# Sea Trout Model description

Index:

[1.1 Purpose 1](#_Toc412759132)

[1.2 Entities, state variables, and scales 1](#_Toc412759133)

[1.3 Process overview and scheduling 3](#_Toc412759134)

[1.4 Design concepts 4](#_Toc412759135)

[1.5 Initialization 6](#_Toc412759136)

[1.6 Input data 7](#_Toc412759137)

[1.7 Submodels 7](#_Toc412759138)

## 1.1 Purpose and patterns

## 1.2 Entities, state variables, and scales

*Entities*:

- Trout

- Patches

*State variables*:

- Trout main state variables: Table A.1

- Patches: habitat (freshwater vs. marine); patches in the marine habitat: parasites? (present or absent)

*Spatial scales*:

To be defined (right now: 100 x 100 patches, 50% fresh water-50% ocean)

*Temporal scale*:

Time step: weekly

Simulation length: user-defined (300 years)

**Table A1.** Entities included in the Sea Trout Model with their state variables and units of measurement.

|  |  |  |  |
| --- | --- | --- | --- |
| **Agent** | **Variable** | **Description** | **Unit** |
| Trout | age | Number of week since the fish was born | weeks |
|  | sex\* | Sex | M/F |
|  | habitat | Compartment where the fish is located | fresh/marine |
|  | state | Health status (whether the fish has parasites or not) | healthy/parasitised |
|  | mother\* | Identity of the fish mother | ID |
|  | father\* | Identity of the fish father | ID |
|  | z\_thresh\* | Phenotypic value of the condition threshold trait | unitless |
|  | GM\* | Genetic matrix (21 loci with 2 alleles coded by 1 or 0) | 21x2 binary matrix |
|  | G\* | Genotypic value for the condition threshold trait | unitless |
|  | e\_thresh\* | Enviornmental component for the condition threshold trait | unitless |
|  | cond\* | Condition trait (energy status?) | unitless |
|  | anadromous\* | Migratory tactic (whether the fish becomes anadromous) | true/false |
|  | quality | Quality | unitless |
|  | start\_quality\* | Quality of the fish when its migratory tactic is set | unitless |
|  | sea-time | Time spent by anadromous fish in the sea since migration | weeks |
|  | mates | Set of mature males selected by a female for reproduction | Agentset |
|  | time-since-repro | Time since last spawning event (for females) | weeks |
|  | FecAcc | Accumulated number of eggs produced by females | number of eggs |
| Patches | habitat\* | Environment | FW/Ocean |
|  | parasites?\* | Whether the patch has parasites or not | true/false |

\* Fixed state variables (do not change during a simulations).

## 

## 1.3 Process overview and scheduling

*Processes*:

- Patches do not perform any active process.

- Trout weekly actions (each time step): mortality, aging, update time counters

- Trout actions at specific times: migration, reproduction

*Schedule*:

0. Observer updates date counters.

1. Trout survive or die:

1.1. Density-dependent mortality (*grim-reaper* procedure)

1.2. Density-independent mortality (*mortality*)

2. Trout update age and other time counters (time-since-repro, sea-time).

3. Anadromous fish migrate (*migrate-to…*):

3.1. Migrate to the ocean (*migrate-to-ocean* week 14)

3.2. Migrate to the fresh water (*migrate-to-freshwater* week 44)

4. Trout reproduce (week 48):

4.1. Resident males change their location in the fresh water

4.2. Resident males try to sneak (*sneaker*) [if the sneaker tactic is turned on]

4.3. Mature females select mates (*choose-mates*)

4.4. Mature females reproduce (*reproduce*):

4.4.1. Egg production and fertilization (*reproduce*)

4.4.2. Genetic transmission of the heritable trait (*reproduce*)

4.4.3. Migratory tactic is set (*set-migratory-behaviour*)

5. Observer updates model graphical outputs and counters in the interface.

## 1.4 Design concepts

Objectives, Learning, Prediction and Collectives concepts do not apply to this IBM.

*Basic principles*:

*Emergence*:

*Adaptation*:

*Objectives*:

*Learning*:

*Prediction*:

*Sensing*:

*Interaction*:

*Stochasticity*:

*Collectives*:

*Observation*: The model produces graphical displays and provide output through counters at the interface. They track: number of fish broken out by sex and migratory tactic, number of fish in the marine habitat, number of parasitised fish, mean, variance and SD of *G* of males and females, mean quality of males and females, and proportion of each migratory tactic broken out by sex.

## 1.5 Initialization

- At initializing a model run, the user must specify the initial date and the length of the simulation. The user must also choose whether resident males can display a sneaker tactic, and the number, if any, of loci wherein there is sexual antagonism through the parameter *n-loci-sign* (parameter descriptions are in **Table A2**). If sexual antagonism is modeled, the *n-loci-sign* first rows of the 21 x 1 matrix of weights *WM* (see submodel for genetic transmission) of males are multiplied by -1.

- The global environment is initialized: the freshwater and marine habitats are created, and a proportion of marine patches set by the parameter *prop-parasites* become infested with parasites. These patches are selected randomly.

- The initial trout population is set by the parameter *n-trout*. All trout individuals are randomly placed in the freshwater habitat and initialized with a healthy state.

- Each individual’s state variable (sex, phenotypic and genotypic values of the condition threshold, condition, quality) is initialized by drawing values from probability distributions describing their variability.

The genome of each initial fish (described by their genetic matrix *GM*) is composed of a sequence of 21 linked loci with binary alleles (values 0 or 1) that are randomly assigned with equal probility.

The migratory tactic of the fish is set as described in the *set-migratory-behaviour submodel*.

## 1.6 Input data

The model does not use input data to represent time-varying processes.

## 1.7 Submodels

1.7.1. Density-dependent mortality in the fresh water (NetLogo procedure *grim-reaper*):

If the population in the fresh water is over its carrying capacity, set by the parameter *carryingCapacity*, trout challenge their survival (in random order) through Bernoulli trials using the proportion of surplus individuals in the freshwater population (population – K / population). The procedure stops once a number of trout equal to the surplus has died and the population is at K.

1.7.2. Density-independent natural mortality (*mortality*):

Each trout challenges its survival by means of a Bernoulli trial using the mortality rate. The mortality rate differs between males (*mortalityM*) and females (*mortalityF*), freshwater and marine (increased by multipliers *anad-death-multiplierM* and *anad-death-multiplierF*) habitat, and between healthy and parasitised (increased by multiplier *parasite-load*) individuals.

1.7.3. Migration (*migrate-to-ocean & migrate-to-freshwater*):

- *Seaward migration*:

Anadromous fish in the fresh water older than 52 weeks (age-1) move to the marine habitat, being placed in a random patch. If the migrant lands in an infested patch, its state changes to "parasitised" and its quality decreases, its new value being drawn from a normal distribution with mean *paras\_quality\_mean* and standard deviation *paras\_quality\_sd*.

- *Return migration*:

Anadromous fish in the marine habitat that have spent there more than 80 weeks (age-2) move to the freshwater habitat, being placed in a random patch, and reset their *sea-time* counter.

1.7.4. *Sneaker*:

Resident males search in a radius set by parameter *sneaker\_radius* and count the proportion of anadromous males relative to residents. If the proportion of anadromous males is greater than the *sneaker\_threshold*, then the resident gets a boost to its quality, defined by the parameter *sneaker\_boost*.

1.7.5. Selection of male mates (*choose-mates*):

Trout are mature after one year (52 weeks). Each female spawner selects in the fresh water the five mature males with the highest quality within a radius defined by the parameter *female-mate-radius*.

1.7.6. Reproduction (*reproduce*):

- *Produce and fertilise eggs*:

Female spawners produce a number of eggs that depends on the the spawner’s fecundity. Fecundity is modeled as a function of quality through a logistic function:

*fecundity* = *L* / (1 + e(- *k* \* (*quality* - *mass0*))

Where *L*, *k* and *mass0* are model parameters.

Each egg is fertilized by a male randomly chosen from the female’s mates, with equal probability of selection across mates,, that becomes the father of the new offspring.

The number of eggs produced by the female was translated into number of fry by assuming that only 10% of the eggs survived to the next stage.

Accumulated fecundity *FecAcc* of the female spawner is updated.

- *Genetic transmission of the heritable trait*:

The model includes a bi-allelic multilocus system for the condition threshold trait. For the trait, two branches representing two chromosomes are attributed with 21 loci, where each locus can take values of either 1 or 0. The last locus is a neutral marker and has no genetic effect. The genome of each fish is represented by a 21 x 2 matrix (*GM*), in which each column represents one branch and each row a locus.

The genome of a newly born individual is determined from the genetic material of its respective parents. One of the two alleles at each locus was randomly chosen to make up a unique branch of code per parent. The two branches from the two parents is then transferred to the new individual to create its *GM*.

1.7.7. Set migratory tactic and quality (*set-migratory-behaviour*):

- *Set migratory tactic*:

The phenotype of the condition threshold *z\_thresh* is defined as the sum of its genotypic value *G* (representing additive genetic variance) and a statistically independent random environmental effect *e\_thresh* drawn from a normal distribution N(0, *Ve*):

*z\_thresh* = *G* + *e\_thresh*

Males and females get the genotypic value for the threshold trait according to their genome, represented by the genetic matrix *GM*. The contribution of each locus to the genotypic value of the threshold trait is defined by the matrix of weights (*WM*), a 21 x 1 matrix in which each row is the weight of the given locus. Weights were estimated according to a negative exponential function, so that their sum equals the population mean of the additive genotypic value at initialization (set to 10). The genotypic value *G* of an individual is then computed as a matrix multiplication:

*G* = *sum-G-matrix* x *WM*

Where *sum-G-matrix* is a 1 x 21 matrix resulting from the matrix addition of the first and second columns (branches) of *GM* and subsequent transposition. *WM* is the matrix of weights.

The value of the condition trait *cond* is drawn from a normal distribution with mean *mu\_cond* and variance *V\_cond*. The condition trait *cond* is compared to the phenotypic value of the condition threshold *z\_thresh* and if an individual’s condition is greater than its threshold value, it becomes resident (i.e., *anadromous* = false), otherwise it becomes anadromous (*anadromous* = true).

- *Set quality*:

Resident individuals get the value of their *quality* state variable from a normal distribution with mean *res\_quality\_mean* and standard deviation *res\_quality\_sd*, while anadromous individuals get the value of their *quality* state variable from a normal distribution with mean *anad \_quality\_mean* and standard deviation *anad\_quality\_sd*.

**Table A2.** Model parameter descriptions and selected values with their sources.

|  |  |  |  |
| --- | --- | --- | --- |
| **Parameter** | **Description** | **Value** | **Source** |
| *n-trout* | Number of trout at initialization |  |  |
| *prop-parasites* | Proportion of marine patches infested with parasites |  |  |
| *carryingCapacity* | Carrying capacity of the freshwater habitat |  |  |
| *mortalityM* | Mortality rate of males in the freshwater habitat |  |  |
| *mortalityF* | Mortality rate of females in the freshwater habitat |  |  |
| *anad-death-multiplierM* | Extra mortality for males in the marine habitat |  |  |
| *anad-death-multiplierF* | Extra mortality for females in the marine habitat |  |  |
| *parasite-load* | Extra mortality due to parasites |  |  |
| *paras\_quality\_mean* | Mean of the normal distribution used to define the quality of infected trout |  |  |
| *paras\_quality\_sd* | Standard deviation of the normal distribution used to define the quality of infected trout |  |  |
| *sneaker?* | Indicates whether resident males use a sneaker tactic |  |  |
| *sneaker\_radius* | Radius within which mature resident males count the number of competing mature anadromous males |  |  |
| *sneaker\_threshold* | Proportion of mature anadromous males inside the *sneaker\_radius* over which a mature resident male becomes a sneaker |  |  |
| *female-mate-radius* | Radius within which mature females select mature males for reproduction |  |  |
| *L* | Parameter of the fecundity logistic function – the maximum value of the curve |  |  |
| *k* | Parameter of the fecundity logistic function – the steepness of the curve |  |  |
| *mass0* | Parameter of the fecundity logistic function – the midpoint of the curve on the x axis |  |  |
| *Ve* | Variance of the normal distribution used to define the environmental effect on the condition threshold trait |  |  |
| *WM* | Matrix of weights defining the contribution of each locus to the genotypic value of the condition threshold *G* |  |  |
| *n-loci-sign* | Number of loci that have a different sign in the males’ matrix of weights *WM* |  |  |
| *Gpm* | Mean genotypic value of the male population at initialization |  |  |
| *Gpf* | Mean genotypic value of the female population at initialization |  |  |
| *mu\_cond* | Mean of the normal distribution used to define trout condition |  |  |
| *V\_cond* | Variance of the normal distribution used to define trout condition |  |  |
| *res\_quality\_mean* | Mean of the normal distribution used to define the quality of resident males |  |  |
| *res\_quality\_sd* | Standard deviation of the normal distribution used to define the quality of resident males |  |  |
| *anad \_quality\_mean* | Mean of the normal distribution used to define the quality of anadromous males |  |  |
| *anad\_quality\_sd* | Standard deviation of the normal distribution used to define the quality of anadromous males |  |  |