Weaver - a modelling tool for complex, uncertain ecological systems: description and testing in the red grouse domain

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Abstract

This paper describes a modelling tool called Weaver designed for modelling and investigating complex, uncertain ecological domains. Weaver integrates machine learning, compositional modelling, and heuristic search methods in order to permit the development of theory about the relative importance of model and parameter uncertainty on the outcome of multiple perspective scenario simulations.

This paper provides an overview of how ecologists might represent knowledge in Weaver and how domain theory may be developed and used. The investigation of red grouse (*Lagopus lagopus scoticus*) population cycles is used as an example.

Keywords: Uncertainty; Scale; Artificial intelligence; Red grouse; Machine learning; Compositional modelling; Artificial life

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1. Weaver

Weaver is a prototype “knowledge discovery environment” (de Jong and Rip, 1997) developed for use in complex, uncertain ecological domains. In terms of categorisation of software support for ecological systems (Lorek and Sonnenschein, 1999), it falls within the category of “modelling tools” in the sense that it supports the "whole process of modelling, experimenting and evaluation". Weaver integrates model composition, experimental simulation, learning and experimental reformulation tools within a process analogous to Popper's scientific method of critical discussion (Popper, 1996a, 1996b). Weaver brings together the following techniques from Artificial Intelligence: Compositional Modelling (Falkenhainer and Forbus, 1991; Rickel and Porter, 1997), Artificial Life Simulation (Langton, 1988), Inductive Learning (Quinlan, 1993) and Heuristic Search. The result is an environment in which the user, as scientist, can test domain uncertainties and assumptions and in so doing develop hypotheses about the domain (a domain theory) through an iterative process of in silico (computer-based) experimentation, theory proposal, criticism, and refinement. To do this, the user is provided with facilities to select and simulate domain models based on sparse and/or conflicting knowledge at a range of different scales.

The paper is divided into eight main sections. Section 2 describes our motivation for developing Weaver. Sections 3-5 explain how Weaver is used, how knowledge is encoded within it, and finally how Weaver's components work together. Section 6 provides an example of the application of Weaver to the domain of the population dynamics of red grouse (Lagopus lagopus scoticus); section 7 compares Weaver to other tools for use in complex ecological domains; section 8 concludes with a discussion of future research directions.

2. Motivation

The development of Weaver has been influenced by two current topics of great interest in the application of ecological modelling to the tasks of natural resource management and integrated assessment: uncertainty and scale. If, as T.F.H. Allen wrote, “Science is not about finding the answers to everything; it is about finding the situations in which one can get away with an assumption” (1998, pp46-47), then the problems of uncertainty and scale increase the number of assumptions that have to be made and thus
worsen the task of finding out which ones “one can get away with”. At EcoSummit 2000, identifying improved ways of tracking assumptions and their impacts on models was viewed as important in establishing the integrity of integrated assessment modelling. The rest of the section reviews the problems of uncertainty and scale and how recognition of these problems has influenced Weaver’s design requirements.

2.1 Dealing with uncertainty in complex uncertain domains

Due to the complexity of the domains being investigated, data, methods and theory may be absent or conflicting (i.e. there will exist multiple perspectives) or their comparative importance in determining system behaviour may not be fully understood. In scientific investigation, these problems are linked to three types of uncertainty (Funtowicz and Ravetz, 1985). The first, technical uncertainty, occurs when it is difficult for scientists to be confident about the accuracy of their measurements. The second, methodological uncertainty bedevils an activity when there is little agreement about the nature of the methods that should be used. Such debates may revolve around the apparatus used to gather data or it may extend to disagreements over representing the domain, for example, on deciding on the scale of description for organisms. Both of these uncertainties undoubtedly contribute to the third, conceptual uncertainty, which undermines the generation of agreed theory and results in contradictory certitudes (Thompson, 1982, cited by Pahl-Wostl et al., 1998), i.e. the existence of theories that may lead scientists to "incommensurable but equally valid conclusions".

Such scientific uncertainties in investigating and understanding the real world lead ultimately to problems and uncertainties in modelling it. Problems of absence and of multiple perspectives all require the making and assessment of numerous alternative model assumptions. When presented with an absence of some datum, one must make an assumption about what information may replace it, if any. When a measurement is difficult to take accurately, one must make assumptions about whether or not it is appropriate to use that measurement in a final model. Similarly, in the face of unresolved conflicts between rival theories or possible model structures, one must make assumptions about which to use in the model.
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Uncertainties in the real world lead to two types of modelling uncertainty which in turn require model assumptions to make: parameter uncertainty (what are the correct values for particular parameters in this model?) and model uncertainty (which processes should be included or which scale used in this model?). Overcoming these uncertainties requires methods that either mitigate the causal problems, i.e. absence and multiple perspectives, or that allow the estimation of the importance of any resulting uncertainty. Approaches to mitigation and importance estimation are not abundant. The following outlines the main methods.

**Absence** – To recap, this is the problem that there is simply neither the data nor the theoretical understanding to build complete models from a single agreed perspective. For many years researchers have recommended the integration of multiple and diverse sources of knowledge to fill knowledge gaps (Hornberger and Spear, 1980; Pahl-Wostl et al., 1998), as well as using the analysis of alternative models to highlight "new hypotheses and profitable avenues" (c.f. Hornberger and Spear, 1980).

**Multiple perspectives** - There is an increasing recognition that models must begin to account for the plurality of opinions and goals in complex systems, particularly in natural resource management tasks that have social and political consequences (Walker and Lowes, 1997). The resolution of conflict will be aided by the development of tools that incorporate and compare opposing alternatives. The concept of model routes has therefore been recently proposed (Pahl-Wostl et al., 1998). This suggests that a modelling environment should present a "road map" of possible trajectories from the present environmental or ecological state to a future one. Such a road map is developed with respect to the alternative data and possible theoretical models. This fits in with the current approach for presenting multiple perspectives in participatory settings (op cit.).

**Importance estimation** - One area of great import in modelling is to determine the importance of model assumptions, based on modelling uncertainties, on model results. Ignoring such uncertainties can lead to underestimation of the level of uncertainty in the model output (Reichert and Omlin, 1997).

Various methods have been proposed for weighting the importance of parameter uncertainties. These include Monte Carlo simulation methods (Hornberger and Spear, 1980; Spear and Hornberger, 1980), First and Second Order Analysis (Perret and Prasher, 1998), Fuzzy Logic (Perret and Prasher, 1998),
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Bayesian updating (Freeze et al., 1990), Kriging (Freeze et al, 1990) and FOSM (a form of Gaussian error propagation (Kunstmann, 1998)). (See Bobba et al. (2000) for further references to uncertainty analysis methods for ecological modelling.) In contrast, less work has been done on providing means of determining the importance of model uncertainties e.g. the impact of the representation of models at different scales or the use of alternative theories or structures. Notable examples of such work include Dowlatabadi et al. (1995) and Massmann and Hagley (1995).

2.2 The importance of scale.

Of enormous importance to ecology is the question of scale. This question can have two forms: how can one understand the interaction of phenomena at different scales of description? (Levin, 1992) and what is the most appropriate scale\(^1\) at which to describe a particular ecological model for a particular task? (Pahl-Wostl et al., 1998). A major modelling decision is to decide on the organisational scale of the model\(^2\). That is, whether one models at the scale of the individual organism or at the scale of the aggregated population. The increase in individual-based modelling in the last 20 years is partly based on the belief that

"much of what we have learned from the state variable [population] models about the theoretical issues … would have to be revised if the discreteness, uniqueness … of individuals were to be taken into account" (Grimm, 1999, p131).

Conclusive answers to the question of what scale to use (and when) have not been forthcoming. This is not merely a problem for ecology. In computational sociology, Doran (1996) also bemoans the fact that the subject is rarely tackled.

\(^1\) The term Pahl-Wostl et al. actually use is "level", but to assure terminological consistency in this paper, the term has been replaced by "scale" according to Levin's (1992) usage of the word. See also the following footnote.

\(^2\) It is a common problem in the communication of science that the same concept can share a number of different terms. For example, in Pahl Wostl, et al, (1998) positions in an organisational hierarchy are termed "levels". In Levin (1992) these positions are termed "scales", and thus he refers to "hierarchical scales of organization" (p.1953). This paper concentrates on scale issues involving such a hierarchy. Therefore, through the rest of this paper we will adopt Levin's term and thus when we refer to the "scale" of a particular model or submodel, e.g. a model at the "individual scale", we mean the position along the organisational hierarchy at which the model is described.
2.3 Modelling tool requirements

In view of these issues, we were therefore motivated to provide a tool that met the following requirements:

Uncertainty and Scale:

- support for the scientific process of knowledge discovery in highly uncertain complex systems;
- integration of diverse knowledge types into multiple perspective models;
- knowledge gap handling;
- analysis of model uncertainty;
- development of knowledge about impacts of assumptions on model outcome;
- multiple-scale modelling: integration of models at different organisational scales;
- comparison of models at different organisational scales
- development of hypotheses aimed at directing future field experimentation.

Model composition and simulation support for uncertain and complex domains:

- specification of models based on explicit assumptions;
- automated selection and construction of models;
- an experimental reformulator to help the user search a potentially vast space of possible parameters and models – the “uncertainty space”.

2.4 Weaver – a software framework and a modelling tool

To meet these requirements, Weaver was developed, in the terminology of Lorek and Sonnenschein (1999), to provide both a software framework and a modelling tool. Accordingly, the use of Weaver is a two stage process. In the first, Weaver is used as a software framework in order to create a knowledge base of the ecological domain. For this purpose, Weaver offers a set of software libraries that provide a structure for representing, integrating, and manipulating diverse and incomplete knowledge sources at multiple scales within a common knowledge base. In the second stage, Weaver is used as a modelling tool to iteratively explore scale and uncertainty issues within models based upon the knowledge base developed. As such a tool, Weaver provides a simple assumption-driven user interface for specifying models; models which it then automatically composes, simulates and analyses. Results of the analysis take
the form of a ‘domain theory’ that indicates the importance of model assumptions on model results. It is through this ‘theory’ that the role of scale and domain uncertainties in models of the system can be ascertained. Weaver finally gives advice on how to search through the uncertainty space. The following sections will explain Weaver in more detail, beginning with Weaver’s role as a modelling tool.

3. Weaver – the modelling tool: an iterative process

Figure 1 illustrates the component architecture and the flow of information between user and tool components during a single iteration of Weaver. The user starts by entering an experimental design consisting of a set of experimental assumptions (1). Figure 2 shows a simple, generic Weaver interface for selecting assumptions and designing the simulation experiment. In this case the chosen assumptions are listed under the headings: ‘Basic Agent Scale’ ‘Significant Processes and their Scales’, ‘Spatial Information’ and ‘Time Step’. The first two headings specify which species are to be included in the model, the scale at which they should be represented and the inclusion and scale of processes affecting them. The generic options are “none” (this species/process is not included in the model) “individual” (the species/process is included at the individual agent scale) and “population” (the species/process is included at the population scale). The last two specify spatial information to be included in the model (whether or not to include coverage information and type of resource distribution) and how much time a single step of the simulation should represent. When required, a further window is brought up to enable the user to enter further simulation model specific assumptions about the value of an uncertain parameter, the result of which appears in the bottom inset pane in the main window. Weaver’s interface can be adapted to represent the specific uncertainties inherent in a chosen domain (see, for example, Figure 5).

When the user presses the “ComposeModel” button on the interface (Figure 2), the compositional modelling tool then interprets the design and generates a model description by integrating the necessary model components contained in the domain knowledge-base (2). The knowledge base represents knowledge (both complementary and conflicting) about the chosen ecological domain. When the “Simulate” button is pressed, the resulting model description (3) is passed to the multiple perspective...
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simulation tool, which converts the model description into an encoded simulation model and then executes that simulation.

The simulations are run on the Swarm complex systems simulation platform (Hiebler, 1994). Swarm provides the resulting simulation with, among many other things, a control panel and time series graphing facilities as well as 2-D viewers of spatial information. The time series generated by the simulation is inspected by the user and manually classified (4), e.g. the population cycles every 6-11 years, cycles every 4-5 years, or reaches equilibrium. Weaver then appends this classification to the original experimental design to generate an experimental case that is added (5) to the case library of previous experimental results.

When the user presses the “Learn” button, the domain theory generator takes this case library (6) and uses an inductive learning tool - C4.5 (Quinlan, 1993) - to generate a domain theory. This is most concisely expressed as a decision tree, which can be expanded into a set of rules defining relationships between assumptions (uncertainties) and simulation results. A rule abstracted from such a domain theory would look like this:

If  

an experimental design includes parasitism processes modelled at the individual scale and territoriality processes modelled at the population scale  

then  

the resulting simulation will generate a population behaviour that tends towards 6-11 year cycles.

The domain theory is then made accessible to the user (7). Pressing the “Advice” button passes the theory on to the experimental reformulator and theory refuter (8). The latter, supported by the knowledge base (9), then uses simple heuristic search to enable it to generate designs for new experiments that will attempt to refute the current theory. This is a way of helping the user navigate through what could amount to be a very large set of possible parameter and model assumptions (i.e. the uncertainty space) and to provide experimental designs which might otherwise not be obvious to the user or which might be arrived at only after lengthy periods of consideration.

A new experimental design suggestion can be generated by pressing “NewModel”. Weaver alters the previous experimental design to conform to its new design suggestion. This is then presented to the user (10) who can then opt, by pressing “ComposeModel”, to have it sent to the compositional modelling tool
to generate new models (11). Of course, the user can also generate his/her own new experiments independently (see step (1)) based on information from the generated domain theory. If new experiments are composed the loop begins again and the results of the new experiments are added to the case library from which another new domain theory can be generated. The current domain theory stands supported if the new domain theory is identical. Otherwise, the altered theory represents the refinement of the old theory in the light of new evidence.

Once a stable domain theory has been generated, i.e. one that cannot be further refined, that theory can be used to direct the design of experiments in the field (12), which will lead to the generation of more and highly relevant knowledge for input into the knowledge base (13).

4. How to encode knowledge using Weaver's software framework

Section 3 described how a scientist would interact with Weaver in its role as a modelling tool. Since Weaver is a generic framework for investigating complex uncertain ecological domains, the specific knowledge and uncertainties in the chosen domain need to be encoded before it can be used in this way. It is the task of a “knowledge engineer” (Feigenbaum, 1977), in conjunction with domain experts, to achieve this with support from Weaver's software framework of libraries.

4.1 Example domain - red grouse population dynamics

This process (and how it works – see Section 5) will be described using the domain of red grouse population dynamics and management. This domain is fascinating for two reasons. First of all, it is a domain that is afflicted by technical, methodological and theoretical uncertainty. Secondly, such uncertainty is the source of scientific and political conflicts that have drawn the attention of the media (Cherfas, 1990; Editorial, 1996). Red grouse are wild game birds that inhabit heather moorland in the uplands of the UK. Red grouse are suffering a long-term decline in numbers and have become listed in the red data book (Brown and Bainbridge, 1995). Various theories have been proposed for their decline (Barnes, 1987); it is clear that ecological, social and economic factors need to be taken into account. The greatest source of scientific conflict, however, lies in the debate about the cause(s) of red grouse
population cycles. The debate is a familiar one within ecology: intrinsic versus extrinsic causes. To paraphrase the debate, one group of researchers (Moss and Watson, 1994; Matthiopoulos, 1997; Matthiopoulos et al., 2000) suggests that that population cycles are caused by density-dependent intrinsic differences in the way that kin and non-kin react to each other when engaged in territory formation. This is known as the kin-facilitation hypothesis\(^3\). The alternative explanation (Potts et al., 1984; Hudson et al., 1992) is the parasite-host hypothesis which states that the cycles are caused by parasitic intestinal worms \((Trichostrongylus tenuis)\) whose effects are dependent upon grouse densities. It is in this area of dispute that we will concentrate our example. An overview of the uncertainties and controversies in the red grouse domain can be found in Lawton (1990). Further general analyses of red grouse ecology can be found in Leslie (1912) and Hudson (1992).

4.2 **Knowledge Engineering: Representing the domain knowledge**

Domain knowledge is represented at two levels in Weaver: influence graphs and simulation code. The influence graphs are a top-level description of the influences between domain variables. This is the representation primarily used to encode domain knowledge contained in the knowledge-base (see Figure 1); it is used by the compositional modelling tool to generate model descriptions. The influence graphs are represented declaratively. In Weaver, an influence is an explicit but unspecified directed relationship between two domain variables. It is coded thus:

\[
\text{Influence(<influence number x>, <variable1>, <variable2>).}
\]

Which means “variable1 influences variable2, in some way, via influence number x” (c.f. Thompson, 1996). Irrespective of the scale at which they operate, variables are also grouped according to the particular domain process in which they are involved e.g. “territoriality”, “parasitism”. As described in Section 3, and illustrated in Figure 2, it is at the level of processes that a user makes model assumptions. If a process is selected, then all variables within that process become candidates for incorporation in the final composed model (more information about model composition is provided in Section 5, below).

\(^3\) Note that in Matthiopoulos (1997) the hypothesis was known in terms of ‘kin-selection’.
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The simulation code is the particular computer algorithm that informs the simulation tool exactly how to simulate the influences represented in the influence graphs. The simulation code is represented by calculation variable objects (CVO) which use an object-oriented methodology called Variable-Centred Object Orientation (see Section 4.3 and Hare, 1999, for more details). The following section describes how different sources of knowledge in the grouse domain have been interpreted by the authors during the knowledge engineering phase and consequently how the knowledge has been represented in Weaver.

4.3 Representation – examples.

Population-based knowledge about influences

This piece of knowledge is a fragment of the kin-facilitation hypothesis model that calculates average minimum territory requirements of the grouse population as a function of average kinship and crowding among grouse. Kinship and crowding are functions of grouse mortality rates, and the number of old and young grouse.

Knowledge: \[ G_r = k(O_r^2/(S^2 Y_r)) \] \[ \quad (1) \]

Source: Matthiopoulos(1997)

\[ G_r = \text{average minimum territorial requirement at time } t \]
\[ O_r = \text{no of old grouse at time } t \]
\[ k = \text{arbitrary constant} \]
\[ Y_r = \text{number of young grouse at time } t \]
\[ s = \text{basic survival rate of young and old} \]

Interpretation: The average potential territory size (avPotential Territory Size) of a grouse population is influenced by the mortality rate of grouse, and the number of old and young within the population. Naturally, the domain process chosen for this variable is “territoriality”. Note that in order to integrate additional domain knowledge about influences on particular domain variables, existing knowledge must sometimes be adapted. For example, in this case, the territory size described as ‘potential’ rather than ‘minimum’ in order to be able to later include the possibility that vegetation structure and fitness also can have an influence on final territory size (see below).

Influence graph representation (see Figure 3):

\[ \text{Influence(78,oldGrouse, avPotential Territory Size).} \]
\[ \text{Influence(79,youngGrouse, avPotential Territory Size).} \]
\[ \text{Influence(86,mortalityRate, avPotential Territory Size).} \]
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**CVO psuedo code:**

\[ \text{AvPotentialTerritorySize} = k \cdot \text{oldGrouse}^2 / ((1 - \text{mortalityRate}) \cdot \text{youngGrouse}) \]

**Individual-based knowledge about influences**

**Knowledge:** fitter grous can have larger territories  
**Source:** gamekeeper knowledge

**Interpretation:** a grous's potential territory size is proportional to its body weight (taken as a measure of fitness). The domain process chosen for this variable is “territoriality”.

**Influence graph representation (see Figure 4):**

Influence(b.bodyWeight, potentialTerritorySize).

**CVO psuedo code:**

```c
for each grouse in population,
    grouse.potentialTerritorySize = grouse.bodyWeight / 15.  endfor
```

[Matt - where does the constant 15 come from? I don't think you can just lob it in without explanation]

**Individual-based knowledge based on spatial information – spatial influences**

Before describing this example, it is necessary to outline how Weaver represents space. It is represented generically as a two-dimensional coverage divided into square cells. In the grous example, the resource in each cell represents a homogenous area of heather of a particular age, containing zero or more heather-dwelling parasites and grous. When the user makes the assumption that space is to be included in the model, such a coverage is provided. If the user then makes assumptions that processes representing grous foraging or territoriality should be individual-based, then grous can move freely around this coverage from cell to cell, foraging on the heather or setting up territories. Natural ageing processes and burning (if included) affect the age of the heather in any particular cell. The following example illustrates how the spatial-layout of heather affects grous territoriality.

**Knowledge:** the chances of a grous being recruited to the current territorial population are influenced by its ability to set up a territory which contains young heather.  
**Source:** gamekeeper knowledge

**Interpretation:** the potential size of a grous's territory can be calculated, but it does not mean that the grous will gain that territory. Whether it can set up this territory and therefore become part of the
territorial population depends on the relative position and availability of young heather. The domain process chosen for this variable is “territoriality”.

**Influence graph representation (see Figure 4):**

\[
\text{Influence}(1, \text{positionYoungHeather}, \text{chanceOfRecruitment}).
\]

\[
\text{Influence}(3, \text{potential Territory Size}, \text{chanceOfRecruitment}).
\]

**CVO psuedo code:**

find no. of young heather cells in heather coverage, h,

take first h grouse agent objects and place in LIST

for each grouse agent object, x, in LIST

choose a young heather cell, p, with coordinates x1,y1, as territory locus not chosen by other grouse

if locus p found

move x to locus at x1, y1

take all cells neighbouring locus, p, up to potential territory size that are not possessed by other grouse

calculate actual territory size of x = number of cells possessed, chance of recruitment = 1.0

else if locus p not found, then kill x, i.e. set chance of recruitment = 0.0

These three fragments of knowledge are parts of the influence graphs describing the domain shown in Figures 3 and 4. These figures illustrate how the alternative theories about the causes of red grouse population cycles, as well as local knowledge about territoriality etc, can be integrated in the same influence graph representation by a knowledge engineer. Note that two scales (individual and population\(^4\)) are represented here - thus this representation can give rise to many possible models. It is the role of the compositional modelling tool to combine the user's assumptions to generate appropriate models.

**Representing uncertain parameters**

Representation of uncertain parameters is simply a case of declaring the possible parameters of that variable. If, as in the basic breeding rate, there is more than one possible value then a list of potential

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\(^4\) Alternative scales could be represented. For example Matthiopoulos et al. (2000) describe a kin-facilitation hypothesis model that operates at the scale of grouse clusters.
values is included. During the use of Weaver, when the value of a parameter is uncertain, the user is invited to choose from a list of these possible values.

**Knowledge:** potential breeding rates of grouse can be 6-12 per pair. **Source:** gamekeeper knowledge

**Interpretation:** the basic potential breeding rate per grouse can be in the range 3-6 chicks. The “basic breeding rate” is assigned to the “breeding” process.

**Representation:** \( \text{param(basicBreedingRate, [3.0,3.5,4.0,4.5,5.0,5.5,6.0])}. \)

Representing knowledge about time

In the following manner, knowledge about timings of events can be encoded in the knowledge-base for use in scheduling the final simulation model.

**Knowledge:** territoriality begins around October or November **Source:** Leslie (1912)

**Interpretation:** the monthly timing of the territoriality process is month 3 (the simulation year starts in August, month 0)

**Representation:** \( \text{atMonth(territoriality, 3)} \)

5. How Weaver's components work: Composing, simulating and comparing models

The development of simulation models is a two-stage process. First the compositional modelling tool generates a model description based on the influence graph, i.e. a description of the nodes and variables to be used in the model. Second it matches the nodes and variables to CVOs which are then linked and scheduled to form a coherent simulation. For the compositional modelling tool to build suitable and non-contradictory models based upon these multiple perspective influence graphs, it needs to be given model constraints by the user. These constraints represent modelling assumptions that the user has to make. The user’s need to understand the importance of particular assumptions will determine the type of the constraints to be applied. Figure 5 illustrates a Weaver interface specific to the domain of red grouse. Illustrated are the types of assumptions constraining model building in this domain. A set of user’s
assumptions constituting an experimental design (called “experiment 1”) for constructing a simulation model is also shown.

5.1 How the model description is built

A compositional modelling approach based upon Rickel and Porter (1997) has been used. However, the approach has been augmented by a novel technique called ‘multiple dynamic scale bridging’. Building the model description depends on finding the exhaustive set of variables that have a direct or indirect influence on the variable of interest. For experiment 1, the variable of interest is the population density of the grouse (see Figure 5). The bold arrows in Figure 6 show all the variables that the compositional modelling tool can find and that influence the variable of interest, given the user’s assumptions.

Note the hashed bold arrows between variables at different scales. These represent the operation of two types of multiple dynamic scale bridging. In the first case, a model can be described that includes influences from different scales, e.g. the integration of population-scale breeding and mortality knowledge with individual-scale foraging. In the second case Weaver can fill in knowledge gaps in order to complete a model description. Of crucial importance here is to note how the user’s desire for modelling territorially at the individual scale has been achieved. This has been done despite the lack of encoded knowledge at this scale: without a desire for weight processes to be represented in the model, there is no knowledge at the individual scale that can be used to calculate the potential size of territory at the individual scale. To fill the gap, the individual scale description has been augmented by knowledge of kin-facilitation effects at the population scale. That is, knowledge about determining the potential size of territory at the population scale is being used to calculate ‘potential size of territory’ at the individual scale (represented in Figure 6 by the dashed link between ‘average potential territory size’ and ‘potential territory size’). The mechanics of multiple dynamic scale bridging are provided in Hare (1999).

5.2 Generating a scheduled simulation model for Swarm

Once the model description has been generated it is a simple task to use the information about the required variables and influences to select the appropriate CVOs for the simulation. The times at which variables are updated are determined (the model is 'scheduled'). The schedule given to a variable by the
compositional modelling tool depends on the process to which the variable belongs. The timing is obtained by the compositional modelling tool from the knowledge base (see Section 4.3) and is dependent on the user's choice of time step. For example, if the time step for the model is 'monthly', then timings for calculating the variables in the territoriality process are provided by a search of the knowledge-base. The search is carried out by the composer in order to find the appropriate piece of knowledge relating to the month in which territoriality occurs. If the time step is yearly, each process occurs at every time step.

5.3 Classifying the results of experiments: creating cases

In defining the results of simulations we use the Hornberger and Spear (1980) approach (for identical reasons relating to uncertainty) of defining a result in terms of whether or not it matches a particular behaviour. The user classifies the results against classes of behaviours. Classification is a matter of great subjectivity. There are many possible metrics that can be used in the grouse domain, e.g. population change, parasite levels, territory size. For this example, however, the classification metric will be the mode population cycle periodicity over 100 years. Amplitude of cycle and other data, e.g. young to old ratio, worm burdens, territory size, will be ignored. The classes are shown in Table 1.

The classification of the four yearly population cycles generated by experiment 1 is thus class I. [Matt - I don't think you've yet described the output from experiment 1 - wouldn't it be worth having a figure showing the output - if only to have one figure which shows the nature of the output] This classification is then added to the experimental design, and stored as a case. It is then placed in a case library along with previous cases carried out by the user. Cases are equivalent to Hornberger and Spear (1980) parameter vectors representing system behaviour outcomes. Once a case library exists we can start to develop understanding about the importance of the different case assumptions in determining behaviour. By doing so, we can learn about the importance of the parameter and model uncertainties; this is achieved by the domain theory generator.

5.4 Domain theory generation

The domain theory generator provides a method of uncertainty analysis for model as well as parameter uncertainty. To do so it uses an inductive learning tool, C4.5 (Quinlan, 1993), to generate a domain theory.
which describes the relationship between key assumption choices in the experimental design and the resultant behaviour of simulations. In this way generalisations can be made about the sensitivity and impact of particular decisions when designing models. The details of how the domain theory generator and C4.5 work are presented in Hare (1999); an overview is provided here.

The domain theory generator takes the initial case library and uses it to develop a classification model that not only correctly classifies the behaviour of simulations using previous experimental designs but also predicts the behaviour of future designs. This model represents the current domain theory. Such a theory consists of a set of hypotheses which state that if certain assumptions are made within an experimental design (the hypothesis conditions), then the experimental simulation based on that design will result in a particular behaviour (the hypothesis consequence). The classification model is developed by finding the most general set of assumptions, that can be used to subdivide the case library into subsets of cases, all or most of whose members share the same classification. The classification model is in the form of a decision tree as shown in Figure 7. Numbers at the start of lines represent sub branches. Numbers 1-3 represent root nodes. Italics represent classified leaf nodes. The numbers in brackets next to the leaf nodes represent the number of cases which have been classified in this way. Bold case represents branches of interest to the following discussion. Each of the fourteen classified leaf nodes in the domain theory in Figure 7 represents the consequences of one of fourteen different hypotheses. The path of assumptions that links the leaf node to the root node represents the conditions of the hypothesis. For example, the path ending at branch 2.1 represents the hypothesis that:

If an experimental design includes parasitism processes modelled at the individual scale and territoriality processes modelled at the population scale

then the resulting simulation will generate a grouse population behaviour that tends towards class II behaviours.

The above hypothesis is called a supported hypothesis because there are (four) cases in the case library that indicate that the hypothesis may be correct. However, the attempt to build a generalised decision tree, i.e., one that can predict the result of simulations based on experimental designs that have not yet been used, means that hypotheses will occasionally be generated which are not supported by any cases within the case library. These are called unsupported hypotheses. For these, C4.5 chooses a classification
for the leaf node based on the class of the majority of cases in the other branches at that decision node. The domain theory in Figure 7 contains only one such hypothesis (branch ending at 3.1). This hypothesis predicts that:

\[
\text{If an experimental design includes no parasitism and body weight processes modelled at the population scale}
\]

\[
\text{then the resulting simulation will generate a grouse population behaviour that tends towards exponential growth behaviours}
\]

One final point to make about the decision tree is that the closer an assumption is to the root node, the more fundamental that assumption is for use in predicting the outcome of a simulation. Hence, in the decision tree in Figure 7, assumptions about parasitism are more important than territoriality process assumptions.

5.5 How the domain theory is used

The experimental reformulator uses the domain theory to generate suggestions for new experiments, and hence guide the user through the uncertainty space. The experimental reformulator uses a simple heuristic that exploits the existence of unsupported hypotheses. The refutation strategy used in the experimental reformulator is one developed by the authors and is simply this:

Unsupported hypothesis refutation strategy: If a hypothesis is generated that says certain classes of assumptions are important in determining simulation behaviour, then attempt to refute this hypothesis. Do this by identifying a rule that has no cases to support it, and generate new experiments based on this rule. The null hypothesis is that the new experiments, once carried out and added to the case library, will change the domain theory, thus indicating that the previous domain theory was inaccurate.

For example, new experiments can be designed based on the unsupported hypothesis described above in Section 5.4 quite simply by finding all existing cases that do not include parasitism and then setting the body weight assumption of these cases to the population-scale.
6. Use of Weaver for a particular task - a simple example

The following section provides a simple example of how Weaver could be useful in solving problems in uncertain ecological domains. Once again the example domain is red grouse population dynamics. The task is to develop better understanding about the conditions in which the parasite-host and kin-facilitation hypothesis models generate cycles.

6.1 Background

Both the competing parasite-host hypothesis and the kin-facilitation hypothesis models have been validated empirically (Dobson & Hudson, 1992; Matthisopoulos, 1997) and thus claim to be an explanation for grouse population cycles. Both are underpinned by a range of modelling assumptions, some of which are based upon conflicting empirical evidence and others of which are artefacts of the chosen modelling paradigm designed to aid analytical tractability.

The assumptions in the kin-facilitation hypothesis model (Matthisopoulos, 1997) supported by conflicting empirical evidence include the assumption that the territorial population (all those birds who manage to gain a territory at the end of the year, through kin-facilitation or otherwise) is a good indicator of the next spring’s breeding population. The empirical evidence supporting this, i.e. evidence supporting the compensatory nature of over winter mortality (Watson and Jenkin, 1968), has been empirically refuted by Hudson (1992). Likewise, the parasite-host hypothesis makes the assumption, based upon empirical evidence, that a direct correlation can be made between the July density of grouse and the parasite burden in the grouse (Hudson et al., 1992). This relationship, in turn, has been empirically disputed by Moss et al. (1993). This conflict is an example of conceptual uncertainty; it is unclear which theory is appropriate to apply as a plausible explanation for the phenomenon of cycles. The conflict also leads to model uncertainty in that it is difficult to know which of these empirically-conflicting assumptions to include in a model. The causes of this uncertainty reside in technical uncertainty (e.g. the difficulties of measuring parasite burdens (Leslie, 1912)) and methodological uncertainty caused by differences in experimental designs between the two research groups. Hudson et al. (1985), for example, suggest that differences in experimental site sizes may be a contributory factor to the conflicting findings.
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Other causes of conceptual uncertainty are the different environmental and ecological conditions in which the research groups have carried out experimental work and data collection in different parts of the country. Since red grouse population cycles have different characteristics in different parts of the UK, this could be an important factor. The kin-facilitation hypothesis model (Matthiopoulos, 1997) has been developed and validated with data from north-east Scotland, whilst the parasite-host hypothesis model was developed and validated predominantly with data from sites in northern England (Dobson and Hudson, 1992). In north-east Scotland, for example, the cycle period is between 6-11 years, whilst in northern England the period is only 4-5 years (Moss et al., 1993; Matthiopoulos, 1997). This leads to the possibility that the two groups could therefore be investigating two different phenomena and, as Moss et al. (1993) write, the “two different [phenomena] may result from different causes” (p208). Hence, the parasite-host hypothesis may represent an explanation for cycles of 4-5 years whilst the kin-facilitation hypothesis represents cycles of 6-11 years.

The artefactual assumptions of both models include the decision to treat the environment as spatially homogenous and to model the grouse at the population scale and thus aggregate the effects of parasites and kin-selection. The use of these assumptions has lead to a certain degree of model uncertainty, since it is not clear what the impact would be on the model results if alternative assumptions were made, such as modelling the population at the individual scale. Matthiopoulos et al. (2000) recognise this uncertainty by acknowledging that there is a need to re-examine the kin-facilitation hypothesis at a higher level of detail and have thus designed a model working at the scale of grouse kin clusters.

Thus there exist, in the field of red grouse population dynamics, technical, methodological and conceptual uncertainties as well as model uncertainty. Unlocking the model uncertainty can be achieved by exploring the importance of assumptions within the models. The conceptual uncertainty can be unlocked by definitively invalidating one or either of the hypotheses. However this is unlikely, given the methodological and technical uncertainties. Alternatively, it can be done by combining the two hypotheses within the same theoretical framework; a framework that describes the environmental and ecological conditions in which the hypotheses explain the empirical findings.
6.2 How can Weaver help?

Weaver can be used to unlock the model uncertainty by allowing the user to explore the impacts of changing modelling assumptions. Weaver also has an indirect role to play in unlocking the conceptual uncertainty. It can be used to try and develop a single domain theory that describes the key assumptions in which both hypotheses in a simulated grouse world can become (im)plausible explanations of population cycles. The domain theory may also highlight the important areas of uncertainty in this modelled world that can lead to a deviation from the expected impacts of parasitism and kin-facilitation-based territoriality. It can then be used to target future fieldwork whose results may lead to a reduction in uncertainty in the real world and allow scientists to resolve conceptual uncertainties.

Specifically the goal of the task is to use Weaver to answer the following questions:

Q1: Can Weaver induce a single domain theory within which both hypotheses are incorporated and which predicts the types of cyclic phenomena (4-5 year or 6-11 year cycles) that the hypotheses are expected to explain?

Q2: What are the key uncertainties (model or parameter) that affect whether or not kin-facilitation and parasite-host models generate cycles?

Q3: What role do assumptions about the model scale play? Does the use of individual-based or population-based models affect the type of cycles produced by the proposed explanatory models?

The next sections will outline the method and results of this task.

6.3 Method

The task began with nine experimental designs chosen by the user. Each was simulated once using a fixed random seed, and classified. During each subsequent iteration of Weaver (see Section 3), the case library was updated with a new set of cases developed, a domain theory was learnt and new experiments generated using the unsupported hypothesis strategy.

Crucial to the use of Weaver is the concept that it provides the guidance, whilst the user makes the decisions. The use of Weaver is a learning process for the user and, as such, the user becomes increasingly
knowledgeable about the uncertainty space that is being navigated. As users become increasingly
certain in that knowledge, they may choose to ignore the suggested experiments in order to guide the
search in their desired direction. Part of the user’s learning process is also in developing the ability to
evolve more appropriate ways of classifying the output (the classification classes). The user was therefore
also permitted to adapt the classification classes. This can improve the clarity of the resulting domain
theory and alter the direction of search, but it means that all previous cases have to be reclassified. In this
example, the classification scheme used was initially as described in Table 1, Section 5.3. By iteration 17 it
was changed according to Table 2.

6.4 Results

While Figure 7 represents the resulting domain theory after the second iteration using the original
classification scheme (Table 1), Figure 8 represents the development of the domain theory after 17
iterations with the scheme in Table 2. Given this domain theory, an attempt can be made to answer the
three questions set in Section 6.2.

Q1: Can Weaver induce a single domain theory within which both hypotheses are incorporated and which
predicts the types of cyclic phenomena (4-5 year or 6-11 year cycles) that the hypotheses are expected to
explain?

A qualified ‘yes’. Figure 8 illustrates a single domain theory that shows that, depending on the model
assumptions, population-scale territoriality models (which include kin-facilitation assumptions) can
generate 6-11 year cycles (class B) (see branches 1.3 & 2.2.5.2) and that population-scale parasite-host
models can generate 4-5 year cycles (class A) (see branches 2.2.1-4). However there appear to be model
and parameter decisions that lead to uncertainties in the outcome of both models.

Q2: What are the key uncertainties (model or parameter) that affect whether or not kin-facilitation and
parasite-host models generate cycles?

In terms of model uncertainty, the choice of whether or not to include foraging in the model appears to
be crucial in determining the outcome of the simulation. When foraging is included (branch 1), decisions
about the absence or scale of territoriality predominantly determine the type of cycle produced. In the
case of no foraging (branch 2), decisions about the absence or scale of parasite model used determine the nature of the cycle produced. The importance of foraging behaviour in the domain theory, however, has to be tempered by the fact that after the 17th iteration, only a small proportion of the cases have used foraging models. Hence, whilst the non-foraging branch of the tree is well supported by cases, the foraging branch is not; more cases are required. However, the importance of foraging on population dynamics, particularly with respect to the effect that movement within a spatially heterogeneous environment has on population cycling and stability, is recognised theoretically (Hassell and May, 1985).

In terms of parameter uncertainty, potential breeding rates are the most important (see branch 2.2). When the basic breeding rate is low, i.e. 2, the population-scale territoriality model can override the effects of parasitism. When basic breeding rate is higher, the dominance of parasitism is restored. However, published data on clutch sizes for a cycling and parasite-infested northern English moor (Hudson, 1992) show that the clutch sizes are lower than the reported clutch sizes for territoriality-induced cycles at a site in the north-east of Scotland (Moss et al., 1993). This would apparently contradict the findings of Weaver. However, care has to be taken in interpreting the assumption features used in Weaver. “Basic breeding rate” represents the maximum potential number of new grouse that can be produced before any effects caused by parasites. The observed clutch sizes are the maximum number of new grouse that are produced after parasitism is taken into account. Hence a more appropriate approach is to compare clutch size data in which parasitism has not taken effect. On parasite infested moors, the only way this can done, is by finding out the clutch sizes of grouse which have been treated for parasites and therefore have a low level of infection when breeding. Using these data, clutch sizes without the effects of parasites, in otherwise parasite-induced cycling populations (Hudson, 1992) are as high or higher than clutch sizes found in territoriality-induced cycling populations (Jenkins, 1969; Moss et al., 1993).

Q3: What role do assumptions about the model scale play? Does the use of individual-based or population-based models affect the type of cycles produced by the proposed explanatory models?

Parasite models tend to be robust in the face of scale changes (see branches 2.2 & 2.3). In the case of territoriality, agent-based models fail to generate class B cycles (see branches 1 & 2.2.5). Once again, care must be taken in interpreting the latter result. No models using agent-based territoriality, unlike those
using population-based versions, incorporate the kin-facilitation hypothesis in its pure form as described in the population-based model. Calculations for potential territory size based on the kin-facilitation hypothesis are only included if there are no body-weight processes included in the experimental assumptions (as occurs in experiment 1 in Figure 6). Even then, location and availability of young heather will temper the actual territory size. Such knowledge suggests that further development of the domain theory by Weaver is required to elicit these subtleties.

7. Comparison of Weaver to existing tools

There are several existing tools designed to aid the investigation of complex domains that share one or more of the AI technologies used in Weaver. The following section provides a summary of the important similarities and differences between Weaver and these tools.

7.1 Modelling tools

There is a range of available modelling tools that provide a generic ecological framework in which to design and execute specific single-model simulations. For artificial life simulations these include Gecko (Booth, 1997), and Herby (Devine and Paton, 1997). For mathematical modelling, they include STELLA (see Costanza et al., 1998 and other articles in same issue) and, although it was originally designed for business decision support tasks, Analytica (Morgan and Henrion, 1998). STELLA and Analytica have an influence-based approach to the representation and encoding of modelling knowledge and a corresponding GUI interpreter that allows simple encoding of models. While Weaver also uses an influence-based representation, the initial setting up of the knowledge base in Weaver (see Section 4) requires the bridging of the type of “modelling gap” of which Lorek and Sonnenschein (1999) are critical. Such gaps occur when a modeller is faced with difficulty in translating ecological knowledge into a specific programming language. Whilst setting up the knowledge base, therefore, Weaver provides a software framework which offers a set of software libraries that provide a structure for the model building process but still require model encoding at the computer programming level. Once the knowledge base has been encoded, however, and Weaver is being used by the scientist for theory development, it becomes a “modelling tool” that provides a simple assumption-driven interface for
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specifying models that are then automatically constructed by the compositional modelling component. In this way, model building is actually easier in Weaver than in either STELLA or Analytica and can result in models that integrate knowledge at multiple scales of agent aggregation.

In terms of support for uncertainty analysis, Analytica provides comprehensive support for modelling parameter uncertainty, whilst STELLA provides rudimentary support through sensitivity analysis. Unlike Weaver, neither tool can represent nor analyse model uncertainty. Both tools’ method of searching through the parameter space (c.f. Weaver’s search through the uncertainty space – Section 5.5) is by carrying out random Monte Carlo sampling. Weaver uses a directed heuristic search based on the principles of critical discussion. Table 3 summarises the comparison of these three modelling tools.

7.2 Integrated AI approaches for managing and understanding ecological systems.

Weaver follows on from the traditions of integrated knowledge-based systems such as COMAX (Lemmon, 1986). The latter used an expert system to select inputs for a cotton management simulation system and then analysed the output to determine the necessary inputs for further simulation runs. COMAX however was a predictive tool, not a domain theory generator. It was able to be predictive because it had enough quality knowledge and data about the domain with which to make analyses and carry out the simulation. Additionally, it had few alternative parameter settings to choose from and limited sets of possible simulations to run and analyse.

Kompare et al. (1994), proposed a tool for developing understanding in complex ecological domains which would make use of the KARDIO (Bratko et al., 1989) approach to knowledge acquisition. This approach was originally used in developing models of the heart. It defines a semi-automated knowledge acquisition cycle that attempts to improve a theory of the system (what they call a deep model ) iteratively through simulation. Kompare et al. suggest that KARDIO can be used in ecological systems without enough expert knowledge to generate a domain theory by starting the cycle at the surface knowledge stage, i.e. data pertaining to actions and reactions within the domain. These facts are then used by an inductive learning tool to generate the domain theory.
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This is an interesting approach because, like Weaver, it iteratively applies machine learning to simulation results in order to generate better understanding of domain knowledge. However, Kompare et al. admit that they have been hindered in the actualisation of such a tool for ecological systems by the lack of data for starting the process off and inducing the deep model. Whilst their approach begins from an assumption that either deep knowledge or data will be available in sufficient quality and quantity to begin knowledge development in a complex ecological domain, Weaver does not make this assumption. Instead, Weaver makes use of all available consistent and inconsistent knowledge and data. These are used to generate simulations from different perspectives on the same domain, rather than from a single unified view. Also, because of the diversity of possible consistent and inconsistent knowledge and data upon which simulation experiments can potentially be based, Weaver provides support in selecting new simulations to help refine the domain theory.

8. Conclusions

We have demonstrated a prototype modelling tool called Weaver that provides support for the scientific process of knowledge discovery in highly uncertain complex systems by tackling the problems of data and knowledge absence, multiple expert perspectives and of determining the impact and importance of modelling assumptions. Specifically, Weaver does this by supporting the integration of diverse knowledge types into multiple perspective models; knowledge gap handling; analysis of model uncertainty as well as parameter uncertainty; the integration and comparison of models at different scales; and the selection of parameters and models in large uncertainty spaces. It uses a hybrid Artificial Intelligence approach based upon Popper’s concept of critical discussion, that integrates several AI techniques such as Compositional Modelling, Artificial Life Simulation, Inductive Learning, and Heuristic Search. Weaver concentrates on assessing the effects of modelling systems with respect to alternative assumptions, rather than on explaining how the domain under consideration actually functions. Answers to the latter are left for empirical investigation, although the claim of this paper is that Weaver could guide such investigations.

Weaver is imperfect in many ways. As explained, the encoding of knowledge is not as easy as it is in tools such as STELLA. Also, there is no statistical support for parameter uncertainty analysis as provided in tools such as Analytica. Furthermore, Quinlan’s inductive learning method used in the domain theory
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generator is not always appropriate for identifying the importance of a dependent variable, if the variable
upon which it is dependent has already been identified. The unsupported hypothesis refutation strategy
for reformulating and identifying experiments for testing domain theory is a rather naïve strategy. It can
lock on to what is, to a human, a clearly unintelligent experimental direction. For example, in tests it
suggested looking into models in which there was no mortality. What is needed, therefore, are basic
ecological rules for describing the essential components of an ecological simulation and for these to be
included in the reformulation strategy in order that bad designs can be automatically identified and
discarded.

Use of Weaver to date has emphasised the importance of allowing the user final control over
experimental design decisions, as well as the importance of choosing correct classification schemes. The
latter particularly affects the clarity of the resulting domain theory, as well as the direction of theory
development. The interface should be developed to allow simple user adaptation of classification schemes
as well as the heuristic search method.

Our next steps in this project include the development of improved experimental reformulation strategies
by trying to model scientists’ own strategies for designing refutation experiments and by encoding basic
ecological rules for defining valid experiments. It is also important for us to compare the qualitative and
quantitative benefits of searching the uncertainty space using a heuristic-based search as used in Weaver
against other approaches such as a Monte Carlo sampling approach. We are also investigating ways in
which the manual classification of simulation output can be automated. Finally, we are interested in
investigating the plausibility of developing Weaver for use with other more established modelling tools,
e.g. STELLA, by integrating one into the position currently held by the multiple perspective simulation
tool.

We hope that this work will provide the foundation for the development and use of ecological modelling
tools that can integrate AI and mathematical modelling techniques. Such tools can help the scientist
design and generate complex models that integrate sub-models at different scales, can contend with
knowledge gaps and can help the user navigate through and understand a potentially vast uncertainty
space.
Acknowledgements

This work was funded by the Scottish Executive Rural Affairs Department (SERAD). It could not have been done without the ability to talk to and discuss ideas with members of red grouse research and management community in north-east Scotland. Thanks go to Gary Polhill for maintaining Weaver and for help in preparing the paper. We would like to thank Claudia Pahl-Wostl, Nick Gotts and Chandana Paul for providing critical feedback on this paper. We also express our thanks to the all the Swarm crew at the Santa Fe Institute, New Mexico, for allowing us to Beta-test their product, which is freely available for downloading at: http://www.swarm.org.

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