



The Bias of combining variables on fish's aggressive behavior studies

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ABSTRACT

Quantifying animal aggressive behavior by behavioral units, either displays or attacks, is a common practice in animal behavior studies. However, this practice can generate a bias in data analysis, especially when the variables have different temporal patterns. This study aims to use Bayesian Hierarchical Linear Models (B-HLMs) to analyze the feasibility of pooling the aggressive behavior variables of four cichlids species. Additionally, this paper discusses the feasibility of combining variables by examining the usage of different sample sizes and family distributions to aggressive behaviour variables. The subject species were: the angelfish (*Pterophyllum scalare*), the tiger oscar (*Astronotus ocellatus*), the *Cichlasoma paranaense* and the Nile tilapia (*Oreochromis niloticus*). For each species, 15 groups of 3 individuals were assigned to daily observations (10-min recordings) for 5 days. Aggressive behavior data was labeled according to its aggressive intensity. The variables chase (C), tail beating (TB), push (P), lateral attack (LA) and bite (B) were classified as high intensity. The variables undulation (U), lateral threat (LT) and frontal displays (FD) were classified as low intensity. These behaviors, however, were not present in all species. Model parameters were estimated by Monte Carlo Markov chains using non-informative priors. B-HLMs were performed to assess the impact probability of each variable in the analysis. Results revealed that when combining variables, the resulting distribution is strongly influenced by only one variable in each category. Moreover, in some cases the aggregate values altered the results, which changed the probabilities of the main variables. Species with low aggressive behavior frequencies, such as *A. ocellatus*, are more sensitive to this bias. LT was the main low intensity variable for all species, while B was the main high intensity variable for the *P. scalare* and the *O. niloticus*. LA was the high intensity category variable that was the most relevant for the *C. paranaense* and *A. ocellatus*. Moreover, combining the variables did not impact the feasibility of reducing the sample size when compared to using the most quantitative variable. For all species a sample size of 12 did not change the study conclusions. With respect to family distribution, based on DIC values the Gaussian model is more suitable for most of the studied species. However, caution should be taken, because the Gaussian posterior probability distribution overlapped 0 in some cases, which is biologically impossible in aggressive behaviors. The only exception is the *A. ocellatus*, which, based on DIC values, was the only species better modeled by a Poisson distribution. Bayesian analysis can be therefore considered a strong tool for analyzing aggressive behavior

1. Introduction

Aggression is an important aspect of behaviour in many social species and it is used to establish a dominance hierarchy and to defend territory (Maan et al., 2001). The aggressive interactions are dynamic

and, depending on the species, can escalate in different time-ranges. However, when prolonged, these interactions can cause bodily harm and increased social stress, leading to impaired growth and welfare (Damsgård and Huntingford, 2012). Because many social species are farmed and fished by the aquaculture and fisheries industries, there is a

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growing body of scientific literature examining the welfare of cultured and wild fishes.

In these studies the behavioral variables are standardized and described in ethograms (e.g. Galhardo et al., 2008; Carvalho et al., 2012). Some typical examples of these variables are bites, lateral attacks, lateral threats, and undulation. These variables are usually either analyzed individually (e.g. Oliveira et al., 2011), partially combined (sum of events based on a given criteria) (e.g. Gómez-Laplaza and Morgan, 1993; Desjardins et al., 2012), or fully combined (sum of all aggressive events) (e.g. Gonçalves-de-Freitas et al., 2008; Maan et al., 2001; Ros et al., 2006; Almazán-Rueda et al., 2004; Castro and Caballero, 2004). Among these types of classifications, the partially combined is the most ambiguous within the literature because it has been classified under many different names, for example: the overt aggression and the restrained aggression (Desjardins et al., 2012; Balzarini et al., 2014), the high and the low intensity attacks (Gómez-Laplaza and Morgan (1993); Werneker and Kramer, 2002; Gonçalves-de-Freitas and Mariguela, 2006), and the Asymmetric high-intensity agonistic attacks (AHI) (e.g. Galhardo et al., 2008). Despite the different classifications, however, these variables all have something in common; they are all based on the energetic costs of aggressive behaviors (e.g. Gómez-Laplaza and Morgan, 1993, Ros et al., 2006; Arnold and Taborsky, 2010). Although plausible, to date no mathematical criteria has been adopted for pooling these variables into a single variable. In fact, pooling variables can generate a bias in data analysis, especially when the combined variables are shown in different temporal patterns during fighting events (Dearing et al., 2001; Noleto-Filho et al., 2017).

In aggressive studies, problems with fully combined variables have previously been acknowledged by Noleto-Filho et al. (2017) for *P. scalare* who have highlighted that the pattern of the most quantitative behavioral variable usually prevails, although there are some exceptions where the other variables (less quantitative ones) cause small deviations to this pattern. It is likely that this problem applies to the partially combined variables, since the variables that are partially aggregated share similar properties with the fully combined variables, such as different frequencies and sometimes different patterns (e.g. Gonçalves-de-Freitas and Mariguela, 2006; Ros et al., 2006). These variables are usually analyzed using the Gaussian distribution. However, they can also be analyzed using a Poisson distribution given that the Poisson distribution is composed of counts and discrete data (Ventura et al., 2015; Sadoul et al., 2016; Slavík et al., 2016). Noleto-Filho et al. (2017) described a suitable approach for using Bayesian Hierarchical Linear Models (B-HLMs) and Raftery's criteria (Raftery, 1995) to measure the impacts of combining aggressive data with a cichlid species. Their results were reliable, although they were sensitive to the number of replicates (Noleto-Filho et al., 2017). Sensitivity was measured by simulating a sample size reduction and checking if conclusions would remain the same. Therefore, they were able to identify how many replicates were necessary to reach the same conclusion.

Table 1

Aggressive behavior in four cichlid species (adapted from Carvalho et al., 2012; Gonçalves-de-Freitas and Mariguela, 2006; Brandão et al., 2015). For √ - aggressive event is present. For 0 - aggressive event is absent.

	Species			
	<i>P. scalare</i>	<i>C. paranaense</i>	<i>A. ocellatus</i>	<i>O. niloticus</i>
Agonistic event				
Attacks				
Chase: one fish follows the opponent that swims in opposite direction.	√	√	√	√
Tail beating: The tail is quickly and sharply struck against the stimulus. Tail must actually contact divider to be scored.	0	√	0	0
Lateral attack: the fish remain alongside each other facing the same or opposite direction and beat their tails sideways.	0	√	√	√
Bites: the aggressor swims toward the opponent and bites its body.	√	√	√	√
Push: A fish with its open mouth nips the lateral flank of its opponent, sometimes displacing the opponent	0	√	0	0
Displays				
Circling: two fish with erected dorsal fin swim following each other, describing a circle, like a very slow chasing.	0	0	0	√
Frontal display: both fish approach frontally each other with head-up posture (around 45°), but without physical contact.	√	0	√	0
Lateral threat: one fish with their fins spread and mouth opened approaches laterally to the opponent, which keeps away.	√	√	√	√
Undulation: only one fish beats its tail side- ways (undulating the body), without spreading its fins.	√	0	0	√

The feasibility of partially combined variables has not yet been explored for cichlids or any other fish families. Within this family, it is common for many species to have dominance hierarchies in either one or both sexes and to have complex social behaviors associated with territoriality and reproduction (Maruska et al. 2014). Also, many of these social species display different aggressive patterns and frequencies (e.g. Carvalho et al. 2012, Gonçalves-de-Freitas & Mariguela 2006, Brandão et al., 2015) which can produce different contexts for data analysis. Therefore, the present study aims to use B-HLMs to check the feasibility of partially combined variables in four cichlids species. Moreover, a second objective of this study is to verify the suitable number of replicates and the more appropriate family distribution to perform aggressive behavior studies, as these are important issues for model accuracies.

2. Materials and methods

2.1. Subjects and maintenance

The subject species were the *Pterophyllum scalare* (Schultze 1823), the *Astronotus ocellatus* (Agassiz 1831), the *Cichlasoma paranaense* Kullander 1983 and the *Oreochromis niloticus* (Linnaeus 1758). These four freshwater cichlids present aggressive relationships which have already been described in laboratories (Carvalho et al., 2012; Gonçalves-de-Freitas and Mariguela, 2006; Brandão et al., 2015; Carvalho et al., 2008). These species were chosen because of their viability (acquisition), differences in frequency and type of aggressive behavior, and therefore improved our data analysis as they provided more contexts for bias evaluation. Regarding the four species, the animals were kept for 15 days in water tanks of 500 L polyethylene (ca. 1 fish/10 L) and fed with food for cichlids (pellets) in the morning and the evening (8:00 and 18:00), until apparent satiety. With the exception of tilapia, no distinction regarding sex was made. The water temperature was controlled at 27–28 °C (Pérez et al., 2003; Kelsch et al., 1990). The water quality was maintained through biological filters (filter 400 L/h) and constant aeration. The photoperiod was kept on 12 h of light (07:00 h to 19:00 h). The tanks were siphoned every week to remove the remnants of food and feces.

2.2. Experimental design

Regarding the four species, 15 groups of three animals each were subjected to 5 days of observation in aquaria (40 × 30 × 40 cm; ca. 48 L). Animal sizes (standard length) were between 3–5 cm, 5–10 cm, 6–8 cm and 5–10 cm for *P. scalare*, *O. niloticus*, *C. paranaense* and *A. ocellatus*, respectively. Aggressive behavior was recorded daily for 10 min. The aggressive interactions were quantified by the frequency of aggressive behavior based on ethograms described for each species (Table 1) (*P. scalare* and *O. niloticus* - Carvalho et al., 2012; *A. ocellatus* -

Gonçalves-de-Freitas and Mariguela, 2006; *C. paranaense* - Brandão et al., 2015). This ethogram is composed of minor variables which are individual events that are classified and combined into two major variables: the attacks (more energetic expense, with body contact) and the displays (less energetic expense, no physical contact) (Table 1). This classification was used because it is a common data pooling criteria in most aggressive behavior studies (e.g. Haller and Wittemberger, 1988; Gómez-Laplaza and Morgan (1993); Werneyer and Kramer, 2002; Gonçalves-de-Freitas and Mariguela, 2006; Arnold and Taborsky, 2010).

2.3. Statistical modeling

Model fitting was carried out with data from each variable using Monte Carlo Markov chains (Metropolis-Hasting algorithm) with non-informative priors (Jeffreys, 1961).

2.3.1. Assessing the possible bias in combining variables

To test the hypotheses of bias in combining variables, we have estimated the posterior distributions of each longitudinal variable by implementing a Bayesian Hierarchical Linear Model (B-HLMs) with a Gaussian distribution (Ventura et al., 2015). In addition, we have assessed the posterior probability of difference in means among days in the minor variables and in their respective major variables (Gelman, 2003; Kruschke, 2012). Since Gaussian distributions allow for negative results, and these are biologically impossible for aggressive behaviors, this distribution was truncated to zero. Additionally, a B-HLM that implemented a Poisson distribution was performed to test the suitability of a different probability distribution on discrete data. Subsequently, the Deviance Information Criterion (DIC) was also calculated as a measure of model fit to compare the statistical models. DIC values are inversely related to the compromise between fit and parsimony (Spiegelhalter et al., 2002). In both models, the Bayesian posterior probability of difference in means was computed (Gelman, 2003; Kruschke, 2012).

The Gaussian model was specified as:

$$\begin{aligned} W_i &\sim N(\theta[Y_i], \tau[Y_i]) \\ \theta_i &\sim N(\mu, t) \\ \mu &\sim N(0, 1.0E - 7)I(,0) \\ t &\sim 1/(\sigma_1^* \sigma_1) \\ \sigma_1 &\sim \text{Uniform}(0, 100) \\ \tau_i &\sim 1/(\sigma_{2i}^* \sigma_{2i}) \\ \sigma_{2i} &\sim \text{Uniform}(0, 100) \end{aligned} \quad (1)$$

where W_i indicates the term for i observations with a normal distribution (N) and θ specifies the mean for each category Y with precision τ . The hyperparameter μ is the overall mean with the precision t . The parameters σ_1 and σ_2 are the standard deviations for the precisions τ and t , respectively.

The Poisson model was as follows:

$$\begin{aligned} W_i &\sim \text{Poisson}(\lambda_i) \\ \log(\lambda_i) &= b[Y_i] \\ b_i &\sim N(\mu, t) \\ \mu &\sim N(0, 1.0E - 7) \\ t &\sim 1/(\sigma^* \sigma) \\ \sigma &\sim \text{Uniform}(0, 100) \end{aligned} \quad (2)$$

where W_i indicates the term for i observations with a Poisson distribution and b specifies the mean for each category Y for parameter λ . The hyperparameter μ is the overall mean with precision t , both specified by a vague prior distribution. The parameter σ is the standard deviation for the precision t .

2.3.2. Sample size suitability

To measure the suitability of the sample size, we used the same

posterior probability of difference models described above. However, we ran the models 10 times at random and took away one replicate from the dataset each time. To reduce the sample size for *P. scalare* and *O. niloticus*, we used the two main minor variables lateral threat (LT) and bites (B), and the two major variables displays (D) and attacks (A). To reduce the sample size for *C. paranaense*, we used the two main minor variables lateral threat (LT) and lateral attacks (LA), and the two major variables displays (D) and attacks (A).

We calculated the Cohen d effect size (1988) to measure the impact of reducing the sample size. We considered values of 0.2, 0.5 and 0.8 for small, medium and large effects, respectively (Cohen, 1988).

2.4. Software and simulations

The models were generated through the online web tool BayesBehav, available at <https://euriconoleto.shinyapps.io/BayesBehav>. This web tool makes it easier to implement Bayesian longitudinal models through the R statistical package “rjags” (Plummer et al., 2006) and the JAGS software (Just Another Gibbs Sampler) (Plummer, 2003). JAGS uses precision as the inverse of variance. The jags code used by the web tool is described in Appendix A.

The parameters were estimated through simulations by using 3 chains and 10,000 iterations in the model convergence process. The Gelman-Rubin criterion (Gelman and Rubin, 1992) was used to check convergence success or failure. The Gelman-Rubin diagnosis (Gelman and Rubin, 1992; Brooks and Gelman, 1998) was used to establish a period of “burn-in” constituted by the disposal of 1000 samples to help model convergence. The 5% level that is standard in statistical practice in much of biostatistics, epidemiology, and other areas of application was considered statistically “relevant” (Gelman, 2013), assuming 95% Bayesian credible intervals.

3. Results

All species presented behavioural variables with very low frequencies that were not suitable to be modeled (*O. niloticus*: Lateral Attack; *A. ocellatus*: bites, frontal display and lateral threat; *P. scalare*: frontal display). Thus, we only described the variables that achieved model convergence and passed model fit criteria (*O. niloticus* and *P. scalare*: bites, chase, lateral threat and undulation; *A. ocellatus*: lateral attack and chase; *C. paranaenses*: lateral attack, chase, push, tail beating and lateral threat).

For all species, only one or two variables provided similar results to the combined variables. Within this context, a reduction of the sample size was only considered to be feasible for the most frequent variables, since using only these variables would have no effect on the study conclusions, as described below. Moreover, for sake of simplicity, results for the species *P. scalare* & *O. niloticus*; and *C. paranaense* and *A. ocellatus*, were presented in pairs due to the similar outcomes they generated.

3.1. Combining variables

3.1.1. *P. Scalare* and *O. Niloticus*

For the major variable attacks (A) of the *P. scalare* and the *O. niloticus* two minor variables stand out: chase (C) and bites (B). When combining these two minor variables in category A, the resulting distribution was strongly influenced by category B for both species (Figs. 1A–C and 2 A, B, C). Similar patterns, close means values and probabilities were also observed, although the latter varied from 1% to 3% (*P. scalare*) or from 3% to 7% (*O. niloticus*), depending on the species. For *P. scalare*, when comparing the major variable attacks with the minor variable bites, the differences between the second-third, and the fourth-fifth days decreased from 77% to 74% and from 94% to 92%, respectively (Figs. 1B and C). Moreover, differences among the third-fourth day increased from 73% to 76%. Both variables increased from

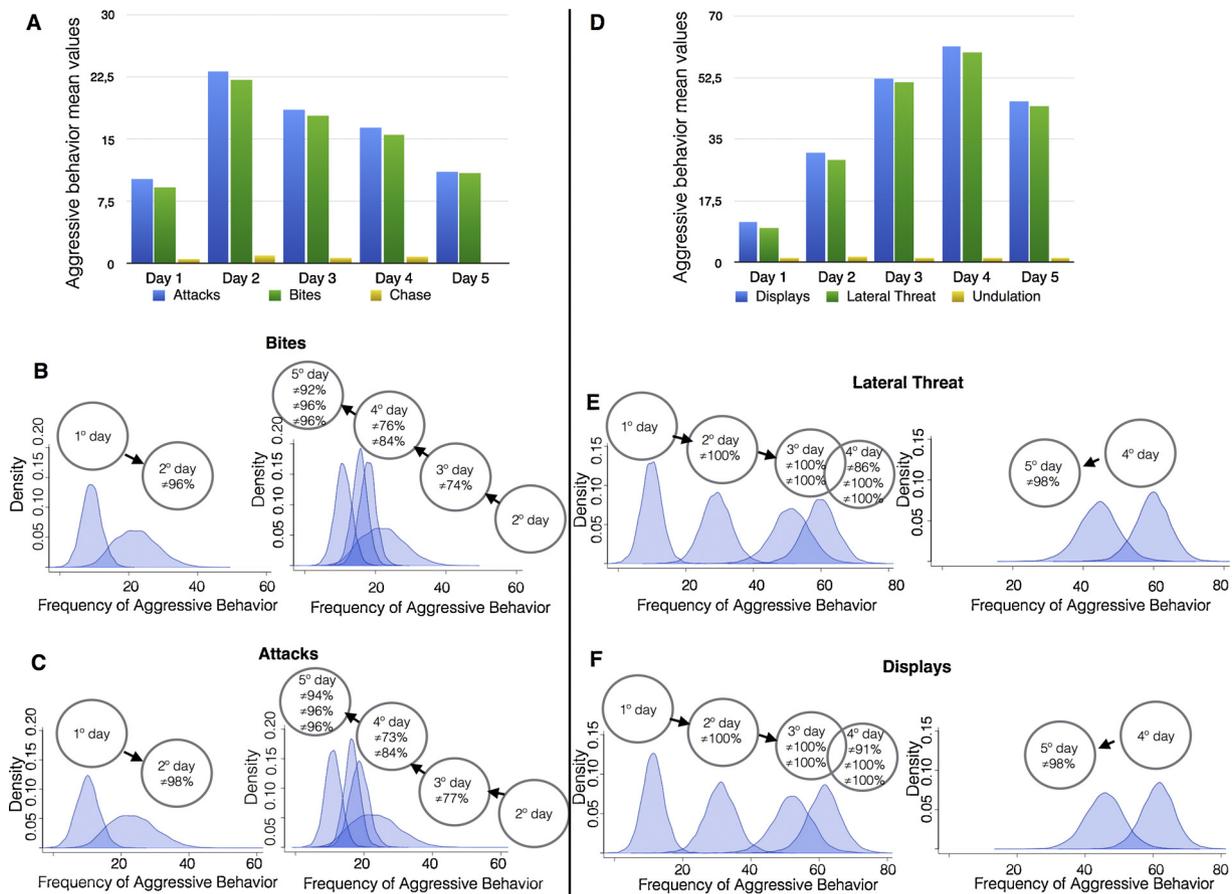


Fig. 1. *Pterophyllum scalare* aggressive interaction in 5 days period. It was observed in 15 min at each day. Each circle contains the probability of difference from the days before. The first probability is from the first day before, the second is from second day before and so on. A - The mean values of the most frequent high intense aggressive variables, individually (Bites and Chase) and the mean value of them combined (Attacks). B and C - The daily aggressive behaviors density distributions of the Bites (B) and Attacks (C). D - The mean values of the most frequent low intense aggressive variables, individually (Lateral threat and Undulation) and the mean value of them combined (Displays). E and F - The daily aggressive behaviors density distributions of the Lateral threat (E) and Attacks (F).

the first to the second day, and decreased by the fifth day. The variable chase was consistent and did not change over time (Fig. 3A). For *O. niloticus*, chase and bites increased until the third day and then decreased until the fifth day (Figs. 2 B and 4 A). For this species, when comparing the major variable attacks with the minor variable bites, the differences between the first-second, the first-third, the second-third, the third-fourth and the fourth-fifth days decreased from 92% to 87%, 95% to 92%, 72% to 64%, 90% to 84% and 87% to 80%, respectively (Figs. 2B, C). The differences between the first and third days were the only ones that affected statistical relevance.

A similar pattern was recorded for the major variable displays (D) for both species, whereby the minor variable lateral threat (LT) and undulation (U) stand out (Fig. 1 and 2). However, the variable LT influenced the distributions of all days and similar patterns, close mean values, and probabilities were recorded (Figs. 1D–F, and 2 D– F). For both species, the variable undulation was consistent, did not change over time, and had very low frequencies (Figs. 3B and 4 B). For *P. scalare*, the only probability that changed was the one between the fourth and fifth days, which is 86% when only considering a lateral threat (LT) or 91% when considering all variables (Fig. 1E, F). In the case of *O. niloticus*, when the major variable displays was compared to the minor variable LT, the differences between the first-second, second-third and fourth-fifth days increased from 91% to 95%, 92%–95% and 64%–72%, respectively (Fig. 2E and F). Hence, combining variables generated a loss of the statistical significance on some days (first-second and second-third).

3.1.2. *C. Paranaense* and *A. Ocellatus*

For the major variable attacks of the *A. ocellatus*, two minor variables stood out: the variables chase (C) and bites (B). Whereas for *C. paranaense*, four minor variables stood out, including lateral attacks (LA), chase (C), push (P) and tail beating (TB). However, when these variables were combined in attacks, the resulting distribution was remarkably influenced by the variable lateral attacks for both species. Indeed, similar patterns, close mean values and probabilities were recorded for LA (Figs. 5 and 6). However, the mean values were lower than attacks (A), and the probabilities varied either from 2 to 8% (*C. paranaense*) or from 1 to 18% (*A. ocellatus*), depending on the species. For *C. paranaense*, when the major variable A was compared to the minor variable LA, differences among the second-third and the third-fourth days increased from 54% to 62% and from 68% to 70%, respectively (Fig. 5B, C). For this species, the variables lateral attacks, chase and push displayed similar patterns, i.e., they decreased from the second day onward. However, the latter two variables displayed much lower frequencies than the former (Fig. 5B and 7 A and B). Tail beating (TB) was consistent, i.e., it did not change over time or in low frequencies (Fig. 7C). For *A. ocellatus*, the LA decreased until the second day and then increased until the fifth day (Fig. 6 B). Chase increased from the third to the fifth day (there were no frequencies on the second day for this variable), with very low frequencies compared to the lateral attacks (Fig. 6C). For this species, when the major variable attacks were compared with the minor variable LA, the differences among the first-third and the third-fifth days decreased from 97% to 78% and from 100% to 88%, respectively. Therefore, when combined variables are

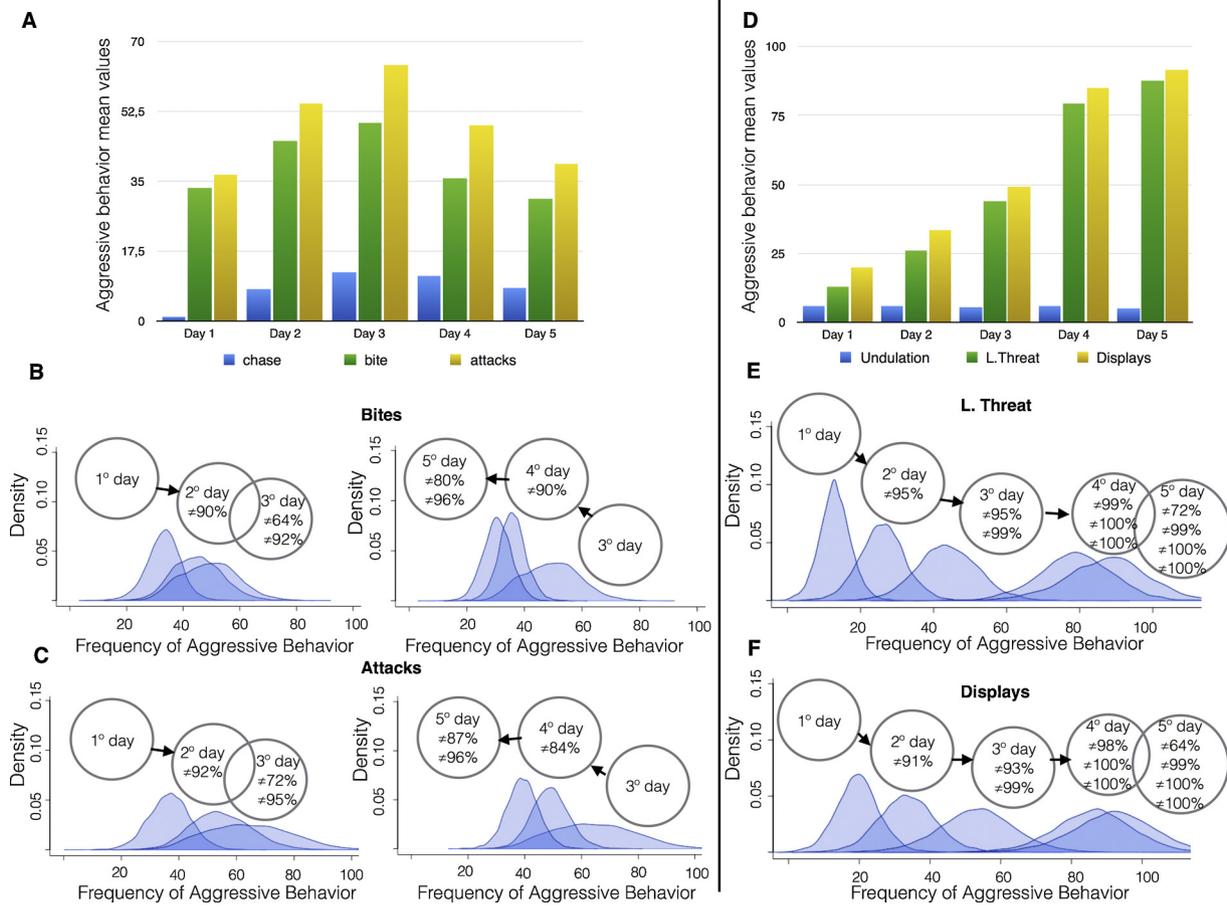


Fig. 2. *Oreochromis niloticus* aggressive interaction in 5 days period. It was observed in 15 min at each day. Each circle contains the probability of difference from the days before. The first probability is from the first day before, the second is from second day before and so on. A - The mean values of the most frequent high intense aggressive variables, individually (Bites and Chase) and the mean value of them combined (Attacks). B and C - The daily aggressive behaviors density distributions of the Bites (B) and Attacks (C). D - The mean values of the most frequent low intense aggressive variables, individually (Lateral threat and Undulation) and the mean value of them combined (Displays). E and F - The daily aggressive behaviors density distributions of the Lateral threat (E) and Attacks (F).

used there is a statistical significance (more than 95% of difference), but not when lateral attacks occur individually. For the major displays, both species presented variables with very few frequencies. As a matter of fact, only the variable lateral threat could be properly modelled from the *C. paranaense*. These variables increased until the fifth day. As only one variable was suitable to be modeled, probabilities did not change even when the very few frequencies from other variables were added.

3.2. Family distribution

With respect to *P. scalare*, for most variables the models with a Gaussian distribution provided better results (based on lower DIC values) than the models that used a Poisson distribution (Table 2). However, for the variables undulation and chase Poisson models provided better fits. Similarly, for all variables, in the case of *O. niloticus* and *C. paranaense* Gaussian distribution models fit better than Poisson distributions (Table 2). Based on these findings, Gaussian distribution models are more suitable for most species, except for *A. ocellatus*, for which the Poisson models were better.

3.3. Reducing sample size

3.3.1. *P. Scalare* and *O. Niloticus*

For lateral Thread (LT) and the displays (D) the reduction of the sample size tended to decrease the posterior probability of difference in means among all the days, for both species. The only exception was found between the third-fourth and fourth-fifth day for *P. scalare* and *O.*

niloticus, respectively. At the inference among these days, the posterior probability pattern was not clear and showed a small effect size (Table 3). In the case of *P. scalare*, for both variables, the difference within the first three days remained the same until the tenth replicate ($\neq 100\%$) (Fig. 8A), which presented a large effect size (Table 3). Regarding *O. niloticus*, for both variables the difference among the first four days remained the same until the twelfth replicate (Fig. 8B). For LT this difference was 95% within the first-second and second-third days and 100% within the third and fourth days. For D this difference was 91%, 93% and 98% within the first-second, second-third and third-fourth days, respectively. For both these variables the degree of effect between these days was considered to be medium (> 0.5) and large (> 0.8) (Table 3).

Regarding bites and attacks among *P. scalare*, a reduction of the sample size tended to decrease the posterior probability of difference in means between the first and second days, and between the fourth and fifth days (Fig. 8A). Between these days there was as medium effect size (Table 3). No clear pattern emerged between the second and fourth days, although a small effect size was observed for both variables (Fig. 8A and Table 3).

With respect to B and A of *O. niloticus*, after reducing the sample size no clear pattern emerged on any of the days. It should be noted that the sample size reduction increased the probability of difference in means for both variables, from the fifteenth to the eleventh replicates, whereas it decreased the probability of difference in means up to the fifth replicate (Fig. 8B). For variable A, this increase generated a non-significant result with fifteen replicates ($\neq 90\%$), but became significant

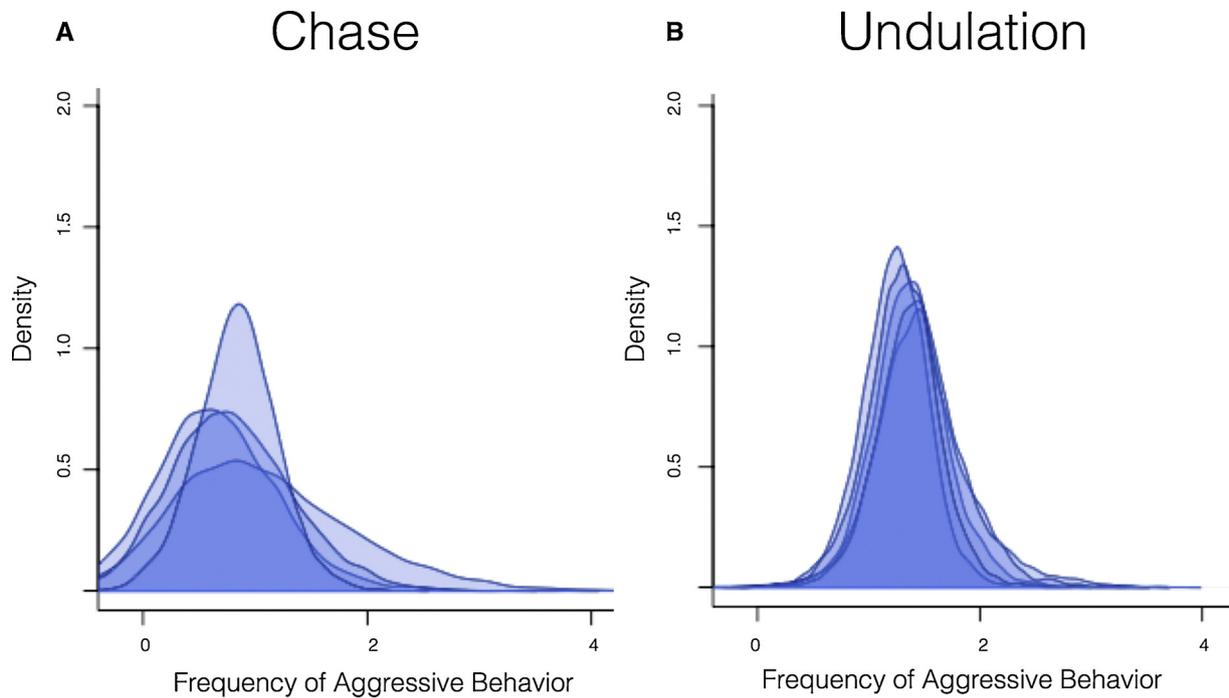


Fig. 3. *Pterophyllum scalare* aggressive interaction in 5 days period. It was observed in 15 min at each day. Each circle contains the probability of difference from the days before. The first probability is from the first day before, the second is from second day before and so on. A - The daily aggressive behaviors density distributions of the Chase. B - The daily aggressive behaviors density distributions of the Undulation.

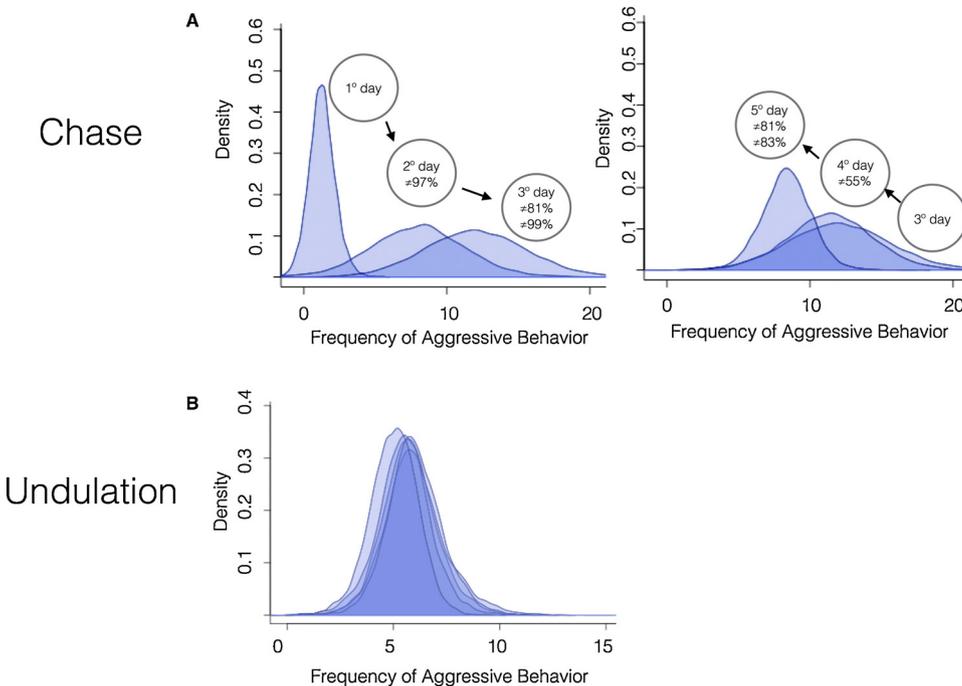


Fig. 4. *Oreochromis niloticus* aggressive interaction in 5 days period. It was observed in 15 min at each day. Each circle contains the probability of difference from the days before. The first probability is from the first day before, the second is from second day before and so on. A - The daily aggressive behaviors density distributions of the Chase. B - The daily aggressive behaviors density distributions of the Undulation.

with eleven replicates (≅ 95). For both variables the differences among all days presented a small effect size (< 0.5) (Table 3).

3.3.2. *C. Paranaense* and *A. Ocellatus*

With respect to lateral threat (LT) and the displays (D), after reducing the sample size no clear pattern emerged between most days (Table 3), and a small effect size was revealed. The only exception was found between the first and second days, whereby a reduction of the data sample size tended to decrease the posterior probability of difference in means. For both variables, the difference among the first and

second days remained the same until the eleventh replicate (≅ 100%) and then decreased until the rest of the sample reduction (Fig. 8C). The effect size between this inference was considered large (≥0.8) (Table 3). Similar to the LT and the D, neither the LA nor the A presented clear patterns between most days, and both had small effect sizes. The only exception was in the inference between the first and second days, with a large effect size (Table 3).

For *A. ocellatus*, a reduction of the sample sizes occurred through the main minor variable, LA. For this variable a reduction of the data sample size has no effect on the posterior probability of difference in

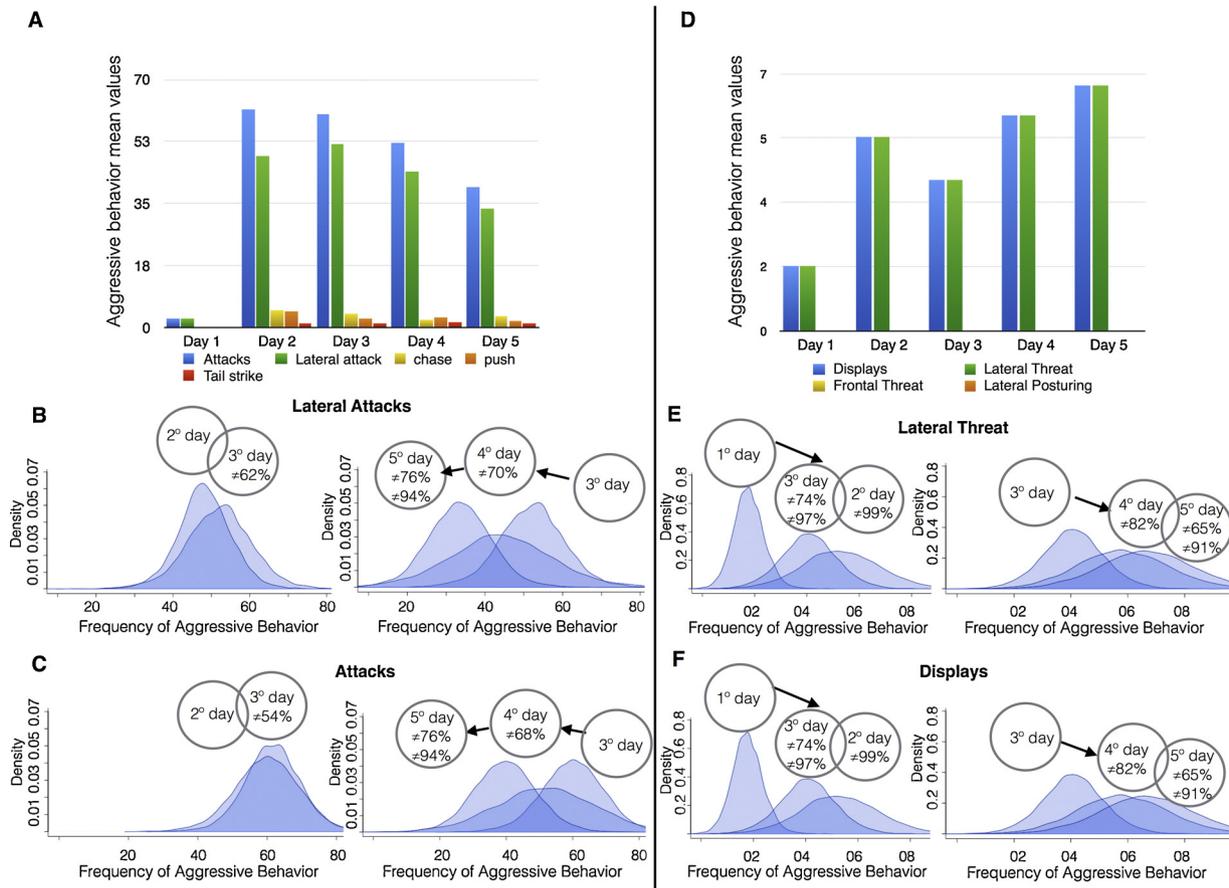


Fig. 5. *Cichlasoma paranaenses* aggressive interaction in 5 days period. It was observed in 15 min at each day. Each circle contains the probability of difference from the days before. The first probability is from the first day before, the second is from second day before and so on. A - The mean values of the most frequent high intense aggressive variables, individually (Lateral attacks, Chase, Push and Tail beating) and the mean value of them combined (Attacks). B and C - The daily aggressive behaviors density distributions of the Lateral attacks (B) and Attacks (C). D - The mean values of the most frequent low intense aggressive variables, individually (Frontal threat, Lateral threat and Lateral posturing) and the mean value of them combined (Displays). E and F - The daily aggressive behaviors density distributions of the Lateral threat (E) and Attacks (F).

means within most of the days. The only exception was found between the fourth and fifth days, in which the posterior probability tended to decrease. This difference remained the same until the ninth replicate ($\neq 100\%$) and decreased afterward for the rest of the sample reduction (Fig. 8D). The effect size was not calculated for this species, given the poor models from zero-inflated data.

4. Discussion

4.1. Combining variables

When two longitudinal variables are combined, two patterns are mixed at the same time. Usually the patterns of the most quantitative variables prevail, whereas the other variables cause small deviances to this trend (Noleto-Filho et al., 2017). For most species the most frequent variables from attacks (A) and displays (D) provided similar results individually as they did when combined with other variables. However, there were two issues: (i) the mean values were lower; and (ii) the difference probabilities in means changed from one to eight percentage points in some cases. The first issue appears to be an advantage of combining variables and, therefore, including information from other variables that also existed in the fight. However, only the temporal pattern of the most quantitative variable was represented. Hence, the mean values increased in comparison to when a single value was used. However, these additional frequencies caused small deviances to the patterns of the main variables, thus leading to the second issue:

deviances generated probabilities gaps, which also caused both a loss and gain of statistical significance on some days when results were combined. These gaps could change our interpretation of biological trends, thus masking patterns of increases/decreases of aggressive behaviours. Therefore, instead of enriching our analysis with data from other variables, we are actually misleading the information of the main one. Noleto-Filho et al. (2017) have already detected this problem when combining A (more intense aggressive behavior) and D (less intense aggressive behavior) in total attacks, and here we saw that the problem deepens for variables that compose Attacks and Displays on their own. This classification in more (A) and less (D) intense aggressive behaviors was described by Hallen & Wittenberger (1987), who observed a substitution of attacks by displays during cohabitation. Subsequently, this classification was adopted in other studies (e.g. Gómez-Laplaza and Morgan (1993); Oliveira and Almada, 1998; Werneyer et al., 2002; Galhardo et al., 2008; Desjardins et al., 2012; Balzarini et al., 2014; Barreto et al., 2015). More intense aggressive behaviors (A) are more associated with high energetic costs than the less intense aggressive behaviors (D), regardless of the frequencies of aggressive events in each category (Ros et al., 2006). In other words, a low frequent aggressive behavior can have a greater impact on metabolism than a more frequent aggressive behaviour can. Consequently, combining variables can hide the pattern of the variable with most impact on metabolism, and lead to extrapolating misleading information from the experiments. Within this context, it is still interesting to categorize the variables by their energetic costs, but without combining them.

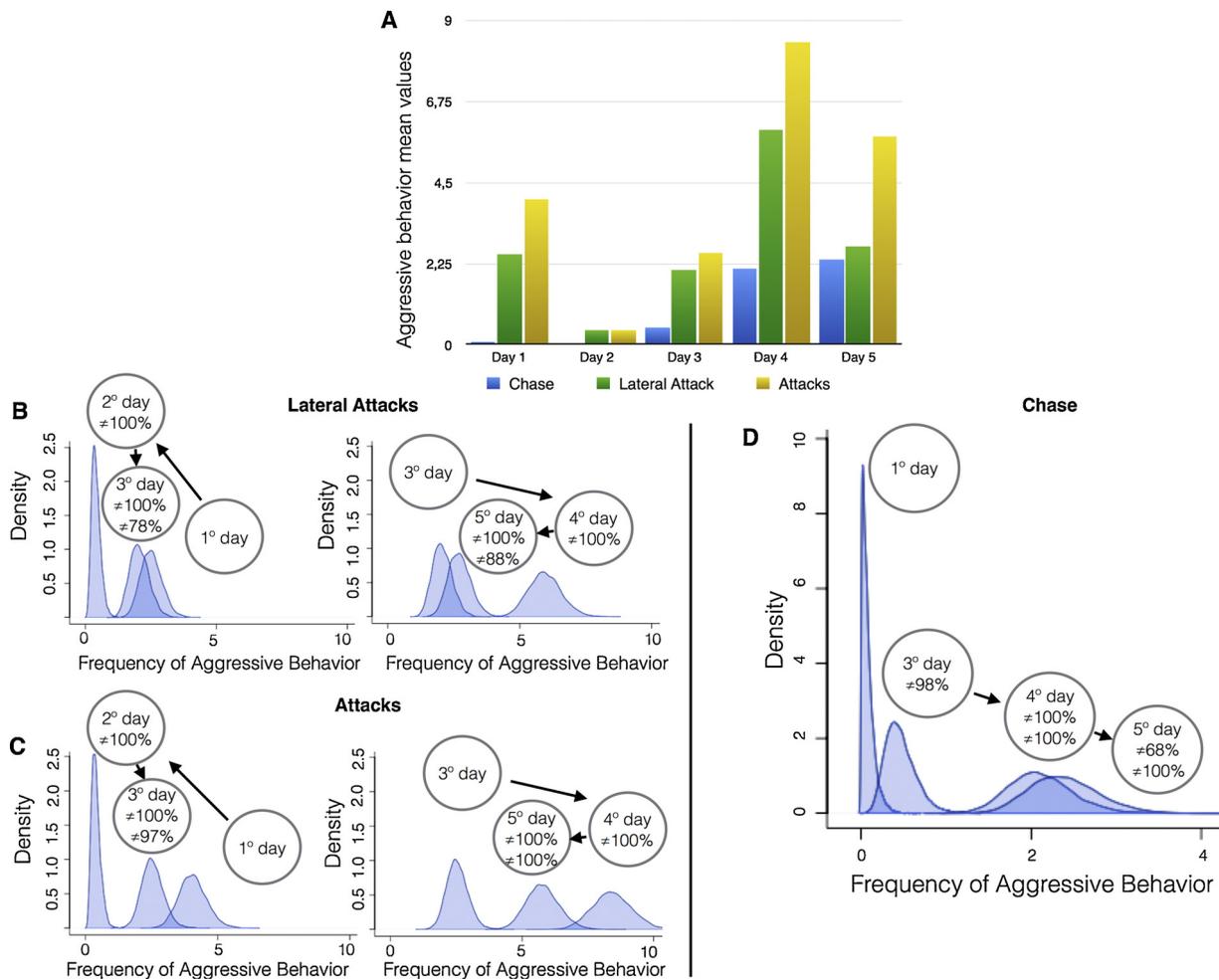


Fig. 6. *Astronotus ocellatus* aggressive interaction in 5 days period. It was observed in 15 min at each day. Each circle contains the probability of difference from the days before. The first probability is from the first day before, the second is from second day before and so on. A - The mean values of the most frequent high intense aggressive variables, individually (Lateral attacks and Chase) and the mean value of them combined (Attacks). B and C - The daily aggressive behaviors density distributions of the L. attacks (B) and Attacks (C). D - The daily aggressive behaviors density distributions of the Chase.

The only species that presented more remarkable differences among the combined variable and the most quantitative variable was *A. ocellatus*. For this species, combining variables increased the difference of some days by up to 18%, compared to when the more quantitative variable was used. This species presented the lowest variable means and standard deviations of all the species in our study, which is probably the reason why it was most susceptible to deviances when variables were combined. For example, if 50 lateral attacks are combined with 2 bites, there is a 3% increase in the amount of aggressive behaviors and it may not be considered a big change. However, if instead only two lateral attacks are combined with 2 bites, there is a 100% increase in the amount of aggressive behaviors and, in this case, it is considered a big change. Hence, combining variables will generate either more or fewer deviances from their minor variables, depending on their frequencies.

Combining aggressive variables for data analysis is also done for other animals, such as mice, birds, bears, lobsters, and others (e.g. Van Loo et al., 2002; Sima et al., 2016; Frederick et al., 2013; Ayres-Peres, 2015, respectively). Therefore, it is possible that the same problem could appear in studies that examine these species. The Bayesian method could also be applied to verify whether combining variables in those cases is feasible, given that in these studies the frequency of aggressive events is also counted and standardized with an ethogram. Researchers can easily apply the proposed Bayesian method using the BayesBehav web tool at <https://euriconoleto.shinyapps.io/BayesBehav>.

4.2. Family distribution

The aggressive behavior data can be viewed as a Poisson distribution because it is composed of counts and discrete data. However, based on DIC values, our results highlighted that Gaussian models were more suitable for most of the species. According to the central limit theorem, Poisson and Gaussian distributions are numerically close when the variables are highly quantitative. The mean of the Poisson distribution is equal to its variance, hence it is more restrictive than the Gaussian model (Ventura et al., 2015). However, in some cases in our study the Gaussian posterior probability distribution overlapped 0, even with a truncated distribution, which is biologically impossible for aggressive behaviors. These negative results were present in the Gaussian distribution variables of almost all species (*O. niloticus*: lateral threat, chase and undulation; *P. scalare*: bites, lateral threat, chase and undulation; *C. paranaenses*: lateral threat, chase, push and tail beating). Hence, to avoid possible biases, the Poisson distribution would be preferred, even with higher DIC values, because it is a proper distribution for counts (Coxe et al., 2009). The *A. ocellatus* was the only species whose main variable (LA) was better modeled using the Poisson distribution with DIC values. This distribution is more suitable for examining low frequencies data and zero-inflated variables (Varona and Sorensen, 2010). Hence, this distribution fits well for species that have low frequencies in their aggressive behaviour, such as the tiger oscar. Other distributions should also be considered in future research such as

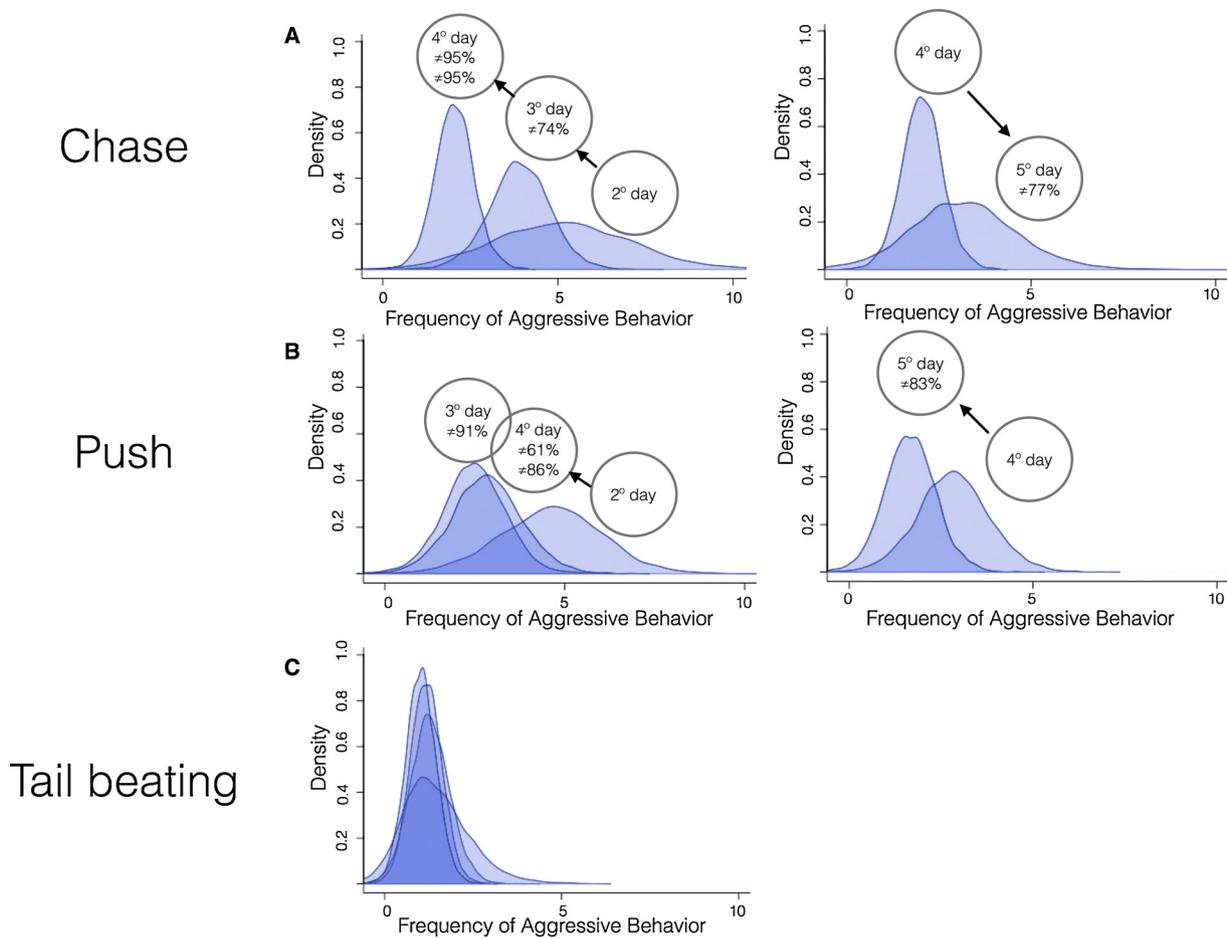


Fig. 7. *Cichlasoma paranaense* aggressive interaction in 5 days period. It was observed in 15 min at each day. Each circle contains the probability of difference from the days before. The first probability is from the first day before, the second is from second day before and so on. A - The daily aggressive behaviors density distributions of the Chase. B - The daily aggressive behaviors density distributions of the Push. C - The daily aggressive behaviors density distributions of the Tail beating.

Table 2
Deviance Information Criterion values from two family distributions (Gaussian and Poisson), of the variables of four cichlids species.

		Gaussian Deviance Information Criterion (DIC)	Poisson Deviance Information Criterion (DIC)
<i>P. scalare</i>	Bites	587	908
	Chase	212	204
	Attacks	656	987
	L.Threat	652	983
	Displays	600	978
<i>C. paranaense</i>	L. Attack	682	1888
	Chase	252	455
	Push	335	351
	Tail beating	285	290
	Attacks	698	2018
<i>O. niloticus</i>	L.Threat	456	563
	Displays	456	563
	Bites	709	1655
	Chase	548	915
	Attacks	745	2056
<i>A. ocellatus</i>	L. Threat	723	1841
	Undulation	520	729
	Displays	764	2182
	L. Attack	154	123
	Chase	NaN	396
	Attacks	617	650

Table 3
Effect size values of the inference of the main time intervals from three cichlids species. Effect sizes were calculated only for the species modeled using the Gaussian family distribution.

		Effect size between days			
		1-2	2-3	3-4	4-5
<i>P. scalare</i>	Bites	0.67	0.24	0.25	0.51
	Attacks	0.64	0.24	0.20	0.60
	L.Threat	1.30	1.10	0.40	0.75
	Displays	1.26	1.94	0.45	0.75
<i>C. paranaense</i>	L. Attack	2.50	0.11	0.16	0.23
	Attacks	2.73	0.04	0.15	0.24
	L.Threat	0.74	0.21	0.31	0.12
<i>O. niloticus</i>	Displays	0.74	0.21	0.31	0.12
	Bites	0.38	0.12	0.48	0.27
	Attacks	0.47	0.20	0.36	0.38
	L. Threat	0.65	0.62	0.98	0.21
<i>A. ocellatus</i>	Displays	0.50	0.52	0.76	0.12
	L. Attack	NaN	NaN	NaN	NaN
	Chase	NaN	NaN	NaN	NaN
	Attacks	NaN	NaN	NaN	NaN

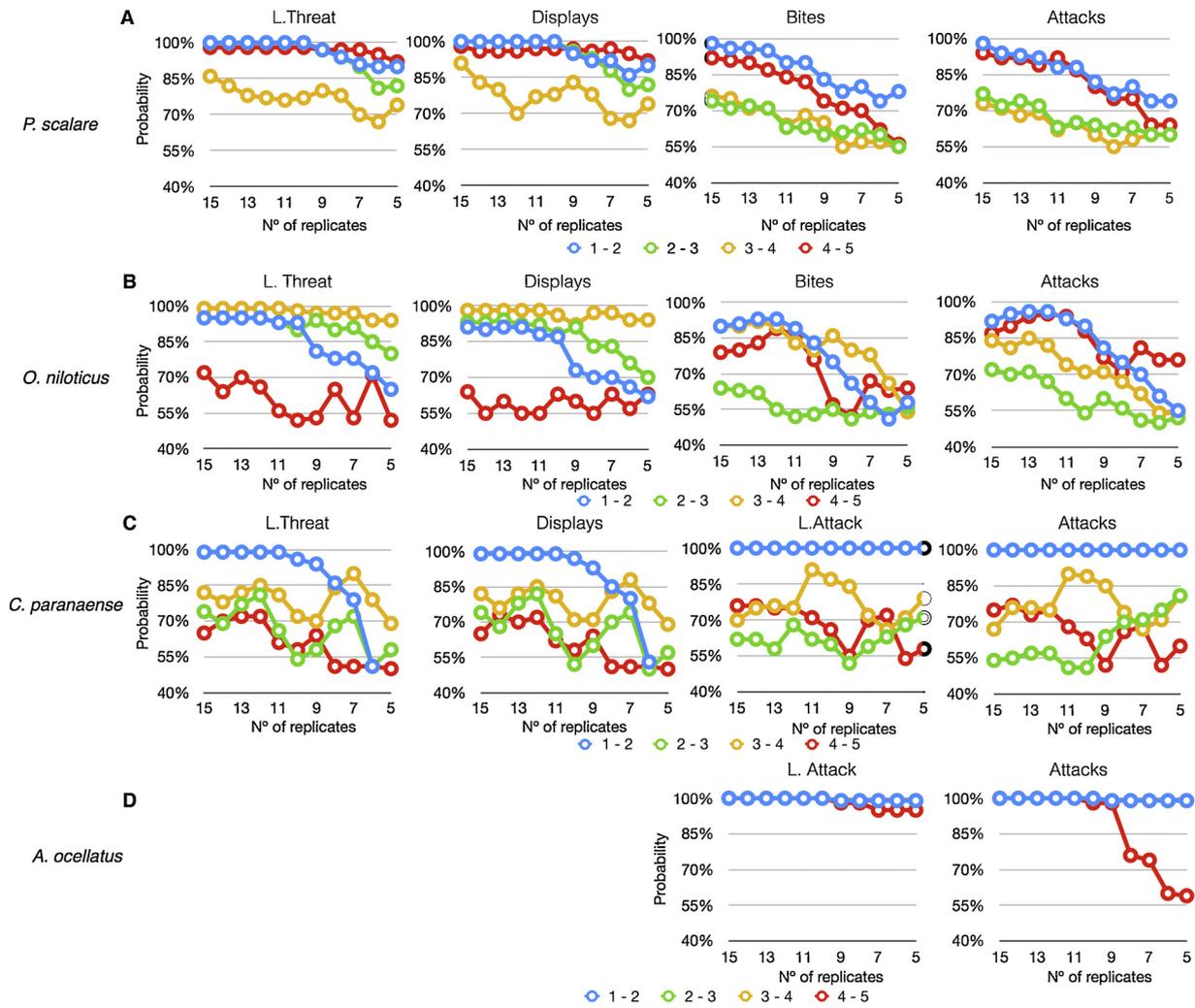


Fig. 8. The distribution of difference between days with different sample sizes of four cichlids species. The species illustrated are the *P. scalare* (A), the *O. niloticus* (B), the *C. paranaenses* (C) and the *A. ocellatus*. The blue line is between the first and second day, the green line is between the second and third days, the yellow is between the third and fourth days and the orange is between the fourth and fifth days.

the quasi-Poisson and negative binomial, which are also appropriated for count data (Ver Hoef and Boveng, 2007).

4.3. Sample size

The required sample size for longitudinal aggressive behavior data is influenced by the degree of overlap in the time intervals, which is related to the effect size (Noleto-Filho et al., 2017). With a large effect size, it is possible to detect an effect in smaller sample, whereas a smaller effect size requires a larger sample size (Sullivan and Feinn, 2012). Within this context, the variables with smaller effect sizes were already expected to be more sensitive to sample sizes. For example, in the variable Attacks of the *O. niloticus*, the inference among the first-second (effect size = 0.47) and fourth-fifth (effect size = 0.38) days were statistically significant with twelve replicates (≠ 96%), but not with fifteen (≠ 92). Thus, a small sample number would have provided a false negative result. In general, effect sizes bigger than 0.7 (medium to large effects) has no effect on results until the 12^o replicate, for the minor variables of all species. However, all species presented at least one variable with small and large effect sizes within the inference of their time intervals. Given that it is unfeasible to disjoin the replicate numbers among time intervals in a longitudinal design, replicates should be based on the inference with the smallest effect sizes. The variable bites of the *O. niloticus* provides a good example of an

appropriate sample size for a small effect size. For this variable, the inference among the first-second days presented a small effect size (0.38), but only changed 2 percentage points from fifteen (≠ 91%) to twelve (≠ 93%) replicates. Hence, this deviance did not change the conclusions and, therefore, it is an appropriate sample size.

Additionally, the most frequent variable from attacks and displays provided similar results individually as it did when combined variables were used. The main minor variables with their respective major variables had already been expected to respond similarly when their sample sizes were reduced. Indeed, the combined variables did not have an impact on the feasibility of reducing the sample size when compared to using the most quantitative minor variable.

5. Conclusions

Results highlight that when behavioral variables are combined the resulting distribution is remarkably influenced by only one variable in each category. Consequently, aggregating values misleads results in some cases by changing the probabilities of the main variables. Moreover, species with low frequency aggressive behaviors are more sensitive to this bias. The variable lateral threat is the main low intensity variable for all species, while bites is the main high intensity variable for *P. scalare* and *O. niloticus*. Furthermore, the variable lateral attack belongs to the high intensity category with the most relevance

for *C. paranaense* and *A. ocellatus*. Combining variables has no impact on the feasibility of reducing the sample size when compared to using the most quantitative minor variable. Effect sizes bigger than 0.7 (medium to large effects) has no effect on results until the 12^o replicate, for the minor variables of all species. Concerning family distribution, based on DIC values the Gaussian model is more suitable for most of the species. However, caution should be taken when using the Gaussian posterior probability because it overlapped 0 in some cases, which is biologically impossible for aggressive behaviors. Based on DIC values, the *A. ocellatus*, was the only species that was better modeled by Poisson distribution. Altogether, we highlight the Bayesian approach as a powerful tool for analyzing behavioral data.

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Appendix A

1 WINBUGS code of the Hierarchical Gaussian model

1. WINBUGS code of the Hierarchical Gaussian model

```

model {
  for (i in 1:N) {
    ataques[i] ~ dnorm(FirstGroup[X[i]], tau[X[i]])
  }
  for (i in 1:B) {
    FirstGroup[i] ~ dnorm(mq, tau1)
    tau[i] <- 1/(sdw[i]*sdw[i])
    sdw[i] ~ dunif(0, 100)
  }

  mq ~ dnorm(0, 0.010E-6)I(0,)
  tau1 <- 1/(sdb*sdb)
  sdb ~ dunif(0,100)
  diff2 <- FirstGroup[C]-FirstGroup[D]
  w1 <- step(diff2)
}

```

2 WINBUGS code of the Hierarchical Poisson model

Ethical note

This study was carried out in accordance with the ethical principles of the National Council for the Control of Animal Experimentation (CONCEA, Brazil) and was approved by the Ethics Committee for Animal Experimentation of the São José do Rio Preto campus of São Paulo State University, known locally as the Universidade Estadual Paulista (UNESP), in Brazil (permit number 169/2017). Data from experiments performed in previous studies were also used. These studies were also carried out in accordance with ethical principles from the CONCEA and the Ethics Committee for Animal Experimentation from the UNESP (permit numbers 077/2013; 083/2013). All fish handling was preceded by anesthesia, and substantial efforts were made to minimize animal suffering, as recommended by the Animal Behavior Society's Guidelines.

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We acknowledge the entire team of the laboratory of Animal Behavior from the State University of São Paulo, Brazil, for helping with the samplings.

2. WINBUGS code of the Hierarchical Poisson model

```

model {
  for (i in 1:N) {
    ataques[i] ~ dpois(FirstGroup[X[i]])
  }
  for (i in 1:B) {
    FirstGroup[i] ~ dlnorm(mq, tau1)
  }
  mq ~ dnorm(0, 0.010E-6)
  tau1 <- 1/(sdb*sdb)
  sdb ~ dunif(0,100)
  diff2 <- FirstGroup[C]-FirstGroup[D]
  w1 <- step(diff2)
}

```

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