

Figure 1: overview of the data generation process

File name: st_1_experimental_details.csv

Content: Experimental details collected from the publications. Unique values are reported for each experiment-treatment.

Header description:

- doi: publication digital object identifier;
- first_author: surname of the first author of the publication;
- *year*: year of the publication;
- facility: name and country of the aquaculture facility;
- experiment: unique identifier for experiment within publication;
- *treatment:* unique identifier for treatment within publication;
- *exp_id*: unique index of the pairs experiment-treatments for the use in the model;
- *included*: binary field, *n* indicates entry has been excluded for model fit;
- reason_for_exclusion: textual description on the rationale for excluding entry form model fit;
- *t_initial*: age at the beginning of the experiment (DAH);
- *t_final*: age at the end of the experiment (DAH);
- *Temperature*: mean of the water temperature during experiment (C°);
- weaning_prey: prey used during weaning (categorical);
- weaning_duration: duration of the weaning (days);
- *main_prey:* prey category used during the treatment (categorical);
- *prey_status*: status of the prey (live or frozen);
- ration_bw_perc: food ration (% body weight day⁻¹);
- egg type: description of the egg and broodstock origin (categorical);
- photoperiod: photoperiod used in the experiment (light hours:dark hours);
- *volume_l:* (volume of water in the experimental tank);
- animal_per_tank: (number of animals per experimental tank);
- *density_animals_liter*: number of animals per liter of water in the experimental tank;
- *notes:* additional annotations.

File name: st2_sample_info.csv

Content: samples information collected from the publications. Data are associated to each experiment-treatment and time of the observation.

Header description:

- *publication_id*: unique identifier for publication;
- *experiment_id*: unique identifier for experiment within publication;
- *treatment_id*: unique identifier for treatment within publication;
- *nsamp*: sample size (numbers);
- t1: age of the observation for w1 (DAH);
- t2: age of the observation for w2 (DAH);
- w1: mean weight at t1 (grams);
- w2: mean weight at t2 (grams);
- *errorw1*: weight standard deviation at t1 (grams);
- *errorw2*: weight standard deviation at t2 (grams);
- *igr.mu*: mean instantaneous growth rate ($\mu_{IGR_{t_i}}$; % weight increase day⁻¹);
- igr.sd: instantaneous growth rate standard deviation ($\sigma_{IGR_{t_{i,i}}}$; % weight increase day⁻¹);
- *fr.mu*: mean feeding rate (% body weight day⁻¹);
- *fr.sd*: feeding rate standard deviation (% body weight day⁻¹);
- *prey_type*: unformatted name of the prey used during the treatment (categorical);
- *exp_id*: unique index of the pairs experiment-treatments for the use in the model;
- *experiment*: unique index of the experiments for the use in the model;
- t: mean age (DAH);

File name: diet info.csv

Content: information on diet and proxy for food ration associated to each experimental treatment

Header description:

- exp_id: unique index of the pairs experiment-treatments for the use in the model;
- *main_prey*: prey category used during the treatment (categorical);
- *Rcomma:* proxy of food ration (relative);
- *Temperature*: mean of the water temperature during experiment (C°);

File name: input_data.csv

Content: data combining other datasets, for replicate *i* of experiment *j*

Header description:

- *publication_id*: unique identifier for publication;
- *experiment_id*: unique identifier for experiment within publication;
- *treatment_id*: unique identifier for treatment within publication;
- *nsamp*: sample size (numbers);
- *t1*: age of the observation for w1 (DAH);
- *t2*: age of the observation for w2 (DAH);
- w1: mean weight at t1 (grams);
- w2: mean weight at t2 (grams);
- errorw1: weight standard deviation at t1 (grams);
- errorw2: weight standard deviation at t2 (grams);
- *igr.mu*: mean instantaneous growth rate ($\mu_{IGR_{t_{i,j}}}$; % weight increase day⁻¹);
- igr.sd: instantaneous growth rate standard deviation ($\sigma_{IGR_{t_{i,j}}}$; % weight increase day⁻¹);
- *fr.mu*: mean feeding rate (% body weight day⁻¹);
- *fr.sd*: feeding rate standard deviation (% body weight day⁻¹);
- *prey_type*: unformatted name of the prey used during the treatment (categorical);
- *exp_id*: unique index of the pairs experiment-treatments for the use in the model;
- experiment: unique index of the experiments for the use in the model;
- t: mean age (DAH);
- *main_prey:* prey category used during the treatment (categorical);
- *Rcomma:* proxy of food ration (relative);
- *Temperature*: mean of the water temperature during experiment (C°);
- case: treatment of partial missing information as described in Table 1.

File name: M1_model_data.csv

Content: subsample of input_data.csv used to fit M1 model variants.

Header description:

- ... variables not described are identical to the file input data.csv;
- z1: z-scored Rcomma (z-score applied to all the values included in input_data.csv);
- z2: z-scored Temperature (z-score applied to all the values included in input_data.csv);
- *Index.t:* unique progressive index associated with treatmens;
- *Index.e:* unique progressive index associated with experiments;
- *Index.no:* single value to fit models with no random effects;
- *Index.food:* unique progressive index associated with prey category;

File name: M2_model_data.csv

Content: subsample of input_data.csv used to fit M2 model variants.

Header description:

- ... variables not described are identical to the file input_data.csv;
- z1: z-scored Rcomma (z-score applied to all the values included in input_data.csv);
- z2: z-scored Temperature (z-score applied to all the values included in input_data.csv);
- *Index.t:* unique progressive index associated with treatmens;
- *Index.e:* unique progressive index associated with experiments;
- *Index.no*: single value to fit models with no random effects;
- *Index.food:* unique progressive index associated with prey category;