; but it would make
sense to change the parameters based on latitude.

parameter(1) = 0.006; % rate moving from susceptible to latent
- alpha / SE
parameter(2) = 1/2; % rate moving from latent to undetected
infectious - beta1 / EI1
parameter(3) = 0.27; % rate of detection - beta2 / I1I2
parameter(4) = 0.80; % rate of early detection to late detection
- beta3 / I2I3
parameter(5) = 0.05; % rate of detected being treated
- gamma1 / I3S

if( 0 ) % change this to a 1 to stop all treatment
parameter(5) = 0.00; % rate of detected being treated
- gamma1 / I3S
end

parameter(6) = 0.20; % rate of removal (includes death by rust and
slash-and-burn but not harvested) - gamma2 / I3R

% these are like production rates to be used in
inter-region transmission. The higher the infection level,
the more spores should be dispersed
parameter(7) = 0.1; % Infection Level 1 - rho1 / I1
parameter(8) = 0.6; % Infection Level 2 - rho2 / I2
parameter(9) = 1.0; % Infection Level 3 - rho 3 / I3

parameter(7:9) =parameter(7:9)*1;

return;
```

## C Octave Code: multiregionSEIRinteraction.m

```
function interaction = multiregionSEIRinteraction(from_node,
to_node,total_columns,Kdist)
% this is the m-file that will run the code that determines the
interaction coefficients for the subregions
if( nargin <= 3 )
    Kdist = 1;
end
xdiff=mod(from_node,total_columns)-mod(to_node,total_columns);
ydiff=ceil(from_node/total_columns)-ceil(to_node/total_columns);

wind_direction=0; % in degrees [N=0, E=90, S=180, W=270]
wind_direction= pi/2-wind_direction*pi/180;

wind_speed=1;

distance = sqrt((xdiff)^2+(ydiff)^2); % calculates the distance
between the two nodes
theta = atan2(ydiff, xdiff); % calculates the angle between the two
nodes [the typical radian measure is rotated so that north=0,
west=pi/2, south=pi, east=3pi/2]

distancefunction = 1/((1+distance/Kdist)^2); % these are the
functions that define interaction strength. they are
changeable, but we might want to do the switch thing so that
we can automate it all from the main m-file
anglefunction = cos(theta-wind_direction)/2+1/2;

if( 0 ) % change this to a 1 to stop all cross-infections
anglefunction=0;
distancefunction=0;
end
if( 1 ) % change this to a 1 to have total cross-infectivity
anglefunction=0.1;
distancefunction=0.1;
end

if (xdiff==0 && ydiff==0) % resets the coefficients for
the region itself
anglefunction=1;
distancefunction=1;
end
interaction = distancefunction*anglefunction;
return;
```

## D Octave Code: multiregionSEIRDynamics.m

```
function delta=multiregionSEIRDynamics(P,tstep,breakdown,A,nodenum)

% this is the m-file that will run the code that determines the
% change in each subregion for every timestep
% (note that this calculates the compartment changes for only one
% subregion at a given timestep)

% breakdown(time, node index, [1:Susceptible, 2:Latent, 3:Infected1,
% 4:Infected2, 5:Infected3, 6:Removed])
% P(node index, [1=SE, 2=EI1, 3=I1I2, 4=I2I3, 5=I3S, 6=I3R,
% 7=I1, 8=I2, 9=I3])
% A(from_node,to_node)

delta=zeros(6); % delta([1:Susceptible, 2:Latent, 3:Infected1,
% 4:Infected2, 5:Infected3, 6:Removed])

% THE DYNAMICS FROM THE SUBREGION ITSELF

S_to_E = 0; %P(nodenum,1)*breakdown((tstep-1),nodenum,1)*
(breakdown((tstep-1),nodenum,2)+breakdown((tstep-1),nodenum,3)+
breakdown((tstep-1),nodenum,4)); % plant gets infected
E_to_I1 = P(nodenum,2)*breakdown((tstep-1),nodenum,2);
% infection progresses
I1_to_I2 = P(nodenum,3)*breakdown((tstep-1),nodenum,3);
% infection progresses
I2_to_I3 = P(nodenum,4)*breakdown((tstep-1),nodenum,4);
% infection progresses
I3_to_S = P(nodenum,5)*breakdown((tstep-1),nodenum,5);
% e.g. fungicide treatment
I3_to_R = P(nodenum,6)*breakdown((tstep-1),nodenum,5);
% death of plant

% THE DYNAMICS FROM INTER-SUBREGION ACTIVITY

for nodenum2=1:size(A,1)
% [P(nodenum,1),A(nodenum,nodenum2),breakdown((tstep-1),nodenum,1)]
S_to_E = S_to_E + P(nodenum,1)*A(nodenum2,nodenum)*
breakdown((tstep-1),nodenum,1)*( ...
P(nodenum2,7)*breakdown((tstep-1),nodenum2,3)+ ...
P(nodenum2,8)*breakdown((tstep-1),nodenum2,4)+ ...
P(nodenum2,9)*breakdown((tstep-1),nodenum2,5));
end

% REBUILD THE DELTA VECTOR
```

```
delta(1) = -S_to_E + I3_to_S;  
delta(2) = +S_to_E - E_to_I1;  
delta(3) = +E_to_I1 - I1_to_I2;  
delta(4) = +I1_to_I2 - I2_to_I3;  
delta(5) = +I2_to_I3 - I3_to_R - I3_to_S;  
delta(6) =+ I3_to_R;  
  
return;
```

## E Octave Code: multiregionSEIRparameteranalysis.m

```
% this is the driving m-file that invokes all of the other
m-files in order to run the model
% this one is to play with the Diff EQ parameters

clear all;
close all;

%%% AMR
pct_vec = -50:10:50;
mult_vec = (pct_vec/100) + 1; % so, for example, +10 becomes 1.10

% SET UP THE REGION

% these are the values to change in order to change the "resolution"
total_rows=10;
total_columns=1;
num_nodes=total_rows*total_columns;

% SET UP THE INITIAL CONDITIONS

breakdown=zeros(1,num_nodes,6); % breakdown(time, node index,
[1:Susceptible, 2:Latent, 3:Infected1, 4:Infected2,
5:Infected3, 6:Removed])
infected_node=num_nodes; % the last node is picked as the initially
infected node. This is changeable (in fact, it would probably be good
to make this a separate function...)

%%% AMR
if( 0 ) % change this to a 1 for just one region, or a 0
for everything infected.
% Infect only one region
experimenttype="Just One Region Infected Initially";
breakdown(1,:,1) = 100;
breakdown(1,infected_node,2)=1;
breakdown(1,infected_node,1)=99;
else
% infect every region equally
experimenttype="Every Region Infected Initially";
breakdown(1,:,1) = 100;
breakdown(1,:,2)=1;
breakdown(1,:,1)=99;
end % if
```

```

% SET UP THE PARAMETERS FOR THE SUBREGIONS

P=zeros(num_nodes,9); % P(node index, [1=SE, 2=EI1, 3=I1I2,
4=I2I3, 5=I3S, 6=ILR, 7=I1, 8=I2, 9=I3])

%%% AMR
labels={'SE','EI1','I1I2','I2I3','I3S','I3R','I1','I2','I3'}
%%% AMR
for npi = 1:9 % iterate across parts of the Parameter vector
for nmi = 1:length(mult_vec) % iterate across different multipliers
parameter=zeros(9);
tmp_mult_vec = ones(size(parameter));
tmp_mult_vec(npi) = mult_vec(nmi); % copy just one
multiplier in to it.
% output some indication of where we are in the looping:
[ npi, mult_vec(nmi)]

for i=1:num_nodes
parameter=multiregionSEIRparameter(i);
%%% AMR
parameter = parameter .* tmp_mult_vec;
for n=1:9
P(i,n)=parameter(n);
end
end

% SET UP THE INTERACTION COEFFICIENTS FOR THE SUBREGIONS

A=zeros(num_nodes,num_nodes); % this is the matrix that will
store the interaction coefficients [A(from_node,to_node)]
from_node=1;
to_node=1;

for from_node=1:num_nodes
for to_node=1:num_nodes
interaction = multiregionSEIRinteraction(from_node,
to_node,total_columns);
A(from_node,to_node)=interaction;
end
end

% RUN THE SEIR DYNAMICS FOR ALL THE SUBREGIONS, CHANGE THE
VALUES, AND LOOP IT OVER DESIRED TIME

```



```

for tstep=2:39
for nodenum=1:num_nodes
%nodenum
delta=multiregionSEIRDynamics(P,tstep,breakdown,A,nodenum);
for i=1:6
breakdown(tstep,nodenum,i)=breakdown((tstep-1),nodenum,i)+delta(i);
end
end
end

% DETERMINE THE WHEAT HARVESTED IN EACH REGION

harvest = zeros(num_nodes,1);
t=tstep;
for i=1:num_nodes
harvest(i)=breakdown(t,i,1)+breakdown(t,i,2)+
breakdown(t,i,3)+breakdown(t,i,4);
end

harvest

%%% AMR
sens_mat(npi,nmi) = sum(harvest);

%%% AMR
% I'm not suggesting we publish this graph, but I'm just curious:
% does the shape of the harvest curve (from north to
south or vice versa)
% change much as we change the parameters?
% Now that I've tried it, it seems like no, the shape
doesn't change much at all.
%plot(harvest);
%hold on;

%%% AMR
end % for nmi loop
end % for npi loop

% GRAPH THE RESULTS

%%% AMR: this whole section is new.
figure ; % open a new figure
plot(pct_vec,sens_mat);
xlim( 1.10*[min(pct_vec), max(pct_vec)] )
%title(experimenttype,'FontSize',14,'FontName','Courier')

```

```

xlabel('Percent Change in Parameter','FontSize',11,
'FontName','Courier')
ylabel('Harvested Number of Wheat Plants','FontSize',
11,'FontName','Courier')

%legend(labels);
% using the legend, it's actually hard to match up
which line is which.
% Consider something like this:
for npi=1:9
% put it on the right
% x = max(pct_vec)*1.05 ; % move the text out just a little
% y = sens_mat(npi,end);
% horizontalalignment = 'left';
% put it on the left
x = min(pct_vec)*0.95; % move the text out just a little
y = sens_mat(npi,1);
horizontalalignment = 'right';
text(x,y,labels{npi},'FontSize',11,'FontName','Courier',
'horizontalalignment',horizontalalignment)
end

```

## F Octave Code: multiregionSEIRparameteranalysis2.m

```
% this is the driving m-file that invokes all of the other m-files
in order to run the model.
% this one is for the K parameter for distance

clear all;
close all;

%%% AMR
pct_vec = -50:10:50;
mult_vec = (pct_vec/100) + 1; % so, for example, +10 becomes 1.10

Kvec = [ .1:.1:6];
maxK=max(Kvec);
minK=min(Kvec);

% SET UP THE REGION

% these are the values to change in order to change the "resolution"
total_rows=10;
total_columns=1;
num_nodes=total_rows*total_columns;

% SET UP THE INITIAL CONDITIONS

breakdown=zeros(1,num_nodes,6); % breakdown(time, node index,
[1:Susceptible, 2:Latent, 3:Infected1, 4:Infected2,
5:Infected3, 6:Removed])
infected_node=num_nodes; % the last node is picked
as the initially infected node.

%%% AMR
if( 0 ) % change this to a 1 for just one region, or a 0
for everything infected.
% Infect only one region
experimenttype="Just One Region Infected Initially";
experiment=1;
breakdown(1,:,1) = 100;
breakdown(1,infected_node,2)=1;
breakdown(1,infected_node,1)=99;
else
% infect every region equally
experimenttype="Every Region Infected Initially";
experiment=0;
```

```

breakdown(1, :, 1) = 100;
breakdown(1, :, 2)=1;
breakdown(1, :, 1)=99;
end % if

% SET UP THE PARAMETERS FOR THE SUBREGIONS

P=zeros(num_nodes,9); % P(node index, [1=SE, 2=EI1, 3=I1I2,
4=I2I3, 5=I3S, 6=ILR, 7=I1, 8=I2, 9=I3])

%%% AMR
for nmi = 1:length(Kvec) % iterate across different multipliers

Kdist = Kvec(nmi)

for i=1:num_nodes
parameter=multiregionSEIRparameter(i);
%%% AMR
% parameter = parameter .* tmp_mult_vec;
for n=1:9
P(i,n)=parameter(n);
end
end

% SET UP THE INTERACTION COEFFICIENTS FOR THE SUBREGIONS

A=zeros(num_nodes,num_nodes); % this is the matrix that
will store the interaction coefficients [A(from_node,to_node)]
from_node=1;
to_node=1;

for from_node=1:num_nodes
for to_node=1:num_nodes
interaction = multiregionSEIRinteraction(from_node,to_node,
total_columns,Kdist);
A(from_node,to_node)=interaction;
end
end

% RUN THE SEIR DYNAMICS FOR ALL THE SUBREGIONS, CHANGE THE VALUES,
AND LOOP IT OVER DESIRED TIME

for tstep=2:39
for nodenum=1:num_nodes

```

```

%nodenum
delta=multiregionSEIRDynamics(P,tstep,breakdown,A,nodenum);
for i=1:6
breakdown(tstep,nodenum,i)=breakdown((tstep-1),nodenum,i)+delta(i);
end
end
end

% DETERMINE THE WHEAT HARVESTED IN EACH REGION

harvest = zeros(num_nodes,1);
t=tstep;
for i=1:num_nodes
harvest(i)=breakdown(t,i,1)+breakdown(t,i,2)+
breakdown(t,i,3)+breakdown(t,i,4);
end

harvest

plot(harvest);
if(Kdist==minK)
x=2;
y=harvest(x);
text(x,y,['\bf K = ',num2str(Kdist)],'FontSize',11,
'FontName','Courier')
elseif(Kdist==maxK)
x=2;
y=harvest(x);
text(x,y,['\bf K = ',num2str(Kdist)],'FontSize',11,
'FontName','Courier')
end
hold on;

%%% AMR
end % for nmi loop
%end % for npi loop

%title(experimenttype,'FontSize',14,'FontName','Courier')
xlabel('Node Number','FontSize',11,'FontName','Courier')
ylabel('Number of Wheat Plants','FontSize',11,'FontName','Courier')
xleft=0.12*num_nodes;
xright=0.98*num_nodes;
y=min(harvest)+5;
yup=y+1.5;
ydown=y-1.52;

```

```
text(xleft,y,['North Dakota'],'FontSize',11,'FontName','Courier')
horizontalalignment = 'right';
if(experiment==1)
text(xright,yup,['Texas (source)'],'FontSize',11,'FontName',
'Courier','horizontalalignment',horizontalalignment)
text(xright,ydown,['of infection'],'FontSize',11,'FontName',
'Courier','horizontalalignment',horizontalalignment)
else
text(xright,y,['Texas'],'FontSize',11,'FontName','Courier',
'horizontalalignment',horizontalalignment)
end
```

## G Octave Code: multiregionSEIRDynamics2.m

```
function delta=multiregionSEIRDynamics2(P,tstep,breakdown,A,nodenum)

% this is the m-file that will run the code that determines the
% change in each subregion for every timestep for a non-adapted
% SEIR model
% (note that this calculates the compartment changes for only
% one subregion at a given timestep)

% breakdown(time, node index, [1:Susceptible, 2:Latent, 3:Infected1,
% 4:Infected2, 5:Infected3, 6:Removed])
% P(node index, [1=SE, 2=EI1, 3=I1I2, 4=I2I3, 5=I3S, 6=I3R,
% 7=I1, 8=I2, 9=I3])
% A(from_node,to_node)

delta=zeros(6); % delta([1:Susceptible, 2:Latent, 3:Infected1,
% 4:Infected2, 5:Infected3, 6:Removed])

% THE DYNAMICS FROM THE SUBREGION ITSELF

S_to_E = 0; %P(nodenum,1)*breakdown((tstep-1),nodenum,1)*
(breakdown((tstep-1),nodenum,2)+breakdown((tstep-1),nodenum,3)
+breakdown((tstep-1),nodenum,4)); % plant gets infected
E_to_I1 = P(nodenum,2)*breakdown((tstep-1),nodenum,2);
% infection progresses
I1_to_I2 = P(nodenum,3)*breakdown((tstep-1),nodenum,3);
% infection progresses
I2_to_I3 = P(nodenum,4)*breakdown((tstep-1),nodenum,4);
% infection progresses
I3_to_S = P(nodenum,5)*breakdown((tstep-1),nodenum,5);
% e.g. fungicide treatment
I3_to_R = P(nodenum,6)*breakdown((tstep-1),nodenum,5);
% death of plant

% THE DYNAMICS FROM INTER-SUBREGION ACTIVITY

for nodenum2=1:size(A,1)

% [P(nodenum,1),A(nodenum,nodenum2),breakdown((tstep-1),nodenum,1)]

S_to_E = S_to_E + P(nodenum,1)*A(nodenum2,nodenum)*
breakdown((tstep-1),nodenum,1)*( ...
P(nodenum2,7)*breakdown((tstep-1),nodenum2,3)+ ...
P(nodenum2,8)*breakdown((tstep-1),nodenum2,4)+ ...
P(nodenum2,9)*breakdown((tstep-1),nodenum2,5));
```

```
end

% REBUILD THE DELTA VECTOR

delta(1) = -S_to_E + I3_to_S; % change in S
delta(2) = +S_to_E - E_to_I1; % change in E
delta(3) = 0; % change in I1 ---> nothing
delta(4) = 0; % change in I2 ---> nothing
delta(5) = +E_to_I1 - I3_to_R - I3_to_S;
% change in I3 ---> I
delta(6) =+ I3_to_R; %change in R

return;
```