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Aim: To attend the International Congress on Modelling and Simulation, University of Western Australia, Perth, 6-10 December, 1993.

Final Report

Mr. Martin Dillon was not able to attend the congress, as it coincided with the birth of his son on 24 November 1993. However, Martin Dillon and Dr. Gary Fitt were co-authors with others, on two papers presented at the congress by Mr. Wayne Rochester. As well as being published in the conference proceedings, both papers were also selected for publication in a special edition of the journal *Ecological Modelling*, and are currently in press. Copies of the papers are attached.

After notifying the CRDC, the travel funds were used for Mr. Martin Dillon to attend the 1994 Conference of the Ecological Society of Australia at Alice Springs, 28 - 30 September 1994. This conference included a special symposium on "Applied spatially dynamic modelling" which was of particular interest to Mr. Dillon and his co-author Mr. Wayne Rochester. A number of valuable contacts were made with Australian and international scientists interested in modelling the spatial dynamics of organisms. A poster paper and an oral presentation were presented at the meeting (abstracts are attached). There were no proceedings published from this conference.

Dillon, ML., Fitt, GP., Hamilton, JG. and Rochester, WA. 1993. A simulation model of wind driven dispersal of *Helicoverpa* moths. Proceedings of the International Congress on Modelling and Simulation, Perth, W.A. 6 - 10 December 1993. pp. 1711-1716.

Rochester, WA., Dillon, ML., Fitt, GP. and Zalucki, MP. 1993. A simulation model of the long-distance migration of *Helicoverpa* spp. moths. Proceedings of the International Congress on Modelling and Simulation, Perth, W.A. 6 - 10 December 1993. pp. 1705-1710.

Dillon, ML., Rochester, WA. and Fitt, GP. 1994. A simulation model of local wind driven dispersal of *Helicoverpa* moths. Poster presentation at the Ecological Society of Australia Conference. Alice Springs, 28 - 30 September 1994.

Rochester, WA., Dillon, ML., Fitt, GP., Gregg PC. and Zalucki, MP. 1994. HERESIS: Using GIS to integrate analysis and modelling tools in the study of *Helicoverpa* spp. dynamics in inland and eastern Australia. Talk presented at the Ecological Society of Australia Conference. Alice Springs, 28 - 30 September 1994.

A SIMULATION MODEL OF WIND DRIVEN DISPERSAL OF *HELICOVERPA* MOTHS.

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1. INTRODUCTION

Two species of highly mobile moths, *Helicoverpa armigera* and *H. punctigera* (Lepidoptera: Noctuidae), have larvae that are the major pests of a wide range of agricultural and horticultural crops. The adult moths move over a range of spatial scales, from continental wide "migration" to localized flights between patches of host plants within agricultural regions [1, 2]. Moth immigration and emigration directly affect the population distribution, density, demography and genetic composition within the regional landscape. Simulating flight behaviour is a crucial component of modelling and forecasting the population dynamics of *Helicoverpa* on a regional basis. This paper describes a simulation model of regional moth flight and dispersal within heterogeneous agricultural regions which forms part of a comprehensive regional population dynamics model known as HEAPS (HElicoverpa Armigera & Punctigera Simulation) [3].

2. REGIONAL *HELICOVERPA* FLIGHT

The flight behaviour of *Helicoverpa*, and the environmental conditions and cues that control the initiation, direction, speed, and termination of flight have been documented by a number of field and laboratory studies [4, 5, 6, 7, 8, 9, 10]. The two most important factors influencing flight behaviour and the displacement of *Helicoverpa* moths are wind speed and wind direction. *Helicoverpa* fly predominantly at night, taking off at dusk. Like many other nocturnally flying insects, if the wind speed is above a minimum threshold, individual moths take up a fixed orientation relative to the wind direction. This results in a distribution of headings on either side of the wind direction with the majority of moths oriented directly downwind [11, 12]. This distribution of flight headings about the wind direction is inversely proportional to the wind speed [11]. Regardless of the heading chosen by individual moths, their displacement relative to the ground is significantly influenced by the wind speed in a downwind direction.

The intra-regional flight of *Helicoverpa* moths is characterized by low undulating flight that is generally between 2 and 10 metres from the ground [7, 13]. *Helicoverpa* moths fly at an average unassisted flight speed of 4 metres second^{-1} (14.4 km hr^{-1}), for up to 5 hours duration [5, 6]. Moths will only take off if the ambient temperature is above 12°C, and if the wind speed over the host vegetation canopy is less than 10 m s^{-1} (36 km hr^{-1}) [14]. The minimum wind speed that influences flight orientation is 1 m s^{-1}, below this threshold moths may fly in any direction, but they still tend to maintain fixed trajectories [7]. Flight of reproductively mature moths is most intense during the first two hours after sunset [7, 8]. While the process of host selection in these moths is poorly understood, it appears that moths are not attracted to patches of host plants over long distances (100's of metres). Rather they seem to only detect hosts over short distances (10's of metres). Therefore the detection of patches of suitable host plants is determined by the mix of crops and vegetation that their flight path happens to transect [4, 7, 8]. In the HEAPS model female moths alight in response to the relative attractiveness of host plants for oviposition. The two species differ to a large extent in their host preferences, and there is evidence to suggest that *H. punctigera* moths may have an initial obligatory flight period during which they are not responsive to host plant stimuli, and therefore will not land close to the source patch [4].

3. MODEL DESCRIPTION

3.1 The spatial framework.

Agricultural landscapes are characterised by a mosaic of patches of crops, pasture, and natural vegetation. The type and growth stage of the vegetation that makes up each patch affect its suitability and attractiveness as a host for *Helicoverpa* moths, eggs, larvae and pupae. The model uses uniform patches of host plants as the base simulation unit (SU), within which the population processes of immigration, birth, development, death and emigration are simulated, and information on the density and demography of *Helicoverpa* can be stored, processed and displayed.

However, moth flight over this mosaic of host patches is simulated at a coarser level of resolution. The region under consideration is divided into a grid of square cells at a user specified scale. Each cell may contain one or more simulation units (uniform vegetation patches). Each night the moths within each cell are flown out from the cell centre in a distribution of trajectories corresponding to current wind conditions. As the moths following each trajectory encounter suitable target cells on their flight path, a proportion of them alight into those cells. The moths landing within a given cell are distributed into its component simulation units on the basis of their attractiveness and proportional area within the cell.

3.2 Processing cells.

Moth take-off is simulated on a daily time step. Each cell may have its own meteorological data, in particular temperature, wind speed and wind direction at dusk. Each cell is processed in turn, and acts as the current source cell. All the moths that are ready to emigrate within the simulation units contained within the current source cell are grouped together at the cell centre ready for outward flight. Moths flying out from this source cell may potentially land in any other cell in the grid, or leave the system altogether. The model only allows individual moths to fly once each night. Therefore as each cell becomes the source cell, only moths that have been resident for at least one day are allowed to fly. If temperature or wind conditions are unsuitable then flight does not take place from the current source cell.

3.3 Flight sectors

As each cell becomes the source cell, emigrating moths are distributed into flight sectors radiating out from its centre. If the wind speed is less than the 1 m s^{-1} minimum threshold that effects orientation, moths will fly out in all directions. Under these calm conditions the model divides the number of flying moths equally into 18 sectors (each 20°) that encompass the full 360° range of possible headings. When the wind speed is above the minimum threshold, the model distributes the moths into 4 sectors on either side of the wind direction, making a total of 8 flight sectors. Emigrating moths are proportionally distributed into the 8 flight sectors on the basis of an assumed normal distribution of flight orientations in relation to the wind direction. The arc of each flight sector represents one standard deviation of the moth orientations away from the mean downwind orientation. The number of flying moths allocated to each sector is representative of the expected proportion of moths orientating within 1,2,3 and 4 standard deviations away from the mean downwind orientation (Figure 1).

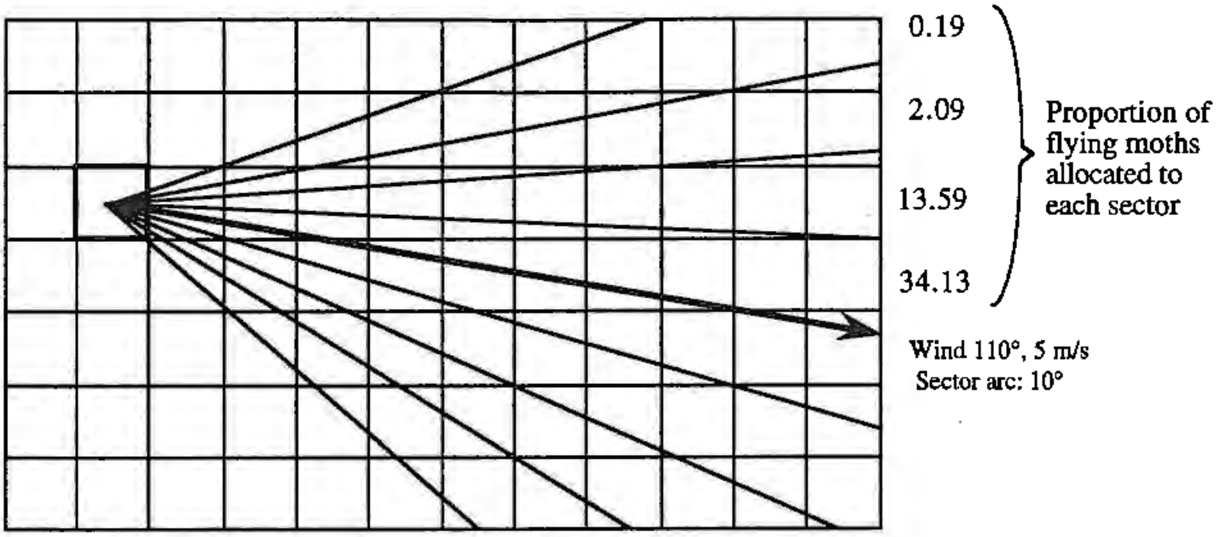

FIGURE 1
A diagrammatic representation of 8 flight sectors extending over part of a 7 x 12 grid, showing the relative proportion of moths leaving the source cell that will fly out along each sector.

The standard deviation of the mean orientation decreases linearly with increasing wind speed, within the range $1.0 < \text{Wind speed} < 5\ \text{m s}^{-1}$, as follows (1).

$$SD(O) = \beta_o - \beta_1 \times WS \qquad (1)$$

Where: SD(O) is the standard deviation of the mean orientation; WS is the average wind speed at dusk; and the initial estimates of β_o and β_1 are 22.5 and 2.5, respectively. This results in a maximum flight sector arc of 20° when the wind speed is 1 m s^{-1} or less, decreasing linearly to a minimum arc of 10° when the wind speed is 5 m s^{-1} or over.

3.4 Adjusting flight sector bearings relative to the ground for the effect of wind speed

The actual bearing of each flight sector relative to the ground will vary from the moth orientations used to define the sectors. This is because as the flying moths maintain fixed headings relative to the wind direction, they will also be blown down wind at the current wind speed. That is, the actual displacement of moths is a product of both flight and wind velocities (Figure 2). The bearings of the new vectors that describe the actual displacement of moths can be calculated with simple trigonometry. The bounds of each flight sector, and the arc of each flight sector, will change. This directly affects the set of host patches that the moths will encounter on their flight paths.

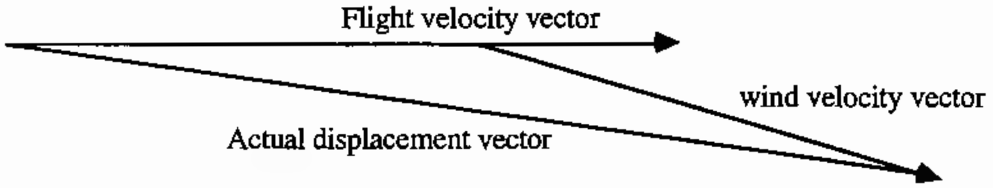

FIGURE 2
Graphical representation of the effect of wind velocity and flight velocity on overall displacement.

3.5 Identifying the target cells enclosed within each flight sector.

Moth flight within each flight sector is simulated as an arc of moths that travels outwards along the sector from the source cell centre. The arc of flying moths intersects target cells, or portions of them, in the order of their distance from the source cell. As the pattern of wind speed and direction is often uniform across large portions of the grid, the same pattern of flight trajectories will apply to many cells. A generic lookup table of target cells that are enclosed by each flight sector is calculated and successively applied to each cell in the grid as it becomes the source cell. Target cells are indexed by their relative displacement in terms of rows and columns from the source cell. Target cells are identified by comparing the angles subtended by the corners of the target cell on the centre of the source cell, with the bearings of the vectors bounding each flight sector. If a change in wind speed or direction is encountered when a new source cell is processed for take-off, then the flight sector bearings will change, and the lookup table of target cells within each sector must be recalculated. The lookup table for each flight sector stores the following details associated with each target cell; (i) the displacement in terms of rows and columns away from the source, (ii) the distance of the target cell centre from the source cell centre, and (iii) the proportion of the flight sector width that the target cell blocks. The average maximum distance that a moth could potentially fly within a given sector is also calculated for each flight sector on the basis of the combined effect of the moth flight speed and heading and the current wind speed and direction.

3.6 Landing moths into target cells.

A proportion of the flying moths alight into each of the target cells that are encountered as the arc of flying moths is moved down a flight sector. The number of moths alighting into a given target cell is determined by four factors; (i) the distance of each target cell from the source cell, (ii) the number of moths still flying in the sector, (iii) the proportion of flying moths that actually encounter the target cell is taken as being equal to the proportion of the flight sector width that is 'blocked' by the target cell, and (iv) of those moths that encounter a target cell, a proportion of them will land in it based on the overall attractiveness of the host patches within the cell.

For example, at a given distance from the source cell, a particular target cell may subtend 50% of the flight sector width. This means that of the remaining flying moths in the arc that spans the sector, only 50% of them will encounter the target cell. If the target cell has an overall attractiveness of 80%, then 80% of the moths that encounter it will alight into that cell. The remaining flying moths that did not encounter the cell, or that did not land in it, move on to encounter other target cells in the flight sector. The moths that land within a given target cell are allocated into the component host patches (or simulation units) contained within the cell on the basis of the relative contribution that each SU made to the overall cell attractiveness. This depends on the relative area of each SU within the cell, and the type and stage of each SU's host vegetation. Specific attributes of the moths, such as age, host plant origin, and genetic composition (for pesticide resistance) are stored as proportional data for the population of moths within each simulation unit.

3.7 Responding to changes in wind speed and wind direction.

Although a daily time step is used for take-off events, a smaller time step can be invoked while flight is in progress. As the arc of flying moths within a flight sector encounters each target cell, the local wind conditions are compared with those that were used to define the flight sector bearings, and the associated lookup table of potential target cells. If the wind conditions have changed at this point, then all of the flying moths that have not landed in the current target cell, are temporarily stored 'above' the target cell for later processing using the changed wind conditions. The model then runs on an hourly time step. Moths that were stored above each cell are processed in turn, and are flown out in newly calculated flight sectors, until the maximum duration of moth flight is exceeded, or until all the moths have landed. The process is identical to that described above, but moths move on from their temporary positions, rather than take off, from a source cell. Each time moths encounter a change in wind conditions and are temporarily stored, the model assumes that another hour of flight time has elapsed. In this way regional changes in wind conditions are applied to moths as they encounter those changes.

4. DISCUSSION

Two simulation studies incorporating localised inter-patch movement of *Helicoverpa* have been published [15, 16]. Neither of these studies incorporated the influence of wind, which has been shown to be the most important factor affecting *Helicoverpa* flight [13]. A number of synoptic models of inter-regional or migratory flight of *Helicoverpa* moths driven by large scale weather systems have been developed [2, 13, 17]. However with respect to localised inter-patch flight within discrete regions, and the effect that wind may have on these movements, there have been no published models for *Helicoverpa*. Some wind driven regional models have been developed for other insects, most notably, the spruce budworm [18], the western tent caterpillar [19] and the boll weevil [20]. These models differ from the present study in the way that flying insects are oriented. In the first two, all of the moths leaving a patch fly out in a single heading, albeit affected by wind direction. The third model distributes the flying beetles into individually assigned random headings between 1° and 360°, that are subsequently affected by the wind velocity. The novel method used in the present study to allocate flying moths into flight sectors distributed about the wind direction is a more realistic, and computationally efficient approach.

The flight model described in this paper, and the overall regional population dynamics model HEAPS, of which it is part, are currently undergoing testing and validation in the Namoi-Gwydir cotton-growing region of NSW, and on the Darling Downs near Dalby, Qld. If the models prove to be sufficiently accurate, it is hoped to produce regular regional forecasts of pest distribution and densities. An equally important use for the models is as research tools, that encapsulate all of our current understanding of *Helicoverpa* ecology. The implementation of these models will aid in the development of regional management strategies for these serious agricultural pests, that take a wider view than the traditional field based controls currently applied by farm managers.

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A SIMULATION MODEL OF THE LONG-DISTANCE MIGRATION OF *HELICOVERPA* SPP. MOTHS

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1. INTRODUCTION

This paper describes a wide-area simulation model of the population dynamics of the migratory moths *Helicoverpa punctigera* and *H. armigera*. In particular, it describes one of the submodels of the wide-area *Helicoverpa* model—a model of the long-distance migration of *Helicoverpa* moths—and the implementation of that model using the generic model GenSIM.

The larvae of *Helicoverpa punctigera* and *H. armigera* are key pests of a variety of agricultural and horticultural crops in Australia [1]. Management of *Helicoverpa* in crops is complicated by the variability in their infestation levels between regions and between years. The infestation levels are affected by climate, host plant abundance and quality, and movements of moths into and out of the crops [2]. A regular source of moths immigrating into the cropping regions of eastern Australia appears to be inland Australia. Large populations of *Helicoverpa* can develop in localised areas of the normally arid inland following rain. These populations can then migrate into the cropping regions on high-level winds associated with large-scale weather systems [3].

The wide-area *Helicoverpa* model is being developed for three purposes: to increase our understanding of *Helicoverpa* population dynamics, and the interactions between the inland populations and those in the cropping regions; to evaluate alternative strategies for managing *Helicoverpa* infestations in crops; and to form the basis of a system for forecasting the levels of infestation of *Helicoverpa* in crops.

The model will include three submodels: a model of the distribution of *Helicoverpa* in inland Australia; a regional model of *Helicoverpa* population dynamics in cropping areas; and a model of the long-distance migration of *Helicoverpa* moths between the inland and cropping regions. The inland distribution model will predict the distribution and abundance of *Helicoverpa* in inland Australia, using estimates of the distribution and abundance of host vegetation. The distribution of host vegetation will be estimated from indices of rainfall and/or vegetation change calculated from GMS and NOAA satellite images respectively [4]. The regional population dynamics model HEAPS (HElicoverpa Armigera and Punctigera Simulation) [5] models the distribution and abundance of *Helicoverpa* within cropping regions. HEAPS is now operational, and currently undergoing testing and validation for the Namoi–Gwydir cotton-growing region of northern NSW. HEAPS takes the number of moths immigrating into the cropping region as one of its input parameters. The long-distance migration model takes the distribution of moths generated by the inland distribution model, and predicts the movements of these moths from the inland to the cropping region considered by HEAPS.

The inland distribution model and the long-distance migration model are being implemented using the generic model GenSIM. GenSIM will also be used to link the three models together to produce the wide-area *Helicoverpa* model. The following two sections briefly introduce GenSIM, and then describe the implementation of the long-distance migration model using GenSIM.

2. GenSIM

2.1 GenSIM overview

GenSIM (Generic Spatial Insect Model) is a generic model of the spatial dynamics of insect populations. It is a combination of GENSECT [6], which is a generic model of insect population dynamics, and a framework for linking together models that have been created using GENSECT or other systems. A key feature of the framework is that it provides spatial and temporal contexts for the models that it manages, by supporting interactions between models that depend on the locations of the domains of the models in space and time. The framework is a set of specifications for writing models to be managed by the GenSIM executive, a library to aid in the development of such models, and software and libraries to provide services to models. The software is implemented in C++. The management and integration of models is implemented using three standard object classes: model elements; entities; and locations. In addition, a random variate generator class is provided for use with parameters that accept random values.

2.2 GenSIM model elements

A GenSIM model is a collection of interacting model elements, which are objects that input and output data. All model elements have a set of standard properties that enable them to interact with other model elements. Similarly, all model elements of a given class have a set of standard properties that enable them to interact with other model elements that recognise their class. Examples of model elements are submodels, interfaces to data management systems, and user interfaces.

2.3 GenSIM entities

GenSIM entities are model representations of real-world entities, such as insects or populations. The properties of a GenSIM entity are defined by its attribute list, which remains with the entity object as it is passed between model elements.

2.4 GenSIM locations

Locations in space and time are defined using an abstract coordinate system. The abstract representation of location enables model elements to manipulate the locations of entities without needing to explicitly support the particular coordinate system on which those entities are located. The abstract coordinate system allows velocities to be assigned to objects, and supports arithmetic operations on locations and velocities.

2.5 GenSIM random variate generators

The values for model parameters that are random variables can be selected using GenSIM random variate generators. The random variate generator for a given random variable is a function that, given uniform random numbers distributed on [0, 1] as input, generates random values with frequencies that fit the distribution of the random variable as output. The random variate generator for a random variable is the inverse of its cumulative distribution function. The random variate generator for a random variable is therefore implemented as the inverse cumulative distribution function of that variable, or an approximation of that function [7].

3. THE LONG-DISTANCE MIGRATION MODEL

3.1 Description of the model

The long-distance migration model predicts the change in the distribution of *Helicoverpa* moths on the ground that results from a period of migration. The model takes an initial distribution of moths, and predicts the resulting distribution by accumulating the end points of a random sample of the flight trajectories of individual moths. A sample trajectory is generated by randomly sampling a moth from the population, and flying the moth along its trajectory. The trajectory is determined by the wind velocities around the moth, and the responses of the moth to the environmental conditions that it experiences during flight. The responses are randomly selected from a set of possible responses, which may change during the course of the flight.

The model has features of both individual- and population-based models. The input and output populations are described at the population level using the spatial distributions of the attributes of the moths in the populations; however, the model generates the output population from the input population by calculating the trajectories of individual moths. To obtain a representative sample of trajectories, the sample of moths that are flown must be representative of the source population. A sample moth is therefore generated by firstly selecting its location using the spatial distribution of moths on the ground, and then randomly selecting, for each attribute type (e.g. maximum flight time), an attribute (e.g. maximum flight time of five hours) using the frequency distribution of the attributes of that type at the selected location.

3.2 Implementation of the model using GenSIM

The long-distance migration model currently includes seven submodels. The relationships between the submodels are illustrated in Fig. 1. The submodels and their functions are:

- Source population distribution model: selects the take-off location of the moth;
- Moth attributes model: selects various biological attributes for the moth;
- Take-off time model: selects the take-off time of the moth;
- Flight behaviour model: selects the flight velocity for the moth at a given location in space and time;
- Wind model: calculates the wind velocity for a given location in space and time;
- Ground velocity model: calculates the velocity relative to the ground of the moth at a given location in space and time;
- Trajectory model: calculates the trajectory of the moth.

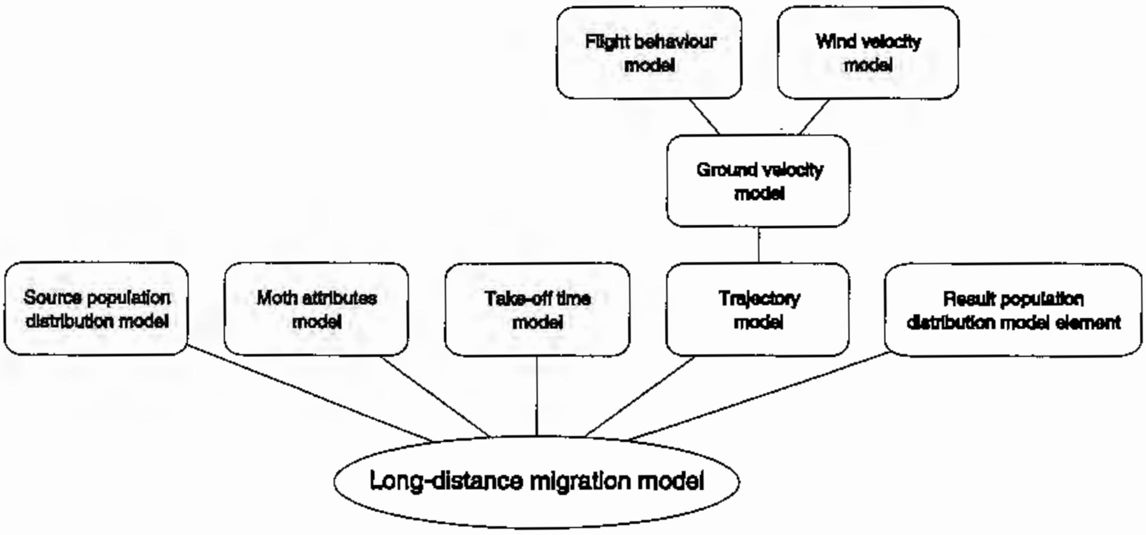

FIGURE 1

The relationships between the submodels and model element of the long-distance migration model

Moths are represented as GenSIM entities, with such attribute types as location, take-off time, maximum flight time and flight velocity. A sample moth is generated by passing it to the models that select the attributes that define the moth—the source population distribution model (for the take-off location), the moth attributes model (e.g. for the maximum flight time) and the take-off time model (for the take-off time). The distribution of the attributes of a given type may depend on what other attributes have been selected; for example, moths from regions with high quality host vegetation might have longer maximum flight times than those from areas with lower quality vegetation. The models select the attributes using GenSIM random variate generators.

The process of the generation a trajectory is represented by the changing state of the moth entity during the simulation of its trajectory. The state of the moth entity is defined by its attributes. The action of models in defining the trajectory of a moth is therefore to alter the attributes (e.g. location) of the moth entity as it passes through them. In determining what values should be assigned to an attribute, a model may look at the current values of the moth's attributes, and may also consult other models for information not carried by the moth entity, such as the environmental conditions being experienced by the moth.

On the completion of the trajectory, the moth is passed to a result distribution model element, which accumulates the end points of the trajectories to calculate the final distribution. Moths are flown until the result distribution stabilises, as determined by comparing the distribution patterns between successive samples of trajectories.

The locations and movements of moths in space are represented using a spherical coordinate system implemented on GenSIM's abstract coordinate system. The origin of the spherical coordinate system is the centre of the earth. A location on the coordinate system is specified by a latitude, longitude and altitude. A velocity on the coordinate system has two components: a horizontal component specified by an angular velocity on a great circle centred on the origin, and a vertical component specified as a rate of change of altitude.

In the current implementation of the source population distribution model, the distribution is represented as a grid. This representation is hidden from the other models, because the interface to distribution model elements describes insect locations as abstract GenSIM locations, rather than as indexes to grid cells. The distribution could therefore alternatively be represented as a probability density function, or simply as the numbers of moths within selected areas.

The flight behaviour model selects the flight velocity for the moth using a random variate generator that varies according to the environmental conditions that the moth is experiencing. The flight behaviour model determines the environmental conditions by determining the location of the moth from its location attribute, and obtaining the environmental conditions at that location from environment models.

The ground velocity model calculates the velocity of the moth relative to the ground by adding the flight velocity to the wind velocity. The ground velocity model is independent of the spherical coordinate system used by the flight behaviour and wind velocity models, because the arithmetic operations that it performs on the velocities are implemented within GenSIM's abstract coordinate system.

The trajectory model is based on the algorithm of Scott and Achtemeier [8]. The algorithm was modified to use GenSIM's abstract coordinate system, so is again independent of the spherical coordinate system used by the other models.

4. DISCUSSION

A number of features of the long-distance migration model lend it towards implementation using GenSIM. The migration model simulates a number of distinct biotic and abiotic processes. The models of these processes will change as development of the migration model progresses. Also, different models of some processes are required for different simulation experiments; for example, some experiments use simulated wind fields, whereas others use wind fields calculated from measured data. The separation of processes into GenSIM submodels enables different models of processes to be easily substituted as required. In addition, the implementation of generic process models (such as wind field models) enables the creation of libraries of models that are immediately available for incorporation into new composite models.

Different submodels of the long-distance migration model examine and influence different attributes of the moths used to generate the sample trajectories. The representation of the moths as GenSIM entities enables the moths and their attributes to be passed between model elements, without requiring that each element have access to a complete list of the attributes that describe a moth. For example, the only attribute that the wind velocity model examines is the moth's location in space and time. The wind velocity model could therefore be as readily applied to any entity with a location attribute as it can to a moth entity of the long-distance migration model.

The long-distance migration model initially used x–y coordinates in metres. The coordinate system was later changed to the spherical system described above. The use of abstract GenSIM coordinates by the trajectory and ground velocity models meant that these models did not need to be changed to use the new coordinate system.

For the long-distance migration model to be a flexible tool for examining the influences of behaviour on long-distance movement, it must be possible to assign arbitrary distributions to the parameters of the model (such as moth attributes and responses to stimuli), and to change these distributions as required. The implementation of variable parameters as GenSIM random variate generators satisfies both of these criteria. The uniform treatment of variable parameters also enables the creation of libraries of generators that may be used for other parameters and in other models, and standardises the way in which parameters are added and removed from models.

Rabbinge [9] describes the process of developing an ecological model in three stages: the development of a conceptual model that describes the way in which underlying processes are thought to govern the behaviour of the system; the development of a comprehensive explanatory model; and the simplification of the comprehensive model to produce a summary model for operational use. It is the summary model that is used for such purposes as forecasting and evaluating management strategies.

We now have a detailed conceptual model of the wide-area population dynamics of *Helicoverpa* in Australia, as a result of the large volume of published work on these species in cropping and non-cropping areas [10]. The wide-area *Helicoverpa* model is a comprehensive explanatory model which incorporates the processes identified in the conceptual model. The implementation of the model in GenSIM will aid in determining how the processes operate, and which processes are most important, due to the ease with which models of processes can be added and removed from the system, and with which the distributions of parameters can be manipulated. GenSIM will also facilitate the creation of a summary model from the comprehensive model, as the models of ineffectual processes can simply be removed, and the random variate generators for parameters to which the model is insensitive adjusted to return nominal values.

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Abstract of poster presented at the Conference of the Ecological Society of Australia, Alice Springs.

A simulation model of local wind driven dispersal of *Helicoverpa* moths.

Martin Dillon, Wayne Rochester, and Gary Fitt.

A model is described that simulates the spatial displacement of populations of moths over a heterogeneous landscape in relation to wind conditions. The model divides the area under consideration into a scalable grid of square cells, each of which contains a known mix of host and non-host habitats. Flight is simulated for each cell in turn, once each night. For each cell, the flight paths of emigrating moths are distributed into sectors radiating from the cell centre and flanking the wind direction. The angle (or width) of the flight sectors on either side of the wind direction is inversely proportional to wind speed. If wind conditions are calm the flight sectors encompass a full 360° arc. The moths within each flight sector are moved out from the cell centre on a front which forms the arc of the sector. As the arc intersects with cells on the underlying grid, a proportion of moths land in each cell. The proportion of moths alighting is determined on the basis of the overall attractiveness of the habitats within each cell, and the proportion of the cell that is intersected by the flight sector. Alighting moths are distributed into the landuse units in target cells according to the relative attractiveness of each landuse, and its relative area within the cell. A daily time step is used between take-off events, while a smaller time step is used while flight is in progress. Wind velocities may vary between cells or time steps, allowing the model to simulate varying spatial wind systems.

Abstract of talk presented at the Conference of the Ecological Society of Australia, Alice Springs.

HERESIS: Using GIS to integrate analysis and modelling tools in the study of *Helicoverpa* spp. dynamics in inland and eastern Australia.

Wayne Rochester, Martin Dillon, Gary Fitt, Peter Gregg and Myron Zalucki.

The *Helicoverpa* Research Support and Simulation Modelling System (HERESIS) aims to support research on the dynamics of the pest moths *Helicoverpa armigera* and *H. punctigera* in inland Australia and the summer cropping regions of eastern Australia. It will form the basis of a proposed system for forecasting and monitoring migrations of *Helicoverpa* moths from the inland breeding habitats to the cropping regions, where they cause significant economic damage. HERESIS consists of a geographic information system integrated with a number of analysis and modelling tools. The areas of *Helicoverpa* research that HERESIS supports include the phenology of key host plants throughout the inland; insect population dynamics in the inland; and long distance migration. Techniques being applied or evaluated in the system include remote rainfall monitoring; satellite image analysis; plant growth modelling; insect population modelling; and long distance trajectory modelling of wind-assisted insect migration.