Asian honey bee Transition to Management Program

Asian honey bee spread modelling

Contents

Summary

This report aimed to fulfil AG3C of the AHB Transition to Management (T2M) Plan, i.e. to "model the population dynamics and drivers of spread", and contribute towards QG2C & QG2D of the AHB T2M Plan, i.e. to "undertake a spatial analysis of the current AHB infestation to guide future surveillance activities". As such, the aim was to (1) conduct preliminary modelling, (2) compare the output of the initial model with the current known infested area of AHB, (3) identify gaps in knowledge where, due to lack of data, input parameters had to be estimated, and (4) identify shortcomings of this initial model and make recommendations to how the model may be improved in the future.

A stochastic, cellular automaton model designed to simulate the spread and control of Asian honey bees in north Queensland was used. It simulates short distance spread as well as long distance jumps (simulating human-assisted spread or other long distance spread). Also incorporated was an estimated habitat suitability for AHB as well as a probability that AHB will be found and destroyed. The model was run for a specified number of replications and for a specified number of time-steps, with each time-step being six months.

When using input parameters for long distance dispersal of 60 km and control effectiveness of 95%, and starting the simulation in 2007, the predicted spread for 2012 somewhat matched the 2012 maximum extent of the known infested area. Unfortunately, an artefact of the model itself (a 'glitch' in the model) was apparent. Due to this 'glitch', any predictions made by the model need to be taken with utmost caution and it is advised to disregard any output of the model until it is repaired.

Suggestions for model improvement include:

- Specifying jump distances that are (a) biologically based e.g. related to swarming distance, and (b) that are human-mediated.

- Allowing more than one jump from each cell in each time-step, based on the density of nests within that cell.

- Incorporating roads; a large number of long-distance dispersal pockets are apparent, most of which are not along roads, i.e. random.

- Using human population density as a predictor of the probability of long-distance spread.

- Incorporating climate data.

Introduction

There are two conceptual approaches to predicting future spread: (1) analysis of, and extrapolation from, past patterns of spread, and (2) computer simulations using data on life-history traits within a mechanistic model (Liebhold and Tobin, 2008).

The former has been explored for the Asian honey bee (AHB) in the report "Spread of *Apis cerana* in Australia, 2007 – 2012" (Koetz, 2013c). The current report explores a computer simulation model designed to simulate the spread and control of AHB in north Queensland. It simulates two types of spread: diffusion into adjacent cells (from short distance swarming) and jumps into cells that may be many kilometres away from originating cells (simulating accidental, human-assisted spread or other long distance spread).

Computer simulation models can be very useful in predicting the spread of an invasive species. However, simulation models are based on a suite of assumptions and often require large amounts of data and knowledge of the species. In particular, one needs to keep in mind that the output will be as reliable as the input data, i.e. if the input data is largely estimated, unknown or unreliable, then the output will also be unreliable.

Nevertheless, a validated simulation model may, in some instances, be more useful than a simple radial-expansion model as was the basis for Koetz's (2013c) report. A simulation model uses knowledge of the biology of the organism and represents that mathematically. The process of developing a simulation model clearly indentifies gaps in the data and knowledge. This can inform further research.

The overall goal was to develop a computer model that may be used to simulate the potential future spread of AHB in Australia. To do so, the aims were to:

- Conduct preliminary modelling using the initial model developed based on expert knowledge of AHB ecology and using original 2007 AHB detection locations.

- Compare the output of the initial model with the current known infested area of AHB, in order to enable modification of the model parameters to improve its predictions.

- Identify gaps in knowledge where, due to lack of data, input parameters had to be estimated. These gaps in knowledge should be addressed by future research.

- Identify shortcomings of this initial model and make recommendations to how the model may be improved in the future.

This report aimed to fulfil AG3C of the AHB Transition to Management (T2M) Plan, i.e. to "model the population dynamics and drivers of spread", and contribute towards QG2C & QG2D of the AHB T2M Plan, i.e. to "undertake a spatial analysis of the current AHB infestation to guide future surveillance activities".

Methods

The Asian honey bee Model (AHBM) is a cellular automaton model designed to simulate the spread and control of Asian honey bees in north Queensland. It simulates two types of spread: spread into adjacent cells (from short distance swarming); and jumps into cells that may be many kilometres away from originating cells (simulating human-assisted spread or other long distance spread).

The probability of establishment in a new cell is dependent upon the habitat suitability within that cell. There is also a combined probability that the locations of AHB within a cell will be found and destroyed within each time-step.

The model is stochastic and is run for a specified number of replications and for a specified number of time-steps, with each time-step being six months.

Output from the model is suitable for importing into ArcMap to produce maps of the potential distribution over time.

Model description

Area

An area in north Queensland, centred around Cairns, was divided into 1 km by 1 km grids, resulting in 119000 cells. This grid size was used as a reasonable size from which AHB may spread into adjacent cells within a 6-month period. Smaller cell sizes would have meant that spread into adjacent cells was at or close to a probability of 1 (always occurring). Larger cell sizes would have meant that the probability of spread into adjacent cells was very low and could not take into account the fine-scale differences in habitat suitability in the region.

Habitat suitability

Habitat suitability was estimated for each cell by the AHB T2M Science team (Table 1; Figure 1) based on current knowledge of the ecology of Asian honey bees and the presence of suitable nest cavities. If the cell was unsuitable, it received a suitability value of 0 (e.g. ocean); if the habitat was highly suitable for AHB, it received a rating of 1 (e.g. urban areas; Figure 1). This was used in the model to determine whether AHB established in a cell if there was potential spread to that cell.

During the simulation, a random number was generated for a cell, compared with the habitat suitability in that cell, and if the random number was equal to or less than the suitability, AHB established in that cell in that time-step.

Table 1: Habitat suitability values for Asian honey bee occurrence in the initial model

Habitat type	Suitability
Urban	1
Mangrove	0.9
Rainforest	0.8
Eucalypt/Savannah woodland	0.8
Agricultural	0.2
Ocean	0

At the start of each time-step, each cell was checked to see whether AHB were present in that cell, and if present, whether they were they found and destroyed. A specified probability of finding AHB was a user input into the model. During the simulation, a random number was generated for each cell and compared with the specified detection/destruction probability. If smaller than the probability then AHB was removed from that cell (simulating a detection and destruction event). If a cell had AHB removed from it, that cell was then available for reinvasion by AHB, at the same probability as any other cell with that suitability.

The time-step for the model was six months, approximating the wet and dry seasons in north Queensland. This enabled different probabilities of spread to be used for the different 'seasons' (Table 2).

Diffusion and long-distance spread

Two types of spread were modelled – spread into adjacent cells (short distance spread or diffusion) and jumps (long distance spread). In assessing diffusion (short distance spread), each cell that is adjacent to a cell with AHB had a user-defined probability of becoming invaded with AHB. For each cell, a random number was generated and compared with the probability of spread and if lower than the specified probability, then AHB could potentially invade the cell. If potentially invaded, another random number was generated and compared with the habitat suitability, and if smaller than habitat suitability, then the cell became invaded with AHB. Thus an adjacent cell may fail to be come invaded because there was no potential spread into the cell or because the habitat was not suitable.

Jumps (long distance movements) were included to represent human-assisted spread. For each cell with AHB, there was a user-defined probability that there would be a jump from that cell in a time-step. A maximum distance was specified with the model, and several maximum distances were tested. If a jump occurred, then that jump was to a cell estimated from a uniform-random distance of spread in the x- and y-directions.

Logic flow within the model

The sequence of calculations is as follows:

1. Does cell have AHB

    - If Yes, then is AHB killed?
    - If not killed, does a jump occur from this cell?
    - If No, then next process

2. Is cell adjacent to cell with AHB

    - If Yes, then is cell invaded by diffusion?
    - If No, then next process

3. Continue until all cells assessed, update all cells, and start on next time step.

4. When all time-steps completed, write output to files.

Model input

The program was written in FORTRAN and compiled into an EXE file, which was run from a DOS prompt. Input data were edited using Microsoft Notepad. Input data files included two text files: user input file and habitat suitability file.

Table 2: Input parameters and corresponding values for the initial AHB spread model. Where parameters were varied in order to improve the model fit with actual AHB occurrence, all values are listed. The value in bold is the one that was used in the improved initial model.

Model input parameters	Input
Number of simulations	100
Time steps (6-monthly)	58 (29 years)
Probability of spread into adjacent cells if suitability is 1.0 (wet season)	0.9
Probability jump from existing infested cell (wet season)	0.8
Probability of spread into adjacent cells if suitability is 1.0 (dry season)	0.6
Probability jump from existing infested cell (dry season)	0.8
Maximum number of cells to jump (equivalent to kilometres)	10, 20, 40, 50, **60**, 70
Maximum mortality/control efficiency[1]	0.1, 0.5, **0.95**

[1] This inherently contains two features: (1) how many nests are known about, and (2) how effective the control of known AHB nests/swarms is. It is assumed that effectiveness of control is 100%. The number of nests known about has been set at 50%.

Output and mapping

The program generated two output files, one specifying detailed AHB presence/absence in each cell in each time-step, and one summary file showing the average number of cells with AHB for each time step over the whole area.

The detailed output file was then opened in Microsoft Excel and a CSV file was generated. The CSV file was then entered into and edited in ArcMap in order to generate maps of the model output.
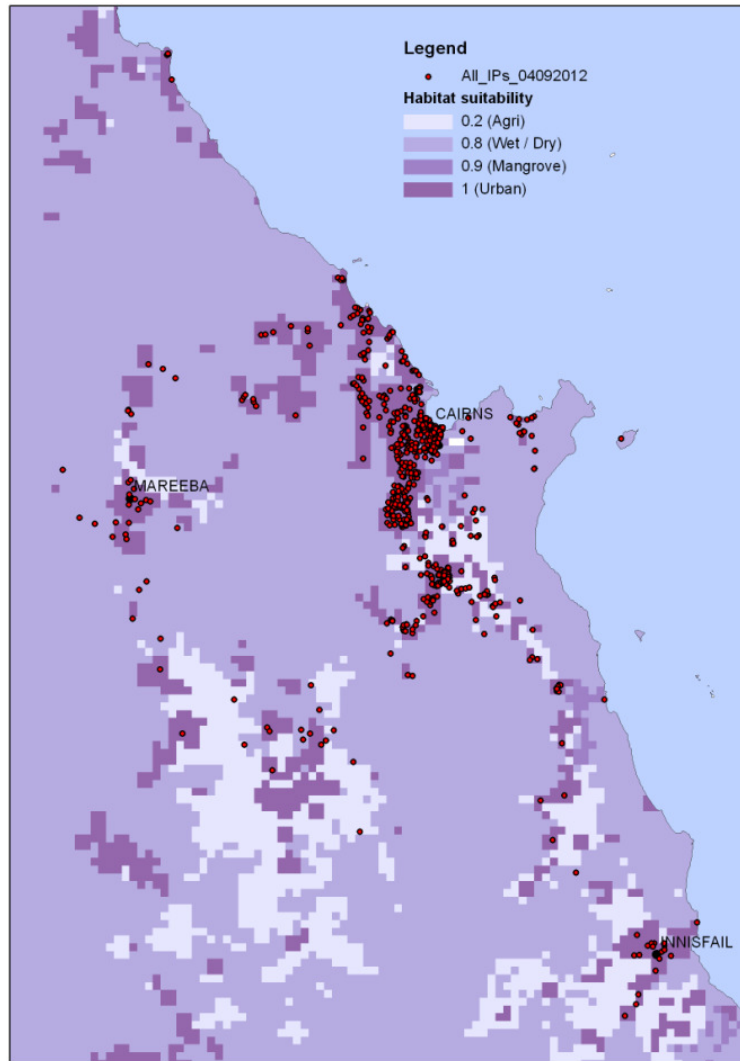
Figure 1: Habitat suitability and locations of Asian honey bee nests across far North Queensland, Australia, found to date.
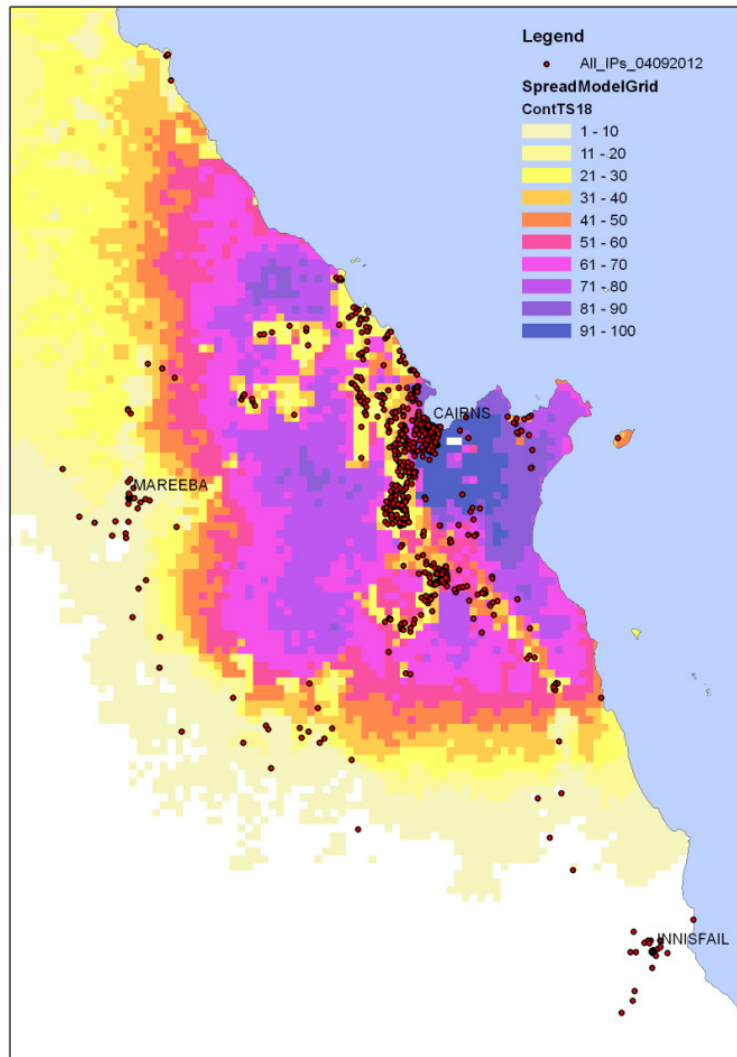
Figure 2: Example map of model output data. Colours on the map indicate the percentage of simulations in which AHB were located in each cell, given current level of control at time-step 18 (year 9). Red dots indicate the location of all AHB nests found to date. Note that areas with high percentage of simulations predicting AHB presence have not been surveyed in detail to indicate whether or not AHB were in fact within these areas. This is an example only and has not been tuned to fit the data.

Results

When the maximum distance for a jump (long distance dispersal) was 60 km (= 60 cells), and the control effectiveness was 95%, the output for time-step 8 (= 2012) gave a reasonable match to the current (2012) maximum extent of the known infested area (Figure 3 a & b).

Large gaps were apparent where the model predicted presence of AHB but no AHB have been detected, or where surveillance has not been done (Figure 3 a & b).

When the model was repeated without control measures (no detection/destruction) but otherwise using the same parameters as the previous analysis, it showed a similar overall predicted distribution of AHB to the previous analysis (Figure 4 a & b). However, the overall probability of AHB presence in each cell was much higher, which is indicated by red and dark red areas (Figure 4 a & b).

Again, large gaps were apparent where the model predicted presence of AHB but no AHB have been detected, or where surveillance has not been done (Figure 4 a & b).

In both simulations, AHB are predicted to spread in a north-westerly direction (Figure 3 & 4) – this is an artefact of the model that needs to be investigated further.
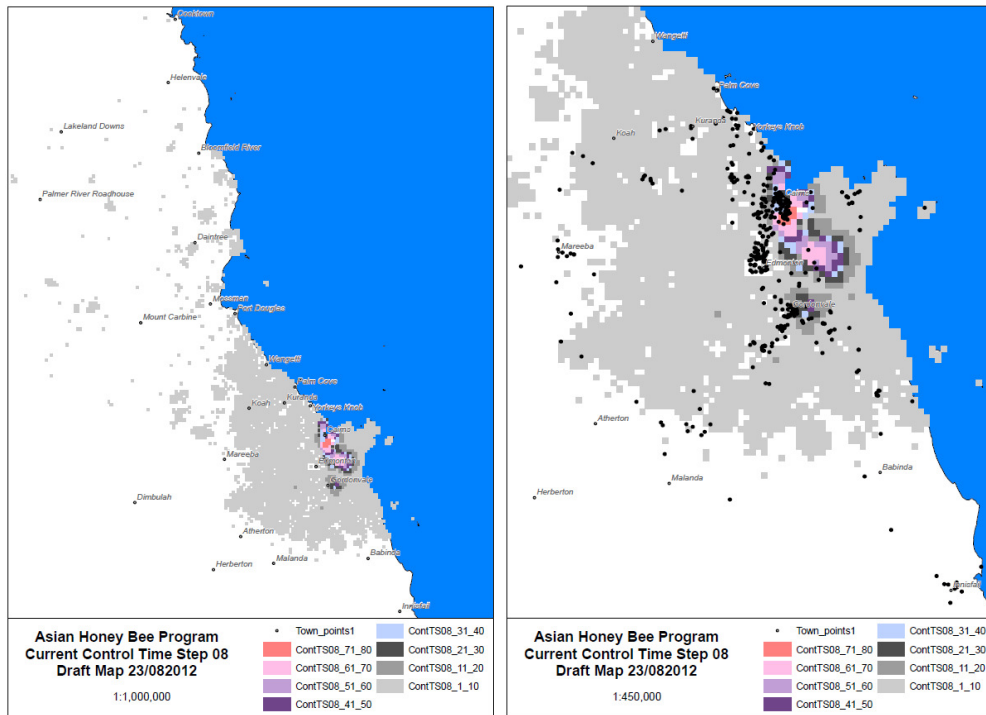

Figure 3:   Map of model output data for time-step 8 (= 2012) with the following input parameters: maximum dispersal – 60 km; control - 95%). Colours indicate the percentage of simulations in which AHB were located in each cell. Black dots indicate the location of all AHB nests found to date. Note that areas with high percentage of simulations showing presence of AHB have not been surveyed in detail to indicate whether or not AHB were in fact within these areas.

Figure 4:   **Map of model output data for time-step 8 (= 2012) with the following input parameters: maximum dispersal – 60km; control – no control). Colours indicate the percentage of simulations in which AHB were located in each cell. Black dots indicate the location of all AHB nests found to date. Note that areas with high percentage of simulations showing presence of AHB have not been surveyed in detail to indicate whether or not AHB were in fact within these areas.**
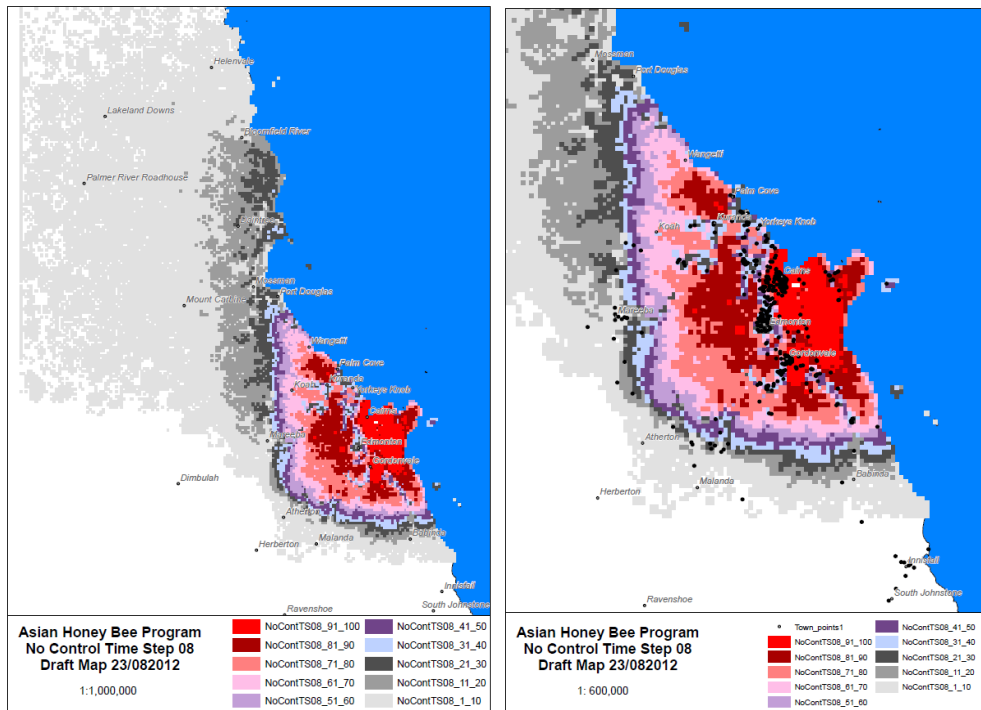
Discussion

When using input parameters for long distance dispersal of 60 km and control effectiveness of 95%, and starting the simulation in 2007, the predicted spread for 2012 somewhat matched the 2012 maximum extent of the known infested area. Simulating historical spread up to the current extent of a species can help determine a specific set of input parameters to use. By trialling different sets of input parameters, the set that results in the most closely matched modelled distribution to the actual extent of the species can be identified. Using these input values, the model can then be used to predict future spread. However, it needs to be noted that different sets of initial input values may give similarly good matches, and the chosen set of values is by no means the only or best one.

Interestingly, the simulated extent of AHB without control measures is no different to the simulated spread with control measures, indicating that detection/destruction has no effect on spread even if it does have an effect on AHB density. However, this outcome would need to be verified and validated.

According to the simulation model, spread appears to occur much more frequently in a north-westerly direction (Figures 3a & 4a). This is not based on any biological or climatic factors. There is no reason to believe AHB should preferentially spread north-west, and climate was not taken into account in this model. Therefore, the north-westerly spread is an artefact of the model itself (a 'glitch' in the model), which will need to be rectified. Due to this 'glitch', any predictions made by the model need to be taken with utmost caution and it is advised to disregard any output of the model until it is repaired.

Furthermore, it has been assumed that AHB occur in the rainforest, which results in a large discrepancy between the model output and the actual locations of AHB (Figure 3). Although there is some evidence that AHB do occur in the rainforest (Commerford and Koetz, 2013; Koetz, 2013a; Koetz, 2013b), this needs to be validated. Without validation, the model is almost useless in terms of comparison of output with the current known distribution as there has been little searching done in the rainforest.

Suggested improvements to the model include:

- specify jump distances that are (a) biologically based e.g. related to swarming distance, and (b) that are human-mediated.

- allow more than one jump from each cell in each time-step, based on the density of nests within that cell. At present, cells are either occupied or free of AHB. If a cell contained 100 nests, then spread from that cell is likely to be higher than if only one nest was present. Such a change to the model is quite a substantial change to structure.

- incorporate roads; a large number of long-distance dispersal pockets are apparent (Figure 3a) – most of these are not along roads, i.e. random.

- use human population density as a predictor of the probability of long-distance spread

- incorporate climate data

- increased surveillance in, or greater understanding of the distribution of, AHB is the rainforest. This would enable a more realistic comparison of model predictions with actual distribution.

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