# SolBeePop*ecotox*
# A population model for pesticide risk assessments of solitary bees

## User Manual

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## INTRODUCTION

The SolBeePop*ecotox* model is an extension of the model SolBeePop. This user manual provides a short overview of the user interface of the SolBeePop*ecotox* model and how simulations can be started. The model code (SolBeePop_ecotox.nlogo with its extension BeeGUTS.nls) and documentation are available from GitHub, a public repository: https://github.com/SolBeePop/SolBeePop.

Beyond the model code, this manual references files available from the SolBeePop*ecotox* respository, including the TRACE documentation (SolBeePop_ecotox_TRACE.pdf) and tables (SolBeePop_ecotox_Tables.xlsx).

To run SolBeePop, the NetLogo software is required (for runs in the current study, NetLogo 6.3.0 was used). NetLogo is available for download free of charge: https://ccl.northwestern.edu/netlogo/6.3.0/. For guidance how to use NetLogo, please refer to the NetLogo website (https://ccl.northwestern.edu/netlogo).

## INTERFACE OVERVIEW

In Figure 1, a screenshot of the user interface of SolBeePop*ecotox* (implemented in NetLogo) is shown. Elements of the interface are indicated by boxes of different colors. These elements are introduced in the following.

After the introduction of the interface and its elements, a short guide is provided to running a simulation with generic settings.
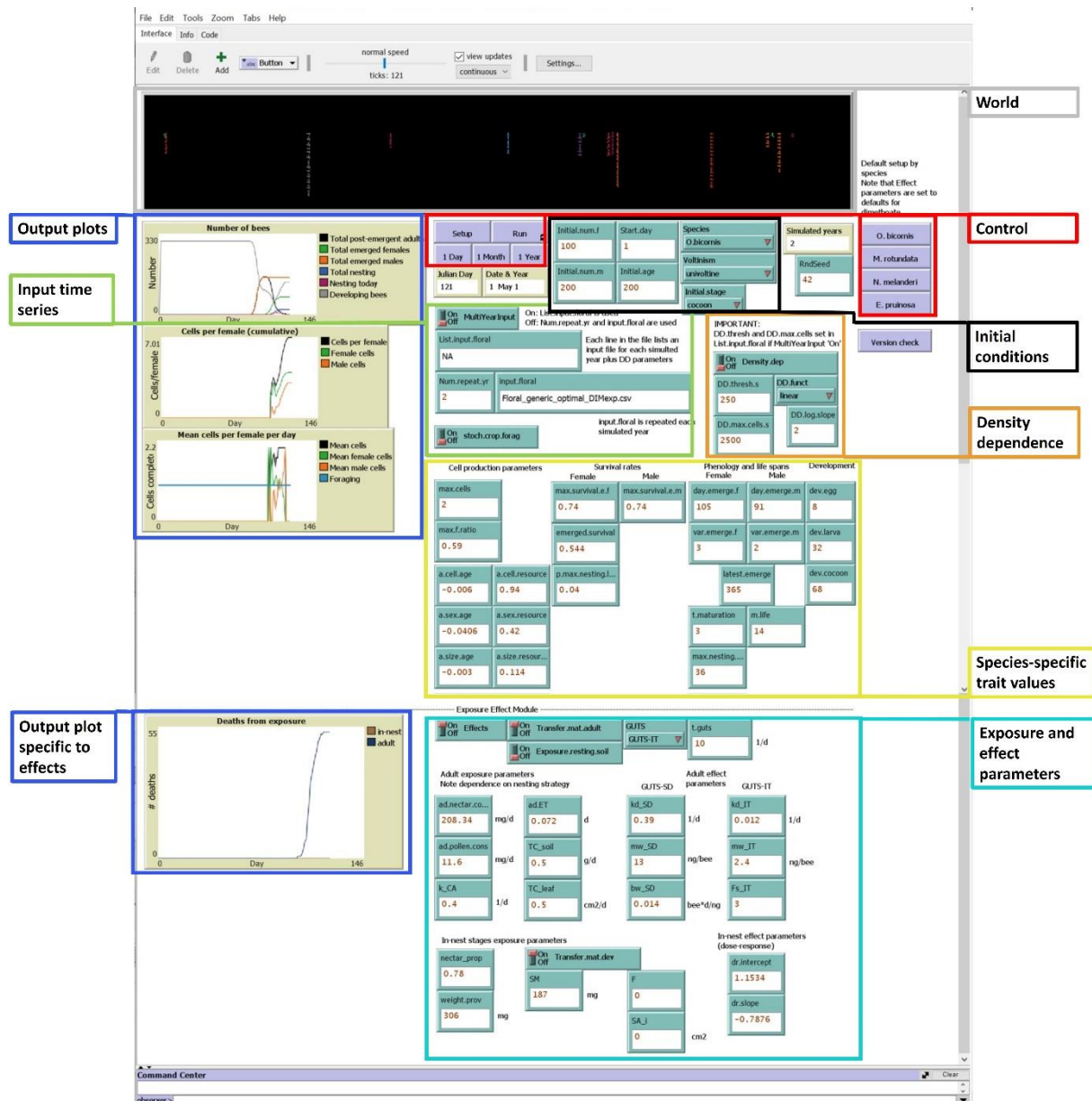
*Figure 1. Screenshot NetLogo interface of the SolBeePop_ecotox model. Colored boxes and descriptions are added and addressed in text below.*

## World

The 'world' shows the bees currently present in the simulation and indicates whether they are postemergent adults (in white) or in an in-nest life stage (random colors). Larger icons indicate females, smaller icons correspond to males. Individuals in in-nest life stages shown in a single column of the same color are the offspring produced by the same female. Note that the model is not spatially explicit, and the bees and their brood are shown in random order on the 'world'.

## Output plots

The output plots show the behavior of the model over time (days since start of the simulation). In the top plot, the number of total bees and bees in various life stages are plotted. The middle plot shows

the average number of brood cells produced across females nesting in the current year plus the numbers by offspring sex. The bottom plot shows the average daily cell production across the currently nesting population. For reference, the foraging availability is also indicated in the plot, foraging availability is read from the input time series and is unitless. It can range between 0 and 1 whereby foraging availability = 0 means that bees cannot forage or no resources are available, foraging = 1 means that optimal foraging conditions occur on a given day. If the ecotox module is used (Effects "On"), an additional output plot shows the cumulative number of bee deaths that occurred due to exposure (in-nest life stages and adults are shown separately in the plot).

Values from all model variables (including all the outputs shown on the interface plots) can be written to file if the model is run using the NetLogo tool BehaviorSpace (https://ccl.northwestern.edu/netlogo/docs).

## Control

The **Setup** button in the left block (indicated with a red box) are used to setup and start a simulation. **Setup** initiates the simulation, reading in all settings on the interface. If settings are changed, **Setup** needs to be called again to take effect. Alternatively, one of species default setups can be used, i.e., buttons **O. bicornis**, **M. rotundata**, **N. melanderi**, or **E. pruinosa**. If clicked, all parameters on the interface are set to generic default values, using the default species-specific trait values (see below) for each species. Subsequently, Setup is run. These options provide a convenient way to achieve default interface settings. Individual values can be changed after using one of the default speciesspecific setup buttons. In this case, **Setup** needs to be clicked again to read the changed settings into the model.

Run the simulation either in increments of single days (**1 Day**), a month (**1 Month**), a year (**1 Year**) or for the entire simulation span (**Run**).

## Initial conditions

The user sets the number of female (**Initial.num.f**) and male bees (**Initial.num.m**) present at the start of the simulation. The **Start.day** is set to the day of year (Julian day) that corresponds to the first day in the simulation. All bees initially present are set to be in the same life stage with the indicated age in days (**Initial.age**). Note that **Initial.age** refers to the days since reaching the indicated life stage (not the total age of the individual).

The species to be simulated is chosen in **Species**. The options included in the current version of SolBeePop include the 7 model species (*N. melanderi, E. pruinosa, M. rotundata, O. bicornis, O. cornifrons, O. cornuta, O. lignaria*). The selection of the species only sets the nesting strategy for all simulated individuals (above-ground or soil nesting) but does not automatically set the speciesspecific trait values. Use the default species-specific setup buttons (see Control) to set traits to default species-specific values. **Voltinism** sets the number of generations per year to one (*univoltine*) or multiple (*multivoltine*). The effective number of generations simulated if set to multivoltine depends on the defined active season and the development times of brood as well as the maturation time of females. The initial stage of all individuals initially present is set by **Initial.stage**. The options include *cocoon*, which summarizes all life stages after feeding is complete but prior to emergence (even in species that do not produce a cocoon). *Emerged* is the life stage after emergence from the nest but prior to the initiation of nesting (in females). If *nesting* is chosen, all females are in nesting stage; this setting does not allow the presence of males upon initialization of the simulation because males die

after the *emerged* life stage in the model. Individuals initially present in the simulation can also be set to *egg* or *larva*, whereby *larva* refers to the larval development stages during which feeding occurs.

Note that simulations are set up to end at the end of a simulated year (corresponding to 31 December). If a start date later than 1 January (**Start.day** = 1) is set, the simulation will run the remaining days of the year and consider this as year 1. For instance, if a simulation is set with **Start.day** = 360 and to run for one year (**Num.repeat.yr** = 1), the simulation stops after 5 days.

Make sure that **Start.day**, **Initial.age** and **Initial.stage** are set to values that could occur together in a population. For instance, if a simulation is set to start on **Start.day** = 1, all model species can be assumed to be in the *cocoon* stage. The initial age should correspond to the estimated average time since the individuals reached the life stage based on the species' active nesting season. Note that the emergence of bees from *cocoon* stage is determined by the phenology trait values (see below), as long as the life stage age is larger than **dev.cocoon**.

## Input time series

If the **MultiYearInput** switch is set to *On*, a file name (csv file) needs to be entered in **List.input.floral**. This input file is a list of csv files that are used by the model for each simulated year. This option makes it possible to simulate multiple years with different time series (e.g., due to different weather and/or resource availability). Note that the total number of years simulated is defined by the number of files in the list (**Num.repeat.yr** and **input.floral** are unused if **MultiYearInput** = *On*).

If the **MultiYearInput** switch is set to *Off*, the number of years in the simulation has to be set in **Num.repeat.yrs** and a file name (csv file) needs to be entered in **input.floral**. If **MultiYearInput** = *Off*, **List.input.floral** remains unused.

Detailed information on the format, generation and use of the input files can be found in the TRACE documentation, Appendix B.

**Stoch.crop.forag** is an option for stochastic foraging on crop vs. off-crop resources by the bees. It only applies if values for *Prop_foraging_crop* in the input time series are set to 0.5 (see TRACE, 2.4.2. Reproduction (nest building)). The option has not been tested systematically or used in simulations presented in the TRACE documentation. We recommend to set **stoch.crop.forag** = *Off*.

## Density dependence

Density dependence can be included in the simulations as an option. Set **Density.dep** = *Off* for simulations without density dependence. In this case, all other settings in this block remain unused. Set **Density.dep** = *On* to include density dependence (see also TRACE, 2.4.3. Density dependence of brood cell production). **DD.thresh.s** corresponds to the threshold number of bees in in-nest life stages in the population. Above this threshold, brood cell production by nesting females is progressively reduced due to increasing brood number. **DD.max.cells.s** corresponds to the hypothetical maximum number of brood cells available for the population. If this number is reached, no further brood cells can be produced by nesting females. **DD.thresh.s** and **DD.max.cells.s** are overridden by year-specific values set in **List.input.floral** if **MultiYearsInput** = *On* (see TRACE, Appendix B, Use of multi-year inputs). Two functions can be used alternatively for the density dependence (*linear* or *log*). Only the *log* function requires the definition of a slope (**DD.log.slope**).

## Species-specific trait (parameter) values

In this block, the species-specific parameters (trait values) are set. Please refer to input parameter table (SolBeePop_ecotox_Tables.xlsx) for description of the parameters and their value ranges.

## Exposure and effect parameters

This block reflects the extension with the ecotox (exposure effect) module. The parameter settings for exposures and effects are applied whereby parameters are organized into a set of parameters defining the exposures and effects of post-emergent adult bees and in-nest life stages. Please refer to TRACE (2.4.4. Exposures and effects of post-emergent females (BeeGUTS), and 2.45 Exposures and effects to in-nest life stages) for the description of the exposure and effect implementation, and to the input parameter table (SolBeePop_ecotox_Tables.xlsx) for description of the parameters and their value ranges. Exposure and effects can be switched off by setting **Effects** to "Off".

# RUN A SIMULATION

- NetLogo needs to be installed (version 6.3.0 used for the model outputs presented).

- Open NetLogo and load SolBeePop_ecotox (File > Open…). Note that the extension file BeeGUTS.nls needs to be present in the same folder as SolBeePop_ecotox.nlogo.

- Set initial conditions, inputs, density dependence and species-specific trait values. See SolBee_ecotox_Tables.xlsx for species-specific values for the model species.

- Make sure that the input files (**input.floral** or **List.input.floral**) are saved in the same path as the SolBeePop_ecotox.nlogo file (or provide the full path in the input field). The generic input files "Floral_generic_optimal.csv" and "Floral_generic_optimal_DIMexp.csv" are provided in the GitHub repository along with the model code. Additional input files that were used for model evaluation and application can be found in the corresponding subfolders.

- Click **Setup**. Note that setup checks for some impossible initial settings or their combinations. If such settings were chosen, the interface gives a warning. In this case, fix the settings and click **Setup** again.

- Alternatively, use one of the species-specific setup buttons, **O. bicornis**, **M. rotundata**, **N. melanderi**, or **E. pruinosa**. If used, default interface settings are applied with species-specific trait values differing according to the selected species. Exposure and effect parameters are set to defaults for dimethoate. The buttons also call Setup. Individual values can be changed after using one of the default species-specific setup buttons. In this case, **Setup** needs to be clicked again to read the changed settings into the model.

- Click **Run** once to run the entire simulation until the end (duration indicated in Simulated years). Simulations can be paused by clicking **Run** a second time. Click (repeatedly) one of the other options in the control block to run the simulation in smaller time increments.

- Simulations stop once the number of years (**Num.repeat.yrs** or number of files listed in **List.input.files**) is reached. Click **Setup** again to start a new simulation.

# VERSION CHECK

The button **Version check** was added to SolBeePop_ecotox.nlogo. The version check can be used if changes were applied to the code. If used, it runs two simulations using the default input files provided in the repository. The outputs of the simulation runs are compared to outputs generated with the version from GitHub. If the outputs are identical, the version check is displayed as successful. If the outputs differ, the version check is displayed as failed.