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Introduction

Models of the control of tsetse and human African trypanosomiasis (HAT) can improve the understanding and planning of field campaigns and clarify research priorities. Ideally, the models should be user-friendly, covering aspects of the basic biology of tsetse, trypanosomes and their hosts, and consider a wide range of control options in simulations of real operational areas. Existing models do not meet all of these requirements. To start filling the gap, a dynamic deterministic model, "HAT-trick", has been developed.

Modelling is conducted at three successive levels. First, the Basic Level covers fundamental aspects of tsetse and trypanosome biology that apply in any situation. Second, the Map Level combines outputs from the Basic level with inputs specific to a particular operational areas, up to 40,000 km², to produce maps for the (i) abundance, distribution, age structure and infection status of tsetse, and (ii) the incidence and prevalence of HAT, before any intervention. Third, the Control Level simulates the impact of tsetse control.

The modelling levels are accessed via blue buttons on the Begin Menu (Fig. 1). Further context-sensitive information is provided by clicking on the Query (?) icons and the 'Help Team member'.

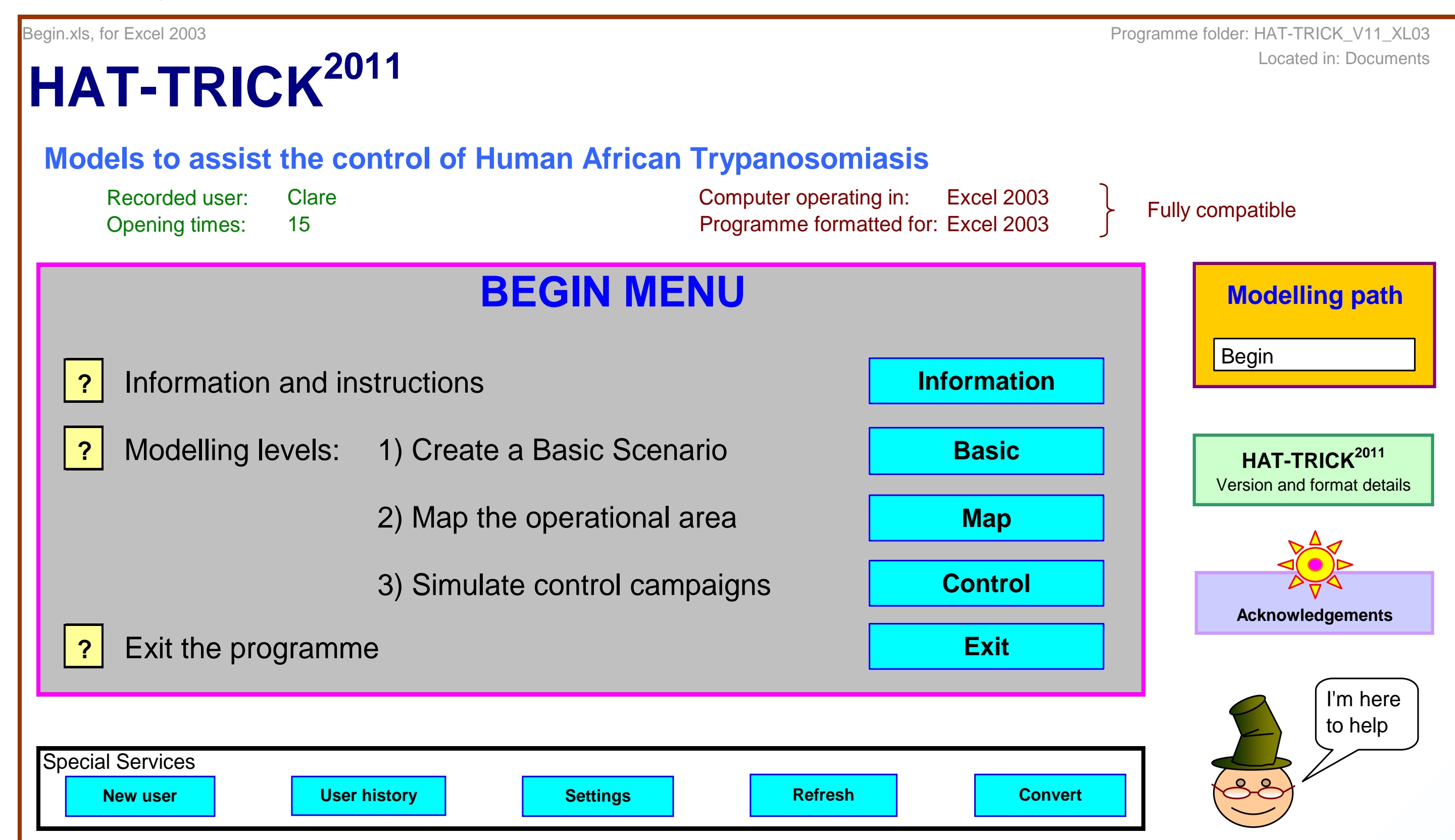


Fig 1. The Begin Menu to access modelling levels, information and services.

Basic Level

The Basic Level deals with the growth, mobility, host-finding abilities and infectivity of a population of a specific tsetse species, and its distribution between vegetation types. The inputs sheet for the growth (Fig. 2) typifies all input sheets in offering suggested inputs via the Suggest button, and comments on the current inputs. After completing all inputs sheets and generating outputs, the combination of input and output data is saved to a Basic Scenario, and to a Report that summarises the scenario.

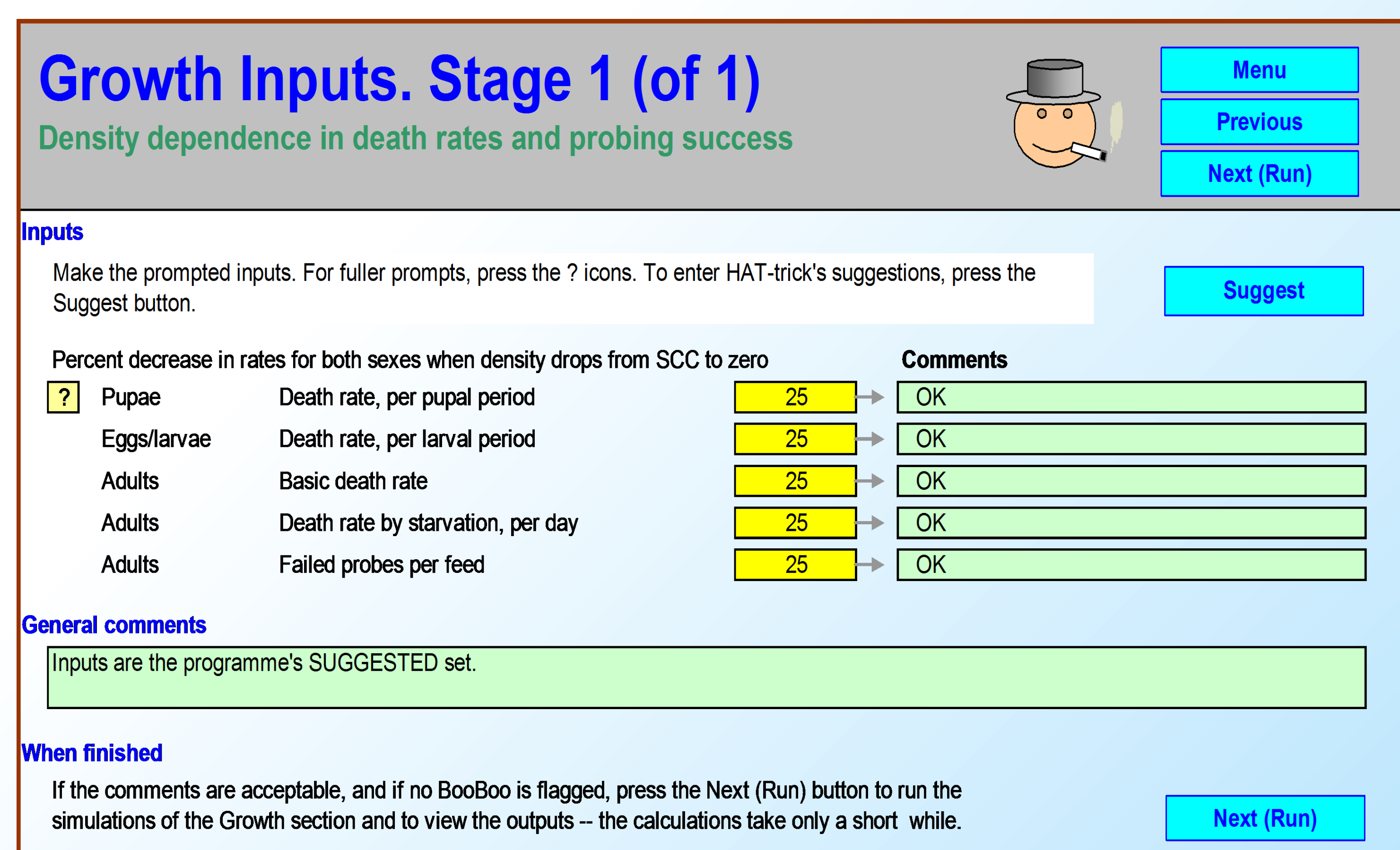


Fig. 2. Inputs sheet for tsetse population growth.

Map Level

The first task of the Map Level is to load the particular Basic Scenario that details the fundamental biological processes within the area to be mapped. Inputs then specify matters such as the distribution of vegetation, humans, cattle, other mammals and reptiles, and the incidence of HAT. Outputs identify the infection rate in non-humans and simulate the distribution of the sexes, age classes and infection states of tsetse, and the incidence and prevalence of HAT in the absence of any control (Fig. 3).

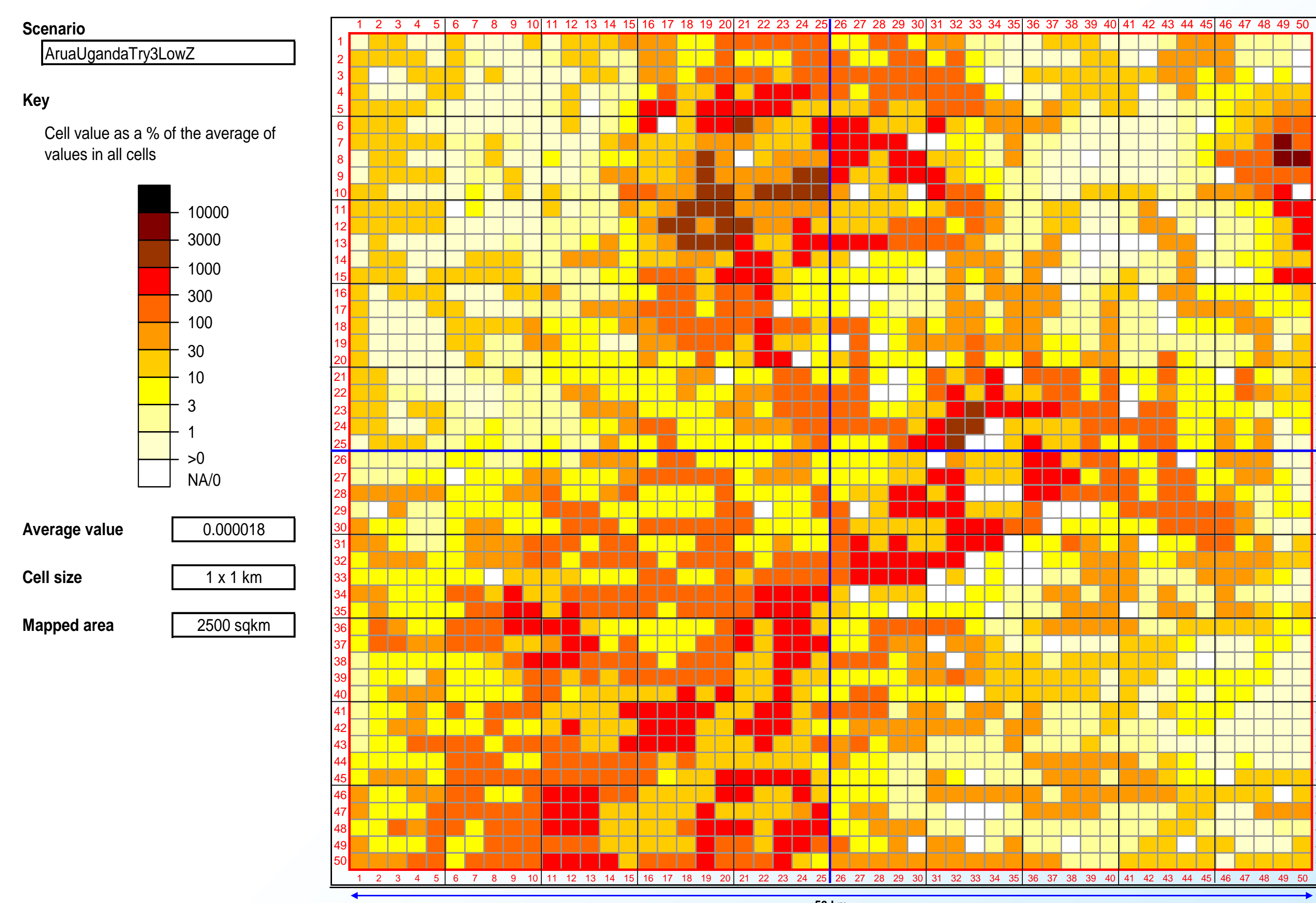


Fig 3. Example of an outputs map: distribution of HAT before control.

Control Level

After loading the Map Scenario that specifies the pre-control situation, inputs are required to cover the type(s), timing, intensity and location of control measures. Control is then simulated, leading to outputs for the resulting distributions of each segment of the tsetse population, and the incidence and prevalence of HAT, and the extent to which these matters have changed over time (Fig. 4). After saving the data to a Control Scenario and Report, a second round of control can be simulated.

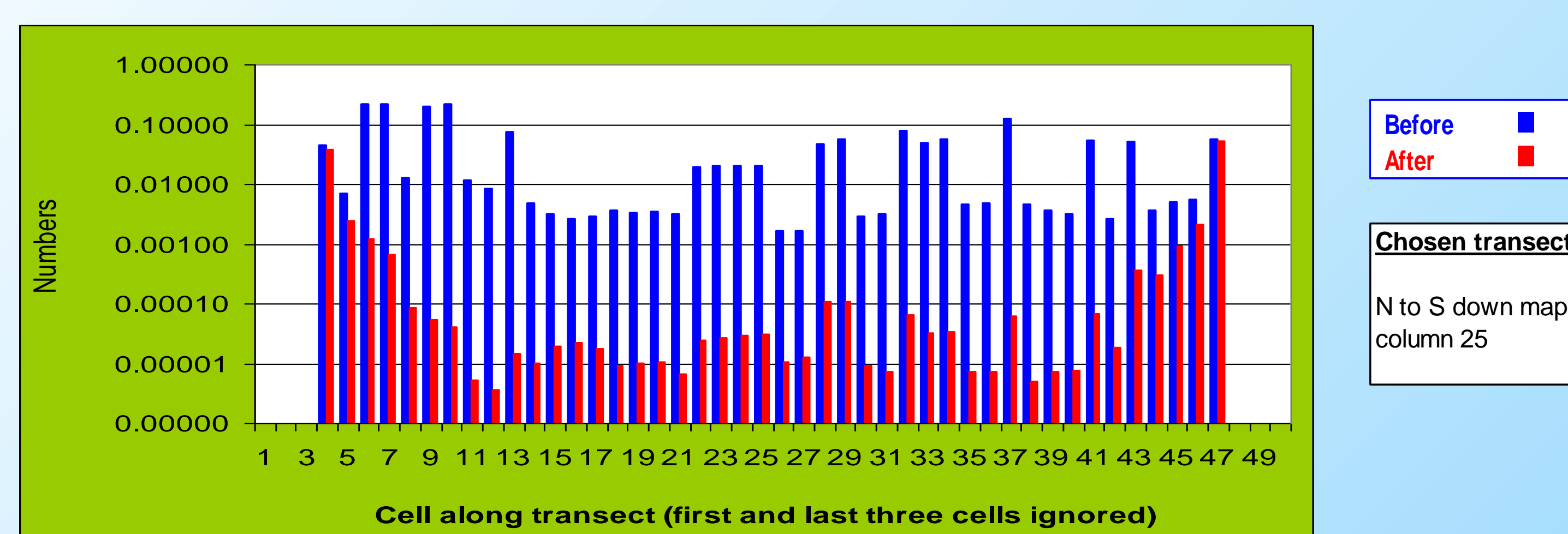


Fig 4. Example of outputs: HAT cases along a transect, before and after control

Use

The model has been used to simulate HAT foci in East, West and Southern Africa, giving outputs consistent with field data. It also offered several suggestions, such as the need to look in the field for 10-90% reductions in HAT risk that are simulated to occur over areas up to six times greater than those where bait control is operated. The degree of man/fly contact under various field circumstances deserves fuller study. It is required to resolve the apparently gross disparity between the seemingly low rates of *Trypanosoma brucei* infections in wild tsetse, and the higher rates in cattle and wild animals.

Future

It is hoped that the model will evolve through use and suggestions by all interested persons -- who are most welcome to become co-authors. In particular, it would be helpful to extend the model to simulate the direct control of trypanosomiasis