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AN AGENT BASED MODEL OF ACUTE BEE PARALYSIS VIRUS AND KASHMIR BEE VIRUS CO-INFECTION WITHIN A HONEYBEE COLONY

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ABSTRACT

The study examined the transmission dynamics of Acute Bee Paralysis Virus (ABPV) and Kashmir Bee Virus (KBV) co-infection in a colony. The study is aim at determining the degree of co-infection between the two honeybee viral diseases "ABPV" and "KBV" using machine learning classification methods. The model is based on the presence of the Varroa mite in a honeybee colony which is a vector of the diseases and as well transmit to a susceptible host (honeybee) only upon adequate contact with an infected host. The study made used of Honeybees Dataset generated from the NetLogo simulation environment. The experiment used 10-fold cross-validation to estimate accuracy of the classification of the co-infection between the two diseases using machine learning approach. It splits the dataset into 10 parts, train on 9 and test on 1 and repeat for all combinations of train-test splits. The result obtained from the study shows that, the co-infection between two diseases is very likely. Further, the study shows that Classification and Regression Tree (CART) fitted most with classification accuracy of 90.38% for more than 100 mites and 82.88% for less than 100 mites on the honeybee dataset for co-infection between the two viruses ABPV and KBV. Thus, the more the mites infesting the honeybees, the more the accurate the model fit.

Keywords: Agent Based Model, ABPV, KBV, Co-infection, Machine learning.

INTRODUCTION

Honey bee is a eusocial, flying insect which belong to genus *Apis* of the bee clade. They are known for construction of perennial, colonial nests from wax, for the large size of their colonies, and for their surplus production and storage of honey, distinguishing their hives as a prized foraging target of many animals, including honey badgers, bears and human hunter-gatherers. The best known honey bee is the western honey bee which has been domesticated for honey production and crop pollination; modern humans also value the wax for candle making, soap making, lip balms, and other crafts (Michael, 1999). Honey bees have three castes: drones, workers, and queen. Drones are males, while workers and queen are females. The western honey bee was one of the first domesticated insects, and it is the primary species maintained by beekeepers to this day for both its honey production and pollination activities. The Western bees are threatened by pests and diseases, especially Varroa mite (Weinstock & Robinson, 2006).

The Varroa mite is the parasite with possibly the most pronounced economic impact on the beekeeping industry (Weinstock & Robinson, 2006). Varroa is considered to be one of multiple stress factors contributing to the higher levels of bee losses around the world. The Varroa mite attaches itself to an unsuspecting bee and sucks its blood which causes harm to the bees (Eberl, Frederick, & Kevan, 2010). This leaves wounds that they easily become infected with various bacteria, fungi, and viruses such as deformed wing virus, acute bee paralysis virus, kashmir bee virus, etc that have the potential to harm the bees even more (de Miranda, Cordoni, & Budge, 2019). Varroa is considered to be one of multiple stress factors contributing to the higher levels of bee losses around the world (Goulson, Nicholls, Botias, & Rotheray, 2015). Therefore, as a result of cohabitants of bees and varroa mites, diseases spreads within the bee colonies, but it is important for the beekeeper to be able to recognize conditions which might be disease or pests related and respond accordingly (Martin, 2001).

Acute paralysis bee virus (APBV) and Kashmir bee virus (KBV) are part of a complex of closely related viruses from the Dicistroviridae and also, they are serologically related viruses that could affect healthy adult bees (de Miranda, et al., 2004). These viruses have a widespread prevalence in honey bee (*apis mellipera*) colonies with no symptoms been attributed to either, whereas APBV is a disease of adults, KBV is reported to cause mortality in brood and adult honey bees (Hung, Shimanuki, & Knox, 1996; Jay, 2001).

Different models were used to study the epidemiology of ABPV (See, Eberl et al., 2010; Ratti et al., 2012; Ratti et al., 2015; Ratti et al., 2017) and KBV (see, (Sumpter & Martin, 2004; Sara & Ezio, 2016). Mathematical Modeling plays an important role in epidemiology by given more insight in understanding the transmission dynamics of infectious diseases and recommend effective control strategies (Hethcote, 2000).

Computational advances are making it possible to develop agent-based models (ABM) in a variety of application areas, including areas where simulation has not been extensively applied. ABM applications range from supply chains, consumer goods markets, and financial markets, to predicting the spread of epidemics and understanding the factors responsible for the fall of ancient civilizations (Charles & Michael, 2018).

Honey bees are susceptible to many diseases, pathogens, etc. As a result of that, the research by Jay (2001) discover the possibility of a bee been coinfected by Acute Bee Paralysis Virus (ABPV) and Kashmir Bee Virus (KBV). Thus, the aim of the study is to measure the classification accuracy of co-infection rate of the two honeybee viral diseases ABPV and KBV. The study wants to know based on the datasets, if all the two viral diseases ABPV and KBV can co-infect some of the honeybee population and if the case, what will be the accurate rate?

The remaining part of the paper is organized as follows; in section 2, we designed and simulate the model. While the result of the simulations is presented in section 3. The conclusion of the paper is given in section 4.

MODEL DESIGN AND ANALYSIS

Description of the Model

The mathematical model is based on the presence of the varroa mite (which is the vector of ABPV and KBV) that transmit diseases to a susceptible host only upon adequate contact with an infected host in honeybee colony. The model follows a compartmental approach, where the honey bees are classified into eight (8) mutually exclusive compartment, while the varroa mites are classified into three (3) mutually exclusive compartment. The agents or variables represent the members of the aforementioned compartments: susceptible brood bees (B_0), susceptible adult bees(H_0), susceptible mites (M_0), brood bees infected with ABPV (B_1), adult bees infected with ABPV (H_1), mites infected with ABPV (M_1), brood bees infected with KBV (B_2), adult bees infected with KBV (H_2), mites infected with KBV (M_2), brood bees co-infected with both virus (B_C) and adults bees co-infected with both virus (H_C). We assume that pupae infected with ABPV die quickly before they develop into adult bees.

Table 1: Model parameter and their description.

Parameters	Description
ϕ_0 (ϕ_2)	The rate at which susceptible (infected with KBV) brood bee's metamorphose to adult bees
$\gamma_1(\gamma_2)$	The rate at which the susceptible brood bees become infected with ABPV (KBV)
θ_1 (θ_2)	The rate at which the susceptible adult bees become infected with ABPV (KBV)
γ_{1C} (γ_{2C})	The rate at which the brood bee infected with ABPV becomes co-infected with KBV (infected with KBV become co-infected with ABPV)
θ_{1C} (θ_{2C})	The rate at which the adult bee infected with ABPV becomes co-infected with KBV (infected with KBV become co-infected with ABPV)
d_b $(d_h)[d_m]$	Natural death rate of the brood (adult) [mite] bees

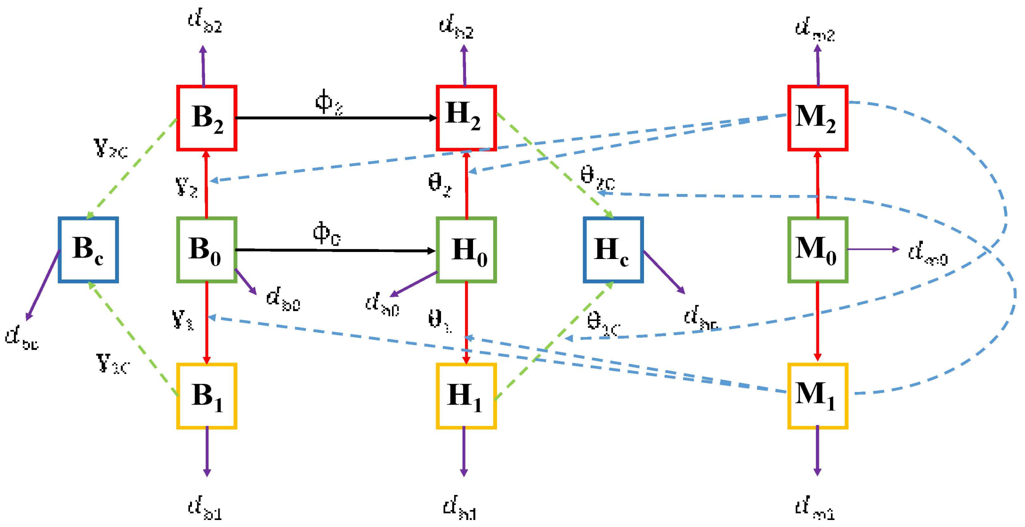


Figure 1: Flow diagram of the model showing the transition of honey bees and varroa mites between mutually-exclusive compartments based on diseases status. The solid line shows the transition while the dashed line shows interaction.

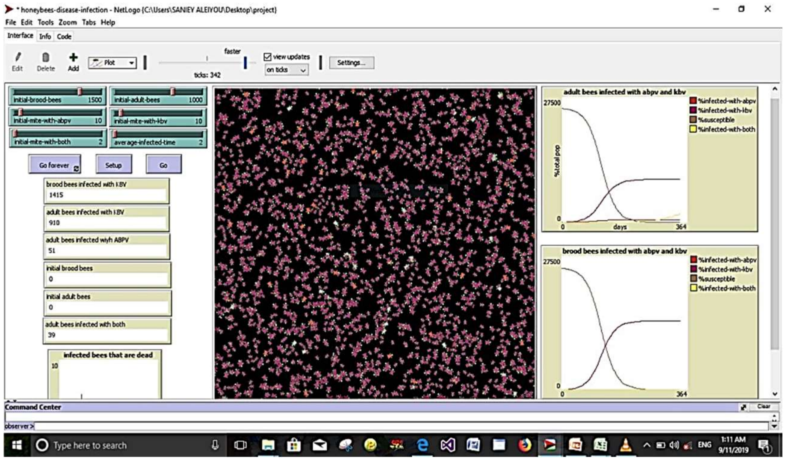
Agent Based Modeling

Agent-based modeling (ABM) and simulation is an approach to modeling systems comprised of autonomous, interacting agents. It consists of agents that interact within an environment. Progress suggests that ABM could have far-reaching effects on how researchers use models as electronic laboratories to identify promising research directions. Some contend that ABM “is a third way of doing science” and could augment traditional discovery methods for creating new knowledge (Charles & Michael, 2018).

Machine learning (ML) is scientific technique where the computers learn how to solve a problem, without been explicitly programmed. Deep learning is currently leading the ML race powered by better algorithms, computation power and large data. Still ML classical algorithms have their strong position in the field (Jason, 2016). The mixture of simple linear algorithms (such as Linear Regression (LR) and Linear Discriminant Analysis (LDA)) and nonlinear algorithms (such as k-Nearest Neighbors (KNN), Classification and Regression Trees (CART), Gaussian Naive Bayes (NB) and Support Vector Machines (SVM)) were used. Furthermore, we reset the random number seed before each run to ensure that the evaluation of each algorithm is performed using exactly the same data splits. It ensures the results are directly comparable. Further, the study depends on data generated from Netlogo software (not a field research).

NetLogo

NetLogo is a programmable modeling environment for simulating natural and social phenomena. It was designed by Uri Wilensky in 1999 and has been in continuous development ever since at the Center for Connected Learning and Computer-Based Modeling (Wilensky, 1999–2019). NetLogo is particularly well suited for modeling complex systems developing over time. Modelers can give instructions to hundreds or thousands of “agents” all operating independently. This makes it possible to explore the connection between the micro-level behavior of individuals and the macro-level patterns that emerge from their interaction. NetLogo is the next generation of the series of multi-agent modeling languages including StarLogo and StarLogoT.



* honeybees-disease-infection - NetLogo {C:\Users\SANIEY ALEIYOU\Desktop\project}

ticks: 342

☑ view updates
on ticks

initial-brood-bees 1500
initial-adult-bees 1000
initial-mite-with-abpv 10
initial-mite-with-kbv 10
initial-mite-with-both 2
average-infected-time 2

brood bees infected with KBV
1415

adult bees infected with KBV
910

adult bees infected wiyh ABPV
51

initial brood bees
0

initial adult bees
0

adult bees infected with both
39

Figure 2: NetLogo simulation environment

RESULTS AND DISCUSSION

Experimental Results

In this section, we simulated the model depicted in Figure 1 using NetLogo 6.0.2 software. We perform two experiments with less 100 mites and 100 mites in a colony.

Experiment I:

A total number of 1500 of brood bees, 1000 adult bees, 10 mites infected with KBV and 10 infected with ABPV were chosen. Simulating this using the setting in Figure 1 for 365 days revealed that, a total of 1278 brood bees become infected with KBV, 796 adult bees infected with KBV, 148 adult bees infected with ABPV and 0 brood bees infected with ABPV because if it infects with ABPV it dies immediately (as assumed in section 2.1), and 56 adult bees co-infected with both viruses.

Experiment II:

A total number of 1500 of brood bees, 1000 adult bees, 100 mites infected with KBV and 100 infected with ABPV were chosen. Simulating the model using the setting as in Figure 1 for 365 days revealed that, a total of 1109 brood bees become infected with KBV, 719 adult bees infected with KBV, 249 adult bees infected with ABPV and 0 brood bees infected with ABPV because if it infects with ABPV it dies immediately (as assumed in section 2.1), and 32 adult bees co-infected with both viruses.

10-Fold Cross Validations

This will split our dataset into 10 parts, train on 9 and test on 1 and repeat for all combinations of train-test splits. The dataset is sub grouped into 10 groups. The 9 groups are used for training and the remaining one is used for testing. The validation is performed ten times. For each validation time, randomly choose 9 groups for training and remaining one for testing. The Average Classification Accuracy (ACA) is calculated over these ten validations.

The experimental results are presented for classifier performance of the algorithm on the dataset. The experiments are performed on the Honeybees Dataset generated from NetLogo simulation environment. We used 10-fold cross-validation to estimate accuracy using the metric of accuracy to evaluate the models. This is a ratio of the number of correctly predicted instances divided by the total number of instances in the dataset multiplied by 100 to give a percentage (e.g. 95% accurate). We will be using the scoring variable when we run build and evaluate each model.

Table 2: Classifier performance on Honeybees Dataset for less than 100 mites over 10-Fold Cross Validations

Honeybees Categories	**10-Fold Cross Validation**						
	Accuracy Rate (%) for Classification Methods						
	ACA	**LR**	**LDA**	**KNN**	**CART**	**NB**	**SVM**
Adult infected with ABPV	0.7971	0.4300	0.6021	0.7587	0.839021	0.7767	0.5507
Adult infected with KBV	0.4118	0.2598	0.3047	0.4088	0.4724	0.4087	0.2264
Adult infected with both ABPV and KBV	0.8254	0.4702	0.5305	0.7728	0.8288	0.7729	0.4105
Brood infected with KBV	0.3824	0.1661	0.2437	0.2954	0.3433	0.3099	0.1660

Table 3: Classifier performance on honeybees dataset for greater than 100 mites over 10-fold cross validations.

Honeybees Categories	10-Fold Cross Validation Accuracy Rate (%) for Classification Methods						
	ACA	**LR**	**LDA**	**KNN**	**CART**	**NB**	**SVM**
Adult infected with ABPV	0.5926	0.3437	0.4823	0.5742	0.6301	0.5647	0.4405
Adult infected with KBV	0.4483	0.3130	0.3522	0.3957	0.4739	0.4043	0.3087
Adult infected with both ABPV & KBV	0.9038	0.3910	0.6583	0.8362	0.9038	0.8652	0.3917
Brood infected with KBV	0.2083	0.0945	0.2837	0.2887	0.3255	0.2992	0.2047

The experimental results for different classification methods on Honeybees Dataset are shown in table 2 and 3 above for variable number of mites.

Honeybees Diseases Visualization for less than 100 mites

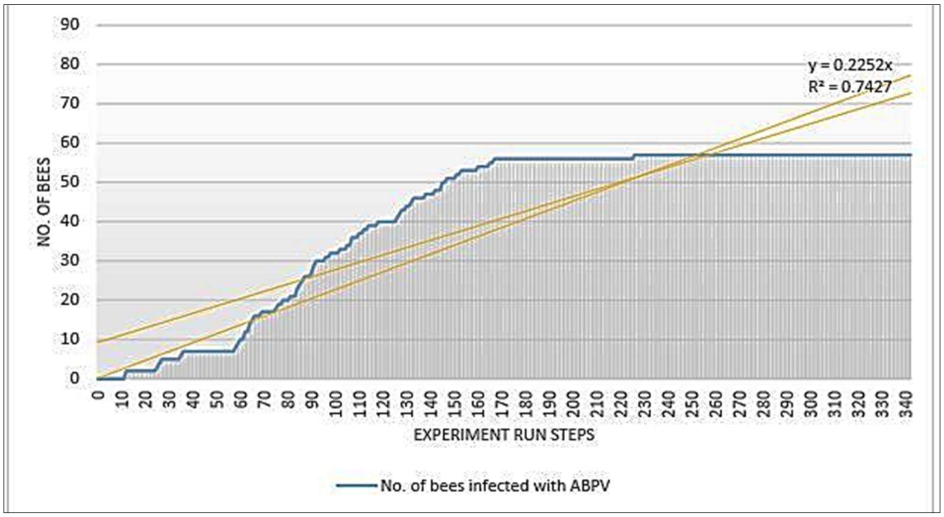


Figure 3: Adult Bees infected with ABPV Viral Disease.

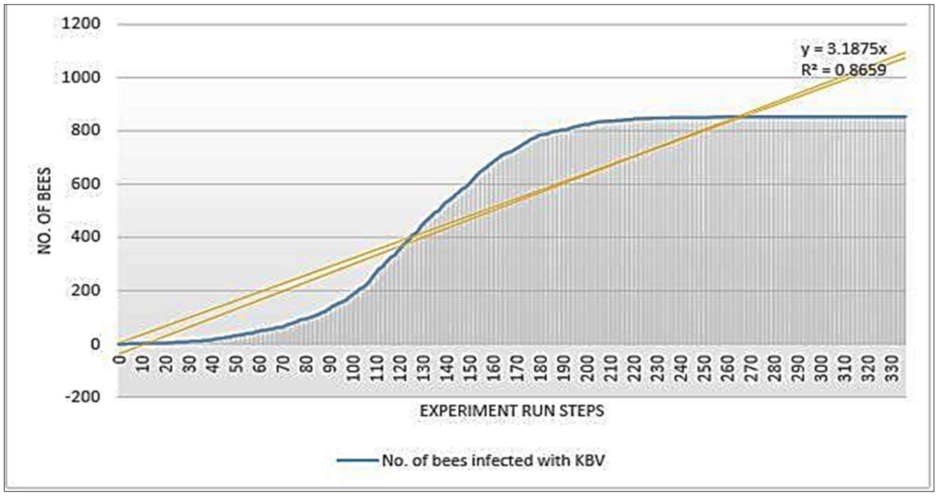


Figure 4: Adult Bees infected with KBV Viral Disease.

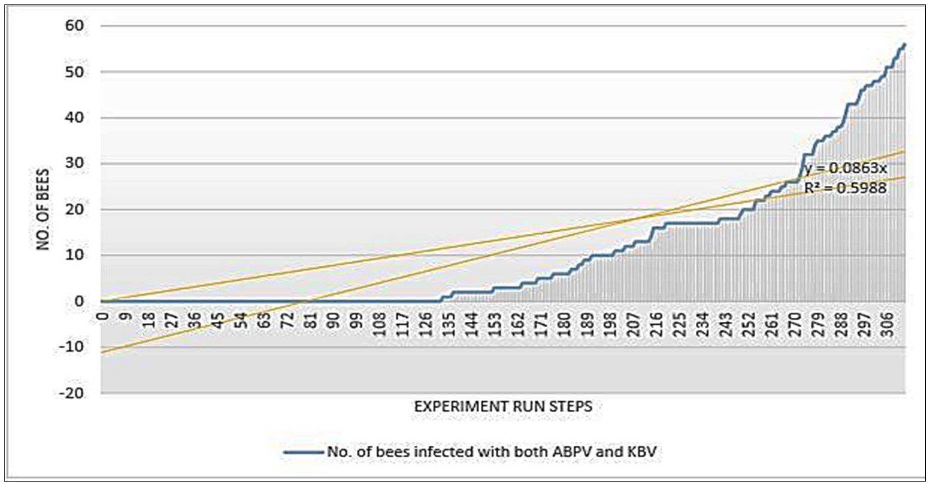


Figure 5: Adult Bees infected with both ABPV and KBV Viral Diseases (Co-infection).

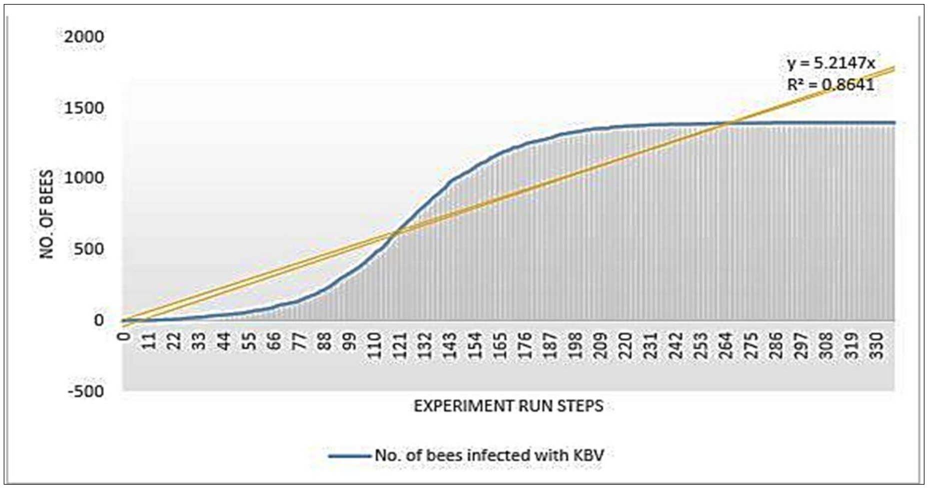


Figure 6: Brood Bees infected with KBV Viral Disease.

Honeybees Diseases Visualization for greater than 100 mites

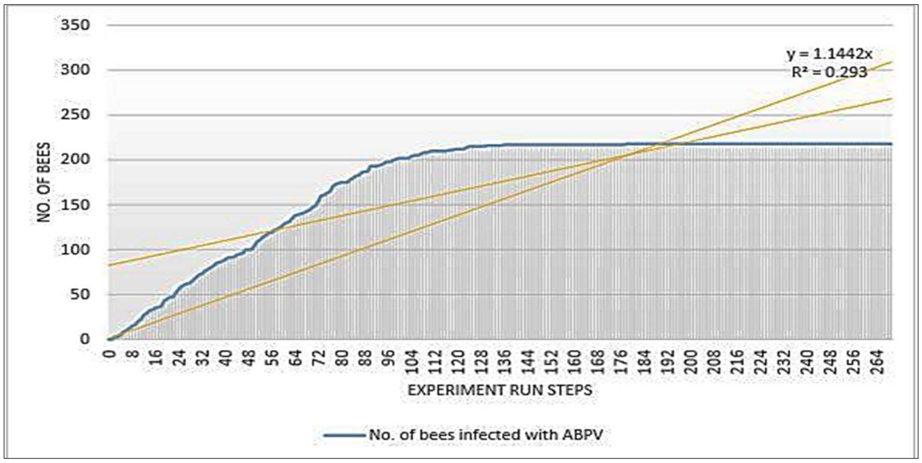


Figure 7: Adult Bees infected with ABPV Viral Disease.

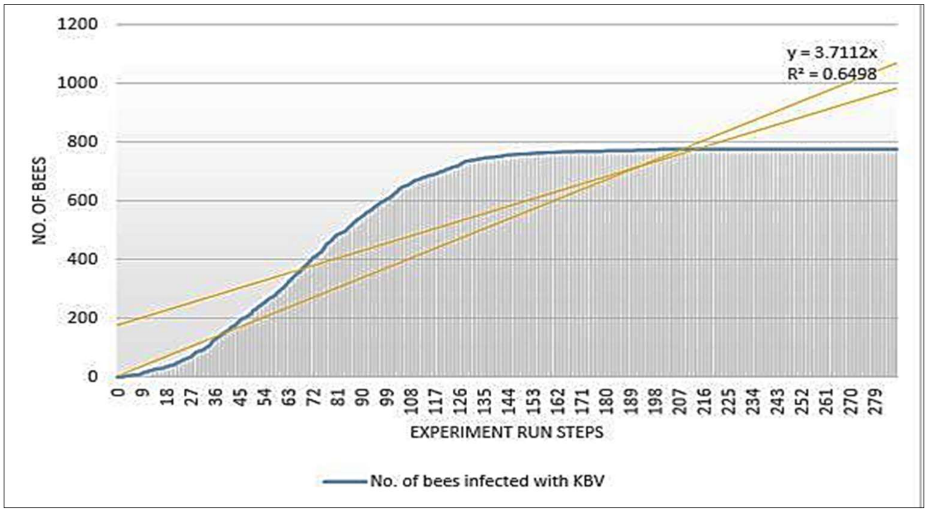


Figure 8: Adult Bees infected with KBV Viral Disease.

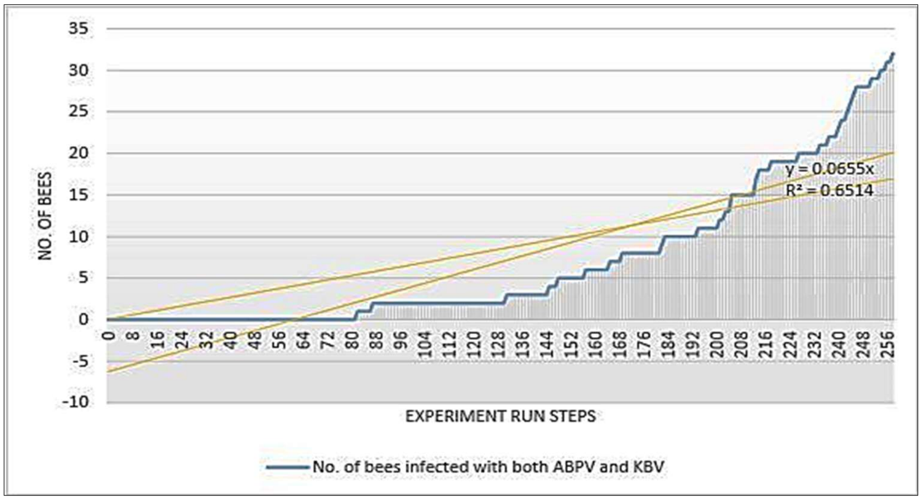


Figure 9: Adult Bees co-infected with ABPV and KBV

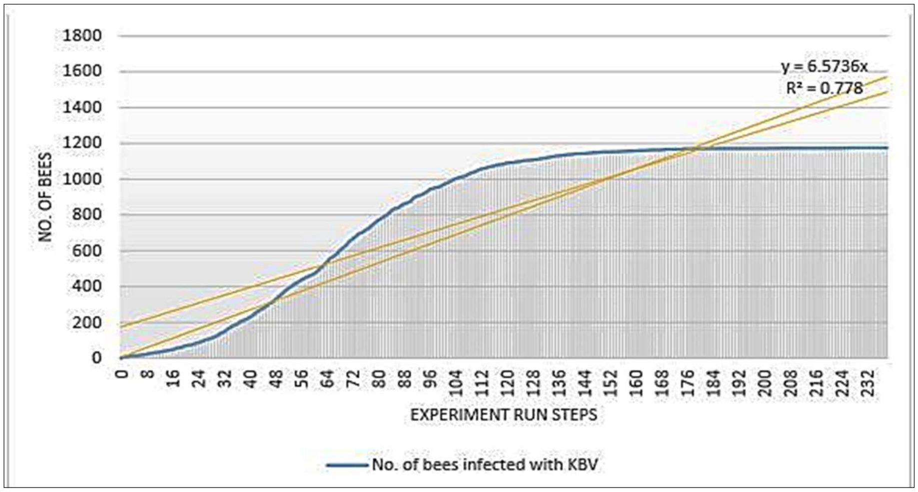


Figure 10: Brood Bees infected with KBV Viral Disease.

In this study, Classification and Regression Tree (CART) has a highest classification accuracy of 90.38% for more than 100 mites and 82.88% for less than 100 mites on the honeybee dataset for co-infection between the two viruses "Acute bee paralysis virus" and "Kashmir bee paralysis virus". Based on this study, the CART classifier is the most fitted model for the problem over 10-fold cross validation.

CONCLUSION

In summary, we proposed and study (via a computational approach) the transmission of ABPV and KBV co-infection within a colony of honey bee. We use an ABM method of computational modeling to study the transmission dynamics with the help of NetLogo. Furthermore, we use a machine learning technique to evaluate the proposed model. Among all available classification methods, the CART has the highest classification accuracy over 10-fold cross validation as discovered in the study. Even though, other remaining classification methods also have acceptable classification accuracy rate and classifier performance. In the study, Classification and Regression Tree (CART) fitted most with classification accuracy of 90.38% for more than 100 mites and 82.88% for less than 100 mites on the honeybee dataset for co-infection between the two viruses ABPV and KBV. Based on that, the CART classifier is the best model for the problem over 10-fold cross validation. Thus, we conclude that the more the mites infesting the honeybees' hosts are, the more the accurate the model will be for honeybees co-infected with both ABPV and KBV. Biologically speaking means, the two viruses are likely to co-infect a honey bee, if the number of mites increase.

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