Sal-Strand-IBM ODD

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Description of the model, IBTRUTTA, follows the Overview, Design concepts and Details (ODD) protocol ([Grimm et al. 2020](#_ENREF_1)).

# Purposes and patterns

The model *SalStrand-IBM* is an individual-based model, created to simulate the effect of hydropeaking on total stranding mortality of populations of juvenile Atlantic salmon (parr) within rivers downstream of hydropower stations. The model was designed to examine the effect of a range of parameters, related to the hydropeaking regime, the morphology of the habitat, and the biological characteristics of the parr population, on total stranding mortality.

# Entities, state variables and scales

Parr are modeled as individual entities. The response of parr is governed by three parameters: (1) *locus movement speed*

* the speed (m timestep-1) at which an individual moves to habitat more suitable than the currently occupied habitat

(2) *territory size*

* the territory (expressed as a diameter, m) that the individual requires

(3) *stranding mortality probability*

* the probability that a stranded individual will die per timestep

Each individual parr is characterized by state variables (Table 1), used for either (1) controlling the processes applied and (2) recording the history of the individual.

Table 1. Parr state variables.

|  |  |
| --- | --- |
| Variable Name | Meaning |
| *ori-xcor* | x coordinate at end of burn-in |
| *ori-ycor* | y coordinate at end of burn-in |
| *xcor* | x coordinate |
| *ycor* | y coordinate |
| *heading* | Direction turtle is facing |
| *flockmates* | Conspecifics within territory size |
| *turtlesinfront* | Conspecifics in a ±45o cone in a 0.5×territory size in turtle *heading* |
| *min-distance* | Minimum distance to *flockmates* |
| *average-distance* | Average distance to *flockmates* |
| *distance-traveled* | Distance from *ori-xcor*, *ori-ycor* |
| *max-distance-traveled* | Maximum of all distance-traveled |
| *distance-bank* | Distance to bank |
| *meanx* | Mean x position of *flockmates* |
| *meany* | Mean y position of *flockmates* |

The model is spatial. The temporal extent is user controlled. The model time-step is 10 min.

# Process overview and scheduling

Processes are modelled by the following routines: (1) Migration to suitable habitat; (2) Migration away from conspecifics; and (3) Mortality from stranding (**Figure 1**).

**Graphical user interface, diagram

Description automatically generated**

**Figure 1. SalStrand-IBM function schematic.**

# Design concepts

## Basic principles

The model addresses how parr mortality is dependent on stranding. Specifically, the model addresses how total stranding mortality is dependent on characteristics of the hydropeaking cycle (ramping speed and length of the minimum flow period), characteristics of parr behavior (locus movement speed and territory size), and the probability of parr dying per unit time (stranding mortality probability).

Parr migrate to the most hydraulically suitable habitat available to them (sub-model: *Migration to suitable habitat*). Parr also migrate away from one another (sub-model: *Migration away from conspecifics*). These two sub-models produce behaviors that counterbalance one another, with the former causing parr to cluster in suitable habitat and the latter dispersing them and limiting the numbers present in this habitat. The sub-model *Migration to suitable habitat* implements a response to hydropeaking-induced down-ramping because it means that parr migrate away from areas that are becoming dewatered (very shallow and very low velocity areas are parameterized as being unsuitable). An additional sub-model, *Mortality from stranding*, implements a stranding mortality probability for those parr in dewatered areas.

## Emergence

Population abundances and dynamics emerge from characteristics of the parr individuals, such as the speed which they can migrate to water-covered habitat during down-ramping, and which they can survive stranding if temporarily stranded.

## Adaptation

Parr individuals do not have modelled learning or prediction.

## Interaction

Interaction between parr individuals is modeled using the function *Migration away from conspecifics*. Individuals sense other conspecifics within a territory size, identify whether there is an available location to flee to, and if such a location is present, flee to that location. This interaction results in individuals dispersing from one another.

## Stochasticity

Parr individuals are randomly distributed to areas with a habitat suitability ≥ 0.9. Routines are partly stochastic. The order in which migration away from conspecifics occurs is dependent on the order of parr selection (which is random).

## Collectives

The model does not include collectives.

## Observation

Data on the parr population are saved using the BehaviorSpace module of NetLogo.

# Initialization

The model is initialized with a user-specified number of parr individuals, and run for a user-specified number of years.

# Input data

The model uses time-series data on discharge, habitat suitability fields, and a field describing the distance to the nearest bank.

Parr populations are simulated for a user-specified time-period. The first years are used as a “burn-in” period ([see Williams et al. 2017](#_ENREF_2)), allowing parr to distribute themselves so as to reach an equilibrium between routines for *Migration to suitable habitat* and *Migration away from conspecifics*. Effects of model conditions on parr dynamics are determined from modelled outputs over the remaining time-steps of the simulation.

Migration to more suitable habitat and total stranding mortality in the *SalStrand-IBM* model are dependent on how the spatial distribution of suitable habitat and the spatial distribution of water-covered area change during the hydropeaking cycle. Habitat suitability in each 1 × 1 m cell is determined using a habitat suitability curve-based approach, based on suitability for velocity and depth (predicted externally by a hydrodynamic model), which changes according to discharge. The status of each cell in terms of the presence of water is calculated for each discharge. A depth > 0 m indicates a water-covered status. Stranding mortality is only applied to parr individuals in cells with a dewatered status (depth = 0 m).

# Sub-models

## Migration to suitable habitat

The parr individual identifies the location that has highest habitat suitability within a range of 5 m, and moves towards that location at a given speed, defined as the *locus movement speed* (*L*), if the suitability of that location is greater than the suitability of the current location the individual occupies and this location is unoccupied by conspecifics. The locus movement speed describes the movement in the locus position (the average holding position of the individual) over the 10 min time-step interval. Implicit in this routine is that parr individuals are able to detect suitable habitat in their proximity (radius of 5 m). To do this, it is assumed that the individual will be swimming around its location averaged across the 10 min time-step of the model (the *locus position*). These short-term, sub-10 min movements, are not explicitly modelled to minimize computational time.

## Migration away from conspecifics

The parr individual identifies if conspecifics (other individuals) are present within its *territory size* (*T*), expressed as a diameter of the circle centered on its locus position. If one or more conspecifics are within its territory size, the individual moves in the opposite distance from the average position of these conspecifics by this territory size. For example, if the territory size is 1 m, and there are two conspecifics in close proximity (< 1 m), one conspecific will move away from the other by a distance of 1 m. The result is that the minimum distance of separation between the conspecifics’ locus positions will be 1 m.

## Mortality from stranding

The parr individual experiences a mortality probability each time-step that it is occupying a dewatered location, defined as a stranding mortality probability (*M*). Locations become dewatered, depending on channel bathymetry and hydraulic conditions. Stranding mortality probability is defined in the model as a probability for a 4 h period (, corresponding to the length of a typical stranding event), but converted within the model to be applied at the model 10 min time-step, using the relationship .

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