

Introduction

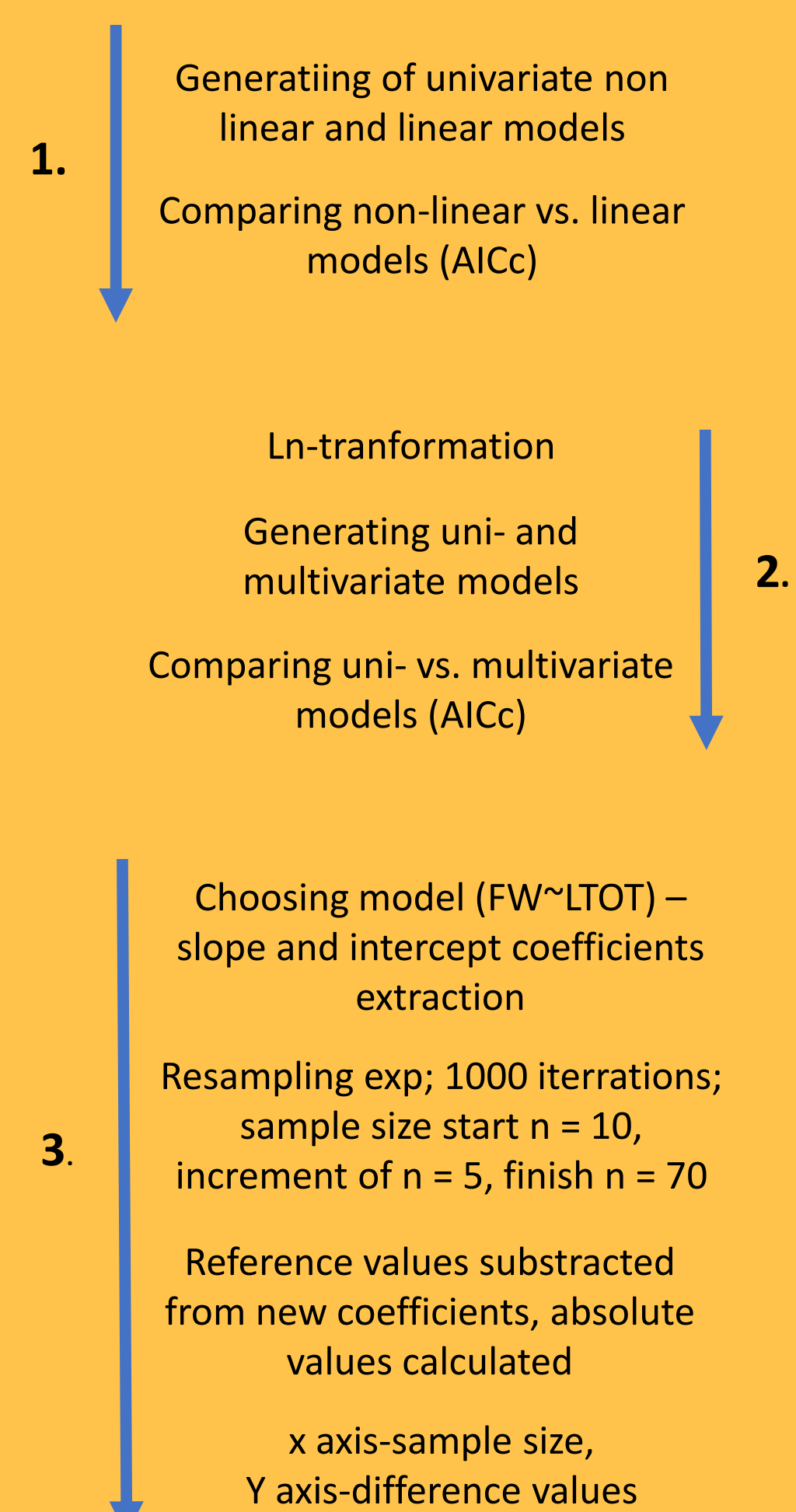
Gongolaria barbata (Fig. 1) is an important canopy-forming macroalga, providing key ecosystem services (together with other canopy forming species from the order Fucales) in intertidal and subtidal zones of the Mediterranean Sea (Blanfuné et al., 2019). In recent times, its populations along the Istrian coast (northern Adriatic Sea) have sharply declined. The only remnant populations are those found in some shallow bays, rockpools and coastal lagoons (Iveša et al., 2022). Therefore, development and application of non-destructive methods for long-term monitoring of remnant populations and future restored populations is to be considered (Orfanidis et al., 2017). This study aimed to generate site-specific (lagoon vs. rockpools) predictive models for estimating wet biomass using different morphometric variables. Non-linear and linear univariate models were compared using the Akaike information criterion (AICc). Then, linear uni- and multivariate models were created for each study population, and best models were selected based on the corrected AICc. Furthermore, a resampling experiment with replacement was conducted using the lagoon dataset to determine the minimum sample size required for creating site-specific predictive models. The results of this study should provide an insight of the basic relationship between wet biomass and morphometric characteristic of *G. barbata* from different sites, and elucidate the knowledge of the potential for developing valuable models for future monitoring of remnant populations.



Fig. 1 *G. barbata* from the lagoon.

Tab. 1 Results (models, AICc and R²) of the comparison between different generated models (uni-/multivariate) for biomass prediction, presented for the lagoon and rockpools dataset.

Model formula	ΔAICc	R ²
Lagoon (n = 70)		
FW ~ 1.119*LTOT - 1.887	0.00	0.88
FW ~ 1.147*LTOT - 0.030*NK - 1.925	2.15	0.88
FW ~ 1.105*LTOT + 0.036*LK - 1.921	2.15	0.88
FW ~ 1.129*LTOT - 0.018*NK + 0.018*LK - 1.927	4.46	0.88
FW ~ 0.759*NK + 0.921*LK - 1.588	26.52	0.83
FW ~ 0.916*NK + 0.215	77.02	0.65
FW ~ 1.349*LK - 1.172	112.64	0.42
Rockpools (n = 36)		
FW ~ 0.457*LTOT + 1.141	0.00	0.51
FW ~ 0.296*NK + 0.430LK + 1.137	0.70	0.52
FW ~ 0.389*LTOT + 0.092*NK + 1.189	2.11	0.50
FW ~ 0.395*LTOT + 0.119LK + 1.090	2.21	0.50
FW ~ 0.110*LTOT + 0.230*NK + 0.331LK + 1.120	3.22	0.50
FW ~ 0.639*LK + 1.200	7.68	0.39
FW ~ 0.442*NK + 1.721	7.84	0.39



Methods

We randomly sampled 70 individuals from a coastal lagoon on the southern Istrian coast (June 2021), and 36 individuals from rockpools on the western Istrian coast (July 2021). We generated univariate linear and non-linear (power function) models for each variable using raw data (morphometry: LTOT-total cauloid length, NK-number of cauloids, LK-cauloid length; FW-biomass), then compared model fit via the corrected Akaike information criterion (AICc). Next, we transformed the given variables and fit uni- or multivariate linear models to the transformed data using single predictor variables and combination of variables, thus getting seven linear models for each study site. Models were compared via AICc, and best models were chosen based on the ΔAICc < 2 condition (Tab. 1). In general, the lower the criterion value, better the model. If values of generated models are within the ΔAICc < 2 condition, the models are considered equal in quality of prediction. Furthermore, a resampling experiment with replacement was done (on FW~LTOT model from the lagoon dataset). Data was ln-transformed, the linear model was generated, then slope and intercept coefficients were extracted from the model and used as reference values for the later comparison with newly generated coefficients related to different sample sizes. The resampling comprised of 1000 iterations, starting with the sample size of n = 10, and increasing the sample size by the increment of 5, all the way to the size of n = 70. The reference slope and intercept coefficient values were then subtracted from the newly generated slope and intercept coefficient values from different sample sizes, then the absolute values were calculated. The obtained absolute slope and intercept difference values were then plotted, each of the value shown on the y-axis, while increments of sample size being presented on the x-axis. The methods of generating and choosing the best models, as well as choosing the minimal sample size are similarly used for predicting fresh weight of *Saccharina latissima* (Laminariales, Phaeophyceae) in Southern British Columbia (Campbell & Starko, 2021). All calculations, models and plots were performed using R software, version 4.2.2 (R CORE Team 2018).

Results

- No difference in model quality (ΔAICc < 2) among non-linear and linear univariate models built from raw data (lagoon data) (Fig. 2a, c, e).
- No difference between linear and non-linear models for the cauloid length (LK; Fig. 2f) metric from raw data using the rockpools dataset (difference for other metrics; Fig. 2b, d).
- Univariate model using total cauloid length (LTOT) raw data from the lagoon dataset explains 88% (R² = 0.88) of the variation in fresh weight (FW; Fig. 2a).
- Univariate model using number of cauloids (NK; Fig. 2d) raw data from the rockpools dataset explains 49% (R² = 0.49) of the variation in fresh weight (FW).
- ln-transformed data (lagoon) – univariate model LTOT shows the best quality of fit (ΔAICc < 2; explains 88 % of the variation in fresh weight; Tab. 1), followed by LTOT+NK, LTOT+LK, LTOT+NK+LK models (as well explaining 88% of the variation; Tab. 1).
- ln-transformed data (rockpools) – univariate model LTOT shows the best quality of fit (ΔAICc < 2; explains 51 % of the variation in fresh weight; Tab. 1).
- Increment in sample size leads to more precise and reliable models (Fig. 3).

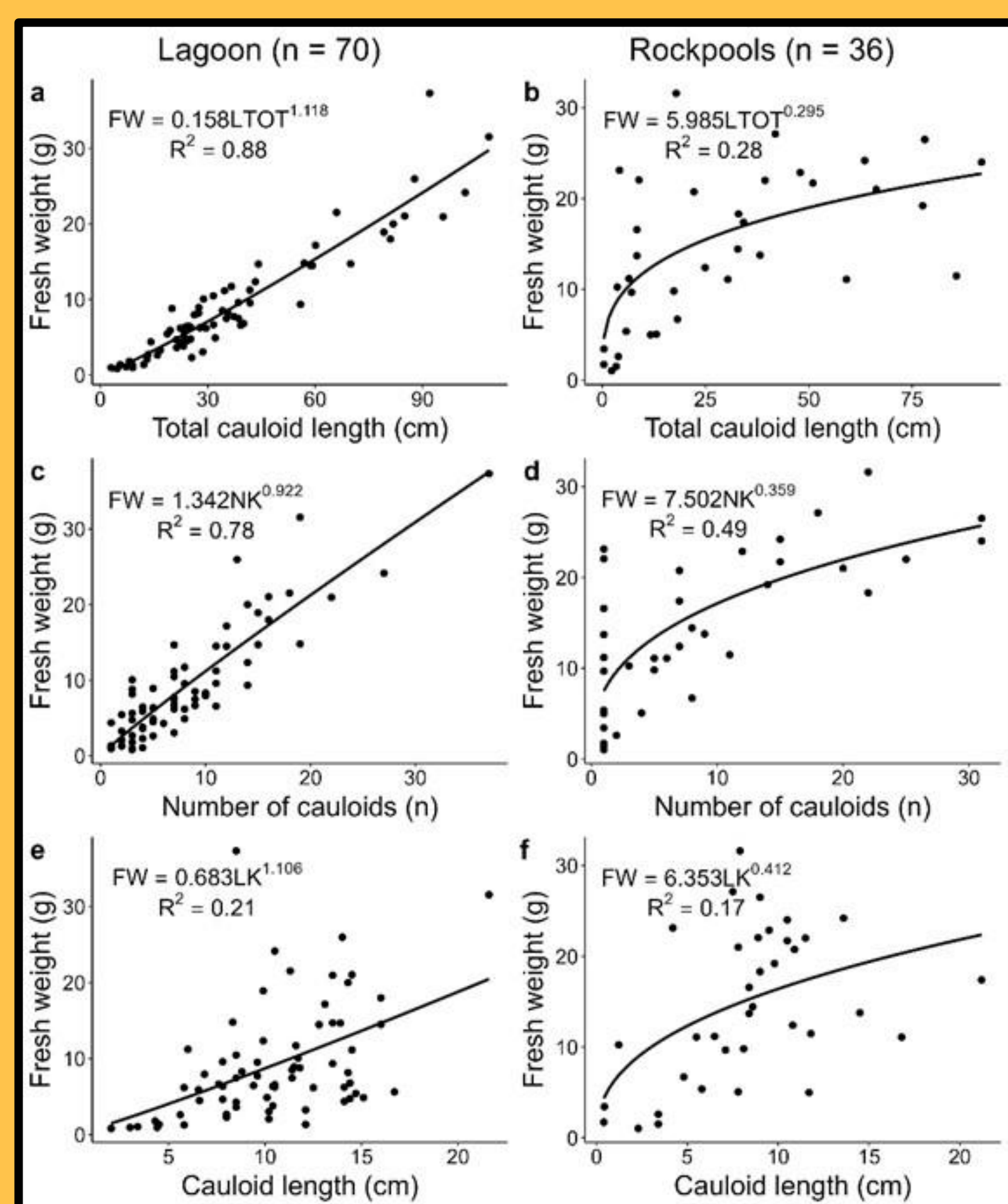


Fig. 2 Non linear univariate models (raw data) showing the relationship between fresh weight and other morphometric variables for *G. barbata* from the lagoon (a, c, e) and from rockpools (b, d, f).

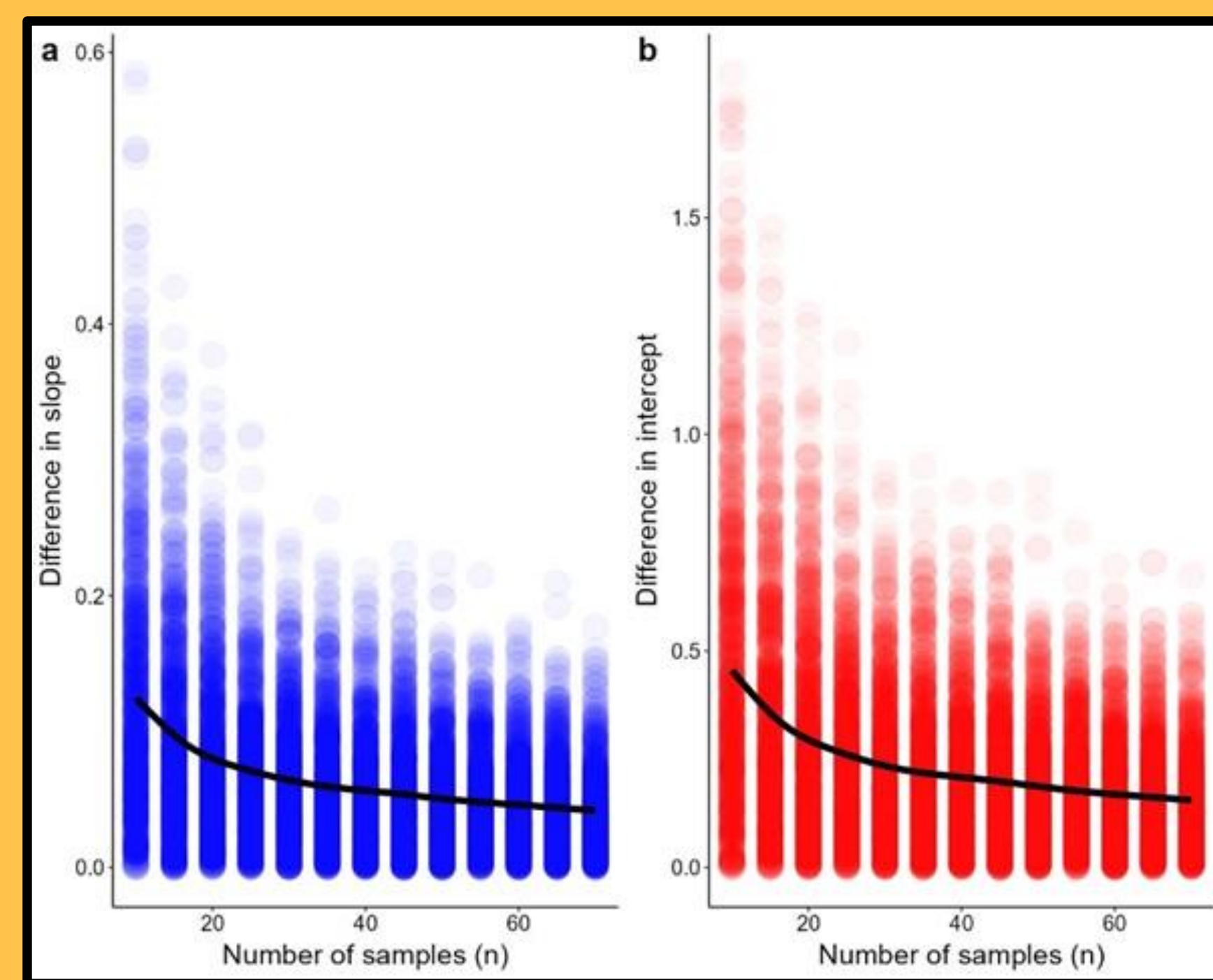


Fig. 3 Differences in slope (a) and intercept (b) from the resampling experiment using 1000 iterations (FW~LTOT model from the lagoon dataset, ln-transformed data).

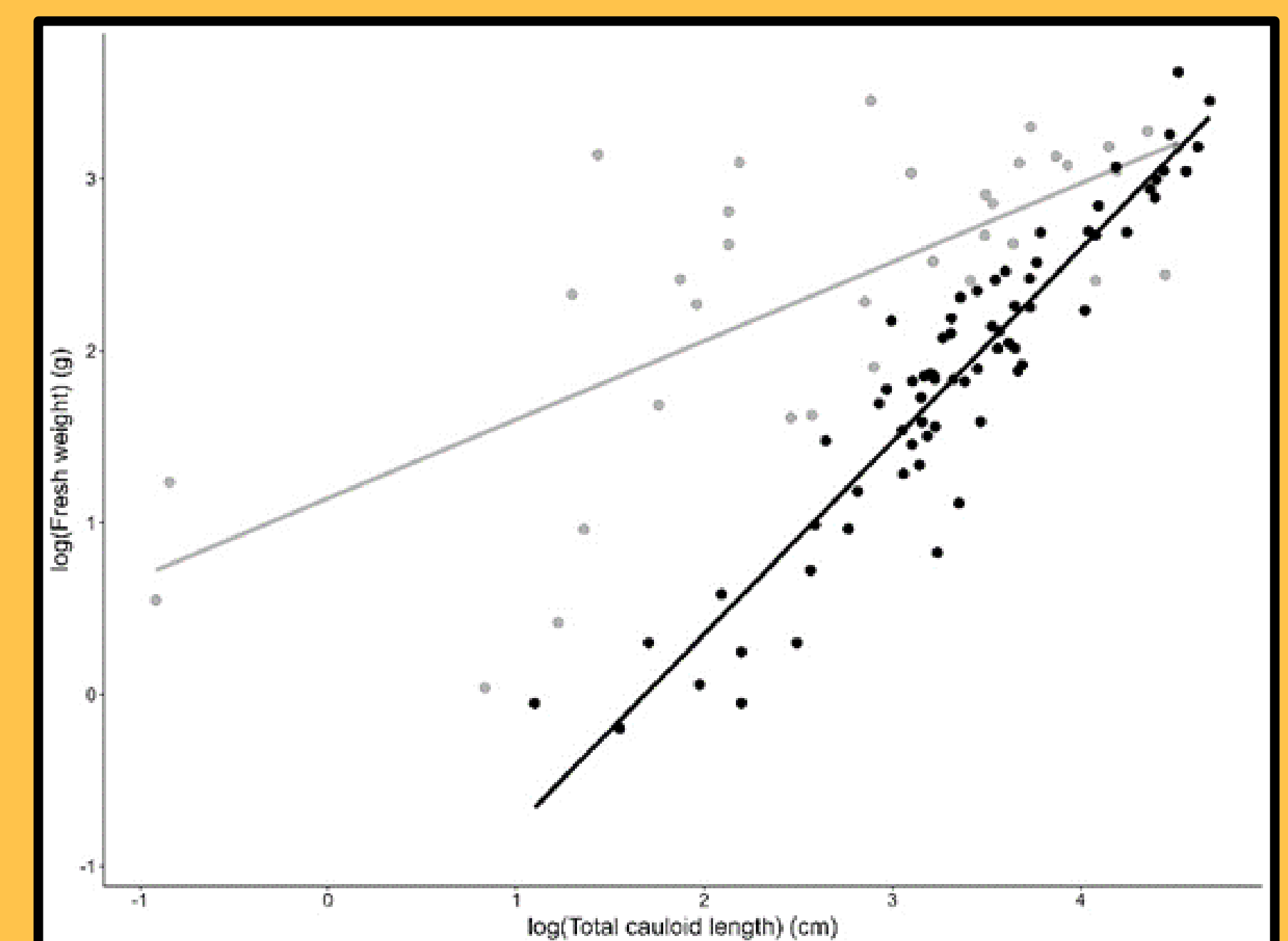


Fig. 5 Relationship between fresh weight and LTOT from the lagoon data (bold dots and line) and from the rockpools data (pale dots and line).

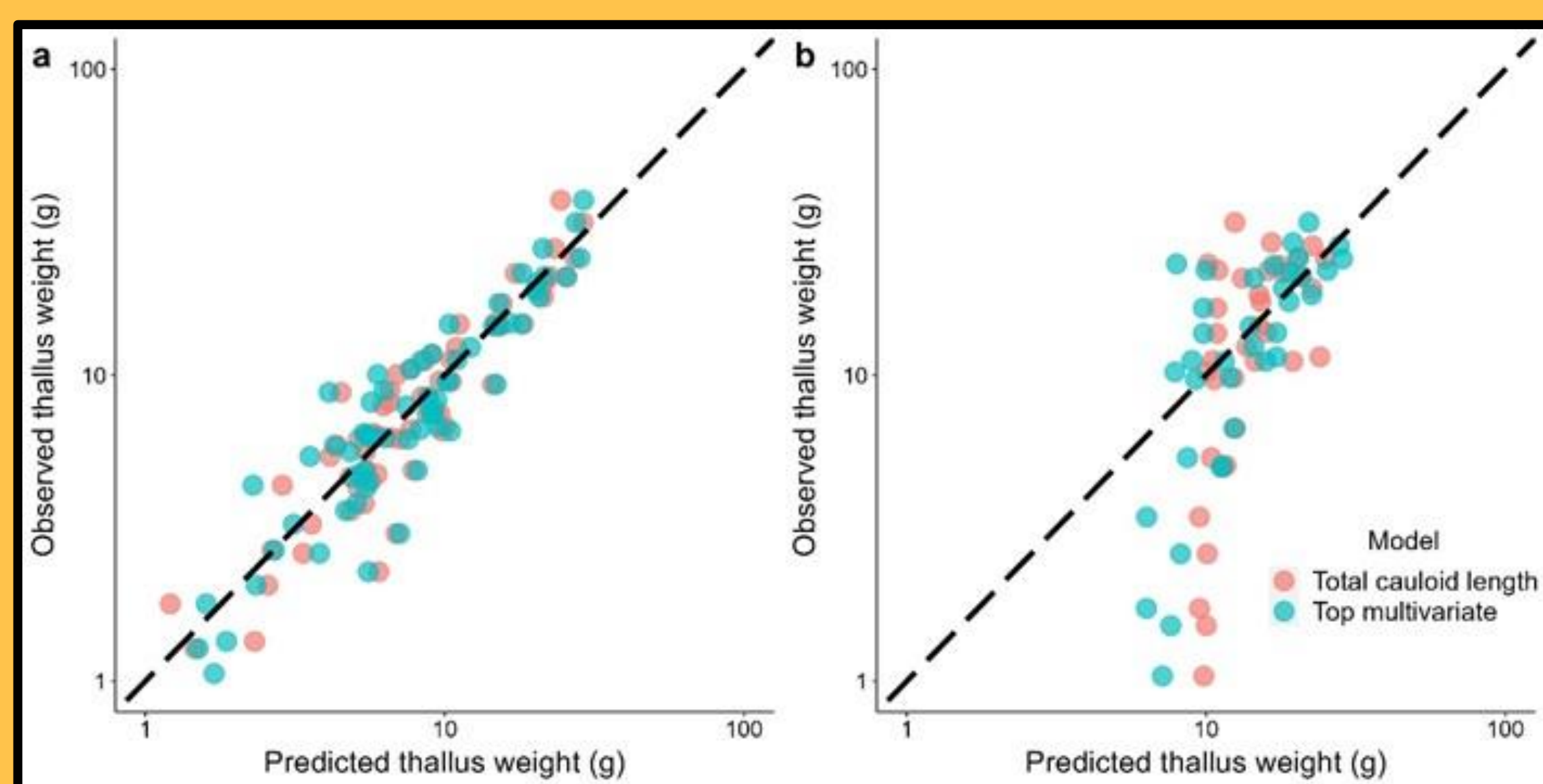


Fig. 4 Relationship of observed fresh weight and predicted fresh weight for the lagoon (a) and rockpool (b) dataset, showing the top univariate and top multivariate model.

Conclusions

- Non-linear and linear univariate models (LTOT) generated using raw data can be used for biomass prediction, but in a site specific context (lagoon; Fig. 5).
- Linear univariate (particularly LTOT) and multivariate models (LTOT+NK, LTOT+LK, LTOT+NK+LK) generated out of ln-transformed data can be used for predicting biomass, but also in a site specific context (lagoon; Fig. 4).
- The relationship of morphometric characteristics with biomass in the rockpools dataset didn't show the potential for biomass to be predicted out of these variables in comparison to the lagoon case.
- The minimal sample size needed for constructing the best fitted univariate model (FW~LTOT) for the lagoonal dataset is found to be between n = 35 and n = 45 (Fig. 3).
- At the moment there is no evidence that a „regional“ model for predicting biomass out of morphometric characteristics is possible (Fig. 5).
- For *G. barbata* populations, models should be build and used (if reliable) in a site-specific context.

References

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