1 FishMet

FishMet — A simulation model of fish feeding and appetite

Synopsis

fishmet.exe [OPTIONS]

DESCRIPTION

FishMet, is a mechanistic, process-based agent-based simulation model of feeding, appetite and growth in fish. It has been engineered from the start to provide extensibility, interoperability and a plugin-like application within a larger digital twin system. FishMet is a discrete time model running over numerous time steps with the resolution of 1 s. The model works at the fine-grained level of individual feed items and individual fish decisions. This will potentially allow for complex simulations with variable feed, complex schedules and stochastic environment.

For more details of the model, see the FishMet model User Manual.

OPTIONS

-h, --help, /h or /help

print brief help

-g, --force-gui, -gui, /gui force the model to start in the GUI mode.

-run, --run-model, /run

force run model at startup with the default parameters from the configuration file and then exit.

-q, --quiet, /q, /quiet

"quiet mode" with minimum output.

-b, --batch, /b, /batch

"batch mode" with no screen output, useful for running script. Note that GUI is always disabled in the batch mode.

ENVIRONMENT VARIABLES

Some global aspects of the program can also be controlled via the system environment variables.

FFA_MODEL_PARAMETER_FILE

Defines the name of the file that keeps global model parameters. If this environment variable is not set, the default name parameters.cfg is used.

FFA_MODEL_GUI

if set to 1 or yes or true will force the model to start in the GUI mode.

FFA_MODEL_OUTPUT_DEST

sets the output destination as output_dest parameter in the model configuration file. The value set by the environment variable takes priority over the configuration file. Note that the outout destination can also be set using the output_dest parameter in the configuration file, but this environment variable takes priority.

FFA_MODEL_OUTPUT_TAG

sets the model tag that is added to all automatically generated files.

FFA_MODEL_OUTPUT_TAG_CONFIG_REV

causes to determine the model tag that is added to all automatically generated file names from the configuration_version parameter in the main parameter configuration file. See configuration_version parameter.

GUI_PLOT_AREA_WIDTH

sets the width of the graphical plotting area. The default value is 110. But if you have a very big computer screen, this may be increased. As an approximate orientation, GUI_PLOT_AREA_WIDTH=150 is adequate for a 75dpi screen 1920x1200i, GUI_PLOT_AREA_WIDTH=200 is okay for 2560x1440.

CONFIGURATION FILE

The configuration file is a text file with various model options that are set as $option_name = value$ format. Any line starting from # is a comment and is ignored. This file is mandatory, the model program will not work without it.

The standard name of the configuration file is parameters.cfg

Program options

interface_graphical

default program interface type, graphical true or command line false.

output_dest

Output destination (usually directory): all plot and output data files will be saved there. The default value is if this variable is absent or directory is not writeable is the current directory. This parameter affects the program behaviour only in the command line user interface and not in the graphical user interface. Note that fish object data save fish_object_data is saved exactly into the fish_object_file because this is non-human readable internal binary data not intended as the model output. The destination can refer to destination directory or output file name prefix. In the former case it should terminate with the operating system specific directory delimiter (e.g. / on GNU/Linux or \ on Microsoft Windows). If the value of output_dest does not terminate this way, it will refer to the file prefix. It is important that the output destination can also be set with the FFA_MODEL_OUTPUT_DEST environment variable, which takes priority over this configuration file parameter. The following outputs are saved to the output_dest:

- output plots produced by save command;
- output arrays by save model_output;
- rate arrays by save rate_output;
- output statistics by output stats and append stats.

time_plots_unit_scale

Scale units for the time-based plots 1=sec, 2=min, 3=hours.

rate_unit_scale

Default time unit scale for calculating rates. Rate unit is set as digit: 1=s-1, 2=min-1, 3=h-1.

plot_scale_relative

define whether to use the raw absolute or relative for some of the time-based plots, e.g. stomach and midgut mass dynamics. true means relative scales, i.e. stomach or midgut food mass plot displays filling relative to the total capacity, false means that absolute food mass is used.

rate_interval

default discretization interval in minutes that is used to calculate rate, e.g. this interval is used to plot the ingestion rate

gui_plot_window_page_size

default page size (height, width) for the GUI plot window in pixels.

gui_plot_area_width

default width of the plot output area in pixels.

gui_plot_area_aspect

default aspect ratio (height/width) of the plot output area.

configuration_version

defines the configuration version tag that is added to all automatically generated output files. The tag should be defined using Subversion "\$Revision: 1234 \$" keyword. It is then parsed to exclude everything except the revision number, adding "conf_r" prefix. (so configuration_version = "\$Revision: 1234 \$" translates to "conf_r1234". Note that this behaviour is enabled if the environment variable FFA_MODEL_OUTPUT_TAG_CONFIG_REV is set to any value and disabled otherwise.

food_provision_file_name

This variable defines the file name that contains the food provision scheduling. This file should be in CSV format or a single-column plain text. In a multi-column CSV file, the last column is assumed to contain the feed scheduling. Scheduling is encoded by **zero** and **non-zero** values by minute (or by second if food_provisioning_file_by_s is set to TRUE). Here any non-zero value means that food is provided during the respective minute interval, zero means that food is not provided. The file is intended to describe the temporal pattern for 24 h, any longer sequence is discarded. All missing values used for filling the remaining minutes to complete the 24 h are zeroes, i.e. food not provided. The pattern is then propagated for all 24 h periods if food_provision_file_repeat is TRUE or applied once if food_provision_file_repeat is FALSE. Note that the file takes priority over the food ononing pattern defined in food_provision_pattern. **Example:** food_provision_file_name = "../file_name.csv"

food_provision_file_repeat

A logical flag that defines if the feed scheduling pattern defined by the food_provision_file_name file will propagate to all 24 h periods or applied just once to the first such period. The default value is TRUE.

Example: food_provision_file_repeat = TRUE

food_provisioning_file_by_s

Global logical flag that defines if the feed scheduling pattern defined by the food_provision_file_name file represents the data for each time step (s) (if TRUE) or by minute (FALSE). The default value is FALSE i.e. data are given for each minute.

Example: food_provisioning_file_by_s = FALSE

stats_output_file

The name of the CSV file to save general output statistics for specific run of the model. The default name is "fishmet_stats.csv" Example: stats_output_file = "data.csv".

stats_output_long

This is a logical parameter that defines if the output stats are saved using the long or short format. In the first case, both the input parameters and the output stats are saved/appended into the CSV file. Note that the default value is TRUE. **Example:** stats_output_long = TRUE

stats_output_prediction_stamp

This parameter define if the prediction timestamp is produced in the output stats file. This timestamp then takes the model execution timestamp and adds the time equivalent to the run_model_hours simulation duration. The default value is FALSE. All timestamps are produced in the following format: 2023/07/21 03:09:50.

Example: stats_output_prediction_stamp = TRUE

fish_object_file

The name of the binary file to save the fish object data, i.e. all data for the model fish allowing to resume simulation from a specific fish state (stomach and midgut content, appetite level etc). The default file name is fishmet_fish_state.bin. Note that the file name must have the .bin file extension, otherwise it is not accepted.
Example: fish_object_file = "persistent_data_1.bin"

stomach_emptying_matrix

The name of the CSV data file that defines the stomach emptying parameter matrix, an interpolation grid matrix that defines how long does it take to process full stomach calacity of the feed until no feed remains in the stomach. The matrix defined in this file determines stomach emptying time for a range of fish body mass (columns) and ambient temperatures (rows).

An example of the stomach emptying matrix is provided below:

,	50,	100,	300,	500
5,	24,	35,	75,	100
10,	15,	20,	50,	75
15,	9,	15,	40,	50
20,	5,	10,	30,	35
22,	4,	8,	29,	33

Here the rows define ambirnt temperatures (5,10,15,20,22 C) and columns refer to the fish body mass (50, 100, 300, 500 g).

Model parameters

The parameters of the model described below can de defined in the parameter file or set during the runtime using the command line or graphical user interface. They can also be defined in a batch script file.

run_model_hours

Total number of hours for which the simulation is run. It translates into the raw time steps internally as $T = H \times 3600$, where T is the number of time steps, H is the run_model_hours parameter and 3600 is seconds per hour. Example: run_model_hours = 24.

daytime_hours

Default daytime duration, hours. The night time duration is defined as 24-daytime_hours. Note that feeding activity occurs only during the day time and not at night. Example: daytime_hours = 12.

day_starts_hour

Default hour at which the daytime is normally started. It is also the initial offset for day at the start of the simulation. **Example:** $day_starts_hour = 6$.

temperature

Ambient temperature °C. Example: temperature = 14.

body_mass

Fish body mass at the start of the simulation, g. Example: body_mass = 10.0.

body_mass_override

Override body_mass value from fish object file (see fish_object_file) with input parameter value.

baseline_activity_day

Baseline locomotor activity, swimming speed SL/s, during the day as defined by daytime_hours parameter. + Example: baseline_activity_day = 2.5.

baseline_activity_night

Baseline locomotor activity, swimming speed, SL/s, during the day as defined by daytime_hours parameter. + Example: baseline_activity_night = 0.5.

stomach_capacity

fish stomach mass, max. filling capacity, g. Example: stomach_capacity = 5.0.

midgut_capacity

fish midgut mass, max. filling capacity, g. Example: midgut_capacity = 10.0.

stomach_midgut_automatic

logical flag determining, when TRUE, that stomach_capacity and midgut_capacity are continuously automatically recalculated based on the body mass body_mass. Note that this can override any fixed parameter values set by the parameter values stomach_capacity and midgut_capacity.

Example: stomach_midgut_automatic = True

absorption_ratio

Absorption ratio in the midgut, relative to the initial mass of food. **Example:** absorption_ratio = 0.7.

ingestion_delay

Delay after ingestion, min. Water uptake occurs during the delay. **Example:** ingestion_delay = 30.

water_uptake

Proportion of water uptake, relative to the initial food item mass. **Example:** water_uptake = 0.20.

water_uptake_a

Water uptake pattern over time is defined by the logistic equation $\frac{c}{1+ae^{-r^2t}}$, where c is the upper limit of the mass, a and r are logistic parameters and e is natural logarithm base. The a and r parameters of the equation refer to the water_uptake_a and water_uptake_r parameters. See also water_uptake_r. **Example:** water_uptake_a = 200.0.

water_uptake_r

Water uptake pattern over time is defined by the logistic equation $\frac{c}{1+ae^{-r^2t}}$, where c is the upper limit of the mass, a and r are logistic parameters and %e is natural logarithm base. The a and r parameters of the equation refer to the water_uptake_a and water_uptake_r parameters. See also water_uptake_a. Example: water_uptake_r = 0.01.

digestion_delay

Delay of digestion, min. This refers to the time interval from the moment the food item gets into the mid-gut until absorption of the food starts. **Example:** digestion_delay = 20.

midgut_maxdur

The maximum duration a food item can be processed in the fish midgut, min. If it stays in the mid-gut for any longer time, it is evacuated. Example: midgut_maxdur = 180.

transport_pattern_t

Grid array defining the food transport pattern in the stomach. This array defines the time grid for interpolation. Note that normally it takes several hours until the food item fully disappears from stomach (gastric emptying time). This parameter can be set either in hours (small numbers) or in raw seconds (large numbers) and the correct time unit is normally autodetected by the program. See also transport_pattern_r.

Example (s): transport_pattern_t = 0 3000 15000 21600
Example (hours): transport_pattern_t = 0, 0.8, 4, 6

transport_pattern_r

Grid array defining the food transport pattern in the stomach. This array defines the proportion of food mass left in stomach at each level of transport_pattern_t array. See also transport_pattern_t. **Example:** transport_pattern_r = 1.0 0.6 0.01 0.0.

appetite_night

Fish appetite at night. This value is normally low because the fish do not feed at night. If the value is absent or negative, fish appetite does not reduce at night.

Example: appetite_night = 0.1

appetite_factor_a

Appetite factor is defined by the logistic equation: $\frac{c}{1+ae^{-r^2t}}$. This parameter refers to *a*. See also appetite_factor_r. **Example:** appetite_factor_a = 50000.0.

appetite_factor_r

Appetite factor is defined by the logistic equation: $\frac{c}{1+ae^{-r^2t}}$. This parameter refers to r. See also appetite_factor_a. **Example:** appetite_factor_r = 20.0.

appetite_threshold_stomach

Protective appetite threshold for stomach: this is the maximum value of the stomach appetite signam when the overall fish appetite level depends only on stomach filling. Setting a sufficiently low value provides a way to protect stomach from overfilling.

Example: appetite_threshold_stomach = 0.2

appetite_energy_rate

Logistic appetite parameter describing defining the energy appetite component dependence on the energy budget. Example: appetite_energy_rate = 40.0

appetite_energy_shift

Logistic appetite parameter describing defining the energy appetite component dependence on the energy budget. **Example:** appetite_energy_shift = 0.2

activity_appetite_factor

Activity appetite factor determining how fish locomotor activity increases with increasing appetite. **Example:** activity_appetite_factor = 0.5

stress

This is an array of time points that define intervention of stress. The array can be defined either in raw s time scale or in minutes depending on stress_is_min parameter. Example: stress = c(1200, 6000).

stress_metabolic_cost

The maximum value of the metabolic cost of stress in units of resting metabolic rate (SMR). The actual metabolic cost at each time step scales depending on the time since stress intervention defined by stress array, following the stress pattern described by the stress_grid_hour and stress_grid_fact arrays. **Example:** stress_metabolic_cost = 0.5

stress_is_min

Defines if stress intervention timing is defined in minutes (TRUE) or raw s (FALSE)). Example: stress_is_min = TRUE

stress_grid_hour

Stress effect interpolation grid array. $stress_grid_hour$ defines the time since the stress intervention occurs. The second array, stress_grid_fact, defines the intensity of the stress effect. Example: $stress_grid_hour = c(0, 10, 20, 40, 50, 72)$

stress_grid_fact

Stress effect interpolation grid array. $stress_grid_fact$ defines the intensity of the stress effect. For example, if it is equal to 1.0, appetite is completely suppressed. The other array, stress_grid_hour defines the time scale (h) for each point. **Example:** $stress_grid_fact = c(1.0, 0.9, 0.7, 0.2, 0.1, 0.0)$

midgut_michaelis_r_max

Michaelis-Meneten food absorption parameter in midgut, r_max, relative to the mass of the food item. Rate is per second, the basic discrete step of the model. E.g. 0.8 means that 80% of the food item mass can be absorbed at maximum. See also midgut_michaelis_k. Example: midgut_michaelis_r_max = 0.9.

midgut_michaelis_k

Michaelis-Meneten food absorption parameter in midgut, K_M, relative to the total midgut capacity (e.g. 0.25 means a quarter of the total midgut mass). See also midgut_michaelis_k. **Example:** $midgut_michaelis_k = 0.25$.

midgut_temp_fact_t

Temperature adjustment for absorption is controlled by the two parameters that define the temperature adfjustment grid factor for the Michaelis-Menten equation: $midgut_temp_fact_t$ and $midgut_temp_fact_m$. This parameter is the temperature grid for Michaelis-Menten absorption process. Example: $midgut_temp_fact_t = c(5.0, 10.0, 15.0, 25.0)$.

midgut_temp_fact_m

Temperature adjustment for absorption is controlled by the two parameters that define the temperature adfjustment grid factor for the Michaelis-Menten equation: $midgut_temp_fact_t$ and $midgut_temp_fact_m$. This parameter is the temperature grid for Michaelis-Menten absorption process. This is the speedup factor grid for the Michaelis-Menten absorption process for the temperatures defined by $midgut_temp_fact_t$.

Example: midgut_temp_fact_m = c(0.4, 0.6, 1.0, 8.0)

smr_oxygen_temp

Interpolation X axis grid defining the SMR function on the temperature °C.

smr_oxygen_o2

Interpolation grid Y axis defining the SMR function on the temperature. SMR unit is $mg O_2 kg^{-1} h^{-1}$.

branchial_energy_factor

A parameter defining branchial and urine (ZE+6UE) energy consumption as a factor to SMR, e.g. 0.3 means (UE+ZE) = 0.3*SMR. This is an alternative to branchial_ammonia_rate. If both branchial_energy_factor and branchial_ammonia_rate are defined, the former parameter always takes priority. **Example:** branchial_energy_factor = 0.1

branchial_ammonia_rate

A parameter defining branchial and urine (ZE+6UE) energy consumption as a fixed ammonia excretion rate, micromol per g body mass per hour. This is an alternative to branchial_energy_factor. If both branchial_energy_factor and branchial_ammonia_rate are defined, the former parameter always takes priority. **Example:** branchial_ammonia_rate = 0.25

sda_absorption_rate_max

Defines the specific dynamic action (SDA) that depends on the absorption rate. There are two parameters that define the linear relationship between absorption rate and SDA increase. This parameter defines the maximum absorption rate when the maximum SDA (defined by sda_energy_factor_max is reached. Example: $sda_absorption_rate_max = 0.0007$

sda_energy_factor_max

Defines the specific dynamic action (SDA) that depends on the absorption rate. There are two parameters that define the linear relationship bet ween absorption rate and SDA increase. This parameter defines the maximum SDA reached at the maximum absorption rate defined by sda_absorption_rate_max. For example, this parameter equal to 2.0 means that SDA = SMR * 2.0 at the maximum absorption rate.

Example: sda_energy_factor_max = 2.0

food_item_mass

Basic dry mass of one food item (g). Example: food_item_mass = 0.25.

feed_gross_energy

Gross energy content of the feed, MJ/kg (= kJ/g) Example: feed_gross_energy = 23.0.

food_input_rate

Rate of food item input, per min. Example: food_input_rate = 6.0.

food_provision_pattern

Food provision patterning is determined by an array defining the time intervals (min) when food is provisioned and not provisioned e.g. a value of 10 230 means 10 min food is given followed by 230 min not given. Note also that any arbitrary food scheduling can be obtained by encoding periods of food provisioning and not provisioning in the food_provision_file_name parameter. **Example:** food_provision_pattern = 10 230.

feed_start_offset

The offset (delay, min) to start feeding at the beginning of the 24 hour period. The feeding pattern defined by food provision pattern starts every 24h period after this offset. For example, if the offset is set to 180 min, this means that the first feeding session defined by the food_provision_pattern begins 3h (180 min) after the start of the day. **Example:** feed_start_offset = 180

stomach_emptying_matrix

The stomach emptying parameter matrix, an interpolation grid matrix that defines how long does it take to process full stomach calacity of the feed until no feed remains in the stomach. The matrix is defined in a file set by stom-ach_emptying_matrix.

USER INTERFACE

The program has two interface modes: command line (CMD) and graphical (GUI). Default parameters of the model and the program are obtained from the configuration file parameters.dat.

COMMAND LINE INTERFACE AND SCRIPTING

By default it starts in the command line (terminal window) interface. This can be changed by the interface_graphical option in the configuration file (set to true).

Basic commands

The command line user interface involves typing commands in the program shell. Alternatively, a set of commands can be provided in a batch script file.

help

Get brief help on the commands. Several subcommands can be used: parameters, plot.

run

Run the model with the default parameters. Alternative alias: start.

reset

Reset all model parameters to the default values from the configuration file. Alternative alias: restart.

R

quit exit the program.

set

Set any model parameter defined in Model parameters. Example: set run_model_hours=24. Another use of the set command is to define the output format for saving plots (see save command): set format or set save_format, then define one of the possible output formats: PDF, PNG, SVG, BMP, GIF, EPS, WMF, CGM. This command is also used to define rate interval: set rate_interval as well as to define override flags.

plot

Produce parameter plots or model output plots. To save a plot to a disk file, use the related save command. Rate plots can have different rate interval using set rate_interval command. Example: plot stomach_transport. Subcommands:

- stomach_transport Stomach transport curve;
- absorption_mm Michaelis-Menten absorption;
- appetite_factor Appetite factor;
- smr_function SMR pattern function;
- total_ingested Cumulative N food ingested;
- mass_ingested Food mass ingested, g;
- ingestion_rate Food ingestion rate;
- absorption_rate Absorption rate;
- not_ingested Cumulative N food not ingested;
- encountered Cumulative N food encountered;
- appetite Overall appetite level;
- total_stomach Total mass of food in stomach;
- total_midgut Total mass of food in midgut;
- absorption Total cumulative absorption;
- energy_balance Energy balance, kJ;
- oxygen_uptake oxygen uptake, mg O2 per kg per hour
- body_mass Body mass, g;
- growth_rate Growth rate, g/min;
- sgr Specific growth rate, g/min;
- activity Locomotor activity, SL/s;
- evacuation Cumulative evacuation.

save

Save a plot defined as in the plot subcommand. This command also requires two additional parameters: plot type as in plot and the file name. **Example:** save stomach_transport plot_01.pdf. Another use of this command is for saving model output data (CSV formatted table):

- model_output, output_arrays or output_data model output arrays;
- rate_output, output_rate, rate_data model rate data (using default rate interval, see set rate_interval command to change it).
- fish_object_data or fish save full fish object data allowing to resume simulation using the load command. Note that the file name for the fish object is defined by fish_object_file.

load

• fish_object_data or fish - load full fish object data allowing to resume simulation. Note that the file name for the fish object is defined by fish_object_file.

show

This command is used to print specific model parameters.

- show params or params: print all parameters of the model;
- show stomach_transport with optional raw or adjust: show stomach transport unadjusted or adjusted to temperatrure and fish mass;
- show stomach_emptying: display the current stomach emptying matrix as obtained from the stomach_emptying_matrix;
- show version: print the program version;
- show timesteps: print the total number of timesteps;
- show stomach_transport raw, show stomach_transport adjust: display the unadjusted and adjusted stomach transport grid arrays: transport_pattern_t and transport_pattern_r;
- show save_format or show format: print the graphic output format (PDF, PNG, SVG, BMP, GIF, EPS, WMF, CGM, CSV).
- show plot_scale_relative: print if the time plots show raw data or relative values (e.g. stomach filling relative to the total stomach capacity).
- show statistics or show stats: show general model output statistics.

adjust stomach_transport

Adjust the stomach transport parameter arrays for the body_mass and ambient temperature. See also stomach emptying matrix.

output statistics

Initiate output of the general model statistics into stats_output_file csv output data file. Note that this results in writing the column headers and the first row of the data. All subsequent data output should use the append statistics command. Warning: The output command will overwrite any existing CSV file, be careful!.

append statistics

Append general statistics data for the current run of the model. Note that the first output should use the output statistics command.

shell

Execute some operating system specific command. This command can be useful, for example, for checking files from within the model program, moving files, deleting temporary files etc. Example: shell dir /w (this will show all files in the working directory on Windows without size, timestamp and other details).

Override flags:

The load command that loads the fish object data to resume simulation works such that when the simulation is resumed, fish parameters (e.g. body_mass) are obtained from the fish object data (see fish_object_file) rather than the model parameters, either defined in the parameter file or set command. This ensures smooth continuous simulation over many "resumes." However, there is a method to override the fish object data parameters with those explicitly defined by set or parameter file. It is done by setting the body_mass_override flag to TRUE with set command.

Example: "set body_mass_override = True": the value of the body_mass will be obtained from input parameter rather than fish object file.

Scripting

Many model runs can be performed by a script that contains a sequence of commands. Any line starting with # is considered a comment and is ignored.

Here is an example of a script:

```
set run_model_hours = 100
# ---
set food_item_mass=0.05
set food_input_rate=30
run
save ingested zz_ingested_005.pdf
save appetite zz_appetite_005.pdf
save output_data zz_ingested_005.csv
# ---
set food_item_mass=0.1
set food_input_rate=15
run
```

save ingested zz_ingested_010.pdf
save appetite zz_appetite_010.pdf
save output_data zz_ingested_010.cs

To run the script issue this command on the terminal:

fishmet.exe < script_file.cmd</pre>

GRAPHICAL USER INTERFACE

The graphical interface uses the menus and buttons to control the program.

To start the mode in the GUI mode, use this commend: fishmet.exe -gui

Note

```
There is a Windows VBS script fishmet.vbs to force the model in the GUI mode suppressing the terminal window completely.
```

EXIT STATUS

0

Success

1

Failure or error

BUGS

Todo

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RESOURCES

Main web site: http://fishmet.uib.no/

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