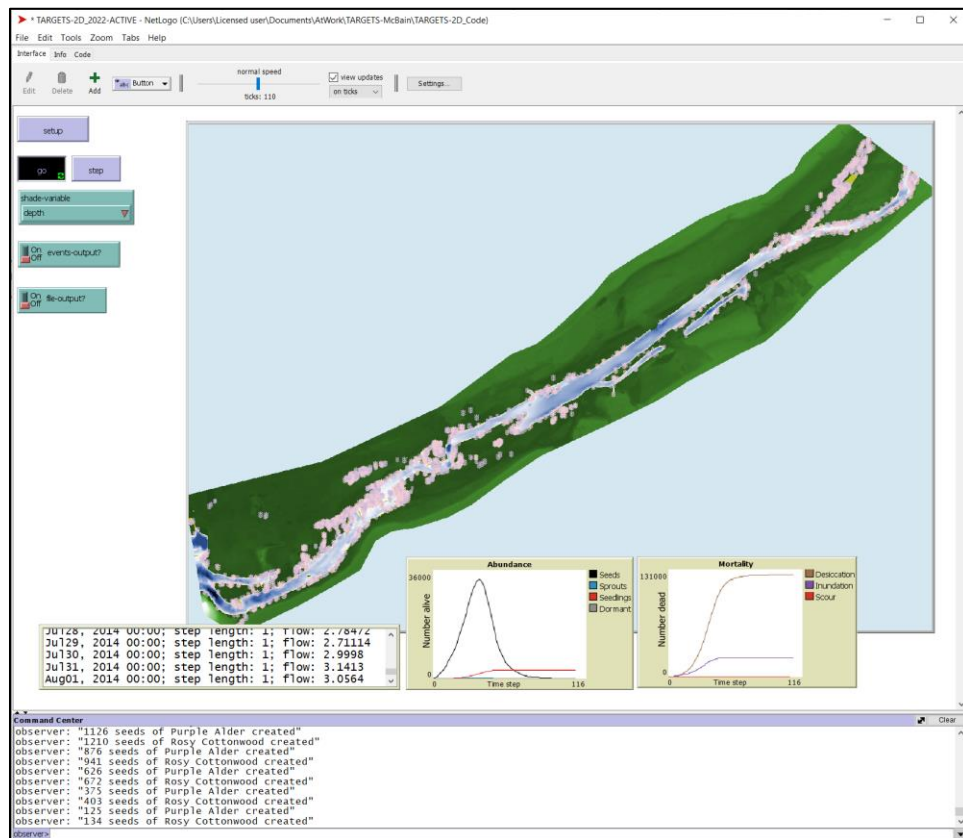


# TARGETS-2D Riparian Vegetation Model



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# 1 Introduction

## 1.1 Report purpose and background

This report describes TARGETS-2D, a new version of the **Tool for Achieving Riparian Germination and Establishment of Target Species**, which is a model of how river flow regimes affect establishment of tree seedlings on riparian habitat. TARGETS-2D differs from previous versions by representing space as a two-dimensional river reach instead of as a line transect.

TARGETS-2D uses the same basic methods for modeling seed establishment and survival as previous versions, e.g., as partially described by Poulsen et al. (2019). However, complete documentation (or source code) of previous versions has not been identified. Therefore, the primary source of methods is the model of Mahoney and Rood (1998), which was also the source for previous versions of TARGETS. The design of TARGETS-2D is also strongly influenced by experience with previous versions and the management questions they were applied to.

Many of the non-biological components of TARGETS-2D are reused from previous two-dimension river management models, especially the InSTREAM 7 trout model (Railsback, Ayllón, and Harvey 2021; Railsback, Harvey, and Ayllón, in prep.) and FYFAM, a frog breeding model (Railsback et al. 2016; Railsback, Harvey, and Ashton 2021).

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## 1.2 Report overview

Sect. 2 provides a complete description of TARGETS-2D, following the “ODD Protocol” of Grimm et al. (2020) for describing individual-based models. The model description starts with an overview of the model’s purposes, entities and scales, and mechanisms (sects. 2.1 to 2.3). Sections 2.5 through 2.7 completely describe how the model is initialized and how its submodels work.

Sect. 3 reports an example parameter sensitivity analysis. That analysis indicates, for one particular application, how strongly each parameter affects the model’s primary results.

The model is implemented in the NetLogo software platform (Wilensky 1999). The software is documented in Sect. 4, which describes installation, the user interface, input and output files, and NetLogo’s automated simulation experiment manager.

## 1.3 Conventions

The following unit conventions are used in the model description and software. Distances and elevations are in meters (m), except that the parameter for root growth are in units of centimeters per day (cm/d). Time is in days (d); and river flows are in cubic meters per second (m<sup>3</sup>/s).

This document uses several text format conventions. Model parameters (constants read from input) are in ***bold and italic*** text. Variables (state variables of model entities; equation variables) are in *italics*. State variables use long names that include the type of entity that the variable belongs to, as in Table 1 and Table 2; temporary variables used in submodel equations have short

symbolic names such as  $E_{gw}$  (cell groundwater elevation). Computer file names, code statements, and input are in Courier font.

## 2 Model Description

### 2.1 Purpose

The purpose of TARGETS is to predict how hydrographs—time series of river flows—and river channel shape and sediment types affect the number and location of riparian tree seedlings. The model addresses tree species that disperse seeds onto riparian areas as those areas are exposed by declining flows, modeling how seed initiation and establishment depend on above- and below-ground water surface elevations. The model is designed to predict where seeds of such species can successfully sprout and survive through their first winter. TARGETS-2D simulates one seed cohort per simulation and ignores interactions among plants; therefore, it is not intended for long-term simulation of riparian forests.

### 2.2 Entities, State Variables, and Scales

This section describes the structure of TARGETS-2D: what things (entities) it represents, what variables characterize each entity, and what spatial and temporal scales it uses. Variables are designated as static or dynamic: static variables represent characteristics assumed not to vary over time and so are constant (e.g., ground surface elevation), while dynamic variables represent characteristics assumed to vary over time and hence are updated during model execution (e.g., flow, water and groundwater surface elevations, plant root depth).

#### 2.2.1 Sites and spatial extent

TARGETS-2D represents one site, a contiguous reach of stream and riparian habitat. The spatial extent of the site is therefore the model's extent. This extent is variable and specified by model input. The site has only one state variable: its flow ( $\text{m}^3/\text{s}$ ).

#### 2.2.2 Habitat cells and spatial resolution

“Cells” represent habitat variation within the site; spatially, the site is made up of rectangular grid of square cells. Habitat conditions can vary among cells but variation within a cell is not represented. All cells are the same size, and this size (the spatial resolution) is specified by the model parameter *patch-width*, representing the width of all cells (m). (This parameter is called *patch-width* because cells are represented as “patches”, NetLogo's built-in square grid cells.)

Because TARGETS-2D assigns the habitat characteristics of each cell from the nearest input node (Sect. 2.5.2), different values of *patch-width* can be used without changing the habitat and hydraulic input. Values of *patch-width* less than the distance between nodes (Sect. 2.5.1) are not recommended because they increase the number of cells without adding information—they would simply produce multiple identical cells, which should have no effect on results. Values of *patch-width* greater than the distance between nodes can be useful because they make the model run faster: the model's execution time depends very strongly on how many cells there are, and increasing *patch-width* reduces the number of cells (in proportion to the square of *patch-width*, so increasing *patch-width* from 1.0 to 2.0 m reduces the number of cells by a factor of 4). Higher values of *patch-width* do of course reduce the level of topographic and hydraulic detail and therefore produce more approximate results. High values of *patch-width* can be useful for, e.g., test runs and model exploration that do not require high resolution.

Cell variables (Table 1) define the elevations of the ground, surface water, and groundwater. Cell locations are defined by NetLogo's built-in patch coordinates *pxcor* and *pycor*, which refer to the cell center and are in units of cell widths. The values of *pxcor* and *pycor* are converted to actual coordinates (m) by multiplying them by *patch-width*. Elevations can be calculated from an arbitrary datum but must be positive.

The variable *cell-shear* is a measure of the shear stress exerted on the streambed by flowing water. Shear stress varies over time with river flow and over space due to variation in bed slope, substrate type, etc. Hydraulic engineers and models use several different measures of shear stress, with different units and magnitudes. (InSTREAM uses the dimensionless Shields stress.) For TARGETS-2D, it does not matter which measure of shear is used as long as the same measure is used in both the input used to determine *cell-shear* (sects. 2.5.2, 2.7.1) and the parameter used to model plant scour from shear (Sect. 2.7.7).

Table 1. Cell variables.

Variable name <sup>1</sup>	Static (S) or dynamic (D)	Type and units	Meaning
<i>cell-elevation</i>	S	real, m	Mean or characteristic elevation of the cell
<i>cell-depth</i>	D	real, m	Mean or characteristic depth of the cell; zero if cell is not submerged
<i>cell-shear</i>	D	real, variable units	A measure of bed shear stress at the current flow, used to model scour (Sect. 2.7.7)
<i>cell-groundwater-depth</i>	D	real, m	Mean or characteristic vertical distance from the ground surface to the groundwater surface; zero if <i>cell-depth</i> > 0
<i>cell-moisture-depth</i>	D	real, m	Mean or characteristic vertical distance from the ground surface to moisture usable to a plant, defined as the top of the “capillary fringe” (Sect. 2.7.1); zero if <i>cell-depth</i> > 0

### 2.2.3 Plants

Plant entities represent tree individuals as they go through the seed to seedling stages. Plants are represented as zero-dimensional objects: points, with locations but no area. Plant state variables (Table 2) represent their development status and root size.

A plant's location is tracked by NetLogo's built-in coordinate variables (*xcor* and *ycor*), which are also the coordinates of the cell the plant occupies. (TARGETS-2D does not represent plant locations at a finer resolution than which cell they are in because it does not include mechanisms—e.g., plant competition for light—that require a finer resolution.)

TARGETS-2D can represent a variable number of plant species, with separate plant parameter values assigned to each species. All plants use the same methods (equations, etc.) but users must

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<sup>1</sup> Cell variables are defined in the `patches-own` code statement. In the code, the *cell-* part of the variable name is omitted, so elevation is simply `elevation`, etc.

provide separate values of all plant parameters for each species. The number of species and their names and parameter values are all specified as user input.

The state variable *plant-stage* identifies which development stage the plant is in. Its value can only be one of these defined stages:

- “Seed” indicates a viable, unsprouted seed. Model plants are created as seeds newly landed on the ground, which transition to the next stage at the time when early roots are assumed to be formed. The seed stage includes seed water imbibement, germination, and early root formation.
- “Sprout” indicates a plant that has begun growing roots, with cotyledons that have emerged and begun to photosynthesize; leaves also form in this stage. This stage ends at the time at which roots are assumed able to grow downwards as groundwater elevations decrease.
- “Seedling” refers to a plant actively producing leaves and growing roots at a rate potentially capable of remaining in contact with declining groundwater elevations.
- “Dormant seedling” indicates a seedling that has entered dormancy for its first winter and stopped root growth.

Table 2. Plant variables.

Variable name <sup>2</sup>	Static (S) or dynamic (D)	Type and units	Meaning
<i>plant-species</i>	S	discrete; text	Name of the plant’s species
<i>plant-stage</i>	D	discrete; text	Values are: “seed,” “sprout,” “seedling,” and “dormant seedling”
<i>plant-root-depth</i>	D	real, m	Vertical distance from ground surface to the plant’s root tip, assumed equal to the depth to which the plant can obtain water
<i>plant-age-in-days</i>	D	real, d	Time in days since the plant was deposited as a seed

#### 2.2.4 Temporal extent and resolution

TARGETS-2D uses a variable time step (temporal resolution). The model is expected to typically use a one-day time step because flow data are typically available as daily mean values and because key model processes (changes in groundwater elevation and plant growth) occur at rates such that daily changes are meaningful but shorter time steps are not necessary to capture important effects. However, shorter time steps can be used to evaluate significant sub-daily flow fluctuations such as those that result from hydropower operations or sun-driven snowmelt. The time step is user-controlled via the flow input file: a new time step begins at each date and time

<sup>2</sup> Plant variables are defined in the `plants-own` code statement.

in that file (Sect. 2.7.1). All model processes use rates and probability values adjusted for time step length, so time step length by itself has no effect on results.

The duration (temporal extent) of a model run is specified by parameters setting the dates on which a simulation starts and ends: *run-start-date* and *run-end-date* (M/d/yyyy format). The first time step begins at midnight at the start of *run-start-date*, and the last time step ends at midnight at the start of *run-end-date*. Therefore, the last time step is labeled with the date just before *run-end-date*: if *run-end-date* is “7/1/2024”, the last time step will represent June 30.

The model can be executed for any duration but simulates only one plant cohort: seed deposition is simulated only in the first year. The model can be run for more than one year, but seeds are created only in the calendar year that *run-start-date* occurs in. Typically, the model is run from the onset of seed deposition in spring through the following winter and spring high flows.

### 2.3 Process Overview and Scheduling

This section describes what happens, in what order, during simulations. On each time step, the following actions are executed in sequence<sup>3</sup>. Each action uses one or more of the submodels described fully in Sect. 2.7. Within each action, the order in which plants execute their submodels is arbitrary because there are no interactions among plants that would be affected by execution order.

1. Time and habitat updates (Sect. 2.7.1): The simulated date and time at which the time step ends are determined from the time series input. The river flow is input and used to update all the dynamic cell variables.
2. Plant stage transitions (Sect. 2.7.2): Each plant determines whether it is ready to change to the next development stage and, if so, makes the transition.
3. Seed deposition: The number of new seeds deposited during the time step is calculated. That number of seeds are created and distributed over space (Sect. □). Seed deposition is scheduled after plant stage transitions to prevent newly deposited seeds from changing stage in their first time step.
4. Root growth: Plants in the seedling development stage grow their roots (Sect. 0).
5. Survival: Each plant is exposed to mortality risks of desiccation (for seeds, equivalent to losing viability), inundation, and scour; with risk depending on cell conditions and plant stage (sects. 2.7.5–2.7.7).
6. Output updates: The state of the model and its plants are written to output files and graphical displays (described in Sect. 0).

### 2.4 Design Concepts

The ODD Protocol’s “design concepts” describe important characteristics of individual-based models not captured by traditional mathematics.

**Basic principles:** TARGETS implements the “box model” concept of Mahoney and Rood (1998), a conceptual model of how riparian seed establishment depends on flow regime. A rectangular “box” region in a plot of elevation vs. time indicates conditions under which

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<sup>3</sup> The schedule of events is coded in the `go` procedure.

establishment is possible because the timing and location of seed deposition coincide with groundwater levels declining at a rate that root growth can keep up with.

**Emergence:** The primary outputs of TARGETS-2D are the number and spatial distribution of seedlings (including dormant ones) remaining alive at the end of a simulation, which can be used to infer where plant establishment is likely under the simulated flow regime. Potentially important secondary results include ages and root sizes of surviving seedlings. These outputs all emerge from complex interactions among landscape topography, flow regime, and the distribution of seeds over time and space.

**Adaptation:** Plant individuals make one very simple adaptive decision, in the seedling development stage. Seedlings decide at each time step whether to continue root growth, considering whether their roots have reached the groundwater table (Sect. 0).

**Objectives, Learning, Prediction:** These concepts are not used.

**Sensing:** Plants are assumed able to sense one variable, whether their roots are below the groundwater table.

**Interaction:** There is no interaction among plants in TARGETS-2D. The survival and development of each plant is assumed unaffected by interactions such as competition for light or nutrients. This assumption is made to avoid substantial additional complexity and because the model is focused on small, young, plants for which competition is relatively unimportant.

**Stochasticity:** Overall, TARGETS-2D is not a highly stochastic model. In seed deposition (Sect. □), the location of each seed is chosen randomly; however, simulating large numbers of seeds assures that they are evenly distributed over the simulated space. Mortality due to desiccation and inundation are simulated as stochastic processes (sects. 2.7.5, 2.7.6), but survival rates are typically not highly affected by randomness unless flows are highly variable.

**Collectives:** This concept is not used.

**Observation:** Simulations are observed via output at the aggregate and individual levels. Output files (Sect. 4.7) provide both summary statistics (e.g., number of surviving plants of each species and development state) and data on simulated individuals (e.g., their location and root depth). The graphical interface allows visual observation of plant distributions over the riparian landscape, overlaid with several views of key habitat variables (Sect. 0).

## 2.5 Initialization

Initialization refers to how model entities are created and have their state variables set before simulations begin<sup>4</sup>.

### 2.5.1 Spatial extent and cell creation

The number of cells and the model's spatial extents, and the static cell variables, are determined from an input file that describes "nodes". Nodes are points in horizontal space where habitat input—elevation, depth, etc.—is provided. Nodes are typically created from hydraulic model

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<sup>4</sup> The procedure `setup` codes the sequence of events during initialization.

output and can be the hydraulic model mesh's nodes, a regular square grid, or an irregular grid with denser nodes near the active channel and sparser nodes in the floodplain. Model cells, in contrast, are always a grid of uniform squares; each cell uses the habitat variables of the node nearest to its center.

Input files provide, for each node:

- A node number, a unique positive integer that must be consistent across input files.
- Its X and Y coordinates, in units of meters with values increasing from west to east and south to north (following UTM conventions). The coordinate system's origin has no effect; it need not be within the simulated space.
- Its elevation, in meters. Elevations can use an arbitrary datum.
- Values of any other static cell habitat variables (TARGETS-2D currently has none).
- Two lookup tables, used to calculate depth and bed shear stress from flow. These tables are typically generated by hydraulic models.

The spatial extent is calculated from the node coordinates<sup>5</sup>. The total extent of the simulated space in X and Y dimensions is determined as the difference between the maximum and minimum node coordinates. The number of cells in each dimension is calculated by dividing the total extent by the value of *patch-width*, rounding up to the next integer if necessary. A rectangular grid of cells is then created, with the distance between adjacent cell centers equal to *patch-width*.

Finally, cells that are not close to any nodes are dropped from the model. If the distance between any cell's center and the nearest node exceeds the value of the model parameter *max-node-distance* (m), then the cell is dropped. This parameter should have a value just less than the highest distance between adjacent nodes; if nodes are on a grid 2 m apart, e.g., *max-node-distance* should be ~1.8 m..

### 2.5.2 Cell initialization

Cells are initialized by setting their static variables (Table 1) and creating the lookup tables used to calculate cell depth and shear stress (Sect. 2.7.1)<sup>6</sup>. Each cell identifies the node closest to its center. (If more than one node is the same distance from the cell, one is chosen randomly.) The cell's static variable values are then copied from that node's input.

The method for creating the depth and shear lookup tables is that used by the FYFAM model and fully described in the FYFAM documentation (Sect. 2.7.1 of Railsback, Harvey, and Ashton 2021). This method estimates depths and shear stresses below and above those in the node's lookup table input but does not estimate which cells become dry at flows below those in the input nor submerged at flows higher than those in the input. Therefore, the node lookup table input should include flows as low and as high as any to be simulated.

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<sup>5</sup> This calculation is in procedure `read-geom`.

<sup>6</sup> Cell variables are read in the procedure `read-cell-variables`. The depth lookup tables are created in `read-hydraulics`.

## 2.6 Input Data

TARGETS-2D uses one set of time-series input to drive simulations: river flows. This input provides a series of date and time values and their associated flow rate. This input not only provides flows but also determines a simulations' time steps (Sect. 2.7.1).

## 2.7 Submodels

This section completely describes how each action in the model's schedule (Sect. 2.3) is executed. The submodels are presented in approximately the order in which they are executed each time step.

### 2.7.1 Time and hydraulic updates

The first action on each time step is to update the simulated time and hydraulic habitat: determine the times at which the new time step begins and ends, read in the river flow, and update cell variables<sup>7</sup>.

The date and time at which the new time step ends, and its river flow, are obtained from the flow input file. Because the rest of this submodel is computationally expensive, it is skipped if the new flow value differs from the previous value by less than 0.01% (if the absolute value of the change in flow divided by the previous flow is less than 0.0001).

Next, each cell updates its depth (*cell-depth*) and shear stress (*cell-shear*) from the new flow value<sup>8</sup>. Cell depth and shear are updated by interpolating (or extrapolating, for extreme flows) values from the cell's lookup tables. The interpolation method is that used for depth in the FYFAM frog model (Sect. 2.7.1 of Railsback, Harvey, and Ashton 2021).

After all cells have updated their depth, each cell updates its groundwater variables *cell-groundwater-depth* and *cell-moisture-depth*<sup>9</sup>. (Because these variables can depend on the depth of nearby cells, they can only be updated after all cells have updated their depth.) For submerged cells (*cell-depth* > 0), *cell-groundwater-depth* and *cell-moisture-depth* are set to zero. For exposed cells (*cell-depth* > 0), the first step is identifying the groundwater surface elevation at the cell,  $E_w$ .

TARGETS-2D does not assume that values of  $E_w$  will be available for dry cells from hydraulic simulations or other sources; instead, it approximates them from river flow and the water surface elevation of submerged cells. One potential approach is approximating the value of  $E_w$  for each unsubmerged cell as the water surface elevation (also  $E_w$ ) of the nearest submerged cell. However, that approach is computationally demanding and results in very slow habitat updates. Instead, TARGETS-2D updates  $E_w$  from the values of adjacent cells, starting with cells adjacent to the wetted channel and working away from it. TARGETS-2D uses this algorithm:

1. For all cells with *depth* = 0.0, set  $E_w$  to -999 and set an update flag *updated?* to false. For cells with *depth* > 0.0, set  $E_w$  to cell-elevation + *depth* and set *updated?* to true.

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<sup>7</sup> Time and habitat updates are programmed in procedures `update-habitat`, `update-hydraulics-for`, and `update-groundwater`.

<sup>8</sup> Depth calculations are in procedure `update-hydraulics-for`.

<sup>9</sup> Groundwater calculations are programmed in `update-groundwater`.

2. Identify the cells with *updated?* = false and at least one adjacent cell with *updated?* = true. (“Adjacent” cells are the up-to-eight cells sharing an edge or corner.) These will be cells adjacent to the wetted channel.
3. For each cell identified in step 2, set  $E_w$  to the mean value of  $E_w$  of its adjacent cells having *updated?* = true.
4. For each cell updated in step 3, set *updated?* to true.
5. Repeat steps 2-4 until all cells are updated.

This algorithm ensures that groundwater elevations are updated from the wetted channel toward the higher floodplain, one row of cells at a time.

After  $E_w$  is updated for all cells, *cell-groundwater-depth* is calculated as *cell-elevation* -  $E_w$ . The value of *cell-moisture-depth* is set to *cell-groundwater-depth* minus the value of the parameter ***cap-fringe-height*** (m), which represents the typical vertical distance between the groundwater surface and the upper limit of capillary moisture. *Cell-moisture-depth* is set to zero if that difference is less than zero (the depth to groundwater is less than *cap-fringe-height*).

It can be possible for a cell’s value of  $E_w$  updated this way to be greater than *cell-elevation*, in low-elevation areas not connected to the main channel (where hydraulic simulations are likely to predict zero depth even though the ground surface is below the nearest water surface). In such cases, TARGETS-2D sets *depth* to  $E_w$  - *cell-elevation*, and *cell-groundwater-depth* and *cell-moisture-depth* to zero.

(Sect. 4.7.4 describes optional output of cell water elevations that can be useful for testing hydraulic input and methods, and for understanding model results.)

### 2.7.2 Plant stage transitions and dormancy

This submodel controls when each plant transitions to the next development stage<sup>10</sup>. It is executed by each plant on each time step. Here, we used the terms “seed”, “sprout”, etc. for plants with *plant-stage* equal to “seed”, “sprout”, etc.

The first step in this submodel is to update the plant’s value of *plant-age-in-days*. This variable is set to the number of days (including fractions, if time steps are not one-day) between the time step on which the plant was created and the current time step (using the date and time at the end of these time steps).

Plants start as seeds and transition to sprouts when they have had time to absorb water, germinate, and form a root. This time is represented simply as a constant specified by the parameter ***plant-seed-to-sprout-time*** (d), plus the requirement that a seed’s cell must be moist (i.e., *cell-moisture-depth* is zero) for sprouting to occur. If the current simulation time equals or exceeds the time at which a seed was deposited plus ***plant-seed-to-sprout-time*** days, and *cell-moisture-depth* is zero, then the seed becomes a sprout.

Likewise, the transition from sprouts to seedlings is represented as requiring a constant time, equal to the parameter ***plant-sprout-to-seedling-time*** (d), with the requirement that the cell is

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<sup>10</sup> This submodel is coded in the procedure `update-stage`.

moist. If the time (in days) between when a plant became a sprout and the current simulation time equals or exceeds *plant-sprout-to-seedling-time*, and *cell-moisture-depth* is zero, it becomes a seedling.

The final transition is referred to as “dormancy”, when plants stop growth in autumn. Dormancy of all plants of a species is assumed to happen on one day, its date specified by the plant parameter *plant-dormancy-day* (M/d). On the first time step on or after the day specified by this parameter, the following transitions occur:

- All seedlings of the species transition to dormant seedlings;
- Any sprouts of the species also transition to dormant seedlings, and have their value of *plant-root-depth* set to 1.0 cm (so the scour survival method of Sect. 2.7.7 does not produce division by zero); and
- Any remaining seeds of the species die of desiccation (Sect. 2.7.5).

### 2.7.3 Seed deposition

This submodel determines how many seeds are created and then initializes the seeds and places them in the simulated space. The submodel is executed for each plant species, each time step.

There are two alternative methods for determining where seeds are placed: distributing them uniformly over all cells vs. representing the “mother” trees that produce seeds and how seeds disperse from those trees. If the model parameter *mother-tree-input?* is set to TRUE, then the second method is used; if FALSE, then the first method is used. In the second of these methods, not all seeds are deposited in the model space; we therefore refer separately to the number of seeds “created” and the number “deposited” on model cells and subsequently simulated; the number deposited can be less than the number created.

#### 2.7.3.1 Uniform deposition

This option simply assumes seeds are uniformly deposited over the model space (all the cells).

The timing of seed deposition is controlled by a set of plant parameters that have separate values for each species. The number of seeds created each year for an entire site is provided by the parameter *seed-number-per-year*. The number of seeds created each time step is controlled by a triangular distribution of deposition rate over time, illustrated in Figure 1. This distribution is defined by parameters *seed-creation-start-day*, *seed-creation-peak-day*, and *seed-creation-end-day*, the days (month and day, M/d) on which seed creation starts, peaks, and ends. The duration of the seed deposition period ( $b$  in Figure 1) is equal to the number of days between *seed-creation-start-day* and *seed-creation-end-day*. The height  $h$  of the triangle is calculated so that the triangle’s area is equal to the total number of seeds created:  $h = (2 \text{ seed-number-per-year}) / b$ .

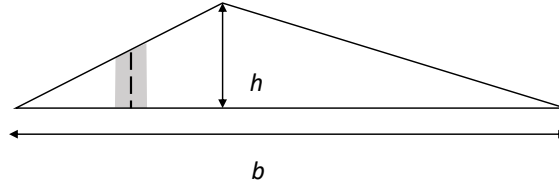


Figure 1. Triangular distribution of seed creation rate over time. The area of the grey trapezoid represents the number of seeds created in one time step; the dashed vertical line indicates the time mid-way through the time step.

The number of seeds created each time step ( $N$ ) is calculated using this algorithm:

- If the current time step starts before midnight at the beginning of *seed-creation-start-day*, no seeds are created ( $N = 0$ ).
- If the current time step ends before midnight at the beginning of *seed-creation-end-day*, then  $N = 0$ .
- If the current simulated calendar year is later than the year that simulations started (as defined by *run-start-date*), then  $N = 0$ . This rule limits each model run to one seed cohort per species; multiple years of seed deposition cannot be simulated.
- Otherwise,  $N$  is set to the time step length ( $d$ ) times the height of the triangle at a time corresponding to the middle of the time step.

For time steps that do not span the peak deposition time (midnight at the beginning of *seed-creation-peak-day*), this calculation of  $N$  is equivalent to using the area of a trapezoid defined by the triangle heights at the beginning and end of the time step (the grey trapezoid in Figure 1). For time steps that do span the peak creation time, this method is an approximation that can cause the total number of seeds in a year to not exactly equal *seed-number-per-year*.

The submodel then creates  $N$  new seeds and “deposits” each by:

- Placing it in a cell selected randomly from all cells, with equal probability per cell regardless of whether cells are submerged or otherwise unsuitable for sprouting. There is no limit on how many seeds can be in a cell.
- Setting its value of *plant-stage* to “seed”.
- Setting its value of *plant-root-depth* to 0.0.
- Setting *plant-age-in-days* to 0.0 days.

#### 2.7.3.2 Mother tree deposition

This option represents how seeds are dispersed from individual “mother” trees that produce them. Any number of mother trees can be represented. The method requires input for each mother tree specifying:

- Its species.
- Its location, as X and Y (east and north) coordinates in the same coordinate system used for habitat nodes (Sect. 2.5.1). This location does not need to be within the area represented by model cells—mother trees can be outside the model’s simulated space.

- The total number of seeds created by the tree.
- The mean dispersal distance: the mean of a random exponential function used to determine the distance from the mother tree to where each seed is deposited. This mean distance could be chosen to vary with tree height or other characteristics that affect dispersal distances.
- The mean and standard deviation of a random normal distribution that determines the compass heading (0 to 360°, with 0° being north) from the mother tree to the deposition site of each seed. For example, a mean of 180° and standard deviation of 20° results in 95% of seeds being deposited between 140° and 220° (mean  $\pm$  two standard deviations) from the mother tree.

On each time step, seeds are created by each mother tree. The number of seeds created is determined using the same method as in the uniform distribution approach except that a separate triangular distribution (Figure 1) is used for each mother tree, with its height  $h$  calculated from the total number of seeds created by the tree.

The deposition site of each seed is determined by:

- Drawing a dispersal distance  $D$  from a random exponential distribution with the tree's mean distance.
- Drawing a dispersal direction  $H$  from a random normal distribution with the tree's mean and standard deviation for direction.
- Identifying the deposition site, a point  $D$  meters from the tree's location in direction  $H$ , and determining if that site is within one of the model's cells.
- If the deposition site is not within a model cell, the seed is not deposited or further represented by the model. Therefore, the number of seeds deposited using this method is typically much lower than the number of seeds created by the mother trees.
- If the deposition site is within a model cell, the seed is placed in that cell and its state variables initialized as in the uniform deposition method (Sect. 2.7.3.1). (There is no limit on how many seeds can be deposited in a cell each time step.)

This method deposits seeds in clusters around each tree, though the clusters can be extensive. The exponential function places most seeds near the mother tree but some seeds are placed many times the mean distance away (Figure 2). High standard deviations in direction can produce near-circular clusters.

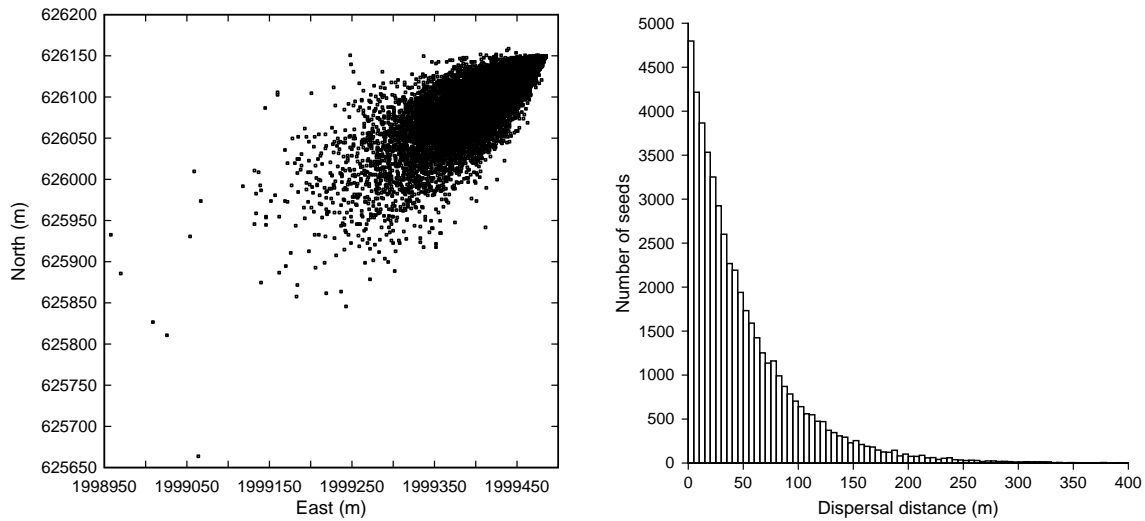


Figure 2. Example seed deposition from mother trees. Left: deposition sites of 50,000 seeds from a mother tree at location 1999485, 626150, with mean dispersal distance of 50 m and heading mean and standard deviation of 230° and 10°. Right: histogram of the dispersal distances, with bin width of 5 m.

#### 2.7.4 Root growth

This submodel represents the rate at which seedling roots grow downwards: how a plant's value of *plant-root-depth* changes. It is executed once per time step, only by plants with *plant-stage* equal to "seedling"<sup>11</sup>.

Root growth is modeled as a constant daily rate of growth in the downward (toward groundwater) direction. Growth for a time step is (a) the parameter *plant-root-growth-rate* (cm/d), (b) divided by 100 to convert its units of cm/d to m/d, and (c) multiplied by the time step length (d).

However, TARGETS-2D assumes that roots do not grow when growth is not necessary to obtain water. This assumption is based on field observations indicating that (a) seedling roots typically do not extend below the water table at lowest summer flow, and (b) seedlings higher on a bank typically have longer roots than do seedlings closer in elevation to the water table. The model assumes roots grow through the capillary fringe but do not grow when the groundwater surface is reached: on any time step when *plant-root-depth* exceeds *cell-groundwater-depth*, then no growth occurs and *plant-root-depth* is unchanged. (Growth resumes if groundwater depth declines past root depth.)

#### 2.7.5 Survival of desiccation

The survival submodels (sects. 2.7.5 through 2.7.7) represent plant mortality due to several causes<sup>12</sup>. They are each executed by each plant on each time step.

<sup>11</sup> Root growth is programmed in the procedure `grow-roots`.

<sup>12</sup> All the survival submodels are programmed in the procedure `survive`.

For each of these kinds of mortality, survival is simulated by first calculating a daily survival probability  $S$  that depends on the states of the plant and its cell. Then the daily probability  $S$  is converted to a probability of surviving the time step, in case time steps of other than one-day length are used; this probability is simply  $S^t$  where  $t$  is the time step length in days. Then whether the plant survives or dies is determined stochastically, as a Bernoulli trial with  $S^t$  as the probability of survival.

“Desiccation” refers to mortality due to lack of moisture. (Previous versions of TARGETS referred to this as “drought” mortality.) For seeds, desiccation mortality is essentially non-viability: the seed may physically still exist but, upon desiccation, is no longer able to sprout and therefore removed from the model. Sprouts and seedlings are assumed to need water and therefore die rapidly when not in contact with groundwater or the capillary fringe, with the rate of mortality dependent on development stage.

Seeds are assumed subject to desiccation if the ground surface is not moist—if *cell-moisture-depth* is greater than zero. Our primary basis for modeling seed desiccation is the seed viability study of Stella et al. (2006). That study evaluated the percentage of seeds remaining viable (capable of sprouting) after being stored in dry conditions for 5 days and then at 2-week intervals for up to ~60 days. They studied Fremont Cottonwood (*Populus fremontii*), Goodding’s Black Willow (*Salix gooddingii*), and Narrowleaf Willow (*S. exigua*). Their results (Fig. 2 of Stella et al. 2006) show a logistic relation between desiccation time and viability, with viability remaining high (80-100% of seeds) for a week or more, then declining steeply with time, but (for cottonwood and Narrowleaf Willow) remaining above zero at the end of the experiment.

By treating the viability results of Stella et al. (2006) as the percentage of seeds that have not died of desiccation, we can model seed desiccation as a daily survival probability that decreases linearly with seed age. The relation between seed age and daily survival probability is defined by the parameter ***plant-surv-desic-seed-S50***, the daily survival probability for a seed with age (*plant-age-in-days*) of 50 days. The daily probability of a seed surviving desiccation  $S_D$  is therefore:  $S_D = 1.0 + m \times \text{plant-age-in-days}$ , where the slope  $m = (\text{plant-surv-desic-seed-S50} - 1) / 50$ . If the value of  $S_D$  is less than 0.0, it is set to 0.0.

This formulation produces a logistic-like decline in percentage viability that can be fit to the observations of Stella et al. Doing so provides values of ***plant-surv-desic-seed-S50*** = 0.78 for Fremont Cottonwood and 0.77 for Narrowleaf Willow.

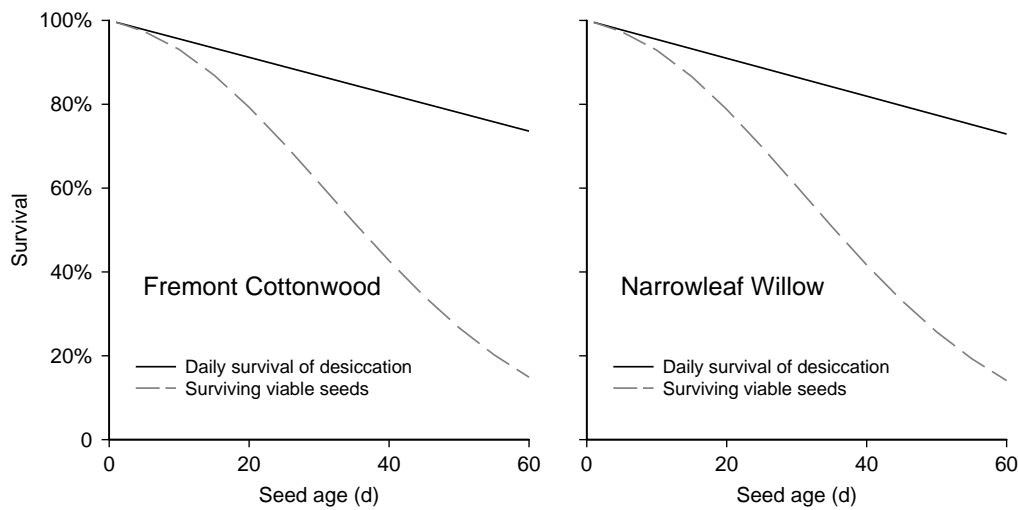


Figure 3. Seed desiccation relations for Fremont Cottonwood and Narrowleaf Willow. The “Surviving viable seeds” curve is comparable to the “percent germination” values in Fig. 2 of Stella et al. (2006).

Sprouts are also assumed subject to desiccation if *cell-moisture-depth* is greater than zero. Their daily probability of surviving without moisture is the parameter *plant-surv-desic-sprout*.

Seedlings are assumed subject to desiccation when their roots are not in contact with the capillary fringe or groundwater: on time steps when their value of *plant-root-depth* is less than *cell-moisture-depth*. On such time steps, the daily survival probability is the parameter *plant-surv-desic-seedling*.

Dormant seedlings are assumed unaffected by desiccation.

#### 2.7.6 Survival of inundation

Inundation refers to the effects of a plant’s cell being underwater (*cell-depth* > 0.0), other than scouring of seedlings, which is treated separately. Those effects include being floated and washed away, drowning (water preventing gas exchange, etc.), and reduced light availability.

Inundation is assumed completely fatal for seeds and sprouts because they are easily washed away. Plants in those stages are assumed to die on any time step when *cell-depth* is greater than zero. Therefore, seeds initially deposited in the water die immediately.

Seedlings and dormant seedlings are assumed able to survive temporary inundation that does not induced scour. Auchincloss et al. (2012) studied inundation of Fremont Cottonwood, finding survival to: (a) be minimal when only roots were submerged, (b) decrease with the duration of inundation, (c) decrease with temperature (11-18°C vs. 18-25° treatments), and (d) be unaffected by seedling age (6 vs. 10 weeks). Because TARGETS does not address temperature directly, we do not model the temperature effect on inundation survival but it can be represented by selecting parameter values appropriate for a site’s temperature regime.

Survival of seedlings and dormant seedlings when inundated is modeled as a Bernoulli trial with daily survival probabilities equal to *plant-surv-inund-seedling* and *plant-surv-inund-dormant*. We define a plant to be inundated when its cell's depth equals or exceeds the plant's root depth ( $cell\text{-}depth \geq plant\text{-}root\text{-}depth$ ), a simple approximation of when depth is sufficient to impair gas and light transfer in the stem and leaves.

Seedlings are assumed less able to survive inundation than dormant seedlings, because they are growing and depend on light and respiration, which inundation interrupts. We estimated a value of 0.96 for *plant-surv-inund-seedling* by fitting the Fremont Cottonwood observations of Auchincloss et al. (2012; mortalities of 22%, 50%, and 71% at 1, 2, and 4 weeks submergence, apparently across both temperature treatments). We estimated a value of 0.99 for *plant-surv-inund-dormant* by assuming mortality of dormant seedlings is 1/3 the values observed by Auchincloss et al. for seedlings. These values produce mortality from 100 days of inundation of 98% for seedlings and 63% for dormant seedlings.

### 2.7.7 Survival of scour

Scour mortality represents the effects of water velocity and shear stress. It applies only to seedlings and dormant seedlings because seeds and sprouts would be killed by inundation before suffering from scour. Scour mortality represents multiple actual processes, including plants being pulled out by the force of water on their stems and leaves, scouring of the sediment in which plants are rooted, and impact damage to stems and leaves from debris in the water. Riparian plant scour has been studied and modeled in detail, e.g., by Pollen and Simon (2005) and Bankhead et al. (2017). TARGETS-2D uses a highly simplified approach that avoids the need for complex assumptions and inputs while still making scour survival depend on the magnitude and timing of high-flow events.

Scour mortality is assumed to be a function of both hydraulic shear stress, which reflects the force of water on both plants and sediment, and seedling root depth, with longer roots offering higher resistance to scour. The formulation is based on (a) the relation between root diameter and the shear stress needed to break roots of Bankhead et al. (2017) and (b) an empirical relation between root depth and root diameter developed from extensive field observations (HVTFD 2021). The HVTFD observations were of several riparian tree species, especially willow, with root depths from 0.5 to over 300 cm. The formulation assumes scour happens whenever the ratio of shear to root depth ( $cell\text{-}shear / plant\text{-}root\text{-}depth$ ) is above a threshold. That threshold is the parameter *plant-surv-shear-threshold*; the analysis of HVTFD (2021) produced a value of 385 Pascals/m. The relationship between root depth and strength differs among plant types (Bankhead et al. 2017).

There are a variety of shear stress measures and units that could be used to model scour survival. The simple threshold approach used by TARGETS allows the use of any shear measure as long as the units of *plant-surv-shear-threshold* are compatible with those of the data used to model shear in each cell (Sect. 4.4.2).

## 2.8 Parameter Summary

All model parameters are briefly described in Table 3. The table includes example parameter values we assembled for two species.

Table 3. TARGETS-2D parameters.

Parameter	Meaning and units	Example value	
Global			
<i>run-start-date</i>	The date on which the simulation starts (M/d/yyyy)	5/1/2010	
<i>run-end-date</i>	The last date simulated (M/d/yyyy)	6/30/2011	
<i>mother-tree-input?</i>	true if seed dispersal is to be non-uniform, using input on individual mother trees; otherwise false	false	
<i>patch-width</i>	Width of square habitat grid cells, m	1.0	
<i>max-node-distance</i>	Maximum distance of cells from an input node, m	1.2	
<i>cap-fringe-height</i>	Height of usable moisture above groundwater surface (m)	0.20	
Plant (separate values for each species)			
<i>species-name</i>	Name of plant species (text)	“Fremont cottonwood”	“Narrowleaf willow”
<i>ind-plant-output-dates</i>	For each species, a list of dates on which individual plant output is written	(list "7/1/2018" "10/31/2018" "6/30/2019")	(list "7/13/2018" "10/31/2018" "6/30/2019")
<i>seed-number-per-year</i>	Number of seeds deposited per year	3.0E06	5.0E05
<i>seed-creation-start-day</i>	Day on which seed deposition begins (M/d)	5/8	6/1
<i>seed-creation-peak-day</i>	Day on which seed deposition rate peaks (mode of the triangular distribution of deposition rate over time; M/d)	5/24	6/21
<i>seed-creation-end-day</i>	Day on which seed deposition ends (M/d)	6/4	7/11
<i>plant-seed-to-sprout-time</i>	Time required for seeds to become sprouts (d)	2.0	2.0
<i>plant-sprout-to-seedling-time</i>	Time required for sprouts to becomes seedlings (d)	19	19
<i>plant-dormancy-day</i>	Day on which seedlings become dormant seedlings (M/d)	10/31	10/31

<b><i>plant-root-growth-rate</i></b>	Maximum rate at which roots can grow downward (cm/d)	2.5	1.0
<b><i>plant-surv-desic-seed-S50</i></b>	Daily probability of seeds surviving desiccation when ground surface is not moist, at seed age = 50 d	0.78	0.77
<b><i>plant-surv-desic-sprout</i></b>	Daily probability of sprouts surviving desiccation when ground surface is not moist	0.1	0.1
<b><i>plant-surv-desic-seedling</i></b>	Daily probability of seedlings surviving desiccation when root is not in contact with groundwater or capillary fringe	0.5	0.5
<b><i>plant-surv-inund-seedling</i></b>	Daily probability of seedlings surviving inundation when submerged	0.96	0.96
<b><i>plant-surv-inund-dormant</i></b>	Daily probability of dormant seedlings surviving inundation	0.99	0.99
<b><i>plant-surv-shear-threshold</i></b>	Ratio of shear stress to root depth above which seedlings and dormant seedlings die of scour (Pascals/m)	385	385

### 3 Parameter Sensitivity Analysis<sup>13</sup>

#### 3.1 Analysis methods

This section describes a set of simulation experiments that examined how strongly individual parameters affect the primary results of TARGETS-2D. There are many kinds of parameter sensitivity analyses and methods for implementing them; we used a very simple approach.

We analyzed one parameter at a time, running the model once for each parameter value over a range of feasible values. All other parameters were kept at their standard value. Results are presented graphically, as plots of model results (number of seedlings alive at the end of a simulation) vs. parameter value. The slopes of these plots are the primary measures of sensitivity: the higher the slope, the stronger the effect of the parameter. Higher coefficients of correlation  $R^2$  also indicate a stronger (relative to the model's stochasticity) or more linear parameter effect.

Parameter sensitivity can vary among simulated sites and hydrographs; for example, parameters for scour mortality can have no effect in simulations with no flow pulses. We used an example study site with a fairly complex channel, illustrated in Figure 20. Simulations ran for over one year, starting on May 1, so they include the seed dispersal period through most of the following winter-spring high flow season. Of the available flow years 2014-19, we chose 2018 (ending on May 31, 2019) because it had a characteristically steep flow recession in spring and early summer, and moderately high flows in late October that could cause inundation or scour mortality (Figure 4). We simulated one species, Fremont Cottonwood, using the parameter values of Table 3. To reduce execution time (discussed in Sect. 3.2), we used a *patch-width* value of 2.0 m.

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<sup>13</sup> Several changes to the model have been made since this sensitivity analysis was conducted, so it does not completely reflect the current model formulation. However, we believe that its conclusions remain valid.

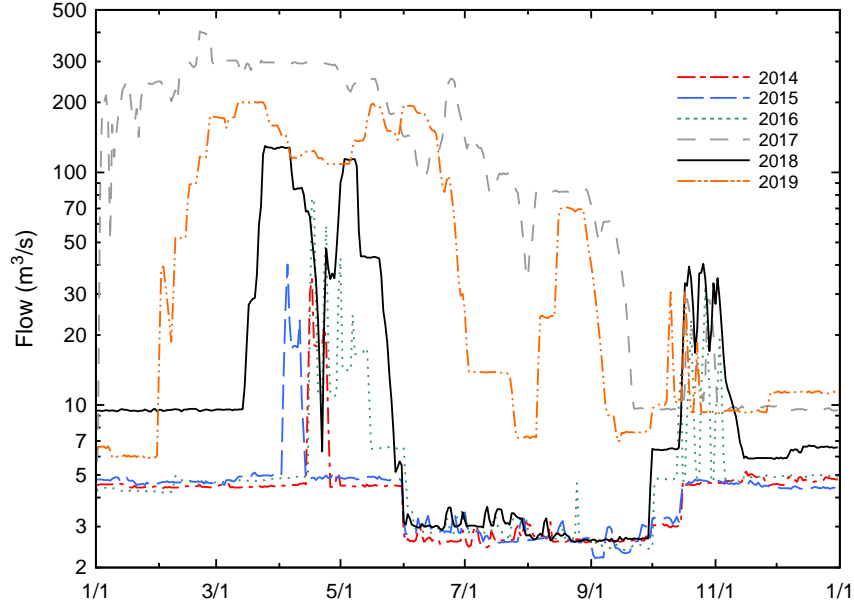


Figure 4. Hydrographs available for the parameter sensitivity analysis.

Understanding survival under standard parameter values (Figure 5) is essential for interpreting the sensitivity analysis results. With standard values for all parameters, 2.2% of deposited seeds survived until sprouting. Of those seeds that died before sprouting, 76% died of desiccation and 22% of inundation (including the seeds deposited onto the water surface). Of the sprouts, 14.3% survived to become seedlings; almost all sprout mortality was by desiccation. Seedling survival to dormancy was 51.3%, with mortality mainly due to inundation. Inundation also killed most (56%) of the dormant seedlings, with 3% also killed by scouring and 41.8% surviving until the end of the simulation. Of all seeds, 0.067% (~1 out of 1500) survived to the end of the simulation.

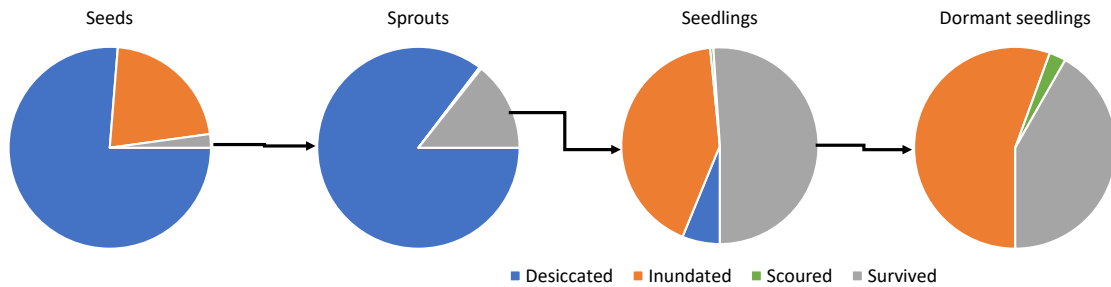


Figure 5. Seed fates under standard parameter values. Each “pie” represents the fate of plants that survived the previous life stage.

### 3.2 Sensitivity results: Global parameters and seed deposition

We examined sensitivity to the model’s spatial resolution (*patch-width*) and the capillary fringe height (*cap-fringe-height*). Results showed very little effect of *patch-width* on final seedling abundance (left panel of Figure 6), even with cells 10 times larger than the 1-m resolution of the site input. This result is important because the spatial resolution very strongly affects

computational and other costs of using TARGETS-2D: small cells take more work to prepare and make TARGETS-2D much slower to execute. (In this sensitivity analysis, patch widths of 2 and 5 m reduced execution times by 76% and 91% from those with 1-m resolution.) The benefits of lower resolution may often have little cost in accuracy, although the effect must be expected to be stronger at smaller streams and sites with more variable topography.

In contrast, the capillary fringe height had very strong effects on results (right panel of Figure 6). **Cap-fringe-height** had by far the strongest effect of any parameter examined (note the difference in Y-axis scale between its graph and those for other parameters). When reduced from its standard value of 0.2 m to 0.1 m, for example, the number of surviving dormant seedlings decreased by almost 80%, while increasing **cap-fringe-height** by 0.1 m more than doubled the number of surviving seedlings.

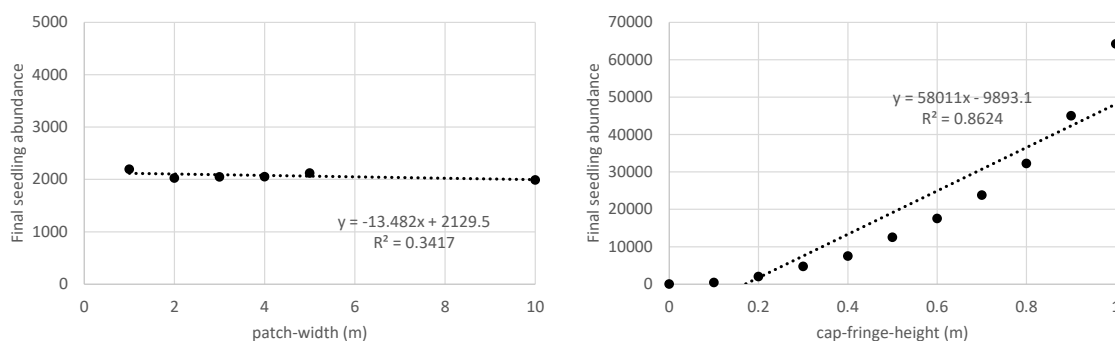


Figure 6. Sensitivity results for **patch-width** and **cap-fringe-height**.

Sensitivity results for the total number of seeds show strong proportionality between **seed-number-per-year** and the number of seedlings alive at the end of the simulation (Figure 7): the correlation is very strong and has a Y-intercept very close to zero. This proportionality is unsurprising given the model's lack of interaction among plants. It appears safe to reduce computational effort (including output file sizes and the effort to analyze them) by reducing **seed-number-per-year** and then assuming final plant abundance is proportional to the number of seeds deposited. (For example, instead of simulating 3 million seeds, simulate 1 million seeds and multiply resulting plant abundances by 3.) In the sensitivity simulations, representing 1 million seeds gives each of the 978,119 cells a 64% probability of having at least one seed; with 3 million seeds, this probability increases to 95%.

The seed number results of Figure 7 also confirm that model results are not highly stochastic; final seedling abundance differed very little among the five replicates of each seed number scenario.

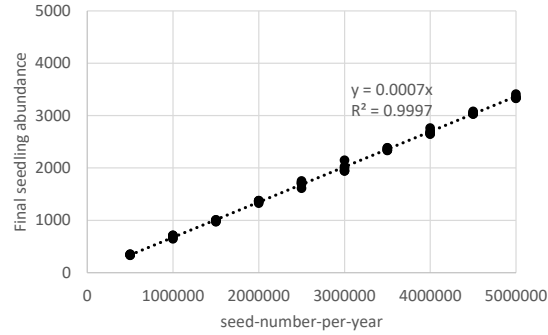


Figure 7. Sensitivity results for *seed-number-per-year*. Unlike all other sensitivity graphs, here the analysis included 5 replicate simulations of each seed number and the regression line was forced to have a Y-intercept of zero.

We examined sensitivity to the dates of seed deposition in two ways. First, we moved the seed deposition date distribution (Sect. □) backwards and forwards in time by adding *date-offset* days to the parameters *seed-creation-start-day*, *seed-creation-peak-day*, and *seed-creation-end-day*, where *date-offset* ranged from -20 to +20 days. Seed deposition dates had strong and complex effects, with the number of surviving dormant seedlings overall increasing with later deposition (Figure 8). With the 2018 hydrograph, later seed deposition produced more seed desiccation, less seed and sprout inundation, and higher mortality of seedlings and dormant seedlings from inundation and scour. The complexity of these results suggests that responses to the date range will be hydrograph-dependent and difficult to predict.

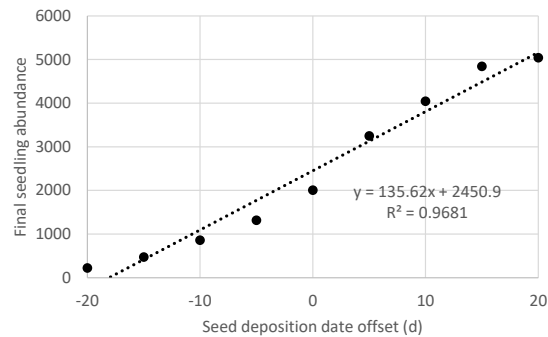


Figure 8. Sensitivity of seedling production to seed deposition timing. The X axis is the number of days added to the start and end of seed deposition.

We also varied the length of the seed deposition distribution by simultaneously increasing *seed-creation-start-day* and decreasing *seed-creation-end-day* by values from -10 to 10 days; this resulted in deposition occurring over 8 to 48 days. The experiment produced a slight decrease in seedling production with increasing length of seed deposition (Figure 9); while more days of seed deposition produced less mortality from most sources, it produced more seed desiccation.

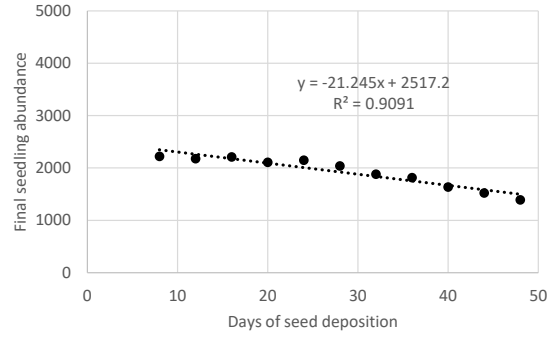


Figure 9. Sensitivity to the number of days of seed deposition.

### 3.3 Sensitivity results: Plant parameters

The two parameters that control the time require for seeds to develop into sprouts and then seedlings had very little effect on the final number of dormant seedlings (Figure 10). *Plant-seed-to-sprout-time* had essentially no effect on results, while *plant-sprout-to-seedling-time* had a consistent but very small negative effect. The lack of sensitivity to these parameters presumably is because (a) the way that flow regime affects survival, via desiccation and inundation, is quite similar across development stages, so the amount of time spent in each stage is not important; and (b) most of a successful simulated plant's life is in the seedling stage.

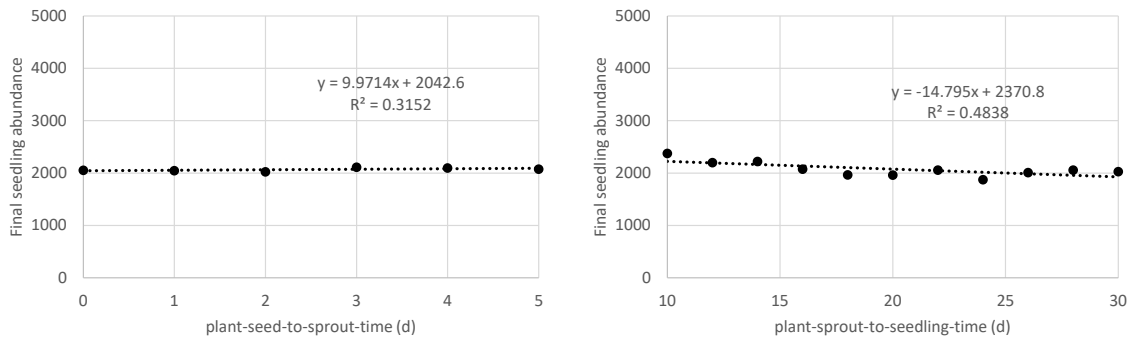


Figure 10. Sensitivity results for development rate parameters.

The parameters for survival of desiccation also had little effect (Figure 11). This lack of sensitivity is largely because many seeds are deposited where there is never moisture and also because when flow decreased, it did so consistently and stayed low for a long period; under these conditions, plant survival of desiccation is unlikely even at high daily survival probabilities. Desiccation remained the dominant mortality source for seeds and sprouts even when *plant-surv-desic-seed* and *plant-surv-desic-sprout* had high values; e.g., even with *plant-surv-desic-seed* set to 0.99, desiccation killed 72% of seeds.

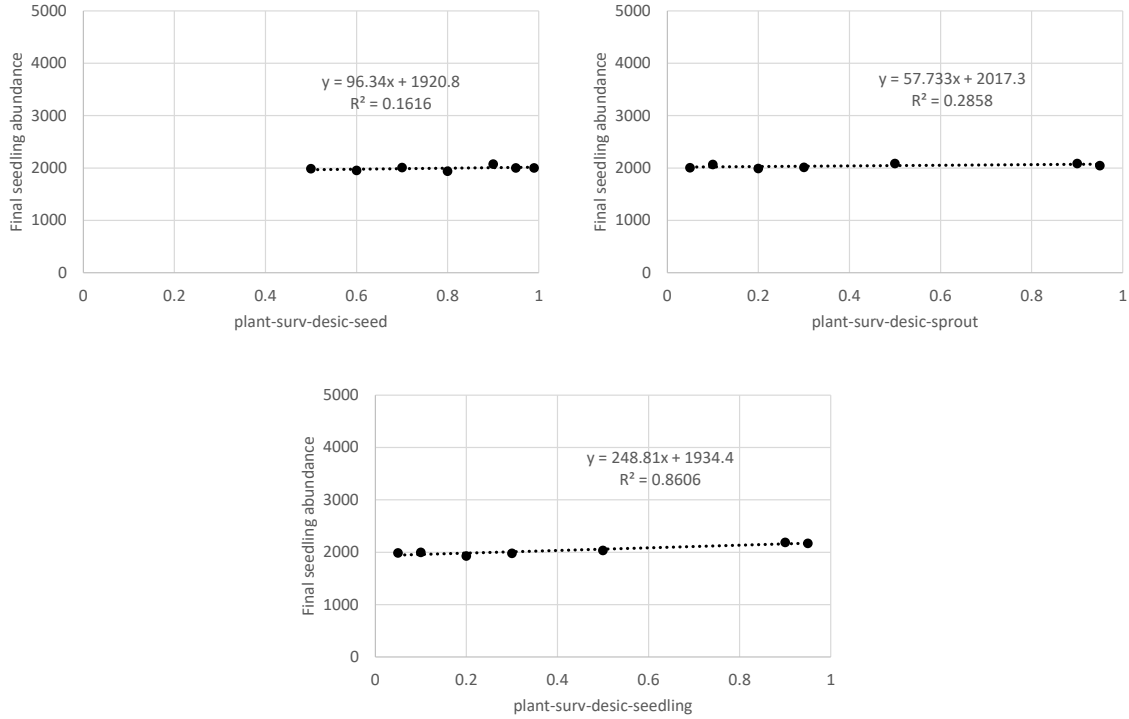


Figure 11. Sensitivity results for desiccation survival parameters.

In contrast to the seed and sprout survival parameters, *plant-surv-inund-seedling* and *plant-surv-inund-dormant* had strong effects on results (top panels of Figure 12). High values of these parameters allowed more seedlings to survive the high flows in October-May of 2018-19 (Figure 4). The value of *plant-surv-shear-threshold*, which controls scour mortality, had little effect on final seedling abundance (bottom panel of Figure 12), even though the number of seedlings dying of scour was very sensitive to values below 500 Pa/m (Figure 13). The lack of sensitivity to *plant-surv-shear-threshold* indicates that plants that are submerged during prolonged high flows are likely to die of inundation if they are not scoured; this effect is illustrated in Figure 13, which shows mortality due to inundation increasing as scour decreases, as the value of *plant-surv-shear-threshold* increases. Understanding the importance of scour mortality may require understanding inundation: scour may not be an important process to model precisely if seedlings are likely to die of inundation anyway, as in prolonged high flows. Flow pulses too short to cause widespread inundation mortality may make scour more important.

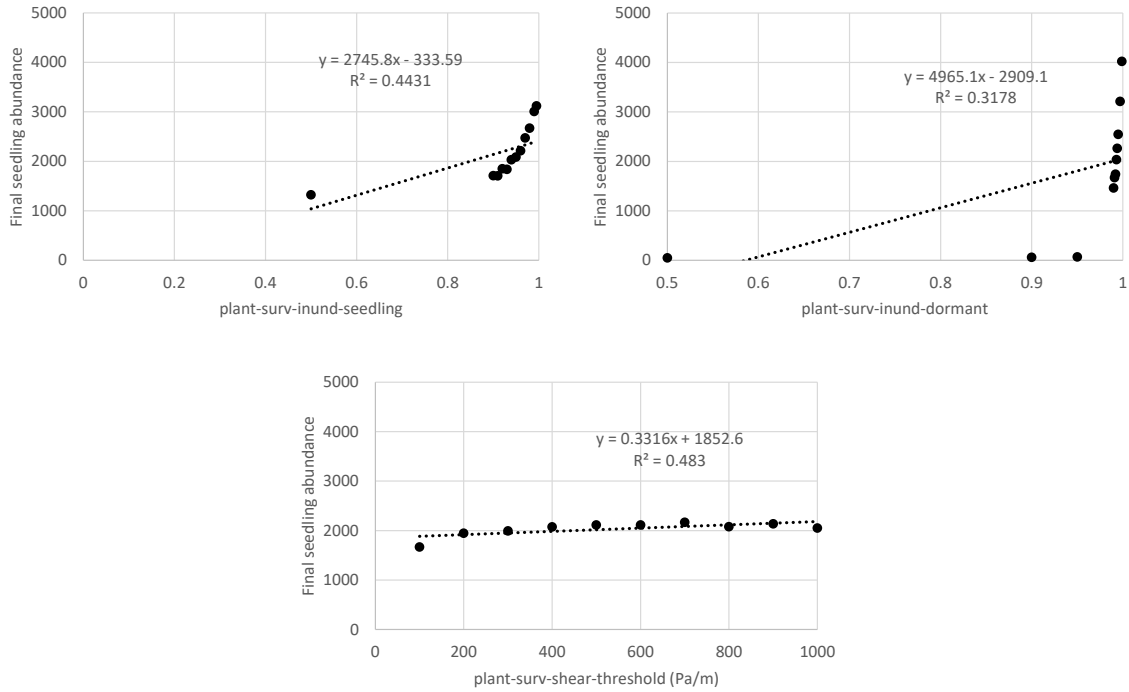


Figure 12. Sensitivity results for seedling and dormant seedling inundation and scour.

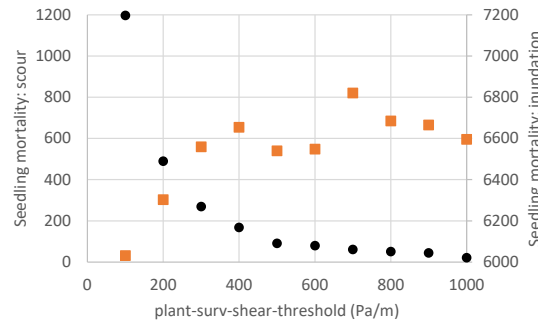


Figure 13. Number of seedlings and dormant seedlings dying of scour (round symbols, left vertical axis) and inundation (square symbols, right axis) under the 10 *plant-surv-shear-threshold* scenarios.

The rate at which plants can grow roots had surprisingly little effect on seedling abundance, though it appears to have some effect on where those seedlings survived (Figure 14). The reason that *plant-root-growth-rate* had negligible effect on seedling abundance appears, from the lower panel of Figure 14, to be because the vast majority of surviving seedlings were in cells where groundwater was never less than 0.3 m below the surface, so even low growth rates allowed plants to survive. However, higher growth rates allowed more plants to survive in cells with groundwater depths that exceeded 0.3 m.

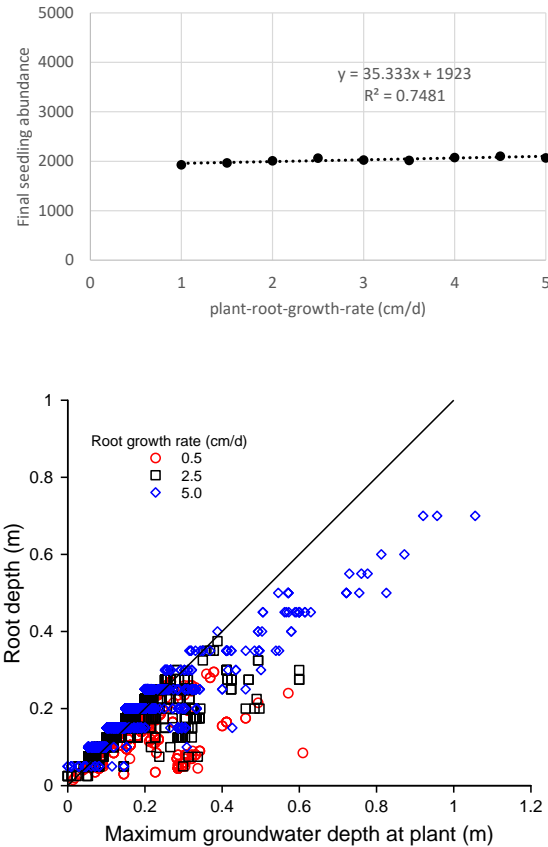


Figure 14. Effects of root growth rate on (top) number and (bottom) location of seedlings. The bottom panel plots the root depth of each surviving seedling as a function of the maximum depth to the groundwater surface at its cell, over the simulation period, for three daily root growth rates. In the bottom panel, the black line indicates root depth if growth stops at the groundwater surface. Note that root depths are always integer multiples of the daily growth rate (Sect. 0).

### 3.4 Sensitivity analysis conclusions

A few simple points are clear from this sensitivity analysis.

First, because sensitivities can change dramatically among sites and flow regimes, it is worth repeating this analysis for each application of TARGETS-2D that supports important decisions. NetLogo's automated simulation tool (Sect. 4.7.4) makes such analyses easy.

Second, sensitivity and other analyses requiring many model runs can be made more feasible, with little loss of accuracy, by using fewer, larger cells and simulating fewer seeds. Larger cells can be created by simply using a higher value of *patch-width*, or by using lower resolution in the hydraulic models and GIS analysis used to prepare input. In the simulations reported here, computation was dominated by updating groundwater elevations (Sect. 2.7.1), so the number of cells had much more effect on execution time than did the number of seeds.

Third, many of the most uncertain parameters do not appear to have strong effects, so reducing the uncertainty in their values could have low priority. These include the parameters controlling development rate and survival for mortality sources other than inundation. Root growth rates

appear to be of intermediate importance, perhaps having more effect on where plants survive (especially, how many establish at higher elevations) than on the total number of surviving seedlings. The parameters for inundation mortality did have strong effects in this case, due to the prolonged high flows that seedlings and dormant seedlings were exposed to. Better understanding of inundation mortality could be an important way to improve TARGETS.

Fourth, the effects of high flows on seedling survival appear to be an interaction between inundation and scour mortality. Sensitivity to scour was low in this experiment because most seedlings that survived scour were killed by inundation; scour will have stronger effects on model results if seedlings are assumed less vulnerable to inundation or if high flows come in short pulses instead of prolonged floods.

Finally, the height of the capillary fringe had very strong effects on seedling abundance. This sensitivity also implies that how groundwater elevation is modeled is important to the results of TARGETS-2D. Therefore, improving the accuracy and detail with which the capillary moisture zone is represented, e.g., by representing how *cap-fringe-height* varies among sites or over space within a site and by testing and improving methods for estimating groundwater elevation efforts, appears important for improving predictions of TARGETS-2D.

## 4 Software Guide

This section describes how to install, use, and modify the TARGETS-2D software. It is modified from the FYFAM software guide (Sect. 3 of Railsback, Harvey, and Ashton 2021); however, there are important differences between the FYFAM and TARGETS-2D software.

TARGETS-2D is implemented in the NetLogo modeling platform (Wilensky 1999), which is free, open-source, widely used, and very well documented and supported. NetLogo is available for all common operating systems, so TARGETS-2D can be used on Windows, Macintosh, and Linux computers.

### 4.1 License

The TARGETS-2D software is copyrighted and licensed under the GNU General Public License (GPL; <https://www.gnu.org/licenses/gpl.html>), which means it is free software that anyone can use, modify, and re-distribute; but it must remain free. A copy of the license is on the “Info” tab of the model’s NetLogo file.

### 4.2 Installation

Installing TARGETS-2D requires two simple steps: installing NetLogo and then copying the model files.

NetLogo is installed by downloading an installer from its web site at Northwestern University: <http://ccl.northwestern.edu/netlogo/>. TARGETS-2D works with versions 6.2.2 and higher of NetLogo.

TARGETS-2D itself is installed by simply copying (or unzipping) a directory containing the code file (with an extension of `.nlogo`; typically named something like `TARGETS-2D.nlogo`) and its input files (described below). The TARGETS-2D directory can be copied anywhere.

TARGETS-2D can then be started by either (a) starting NetLogo (the same way any other installed software package is started) and using “File > open” in NetLogo to find and open the TARGETS-2D code file, or (b) simply double-clicking on the code file.

### 4.3 TARGETS “Projects” and file management

The TARGETS-2D code file and input files are relatively small. Therefore, we recommend users make a separate copy of the entire directory of code and input files (and, after the model is run, output files) for each scenario modeled. We call each such directory a “project”; each project should contain the code, input, and results for one simulation experiment and therefore document and archive the experiment completely. The name of the NetLogo code file should be changed to reflect the project, e.g., `TARGETS-2D_BigCreek_FlowAlternative4.nlogo`. Keeping a separate project for each simulation experiment reduces the potential for mistakes and confusion about which model runs produced which results.

### 4.4 Input files

TARGETS-2D uses several input files, plus a file of parameter values. Examples of these files are distributed with the model, but users typically simulate new sites or management scenarios by creating new files.

All the input files except the parameter file (Sect. 4.5) can have any name, because the file names are specified in the parameter file. The user can give input files any name but must edit the parameter file to provide the name of each input file.

**All input files must be in CSV format.** CSV files are easily opened and edited in spreadsheet and statistical software. From Excel, these files must be saved in Excel’s “CSV” format, not “CSV UTF-8”.

#### 4.4.1 Habitat input file

This file provides the coordinates of the centers of the “nodes” used to create habitat cells (Sect. 2.5.1), and the values of cell-specific habitat variables (the static variables in Table 1). The current version of TARGETS uses only one such habitat variable, *cell-elevation*. Figure 15 provides an example excerpt from a habitat input file when open in a spreadsheet.

Habitat input file for Big River at Zaynee			
Irregular grid (CA StatePlane NAD83 2011	Zone III	meters) 17 August 2021	
Node ID	X	Y	ElevationM
1	1997733.838	624925.6674	45.02468
2	1997734.838	624925.6674	45.69143
3	1997735.838	624925.6674	46.39628
4	1997736.838	624925.6674	47.00588

Figure 15. Example cell input file

This file must contain:

- Three header lines, which the code ignores. The third line should be column headers.
- One row for each node. Rows do not need to be in order of identification number. The values (columns) in these rows are:
  - The node identification number or code, which can be either a number or text value;
  - The node’s X coordinate (explained below);
  - The Y coordinate; and
  - The node elevation, in meters.

The node coordinates must follow these conventions, which are based on the UTM system:

- Coordinates must be in units of meters.
- For display, X coordinates increase from left to right (west to east) and Y coordinates increase from bottom to top (south to north).
- The nodes do not need to make up a square space.

#### 4.4.2 Depth and shear files

The depth and shear files provide lookup tables of water depth and shear stress (sects. 2.7.1; 2.7.7) for a range of flows, for each node. These files are usually generated from output from a

hydraulic model. The number of flows in the tables is not fixed, and the depth and shear files can each use different flows and different numbers of flows.

The flows must be in units of cubic meters per second and depths in meters; shear units must be consistent with those used to model scour survival (Sect. 2.7.7). The node identifiers must exactly correspond to those in the habitat input file.

The two files have the same format (Figure 16):

- Three header lines that are ignored by the computer;
- One line that contains only a single (integer) number: the number of flows for which depths/shear values are provided;
- One line that contains each of the flows, in ascending order; and
- One line for each node, containing the node's identifier code and its depth or shear for each of the flows.

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q
1	Depths loc	Big River at Zaynee															
2	ASH 17 Au	Flows in n	depths in m														
3	First	a row with cell number and depths (m) for each flow															
4	16																
5		2.27	3.11	4.25	8.5	14.16	17.92	21.24	22.65	28.32	32	44.74	84.95	152.91	199.63	271.84	325.64
6	1	0	0	0	0	0.18	0.26	0.32	0.34	0.44	0.56	0.65	1.04	1.43	1.59	1.78	1.91
7	2	0	0	0	0	0.23	0.31	0.38	0.40	0.49	0.62	0.71	1.10	1.49	1.65	1.84	1.97
8	3	0	0	0	0	0.19	0.28	0.34	0.36	0.45	0.58	0.67	1.06	1.45	1.61	1.80	1.93
9	4	0	0	0	0	0.00	0.00	0.05	0.08	0.17	0.30	0.39	0.78	1.16	1.32	1.51	1.65
10	5	0	0	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.44	0.83	0.99	1.18	1.31
11	6	0	0	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.13	0.51	0.67	0.86	1.00
12	7	0	0	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.19	0.35	0.54	0.67
13	8	0	0	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.17
14	9	0	0	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
15	10	0	0	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
16	11	0	0	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
17	12	0	0	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
18	13	0	0	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Figure 16. Example depth input file, viewed in a spreadsheet.

#### 4.4.3 Flow time series file

One file provides the flow time series that drives TARGETS-2D. This file also specifies the model's time steps, as explained in Sect. 2.7.1. The file must contain values for the entire time period to be simulated; it can also contain times before and after the simulated period, which are ignored. (This file can contain additional time-series variables like temperature, which are ignored by TARGETS; time-series input files for FYFAM can be used in TARGETS-2D.)

The time series file (Figure 17) can start with as many header lines as desired, each starting with the semicolon character “;”. These header lines are ignored by the computer. The next line must contain only the text names of the input variables, including `Time` and `flow`. (The for the flow input here must be exactly `flow`; it is case-sensitive.) The remaining data lines each contain a date-time and flow value:

- A date and time, in the “m/d/yyyy h:mm” format (for example, midnight at the start of May 5, 2010 is: 5/5/2010 0:00. One p.m. on the same day is: 5/5/2010 13:00); and

- The flow, in cubic meters per second.

```
;TARGETS time-series input for Big River
;Flow from USGS gage 11289650, converted to cms
Time,flow
1/1/2018 0:00,9.4522
1/2/2018 0:00,9.4522
1/3/2018 0:00,9.4522
1/4/2018 0:00,9.4239
1/5/2018 0:00,9.4522
1/6/2018 0:00,9.5088
1/7/2018 0:00,9.4522
```

Figure 17. Example time series input file, as viewed in a text editor. Here, each time step represents one day, starting at midnight.

For typical one-day time steps and daily mean flows, the hour and minute values are unimportant as long as they are the same for each day; midnight (0:00) or noon (12:00) are convenient.

#### 4.4.4 Mother tree input

If the mother tree method for seed deposition is used (Sect. □), then this file must be provided. It contains one line per mother tree (Figure 18), with columns for:

- Tree species, a text species names corresponding to those in the `set species-names` statement (Sect. 4.5.6). If the species name here is not in the `set species-names` statement, then the line is ignored.
- X coordinate of the tree's location, in the same units (m) and coordinate system as node locations (Sect. 4.4.1).
- Y coordinate of tree location.
- The total number of seeds produced by the tree.
- The mean of the exponential distribution representing distance from the tree that each seed is deposited.
- The mean of the normal distribution representing the direction (compass heading) each seed is deposited.
- The standard deviation of the direction distribution.

	A	B	C	D	E	F	G
1	; Mother tree seed source input						
2	; Species	X-Coord	Y-Coord	NumSeeds	Mean dispersal	Direction-Mean	Direction-SD
3	Fremont Cottonwood	1998983	625049	5.00E+04	296	120	45
4	Fremont Cottonwood	1997818	625997	5.00E+04	161	120	45
16	Narrowleaf Willow	1998791	626179	5.00E+04	50	120	45
17	Narrowleaf Willow	1999874	624944	5.00E+04	69	120	45
18	Narrowleaf Willow	1999429	626135	5.00E+04	78	120	45
19	Narrowleaf Willow	1997949	625802	5.00E+04	100	120	45
20	Narrowleaf Willow	1999846	625985	5.00E+04	96	120	45

Figure 18. Example mother tree input file, displayed in Excel.

## 4.5 Parameter file

### 4.5.1 General characteristics

The values of TARGETS-2D's parameters are specified in the parameter file. This file is actually part of the model's NetLogo code: the file contains a NetLogo procedure named `set-parameters` that sets the values of all the model's global variables. The file is plain text and can be edited in a text editor, or within NetLogo (via the "Includes" button on the Code tab). If edited in a text editor, the parameter file must be saved before opening the NetLogo file and setting up a simulation (Sect. 0).

The parameter file is named something like `TARGETS-parameters.nls` but its name should be modified to identify the project (e.g., `parameters_BigCreek_FlowAlt3.nls`). When the name of the parameter file is changed, it must be updated in the code file: when the NetLogo code file is open, click on the Code tab and edit a line near the very top that reads:

```
__includes [ "parameters_ASite.nls" ]
```

The parameter file must be in the same directory as the TARGETS-2D NetLogo code file.

The parameter file contains many lines with the same format:

```
set parameter-name value ; description.
```

Each such line sets the value(s) of one parameter. Examples are:

```
set habitat-file-name "BullCreek_Nodes.csv"      ; Node input file name

set cap-fringe-height 0.2 ; Vertical distance (m) between groundwater...
```

A parameter value can be changed by finding the parameter name in the file (see the list of parameters at Table 3) and editing its value. Parameter values that are text values (including file names) must be in double quotes. Text following semicolons are comments that are ignored by the computer. The `set` statements do not need to be in any particular order.

### 4.5.2 Model control parameters

Three parameters control the simulation time period (Sect. 2.2.4) and the seed deposition method (Sect. □). They are set via statements like these:

```
; Simulation period
set run-start-date "5/1/2018" ; Date on which simulation starts
set run-end-date   "7/1/2019" ; Last date simulated

; Source of seed input
set mother-tree-input? true ; TRUE to model mother tree seed deposition
```

### 4.5.3 Input file names

The parameter file includes not just the model parameters of Table 3 but also information used to set up and control the simulation. One block of `set` statements provides the names of the input files:

```

; Setup file names
set habitat-file-name "Input-BigCrk/BigCrk_HabitatInput.csv"
set depth-file-name  "Input-BigCrk/BigCrk_Depths.csv"
set shear-file-name   "Input-BigCrk/BigCrk_Shear.csv"
set time-series-file-name "Input-BigCrk/BigCrk_Flows.csv"
set mother-tree-file-name "Input-BigCrk/BigCrk_MotherTrees.csv"

```

The file names must be in double quotes. They can refer to subdirectories by using “/”: in the above examples, the input files are in a subdirectory named `Input-BigCrk` below where the NetLogo file is. File names can also use “..” to refer to the directory above where the NetLogo file is; for example, `"../Input-BigCrk/BigCrk_Flows.csv"` points to a directory `Input-BigCrk` that is a subdirectory of the directory above the NetLogo file’s.

If `mother-tree-input?` is set to `false`, then the value of `mother-tree-file-name` is ignored and its `set` statement can be arbitrary or omitted.

#### 4.5.4 Display parameters

Display parameters have no effect on simulation results but control the graphical interface described in Sect. 0. These parameters are not described elsewhere in this document.

`max-shade-depth`: When submerged cells are shaded by depth (Sect. 0), shading ranges from white at `depth = 0` to deep blue when `depth` equals `max-shade-depth` (m). Cells with `depth` greater than `max-shade-depth` all have the same deep blue color.

`max-shade-shear`: Cells shaded by shear range in color from yellow at zero shear to deep red at `max-shade-shear` (in the same units used to model shear and scour survival; Sect. 2.7.7).

`max-shade-groundwater-depth`: Cells shaded by depth to groundwater range from white at zero depth to dark grey at `max-shade-groundwater-depth` (m/s).

`seedling-scale`: This parameter controls the display size of seedlings. Each seedling is displayed as a plantlike shape with size proportional to its root depth (*plant-root-depth*). `seedling-scale` is the size (in screen pixels) of a seedling with *plant-root-depth* = 1.0 m. Increasing or decreasing this parameter makes seedlings bigger or smaller on the display.

`write-frames?`: When set to `true`, TARGETS-2D will write a graphics file of the model interface at the end of each time step. These files are in .PNG format with file names indicating the time step. They can be assembled into .GIF animations of model runs, using separate software for that purpose.

#### 4.5.5 Global parameters

Global parameters include those controlling the model’s spatial resolution and habitat parameters that affect all cells: *patch-width* (Sect. 2.2.2), *max-node-distance* (Sect. 2.5.1), and *cap-fringe-height* (Sect. 2.7.1).

#### 4.5.6 Plant parameters

Separate parameter values must be provided for each plant species. All plant parameters are defined as lists with one value for each species. For example, this code in the parameter file:

```

; Plant parameters
; These are lists with values for each species
set species-names (list "Purple Alder" "Rosy Cottonwood") ; Species names
set species-colors (list violet pink) ; Display colors

; Seed deposition
set seed-number-per-year (list 1E6 5E5) ; Number of seeds deposited

```

means that there are two species: Purple Alder will be displayed as violet and have one million (1E6) seeds created, and Rosy Cottonwood will be displayed as pink and have 500,000 seeds.

One plant parameter deserves special attention because it is especially complex: *ind-plant-output-dates*. This parameter is a list of dates on which individual plant output (Sect. 4.7.3) is written, and separate dates are specified for each species. The parameter file's value of `ind-plant-output-dates` can include any number of dates, in M/d/yyyy format in double quotes. Any dates before `run-start-date` are ignored, as are any dates on or after `run-end-date`. Individual plant output for the last simulated day is obtained by including the day before `run-end-date` in `ind-plant-output-dates`. If the interface switch controlling individual plant output is set to off, the dates in `ind-plant-output-dates` are ignored, or its value can be set to an empty list: `set ind-plant-output-dates (list)`. The statement setting the values of *ind-plant-output-dates* produces a list of lists; for a two-species simulation it looks like this:

```

; Individual plant output dates
; For each species, a list of dates (M/d/yyyy) for individual plant output
; These must be in date order; dates must be *before* run-end-date
set ind-plant-output-dates (list
  (list "6/6/2018" "6/25/2018" "10/31/2018" "6/30/2019") ; for cottonwood
  (list "7/13/2018" "8/1/2018" "10/31/2018" "6/30/2019") ; for willow
)

```

#### 4.6 Starting and controlling simulations

When TARGETS-2D is opened in NetLogo, its graphical interface appears (Figure 19). The user controls the model and several options via this interface. (The interface is easily modified, so different versions of the model will likely have different controls and displays.)

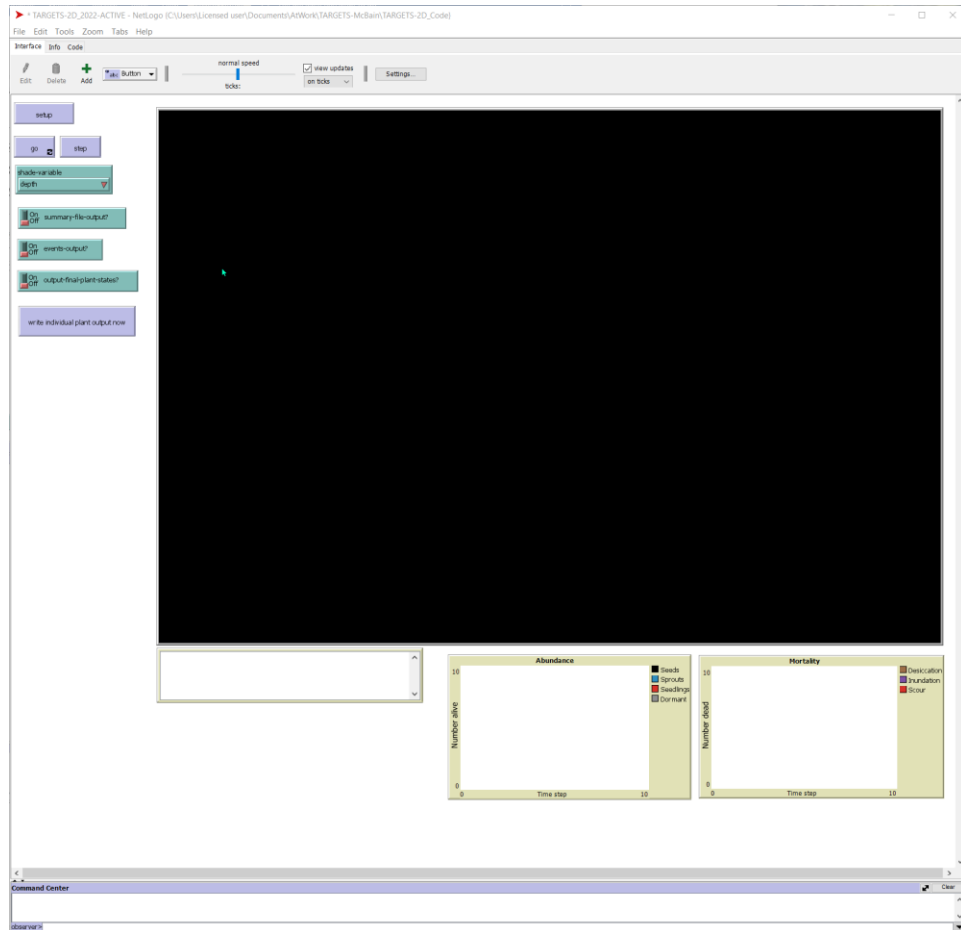


Figure 19. The TARGETS-2D user interface before setup.

From this interface, users can:

- Click on the `setup` button to initialize the model: read input files, create the habitat, and prepare for execution to start. It normally takes several seconds for setup to complete; the button turns black until setup is complete.
- Click the `go` button to start model execution, after setup is complete. Subsequent clicks on this button pause, then re-start, execution.
- After the model is set up, or when it is paused, click the `step` button to execute just one time step.
- Use the `shade-variable` chooser to determine whether, on the display, cells are shaded by water depth or velocity, groundwater depth, etc. (explained below).
- Turn the three output files (Sect. 4.7) on or off. Output files are written only when turned on. The model must be re-initialized via the `setup` button after the `file-output?` or `events-output?` switches are changed, but turning `output-final-plant-status?` on does not require re-initialization.
- Writing the current state of each individual plant to an output file, at any time during a simulation. Click `go` to pause execution, then click on the button labeled `write individual plant output now`.

Once the model is set up and running (Figure 20), the animation display (the “world” in NetLogo terminology) shows cells shaded by whatever scheme is selected using the “shade-variable” selector<sup>14</sup>. The available schemes are:

- Depth: Submerged cells are shaded by *cell-depth*, from white to dark blue as depth increases. The model parameter ***max-shade-depth*** is the depth above which all cells are the same darkest blue. Cells above water are shaded by *cell-elevation*, from lighter to darker green as elevation increases. However, cells with moisture at the ground surface (both *cell-depth* and *cell-moisture-depth* are zero) are colored yellow.
- Velocity: Submerged cells are shaded by *cell-velocity*, from yellow to dark red as velocity increases. The parameter ***max-shade-velocity*** sets the velocity above which cells are the same darkest red. Cells above water are shaded as in the depth scheme.
- Groundwater depth: Submerged cells are shaded by *cell-depth*. Unsubmerged cells are shaded by *cell-groundwater-depth*, from white to dark gray as depth to groundwater increases.
- Water elevation: All cells are shaded by water elevation. For submerged cells, water elevation is *cell-elevation* + *cell-depth*; for other cells, water elevation is *cell-elevation* – *cell-groundwater-depth*. However, cells on the channel margin (with depth > 0 and at least one adjacent cell with depth = 0) are colored black to indicate the wetted channel. Shading is light to dark gray as water elevation increases.

Seeds appear as small dots and sprouts as triangles, although both can be too small for the shape to be distinguishable. Seedlings have a plant shape that grows in proportion to *plant-root-depth*<sup>15</sup>. Seedlings turn grey when they turn into dormant seedlings.

Users will likely need to change the “patch size”, which is the size of cells (screen pixels per cell) on the animation display. During setup, the model adjusts the dimensions of this display to match the simulated area represented in the habitat input file. However, the size of the display depends on the computer screen resolution and the patch size as well as the habitat area. Users may want to reduce patch size to make the entire simulation reach visible, or increase patch size to zoom in on a particular area. To adjust patch size, click the “Settings” button near the top the interface and edit its value in the dialog box that opens. (Patch sizes < 1 pixel are allowed, but NetLogo does not save the display size correctly when they are used.) To accommodate different site shapes and sizes, the whole NetLogo window can be stretched, and individual items on the interface can be selected (by dragging the cursor over them or by right-clicking on them) and moved.

---

<sup>14</sup> Shading schemes are programmed in the procedure `shade-patches`.

<sup>15</sup> Seed display variables (shape, size, color) are set in `deposit-seeds`. Sprout and seedling shapes are set in `update-stage` and seedling display size is updated in `grow-roots`.

Changes to the model interface (or parameters) can be made permanent by clicking on “File” and “Save”.

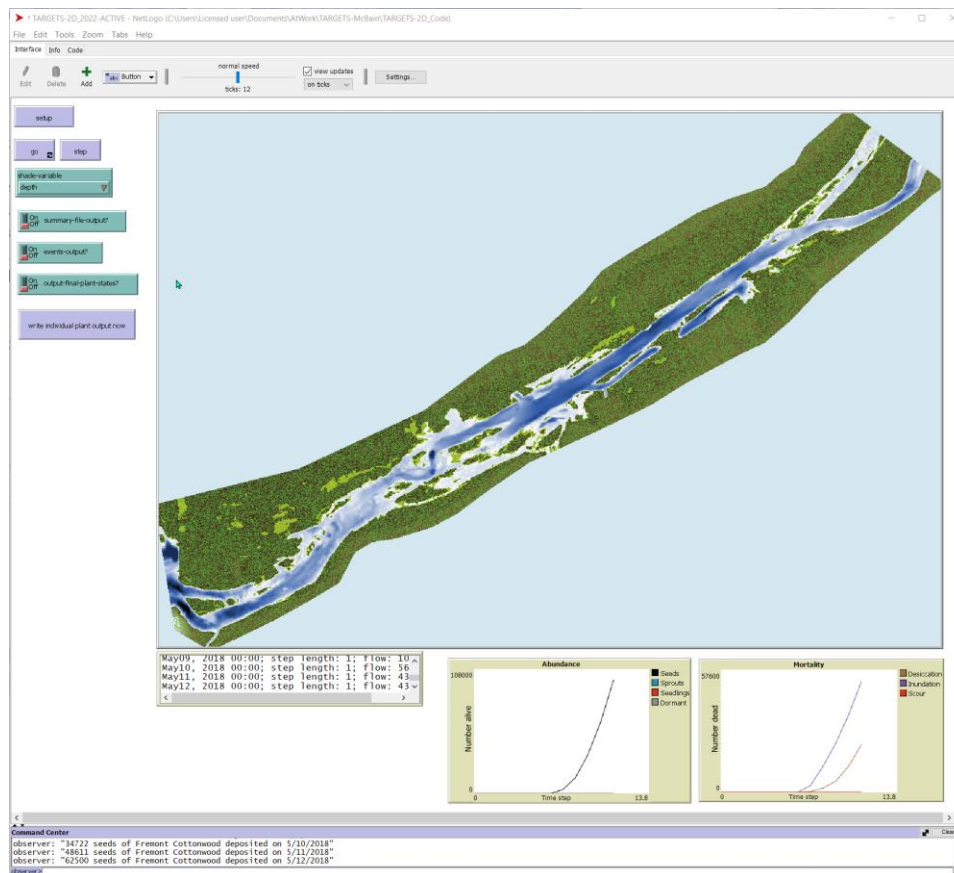


Figure 20. The model interface during execution. (Execution is temporarily paused; hence, the go button is not black.)

## 4.7 Output files

TARGETS-2D can produce three output files, with switches on the interface determining which outputs are produced<sup>16</sup>. The files are written to the file directory where the program file (TARGETS\*.nlogo) resides. For test runs and simply exploring the model, it is convenient to turn output files off so they do not clutter the project directory. For some simulation experiments, the summary output is sufficient, while the “events” and individual plant output files are much larger and provide much more detail. The files are in CSV format and easily opened in spreadsheet or statistical software.

### 4.7.1 Summary output

When the `summary-file-output?` switch on the Interface is turned on, TARGETS-2D produces a summary output file. The summary file reports one line of output for each species on each time

<sup>16</sup> The summary and events output files are written by the procedure `update-output`. The individual plant output is written by `output-individual-plants`.

step (Table 4; output file contents are easily modified so this table may not be accurate for all versions of the model code).

The summary output file name is generated by the code from the system date and time, so each model run produces a unique output file. The file name starts with the word “Output”, e.g., `Output-01-16-15.763PM21-Aug-2023.csv`.

Table 4. Summary output file contents.

Column label	Output
Start of time step	Date and time at the start of the time step
Flow	The flow (m <sup>3</sup> /s) on the current time step
Species	The plant species that the line reports
Seeds Sprouts Seedlings Dormant seedlings	The number of plants alive at the end of the time step, by development stage
Died-desiccation-seed, etc. Died-inundation-seed, etc. Died-scour-seedling, etc.	The number of plants that died during the time step of each mortality source; broken out by development stage

The summary output file therefore makes it easy to produce time-series plots of flow and abundance or cumulative mortality.

#### 4.7.2 Events output

The events output file is turned on by a separate switch because it is typically much larger than the summary output file. It has the same name as the summary output file but with the word “-Events” appended to it (e.g., `Output-01-16-15.763PM21-Aug-2023-Events.csv`). This file reports the time and location at which each plant in the model transitions from one development stage to the next or dies. (It is very easy to modify the code to report other kinds of events in this file.)

The file contains one line per event, reporting the date and time at the start of the time step when the event occurred, the plant’s unique identity number, the node identifier (Sect. 4.4.1) and X and Y coordinates of the cell where the event occurred (actual coordinates from the habitat input file), the cell’s values of *cell-depth* and *cell-moisture-depth*, the plant’s values of *plant-stage* and *plant-root-depth*, the date and time at which the plant was deposited as a seed, and the event type. Event types are self-explanatory, e.g., *became-seedling* and *died of desiccation*<sup>17</sup>.

(The TARGETS-2D code includes an optional procedure to summarize an events output file into the number of events, by type, that occurred in each cell. This procedure can only be executed by typing its name, `summarize-events-output`, into the Command Center on the NetLogo Interface tab. It will only work after a simulation has completed or been paused via the `go`

<sup>17</sup> The kinds of events reported in the events output file can be identified and changed by searching the code for the command `save-event`. The exact information written to the file is specified in the procedure `save-event`.

button, but not after setup has been executed again and not if NetLogo is closed and reopened. This procedure writes a new output file with its results. It is relatively memory-efficient but can take extremely long to execute. It produces output in the Command Center reporting its completion status. We expect that statistical software will often be a more efficient way to produce the same analyses.)

#### 4.7.3 Individual plant output

The individual plant output files report the status of each plant alive, on specific dates chosen by the user. A separate file is written for each plant species because different output dates are typically most meaningful for different species. Each such output file contains one line of output for each plant, for each of the selected dates. These lines contain the simulation date of the output and the plant's location, species, development state, root depth, and age. Producing the output only at user-chosen simulated dates makes the files easier to analyze. Those dates are chosen via the plant parameter *ind-plant-output-dates* (Sect. 4.5.6). The individual plant output dates might typically include a day when all seeds have been deposited and had time to sprout, the date at which all seeds have had time to become seedlings, the day at which seedlings go dormant, and the last simulated day. (To produce output on the last simulated day, *ind-plant-output-dates* must include the date preceding *run-end-date*, not *run-end-date* itself.)

The interface switch `output-final-plant-status?` controls whether this output is produced. The output file has the same name as the summary output file but with “-IP-” and the species name appended to it (e.g., `Output-01-16-15.763PM21-Aug-2023-IP-Narrowleaf Willow.csv`)

#### 4.7.4 Optional output of cell water and groundwater elevations

Testing and understanding simulations can require output of water elevations (surface water or groundwater, for cells that are and are not submerged) so they can be examined, e.g., in GIS. To facilitate this, the TARGETS-2D code includes a procedure to output simulated water elevations at each of several flows. This procedure is called `export-water-elevations-for-flows`. It can be used only by typing a command such as:

```
export-water-elevations-for-flows (list 1 2 5 10 20)
```

in the Command Center, any time after `setup` has been executed and the model is not running (the `go` button is not black). (The Command Center is the terminal-like window at the bottom of the Interface tab, as in Figure 20.)

In this command, the numbers following `list` are the flows (in  $\text{m}^3/\text{s}$ ) at which water elevations will be output. Any number of flows (including just one) can be entered.

When this command has been entered, the TARGETS-2D code updates the simulated hydraulics and groundwater elevations and writes an output file, for each of the flows. (A separate file is written for each flow.) The files have names such as `GroundwaterElevationsForFlow5.csv` where the number in the file name indicates which flow it is for. These output files are in .csv format; Figure 21 illustrates the file open in a spreadsheet.

The file includes one row for each model cell (Sect. 2.2.2), sorted by node number, containing:

- The hydraulic node used by the cell (Sect. 2.5.2; because more than one cell can use the same node, the same node number can appear in more than one row);
- The node's X and Y coordinates, in the GIS shapefile's coordinate system;
- The cell's ground surface elevation; and
- The water/groundwater surface elevation at the flow. If the cell is submerged (*cell-depth* > 0) this value is the ground surface elevation plus *cell-depth*. If the cell is not submerged, this value is the groundwater surface elevation (elevation minus *cell-groundwater-depth*).

	A	B	C	D	E
1	Water elevations for flow:	4.78			
2	Node number	X coordinate	Y coordinate	Elevation	Water elevation
3	1	1997733.838	624925.6674	45.024675	43.81498117
4	1	1997733.838	624925.6674	45.024675	43.81497649
5	2	1997734.838	624925.6674	45.691425	43.81498882
6	3	1997735.838	624925.6674	46.396275	43.81505258
7	4	1997736.838	624925.6674	47.005875	43.81523679
8	5	1997737.838	624925.6674	47.64405	43.81566252

Figure 21. Example water elevation output file.

#### 4.8 Automated simulation experiments with BehaviorSpace

NetLogo includes a very powerful tool for setting up and executing simulation experiments, called BehaviorSpace. BehaviorSpace is quite simple and intuitive to use, and comprehensive instructions for using it are provided in the NetLogo documentation and by Railsback and Grimm (2019). It can very easily be used, for example, to run replicate simulations (the same scenario with different random numbers); multiple years, but one year at a time; several replicates each of multiple flow scenarios; and sensitivity experiments to examine effects of specific parameters or inputs. BehaviorSpace automatically generates the model runs and executes them in parallel on all available processors.

BehaviorSpace is accessed via NetLogo's "Tools" menu, and is menu-driven: users fill out a menu defining what simulation experiments are to be executed and what output is to be saved from them. Each experiment configuration ("Experiment") can be saved as part of the model's NetLogo file. TARGETS-2D is packaged with an example BehaviorSpace experiment (Figure 22), which users can duplicate and modify for their own experiments.

Experiment

Experiment name
ExampleExperiment

Vary variables as follows (note brackets and quotation marks):  

```
[
  "summary-File-output?" false]
[
  "events-output?" false]
```

Either list values to use, for example:  

```
["my-elder" 1 2 7 8]
```

or specify start, increment, and end, for example:  

```
["my-elder" [0 10]]
```

(note additional brackets)  
to go from 0, 1 at a time, to 10.  
You may also vary `min-pyccor`, `max-pyccor`, `min-pyccor`, `max-pyccor`, `random-seed`.

Repetitions
5

run each combination this many times

☒ Run combinations in sequential order

For example, having `[Var 1 2 3]` with 2 repetitions, the experiments "var" values will be:  
sequential order: 1, 1, 2, 2, 3, 3  
alternating order: 1, 2, 3, 1, 2, 3

Measure runs using these reporters:

```
count plants with [plant-species = "Purple Alder" and plant-stage = "dormant"]
count plants with [plant-species = "Rosy Cottonwood" and plant-stage = "dormant"]
table:get-or-default (table:get fate-table "Purple Alder") "seeds-deposited" 0
table:get-or-default (table:get fate-table "Purple Alder") "died-desic" 0
table:get-or-default (table:get fate-table "Purple Alder") "died-inund" 0
table:get-or-default (table:get fate-table "Purple Alder") "died-scour" 0
table:get-or-default (table:get fate-table "Rosy Cottonwood") "seeds-deposited" 0
table:get-or-default (table:get fate-table "Rosy Cottonwood") "died-desic" 0
table:get-or-default (table:get fate-table "Rosy Cottonwood") "died-inund" 0
table:get-or-default (table:get fate-table "Rosy Cottonwood") "died-scour" 0
```

one reporter per line; you may not call a reporter  
across multiple lines

☐ Measure runs at every step

if unchecked, runs are measured only when they are over

Setup commands:

```
setup
```

Go commands:

```
go
```

☒ Stop condition:

the run stops if this reporter becomes true:

Time limit
0

stop after this many steps (0 = no limit)

☒ Final commands:

run at the end of each run

OK

Cancel

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