

Habitat complexity reduces the feeding strength of freshwater predators (CRITTER)

Supplemental Statistics Report

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Overview

Summary

This statistics report is a supplement of our preprint article by Aranbarri et al. (2025) in which we investigate how habitat affects the strength of the feeding functional response of two freshwater invertebrate predators. Find below information on related works and the location of the data and code.

License

This report is published under the [Creative Commons BY 4.0](#) license. The underlying code is licensed under the [GNU General Public License 3](#).

How to cite this report

If you want to refer to our report, please cite:

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Related Works

- [Data on Zenodo](#) (Flores et al., 2025)
- [Data on GitHub](#)
- [R-Code on Zenodo](#) (Rall et al., 2025b)
- [R-Code on GitHub](#)
- [Statistical Report on Zenodo](#) (Rall et al., 2025a)
- [Statistical Report on GitHub](#)
- [Scientific Preprint Article](#) (Aranbarri et al., 2025)

Methods

Theoretical Background

The feeding functional response describes how a consumer's feeding rate reacts to its resource density (Holling, 1959a). The most basic shape of the feeding functional response is a hyperbolic curve, also called the type II functional response (Jeschke et al., 2002). The attack rate, a , controls the initial increase in the feeding rate, F , with increasing resource density, N (Holling, 1959a), and the handling time, T_h controls the satiation of the curve:

$$F = \frac{aN}{(1 + aT_hN)}. \quad (1)$$

If the attack rate is a function of resource density, the functional response becomes s-shaped (Holling, 1959b; Kalinkat et al., 2023). In the simplest form of this **type III functional response**, the attack rate is a linear function of resource density (Juliano, 2001):

$$a = bN, \quad (2)$$

in which b is the attack coefficient. The functional response becomes

$$F = \frac{bN^2}{(1 + bT_h N^2)}. \quad (3)$$

(Real, 1977, 1979) presented an alternative formulation of the functional response inspired by chemical reactions and the Michaelis-Menten kinetics (Barcroft & Hill, 1910). By substituting

$$T_h = \frac{1}{F_{max}} \quad (4)$$

and

$$a = \frac{F_{max}}{N_{half}}, \quad (5)$$

the **type II functional response** becomes

$$F = \frac{F_{max}N}{N_{half} + N}. \quad (6)$$

Here, the curve's satiation is controlled by the maximum feeding rate, F_{max} , and the half saturation density, N_{half} controls the steepness of the functional response curve. The **type III functional response** written in this style is as follows:

$$F = \frac{F_{max}^2 N}{N_{half}^2 + N^2}. \quad (7)$$

The above-described **type III functional response** model has a linearly increasing attack rate, but the attack rate can also be a more complex function of resource density (Juliano, 2001; Kalinkat et al., 2023). A commonly used version is a power law function of the resource density (Kalinkat et al., 2023; Rall et al., 2008; Williams & Martinez, 2004):

$$a = b^q. \quad (8)$$

The Holling-style functional response becomes (Vucic-Pestic et al., 2010):

$$F = \frac{bN^{1+q}}{(1 + bT_h N^{1+q})}, \quad (9)$$

and the Real-style functional response becomes (Rall et al., 2008; Williams & Martinez, 2004):

$$F = \frac{F_{max}^{1+q} N}{N_{half}^{1+q} + N^{1+q}}. \quad (10)$$

We will refer to the above-mentioned functional response models as either the Holling-style or the Real-style **generalized functional response** model. Note that many other functional response models exist, but the ones presented above are most practical and most often used to analyze laboratory functional response experiments (Jeschke et al., 2002; Juliano, 2001; Kalinkat et al., 2023). In our analyses, we will focus on the **generalized functional response** models and, if statistically appropriate, on the **type II or type III functional response** models.

Functional response statistics

Independence of variables

Scientific laboratory experiments are designed to manipulate one or more external variables that are typically called the **independent** or **explanatory variables**. We measure a response of our experimental system, and this measure is normally called the **dependent**, or **response variable**. See, e.g., Zar (2010), chapter 17, or Crawley (2012) chapter 10, for details. In functional response experiments, we manipulate the resource density, N , and measure the number of prey eaten, N_{eaten} , at the end of the experiment. This means that during the experiment, the prey density decreases over time. In contrast, in all the above-mentioned functional response models, the feeding rate, F , depends on a constant prey density, N . To account for the decay of resource density over time, we set up a differential equation, describing the temporal process:

$$\frac{dN}{dt} = -F. \quad (11)$$

The **change of resource density**, dN , over a given **time span**, dt , is described by the negative of the feeding rate F . F can be any of the functional response models introduced above (or described elsewhere). This differential equation model can not be fitted directly to data, but it needs to be solved beforehand. The solution depends on the type of functional response. For a **type II functional response**, the solution is (Rogers, 1972; Rosenbaum & Rall, 2018; Royama, 1971):

$$N_{eaten} = N_{initial}(1 - e^{a(N_{eaten}T_h - Pt)}). \quad (12)$$

The number of resources eaten, N_{eaten} at the time t (e.g., the end of the experiment) depends on the initial number of resources, $N_{initial}$. All other parameters are as described above. This equation is commonly known as **Roger’s Random Predator Equation** (RRPE). By substituting $T_h = \frac{1}{F_{max}}$ and $a = \frac{F_{max}}{N_{half}}$ into Roger’s Random Predator Equation, we get the version for the Real-style functional response model:

$$N_{eaten} = N_{initial}(1 - e^{\frac{N_{eaten}}{N_{half}} - \frac{Pt}{F_{max}}}). \quad (13)$$

Model parameters are as described above.

These equations share the issue that N_{eaten} appears on both sides of the equation. Traditionally, this problem is solved using Newton’s method, an iterative numerical procedure (Juliano, 2001; Vonesh & Bolker, 2005), but Bolker (2008) found that the Lambert **W** function (Corless et al., 1996) allows for an analytical solution:

$$N_{eaten} = N_{initial} - \frac{W(aT_hN_{initial}e^{-a(Pt - T_hN_{initial})})}{aT_h}. \quad (14)$$

The Real-style version is:

$$N_{eaten} = N_{initial} - \frac{W(\frac{1}{N_{half}}N_{initial}e^{-\frac{F_{max}}{N_{half}}(Pt - \frac{N_{initial}}{F_{max}})})}{\frac{1}{N_{half}}}. \quad (15)$$

All parameters are as described above.

Neither the type III nor the generalized functional response can be solved analytically and must be solved using numerical simulations (Rosenbaum & Rall, 2018). We follow the methods published by Rosenbaum & Rall (2018), but find more details in the section “Brief Code Description” below.

Data distribution

So far, we described the mathematical model describing the average number of resources eaten throughout the experimental trials. Each experimentally derived replicate, however, must deviate from this overall model mean (see, e.g., Zar (2010), chapter 17, or Crawley (2012) chapter 10, for assumptions of regression statistics). Our dependent data, N_{eaten} , has the following characteristics: integer numbers (0, 1, 2, ..., n), and the number of prey eaten cannot exceed the number of initially available resource items ($N_{initial}$). Data following these characteristics are known as proportion data and well described by a binomial probability distribution; see

Crawley (2012) chapter 16 for further explanations. We also apply this distribution to our data, as it is commonly used for functional response fitting (Bolker, 2008; Rosenbaum & Rall, 2018). Please also read the description of our code in the corresponding README file, either directly in our [repository](#) or download it from Zenodo (Rall et al., 2025b).

Functional response type selection

As the initial step, we analyzed which functional response type describes our data best (Juliano, 2001). We used two methods: (1) the phenomenological test after Juliano, implemented in the **frair** package (Juliano, 2001; Pritchard, Paterson, et al., 2017)[¹]; and (2) by fitting the Real-style **generalized functional response model** and test if q is significantly different from zero (Rall et al., 2008; Rosenbaum & Rall, 2018; Vucic-Pestic et al., 2010; Williams & Martinez, 2004). If the tests suggest, that at least one functional response treatment is not of type II, we will analyze our data further using the **generalized functional response** model. If the tests suggest that **all** treatments are type II, we will analyze our data further using the **Roger's Random Predator Equation** models.

Habitat complexity as an independent variable

The main scientific question of this project is to figure out how habitat complexity affects the interaction strength of two freshwater invertebrate predators (the consumers) on their prey (the resources). We have three different ways to address this question given the data: (1) the absence and presence of habitat; (2) the amount of habitat (either 0, 2, or 3 plastic ring structures); (3) five levels of complexity (0 to 5). The complexity levels originate from different spatial arrangements of the artificial ring structures, where 0 rings are complexity level 0, 2 rings comprise complexity levels 2 and 3, and 3 rings comprise complexity levels 4 and 5. See Flores et al. (2016) and Aranbarri et al. (2025) for further details. Contrasting the above-described analysis of the functional response type, we use here all data at once, separated by predator species. Each functional response parameter can react to habitat independently of the other parameters. For example, the attack rate can be different for all five complexity levels, whereas the handling time is a function of ring number. For each parameter, we can formulate the following hypotheses:

- H_0 : Habitat has no effect on the functional response parameters.
- H_1 : The sheer presence of habitat changes the functional response parameters.
- H_2 : The amount of habitat structure (number of rings, continuous) alters the functional response parameters.
- H_3 : The spatial arrangements modify the functional response parameters in addition to the amount of habitat structure.

Any functional response parameter independently can fulfill one of the above-stated hypotheses. If we want to test all possible combinations, we need 4×4 models (4 hypotheses per parameter) for each functional response style (Real-style and Holling style), in the case of a **type II functional response**, resulting in 32 statistical models per predator species. In the case of **generalized functional response**, we would have to test 64 statistical models for each functional response style, resulting in 128 models per species. Note that some of these models of how habitat affects the functional response are interchangeable, but not all. We will show for which models this is true in the results part below ([Habitat presence, amount, and complexity statistics]).

Data Availability

You can either download the data from our data publication on [Zenodo](#) (Flores et al., 2025), or from our [GitHub repository](#).

Code availability

You can either download the code from our code publication on [Zenodo](#) (Rall et al., 2025b), or from our [GitHub repository](#).

Results

The functional response type

Using the phenomenological test

Table 1: The results of testing for the functional response type by using the phenomenological test (Juliano 2001, Pritchard et al. 2017). We found for all unique treatments (complexity times predator identity) that a type II functional response explains the data best.

Predator	Complexity	Linear (Q)	Quadratic (Q)	Linear (L)	Type
<i>Ischnura elegans</i>	0	-(n.s.)	+(n.s.)	-(*)	II
<i>Ischnura elegans</i>	1	-(n.s.)	+(n.s.)	-(*)	II
<i>Ischnura elegans</i>	2	-(n.s.)	+(n.s.)	-(***)	II
<i>Ischnura elegans</i>	3	-(n.s.)	+(n.s.)	-(**)	II
<i>Ischnura elegans</i>	4	+(n.s.)	-(n.s.)	-(**)	II
<i>Notonecta glauca</i>	0	-(***)	+(***)	-(***)	II
<i>Notonecta glauca</i>	1	-(***)	+(***)	-(***)	II
<i>Notonecta glauca</i>	2	-(***)	+(**)	-(***)	II
<i>Notonecta glauca</i>	3	-(n.s.)	-(n.s.)	-(***)	II
<i>Notonecta glauca</i>	4	-(*)	-(n.s.)	-(***)	II

We analyzed our data using the so-called the phenomenological test by fitting this test to all ten treatments separately, i.e., two predators with five complexity levels each (Juliano, 2001; Pritchard, Paterson, et al., 2017; Pritchard, Barrios-O'Neill, et al., 2017; Rall et al., 2025b). The only case in which the results suggest a hump-shaped pattern in the proportion data is *Ischnura elegans* at the complexity level of 4, as the linear term is positive, and the quadratic term is negative (table 1). However, both estimates are not significant. The complexity levels 3 and 4 for *Notonecta glauca* show a negative quadratic term, which could also indicate a type III functional response, but both results are not significant. All other treatments have both a negative linear and a positive quadratic term, indicating in all these cases a declining proportion of eaten prey and therewith type II functional responses (table 1).

Direct shape estimation using the generalized functional response model

Table 2: The significance of the shape parameter q of all ten separately fitted generalized functional response models.

Predator Name	Complexity	q	Significance	Type-o-Response
<i>Ischnura elegans</i>	0	0.116	n.s.	II
<i>Ischnura elegans</i>	1	0.047	n.s.	II
<i>Ischnura elegans</i>	2	-0.001	n.s.	II
<i>Ischnura elegans</i>	3	-0.001	n.s.	II
<i>Ischnura elegans</i>	4	0.193	n.s.	II
<i>Notonecta glauca</i>	0	-0.011	n.s.	II
<i>Notonecta glauca</i>	1	-0.006	n.s.	II
<i>Notonecta glauca</i>	2	0.194	n.s.	II
<i>Notonecta glauca</i>	3	-0.002	n.s.	II
<i>Notonecta glauca</i>	4	-0.001	n.s.	II

We analyzed our data using the generalized functional response model by fitting this model to all ten treatments separately, i.e., two predators with five complexity levels each (Rall et al., 2008; Rosenbaum & Rall, 2018; Vucic-Pestic et al., 2010; Williams & Martinez, 2004). The shape parameter q is not significantly different from zero (see table 2). This means that in all cases, a simpler type II functional response can be used to describe the

data properly. This is in line with the phenomenological test shown above, and we will subsequently use the Roger's Random Predator Equation.

Habitat presence, amount, and complexity results

As the type II functional response model is the most appropriate model to describe our data across all treatments (see section “The functional response type” above), we continue our analyses using this functional response model. Based on our hypotheses (see section “Habitat complexity as an independent variable” above), we need to test in total 64 statistical functional response models: 16 models for the Holling-style and 16 models for the Real-style RRPE, resulting in 32 models, and we repeated these 32 models for the two predator species. In the following, we present the description of the 32 models and how habitat affects the functional response parameters:

- Model 01h | 01r: Habitat has no effect on F_{max} | T_h , (H_0), and N_{half} | a is also not affected by habitat presence (H_0).
- Model 02h | 02r: Habitat has no effect on F_{max} | T_h , (H_0), and N_{half} | a is affected by habitat presence (H_1).
- Model 03h | 03r: Habitat has no effect on F_{max} | T_h , (H_0), and N_{half} | a is affected by the amount of habitat structure (H_2).
- Model 04h | 04r: Habitat has no effect on F_{max} | T_h , (H_0), and N_{half} | a is affected by complexity (H_3).
- Model 05h | 05r: Habitat presence affects F_{max} | T_h , (H_0), and N_{half} | a is not affected by habitat presence (H_0).
- Model 06h | 06r: Habitat presence affects F_{max} | T_h , (H_0), and N_{half} | a is affected by habitat presence (H_1).
- Model 07h | 07r: Habitat presence affects F_{max} | T_h , (H_0), and N_{half} | a is affected by the amount of habitat structure (H_2).
- Model 08h | 08r: Habitat presence affects F_{max} | T_h , (H_0), and N_{half} | a is affected by complexity (H_3).
- Model 09h | 09r: The amount of habitat affects F_{max} | T_h , (H_0), and N_{half} | a is not affected by habitat presence (H_0).
- Model 10h | 10r: The amount of habitat affects F_{max} | T_h , (H_0), and N_{half} | a is affected by habitat presence (H_1).
- Model 11h | 11r: The amount of habitat affects F_{max} | T_h , (H_0), and N_{half} | a is affected by the amount of habitat structure (H_2).
- Model 12h | 12r: The amount of habitat affects F_{max} | T_h , (H_0), and N_{half} | a is affected by complexity (H_3).
- Model 13h | 13r: Complexity affects F_{max} | T_h , (H_0), and N_{half} | a is not affected by habitat presence (H_0).
- Model 14h | 14r: Complexity affects F_{max} | T_h , (H_0), and N_{half} | a is affected by habitat presence (H_1).
- Model 15h | 15r: Complexity affects F_{max} | T_h , (H_0), and N_{half} | a is affected by the amount of habitat structure (H_2).
- Model 16h | 16r: Complexity affects F_{max} | T_h , (H_0), and N_{half} | a is affected by complexity (H_3).

The maximum feeding rate, F_{max} , and the handling time, T_h are always interchangeable as $F_{max} = \frac{1}{T_h}$. However, the attack rate, a , is not only a function of the half saturation density, N_{half} , but also a function of the maximum feeding rate: $a = \frac{F_{max}}{N_{half}}$, $N_{half} = \frac{F_{max}}{a}$. This circumstance leads to the fact that the interchangeability of these parameters is context-dependent:

1. Attack rate and half saturation density are interchangeable if the maximum feeding rate is a constant across treatments (models 01 to 04).

2. Attack rate and half saturation density are also interchangeable if we fit a model testing for all complexity levels (H_3) for the half saturation density (models 04, 08, 12, and 16).
3. Attack rate and half saturation density are also interchangeable if we fit a model testing for the same hypothesis (models 01, 06, 11, and 16).

The remaining models (5, 7, 9, 10, 13, 14, 15) will deliver different results.

We will compare all models using common information criteria, the AIC, and the BIC (Akaike, 1974; Schwarz, 1978). The AIC selects models with more parameters, whereas the BIC tends to select models with a lower number of parameters (Schwarz, 1978). Please find the results of all fits saved as *.rds files in the folders results_hab_ie and results_hab_ng online (<https://github.com/b-c-r/CRITTERstatistics>).

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Ischnura elegans results

Table 3: AIC / BIC table of the six most parsimonious out of 32 possible models for *Ischnura elegans*. Find all results below in table .

Model (AIC)	df	dAIC	Model (BIC)	df	dBIC
Model 5r	3	0.000	Model 5r	3	0.000
Model 7r	4	0.265	Model 5h	3	1.583
Model 6h	4	0.952	Model 7r	4	2.731
Model 6r	4	0.952	Model 6h	4	3.418
Model 5h	3	1.583	Model 6r	4	3.418
Model 13r	6	2.107	Model 7h	4	4.718

The most parsimonious model according to AIC and BIC is model 5r (table 3). The maximum feeding rate in the case of no habitat is $28.08 \left[\frac{\text{items}_{\text{prey}}}{\text{day}} \right]$ and in the case of habitat present $14.58 \left[\frac{\text{items}_{\text{prey}}}{\text{day}} \right]$, which is a drop of about half (table 4). Expressed as handling time, T_h , *I. elegans* predators need $0.04 \left[\text{days} \right]$ if no habitat is present and $0.07 \left[\frac{\text{days}}{\text{items}_{\text{prey}}} \right]$ if habitat is present to subdue and feed on a prey item. The half saturation density, N_{half} is not affected by habitat at all ($N_{\text{half}} = 57 \frac{\text{items}_{\text{prey}}}{\text{volume}_{\text{arena}}}$, table 4). As the attack rate a depends on both, the maximum feeding rate F_{max} and the half saturation density N_{half} , we can calculate two attack rates for (1) no habitat ($a = 0.49 \left[\frac{\text{volume}_{\text{arena}}}{\text{days}} \right]$) and (2) for the case that habitat is present ($a = 0.26 \left[\frac{\text{volume}_{\text{arena}}}{\text{days}} \right]$). Note that the change in attack rate matches the change in maximum feeding rate, resulting in the fact that the strength of feeding is influenced equally across the whole range of prey densities (as N_{half} is constant).

We found four more models within a range of two delta units of both information criteria, all with three to four parameters (3), and we will discuss these models below. Please find the full table 18 in the Appendix below.

Table 4: Results of model 5 (Real style) fitted to the data of *Ischnura elegans*.

Parameter Name	Point Estimate	Lower CI	Upper CI
F_{max} (habitat absent)	28.081	19.462	41.043
F_{max} (habitat present)	14.578	10.796	19.989
N_{half}	57.000	34.949	95.128

The models within 2 delta AIC/BIC units

Model 7r (table 5) is more complex than model 5r by one degree of freedom (i.e., one more model parameter). Not only F_{max} depends on the presence of the habitat, but also N_{half} is a negative function of habitat amount

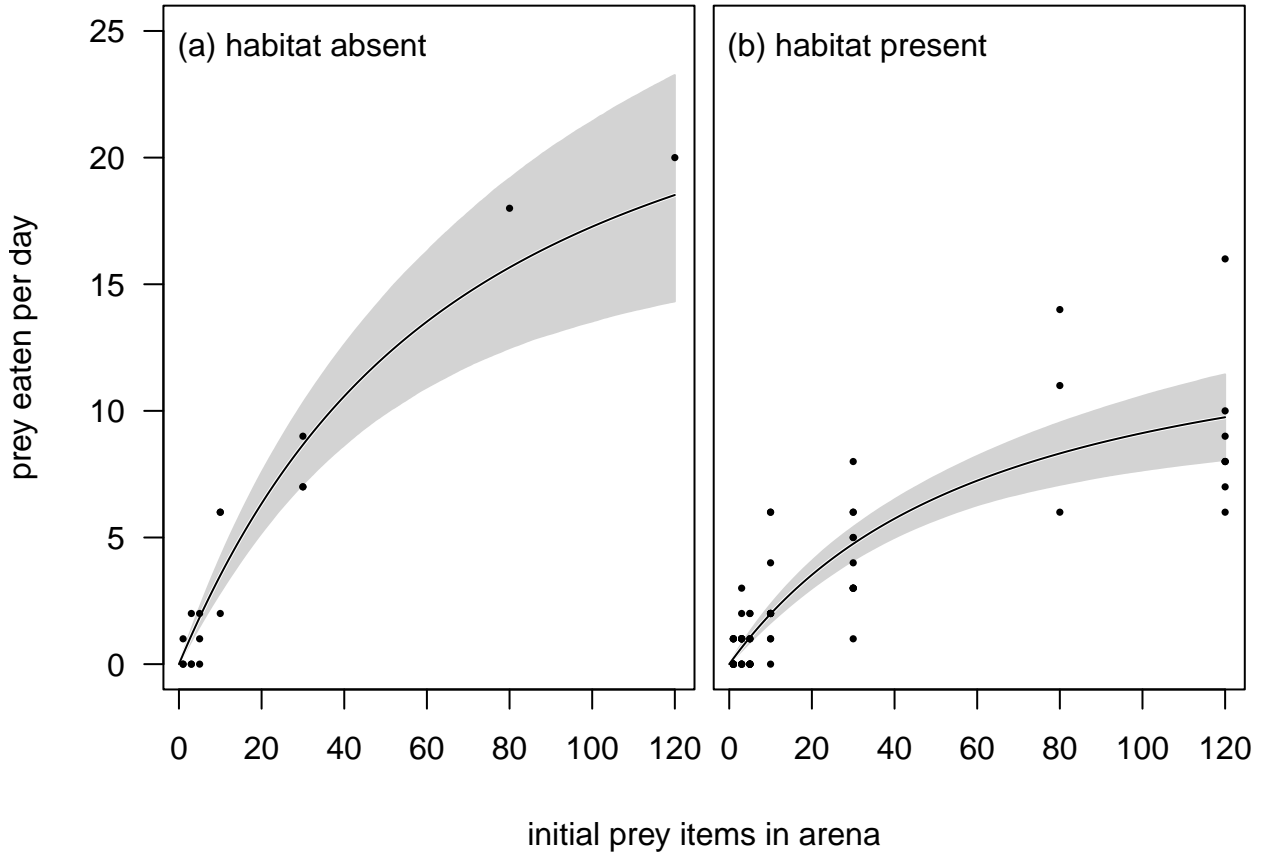


Figure 1: The feeding functional response of *Ischnura elegans* as function of the density of *Asellus aquaticus*. We found that model 5r was the most appropriate to describe the data (table 3). This model includes a unique maximum feeding rate for the cases if habitat is absent (a) or present (b) and a half saturation density that is not affected by habitat (table 4). The regression lines of the best fit point estimates are displayed in black, and the light gray area shows the 95% confidence limits of the best fit.

(the number of rings). However, the slope of this relationship (-0.09) is not significant ($p = 0.203$). In addition, a likelihood ratio test reveals, that adding this model parameter doesn't make the fit significantly better compared to model 5r ($p = 0.188$).

Table 5: Results of model 7 (Real style) fitted to the data of *Ischnura elegans*.

Parameter Name	Point Estimate	Lower CI	Upper CI
F_{max} (habitat absent)	36.596	19.832	66.166
F_{max} (habitat present)	13.563	9.854	18.704
$N_{half}(intercept)$	86.008	36.616	197.422
$N_{half}(slope)$	-0.094	-0.234	0.052

Model 6h (table 6) is more complex than model 5r by one degree of freedom. Model 6h is interchangeable with model 6r below. Not only T_h depends on the presence of the habitat but also a . If habitat is present, the attack rate is reduced from $0.42 \frac{items_{prey}}{volume_{arena}}$ to 0.27. A likelihood ratio test reveals, that adding this model parameter doesn't make the fit significantly better compared to model 5r ($p = 0.306$).

Table 6: Results of model 6 (Holling style) fitted to the data of *Ischnura elegans*.

Parameter Name	Point Estimate	Lower CI	Upper CI
T_h (habitat absent)	0.026	0.012	0.058
T_h (habitat present)	0.075	0.053	0.104
a (habitat absent)	0.419	0.275	0.635
a (habitat present)	0.275	0.204	0.365

Model 6r (table 7) is more complex than model 5r by one degree of freedom. Model 6r is interchangeable with model 6h above. Not only F_{max} depends on the presence of the habitat but also N_{half} . If habitat is present, the half saturation density drops from $90.24 \frac{items_{prey}}{volume_{arena}}$ to 48.65. A likelihood ratio test reveals, that adding this model parameter doesn't make the fit significantly better compared to model 5r ($p = 0.306$).

Table 7: Results of model 6 (Real style) fitted to the data of *Ischnura elegans*.

Parameter Name	Point Estimate	Lower CI	Upper CI
F_{max} (habitat absent)	37.807	16.856	83.438
F_{max} (habitat present)	13.361	9.493	18.635
N_{half} (habitat absent)	90.245	28.980	279.834
N_{half} (habitat present)	48.647	27.185	85.927

Model 5h (table 8) is as complex as model 5r, and both have three model parameters. T_h depends on the presence of the habitat, and a is not affected by habitat at all ($0.32 \frac{items_{prey}}{volume_{arena}}$). The respective half saturation densities are for the case without habitat: $N_{half} = 195.409$; and with habitat: $N_{half} = 38.273$. Especially the half saturation density for the case without habitat seems highly unlikely as it is above the tested range of prey densities. We did not apply a likelihood ratio test, as both models share the same number of parameters.

Table 8: Results of model 5 (Holling style) fitted to the data of *Ischnura elegans*.

Parameter Name	Point Estimate	Lower CI	Upper CI
T_h (habitat absent)	0.016	0.005	0.047
T_h (habitat present)	0.082	0.062	0.110
a	0.317	0.249	0.404

In summary, all models in the range of 2 delta AIC units suggest that (1) the maximum feeding rate drops dramatically by up to 50% when adding habitat structure. The half saturation density is likely to be habitat-

independent, according to the most likely model 5r. Eventually, the half saturation density may also decrease by adding habitat (model 6r), or may even decrease as a function of habitat amount (model 7r), which leads to a decrease in attack rates that is less pronounced as the drop of maximum feeding rates (model 6h) or the attack rate may be constant (model 5h). This result would indicate that the effect of habitat is predominantly acting at high prey densities. However, the alternative models are not contributing significantly to the explanation of the data (see above), leaving this phenomenon open for discussion. The results, however, show, that the higher-order complexity of the habitat structure does not influence the feeding rate of *Ischnura elegans*.

Notonecta glauca results

Table 9: AIC / BIC table of the seven most parsimonious out of 32 possible models for *Notonecta glauca*.

Model (AIC)	df	dAIC	Model (BIC)	df	dBIC
Model 15h	7	0.000	Model 15h	7	0.000
Model 16h	10	1.274	Model 9r	3	1.004
Model 16r	10	1.274	Model 11h	4	1.485
Model 15r	7	1.990	Model 11r	4	1.485
Model 14r	7	4.189	Model 13r	6	1.507
Model 13r	6	4.854	Model 15r	7	1.990
Model 12h	7	8.352	Model 7h	4	2.516

Both, AIC and BIC select for model 15h as the most parsimonious choice (table 9). Within two delta AIC units, models 16h, 16r, and 15r were selected. These models have 7 or more parameters, and in all cases either F_{max} or T_h are affected by habitat complexity. We found the models 9r, 11h, 11r, 13r, and 15r within two delta BIC units, all of them have equal or fewer parameters compared to model 15h (table 9, but see also the full table 19 in the Appendix). These selections highlight the quality of model 15h, as BIC is known to rather select models with fewer parameters (Schwarz, 1978).

Table 10: Results of model 15 (Holling style) fitted to the data of *Notonecta glauca*.

Parameter Name	Point Estimate	Lower CI	Upper CI
T_h (C0)	0.032	0.028	0.038
T_h (C1)	0.057	0.048	0.068
T_h (C2)	0.036	0.030	0.042
T_h (C3)	0.046	0.037	0.057
T_h (C4)	0.053	0.043	0.065
$a(intercept)$	1.280	1.010	1.620
$a(slope)$	-0.144	-0.191	-0.097

In model 15h, complexity affects the handling time (one measure of handling time per complexity level, table 10). The corresponding maximum feeding rates are $30.84 \left[\frac{items_{prey}}{day} \right]$ (C0), $17.5 \left[\frac{items_{prey}}{day} \right]$ (C1), $28.06 \left[\frac{items_{prey}}{day} \right]$ (C2), $21.65 \left[\frac{items_{prey}}{day} \right]$ (C3), $18.9 \left[\frac{items_{prey}}{day} \right]$ (C4). The maximum feeding rates are generally lower if habitat is present (complexity levels 1-4), but especially at level 2, the value is rather comparable to the case without habitat.

The attack rate, a is a decreasing function of the amount of habitat (table 10) with an intercept of ($a_{intercept} = 1.28 \left[\frac{volume_{arena}}{days} \right]$). The intercept is the attack rate when the habitat is absent. The slope of the attack rate is -0.14, indicating that the successful search and attack of prey at low densities decrease with increasing amounts of habitat.

The half saturation density N_{half} depends on both, the handling time T_h and the attack rate a ($N_{half} = \frac{1}{aT_h}$) leading to five half saturation densities, one for each complexity level: $24.1 \left[\frac{items_{prey}}{volume_{arena}} \right]$ (C0); $26.57 \left[\frac{items_{prey}}{volume_{arena}} \right]$ (C1); $42.6 \left[\frac{items_{prey}}{volume_{arena}} \right]$ (C2); $45.81 \left[\frac{items_{prey}}{volume_{arena}} \right]$ (C3); $39.99 \left[\frac{items_{prey}}{volume_{arena}} \right]$ (C4).

In general, the half saturation densities are increasing with increasing amounts of habitat, highlighting the effect of a decreasing hunting success at lower prey densities.

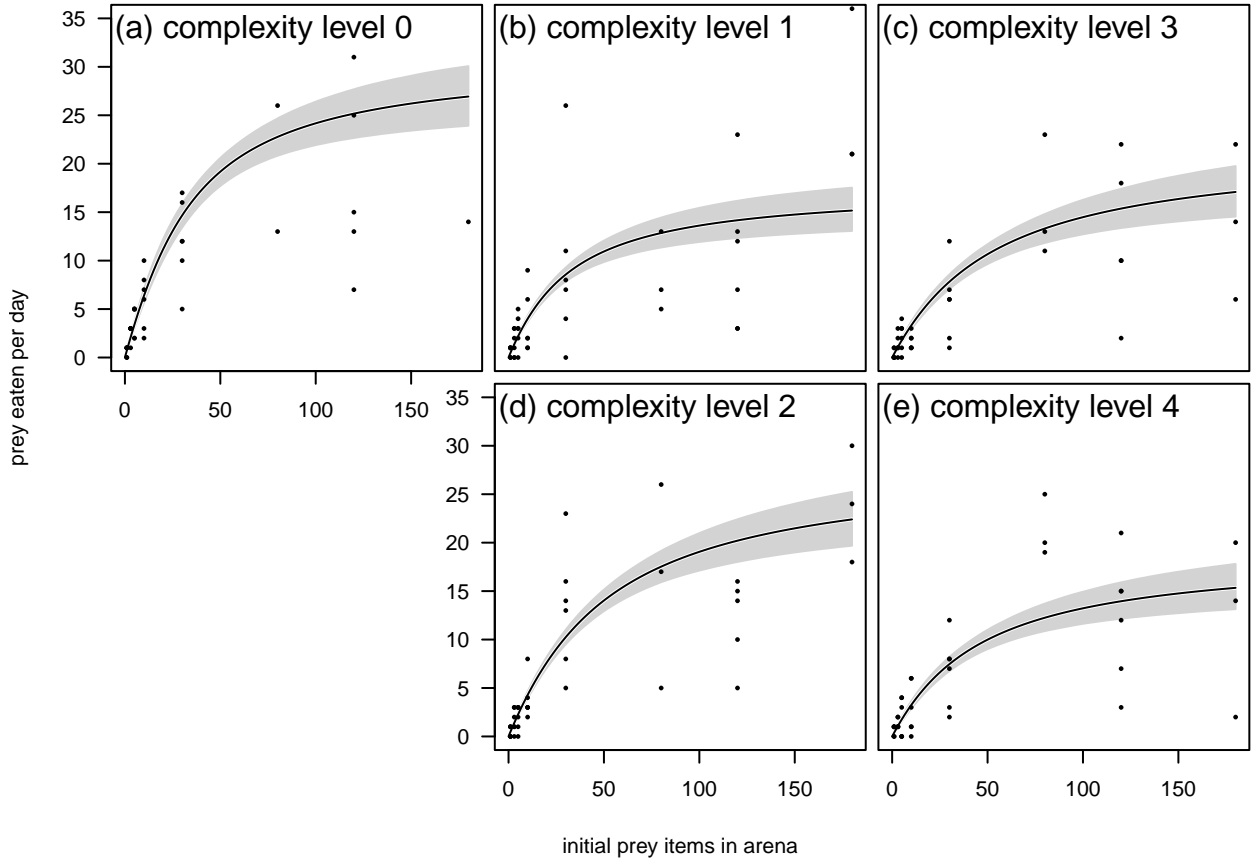


Figure 2: The feeding functional response of *Notonecta glauca* as function of the density of *Asellus aquaticus*. We found that model 15h was the most appropriate to describe the data (table 9). This model includes a unique maximum feeding rate for each complexity level and a decreasing attack rate as a function of the amount of habitat (table 10). The complexity levels (0-4) are displayed in the separate subplots: (a) = 0; (b) = 1; (c) = 3; (d) = 2; and (e) = 4. The amount of habitat structure increases from left to right, whereas the results for 0 rings are displayed in (a), 2 rings are displayed in (b, d), and 3 rings are displayed in (c, e). The regression lines of the best fit point estimates are displayed in black, and the light gray area shows the 95% confidence limits of the best fit.

The models within 2 delta AIC/BIC units

Model 16h and model 16r are interchangeable and are the most complex models we could fit to data. Both functional response parameters are affected by complexity level (see tables 11 and 12). The patterns of how habitat affects the parameters are similar to model 15h, i.e., handling time increases and maximum feeding decreases with increasing complexity, but we see an up-and-down pattern around this general trend. Attack rates are much higher when habitat is absent, complexity levels 1 and 2 (2 habitat rings in model 15h) show an intermediate attack rate, and complexity levels C3 and C4 have the lowest attack rates (3 rings in model 15h). The effect on half saturation densities is rather neutral, with a slight tendency to increase, in line with the fact that the general decrease in attack rates is more pronounced than the increase in attack rates with an increase in levels of complexity.

Table 11: Results of model 16 (Holling style) fitted to the data of *Notonecta glauca*.

Parameter Name	Point Estimate	Lower CI	Upper CI
T_h (C0)	0.032	0.027	0.037
T_h (C1)	0.059	0.048	0.072
T_h (C2)	0.038	0.031	0.045
T_h (C3)	0.039	0.029	0.053
T_h (C4)	0.055	0.044	0.069
a (C0)	1.212	0.947	1.562
a (C1)	0.707	0.507	0.987
a (C2)	0.750	0.578	0.966
a (C3)	0.363	0.268	0.491
a (C4)	0.526	0.389	0.722

Table 12: Results of model 16 (Real style) fitted to the data of *Notonecta glauca*.

Parameter Name	Point Estimate	Lower CI	Upper CI
F_{max} (C0)	31.487	26.903	36.619
F_{max} (C1)	17.046	13.982	21.031
F_{max} (C2)	26.492	22.082	31.860
F_{max} (C3)	25.453	18.921	34.233
F_{max} (C4)	18.057	14.536	22.420
N_{half} (C0)	25.971	17.868	37.286
N_{half} (C1)	24.113	15.074	39.146
N_{half} (C2)	35.334	23.830	52.369
N_{half} (C3)	70.211	40.749	120.865
N_{half} (C4)	34.349	21.529	55.246

Model 15r (table 13) is in line with the above-mentioned models and shows a general increase of F_{max} with the up-and-down pattern with increasing complexity levels as for the models above. The half saturation increases slightly with an increasing amount of habitat. This effect is similar to the effect of complexity in model 16r above.

Table 13: Results of model 15 (Real style) fitted to the data of *Notonecta glauca*.

Parameter Name	Point Estimate	Lower CI	Upper CI
F_{max} (C0)	30.741	26.512	35.664
F_{max} (C1)	19.646	17.096	22.542
F_{max} (C2)	26.474	23.387	30.066
F_{max} (C3)	20.181	17.050	23.980
F_{max} (C4)	19.703	16.704	23.358
N_{half} (intercept)	24.285	17.109	34.158
N_{half} (slope)	0.081	0.010	0.153

Model 9r (table 14) is the by far the simplest model and chosen by the AIC, and not by the BIC selection. It comprises a decreasing maximum feeding rate with an increasing amount of habitat and a constant half saturation density. The generally decreasing trend of maximum feeding rate with increasing amount of habitat is in line with the models above, only ignoring the up-and-down with complexity levels. We also already saw above (e.g., models 15r and 16r) that the effect of habitat on half saturation is rather weak.

Table 14: Results of model 9 (Real style) fitted to the data of *Notonecta glauca*.

Parameter Name	Point Estimate	Lower CI	Upper CI
F_{max} (intercept)	34.831	31.159	38.947
F_{max} (slope)	-0.094	-0.111	-0.077
N_{half}	33.937	27.975	41.408

Model 11h and model 11r are interchangeable, and the functional response parameters both depend on the amount of habitat present (tables 15 and 16). Handling time increases, and, of course, maximum feeding rate increases with the same strength. Attack rates decrease, while half saturation densities increase slightly. These results are in line with the above-mentioned models, only missing the up-and-down with complexity levels as in the more complex models.

Table 15: Results of model 11 (Holling style) fitted to the data of *Notonecta glauca*.

Parameter Name	Point Estimate	Lower CI	Upper CI
T_h (intercept)	0.033	0.028	0.038
T_h (slope)	0.063	0.030	0.094
a (intercept)	1.265	0.997	1.597
a (slope)	-0.144	-0.191	-0.096

Table 16: Results of model 11 (Real style) fitted to the data of *Notonecta glauca*.

Parameter Name	Point Estimate	Lower CI	Upper CI
F_{max} (intercept)	30.745	26.495	35.686
F_{max} (slope)	-0.063	-0.095	-0.030
N_{half} (intercept)	24.304	17.134	34.414
N_{half} (slope)	0.081	0.009	0.151

Model 13r (table 17) shows the well-known up-and-down pattern of maximum feeding, including a general increase with increasing complexity level. The half saturation density is constant, in line with the rather weak (but significant) positive effect of habitat amount in the models above.

Table 17: Results of model 13 (Real style) fitted to the data of *Notonecta glauca*.

Parameter Name	Point Estimate	Lower CI	Upper CI
F_{max} (C0)	34.784	30.956	39.020
F_{max} (C1)	19.350	16.863	22.207
F_{max} (C2)	26.070	23.003	29.504
F_{max} (C3)	18.371	15.974	21.190
F_{max} (C4)	17.969	15.639	20.651
N_{half}	33.928	27.871	41.275

In summary, all models in the range of 2 delta AIC and BIC units suggest that (1) the handling times increase with increasing amount of habitat available, altered by complexity levels. This leads to a decrease in maximum feeding rates, with the mirrored up-and-down effect of habitat complexity. We compared models 15h (the

most parsimonious model) with model 11h (the next simple model nested in model 15h) and found that if the amount of habitat is medium (2 rings), the results for complexity levels 2 and 3 differ from the prediction of the simpler model (figure 3). The attack rates decrease with increasing amounts of habitat, and this effect is slightly stronger than the effect on handling time, leading to a slightly increasing half saturation density. An even more complex effect of habitat complexity is given as models 16h and 16r are also within 2 delta AIC units, but as the AIC rather selects models that overfit data, we consider this effect as rather irrelevant.

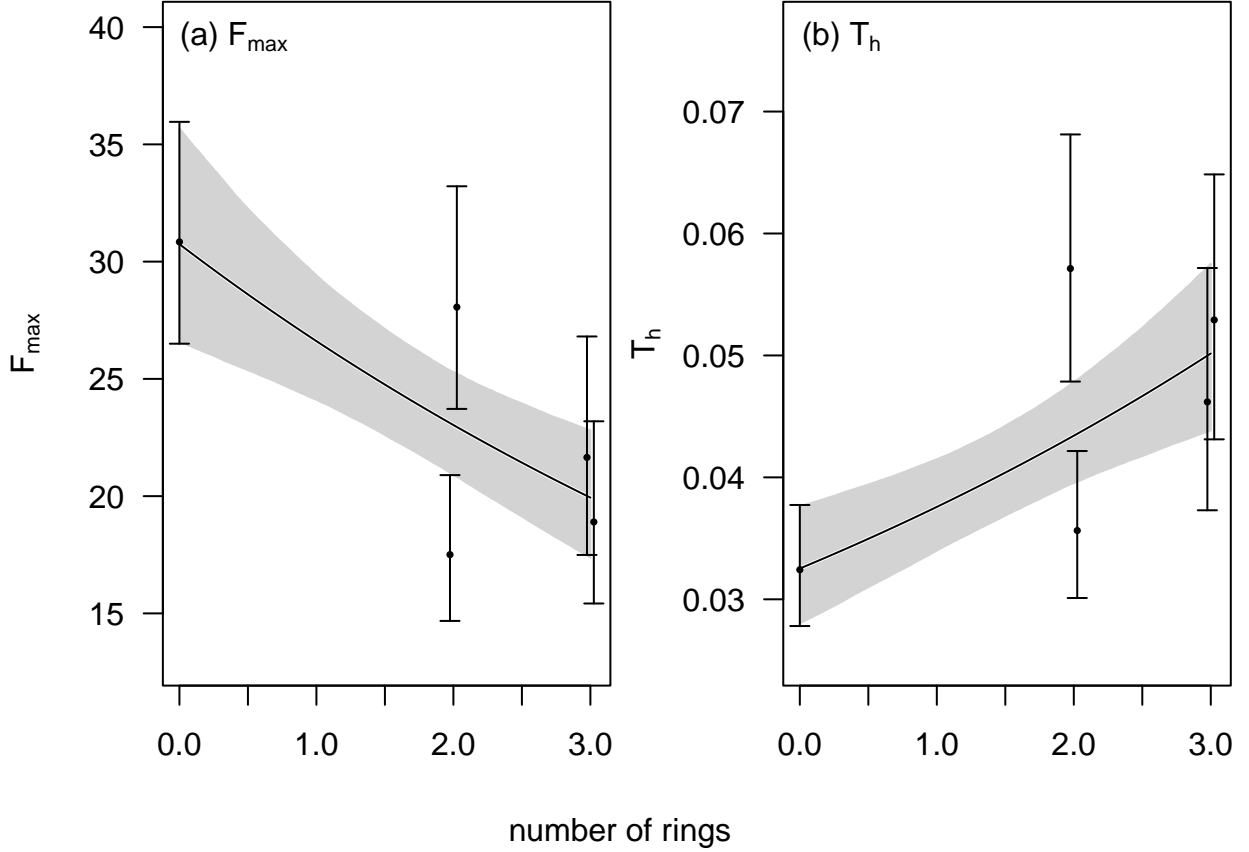


Figure 3: The functional feeding response parameters F_{max} (a) and T_h of *Notonecta glauca* feeding on *Asellus aquaticus*. We found that model 15h was the most appropriate to describe the data (table 9). This model includes a unique maximum feeding rate for each complexity level and a decreasing attack rate as a function of the amount of habitat provided (table 10). The next simpler model, including the decreasing attack rate with ring count, is model 11h (table 15). We consider the complexity levels as variants of the respective ring levels.

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Appendix

Phenomenological Test Rationale

Instead of fitting the number eaten prey items as depended variable as a function of the initial prey density, the ratio of prey eaten and initial prey items is used as depended variable (Juliano, 2001; Pritchard, Paterson, et al., 2017; Pritchard, Barrios-O'Neill, et al., 2017). In the case of a type II functional response, the proportion of eaten prey is constantly declining with increasing prey density, whereas in the case of a type III functional response, the proportion of prey eaten increases at low prey densities and declines after reaching a maximum proportion rate. The main trend of any functional response, if looking at the proportion data, is negative. This negative trend is caused by the fact, that initial prey density linearly increases, whereas the eaten prey items are leveling off. Please see Juliano (2001) for a full description. Pritchard, Paterson, et al. (2017) implemented this test using generalized linear models with a binomial distribution, a standard method to analyze proportion data based on yes/no data (i.e., whether a prey item is eaten or not eaten), but see Crawley (2012), chapter 16, for an introduction on this topic.

We use here the customized function `phen_type_test()` which is a wrapper around the `frair_test()` function from the `frair` package (Pritchard, Barrios-O'Neill, et al., 2017). `phen_type_table()` creates a high-quality PDF report table based on the output of `phen_type_test()`. Both functions are located in the project's sub-folder `functions`.

Full AIC / BIC tables

Ischnura elegans

Table 18: AIC / BIC table of all 32 possible models for *Ischnura elegans*.

Model (AIC)	df	dAIC	Model (BIC)	df	dBIC
Model 5r	3	0.000	Model 5r	3	0.000
Model 7r	4	0.265	Model 5h	3	1.583
Model 6h	4	0.952	Model 7r	4	2.731
Model 6r	4	0.952	Model 6h	4	3.418
Model 5h	3	1.583	Model 6r	4	3.418
Model 13r	6	2.107	Model 7h	4	4.718
Model 7h	4	2.252	Model 2h	3	7.001
Model 8h	7	2.446	Model 2r	3	7.001
Model 8r	7	2.446	Model 9r	3	7.189
Model 14r	7	2.928	Model 10h	4	7.768
Model 15r	7	3.495	Model 13r	6	9.505
Model 14h	7	3.834	Model 10r	4	10.128
Model 13h	6	4.026	Model 9h	3	11.069
Model 15h	7	4.039	Model 13h	6	11.424
Model 12h	7	5.271	Model 11h	4	11.468
Model 12r	7	5.271	Model 11r	4	11.468
Model 10h	4	5.303	Model 3h	3	11.887
Model 16h	10	5.945	Model 3r	3	11.887
Model 16r	10	5.945	Model 8h	7	12.309
Model 2h	3	7.001	Model 8r	7	12.309
Model 2r	3	7.001	Model 14r	7	12.791
Model 9r	3	7.189	Model 15r	7	13.358
Model 10r	4	7.663	Model 14h	7	13.697
Model 4h	6	8.317	Model 15h	7	13.902
Model 4r	6	8.317	Model 12h	7	15.135
Model 11h	4	9.002	Model 12r	7	15.135
Model 11r	4	9.002	Model 4h	6	15.715
Model 9h	3	11.069	Model 4r	6	15.715
Model 3h	3	11.887	Model 1h	2	19.128
Model 3r	3	11.887	Model 1r	2	19.128
Model 1h	2	21.594	Model 16h	10	23.206
Model 1r	2	21.594	Model 16r	10	23.206

Table 19: AIC / BIC table of all 32 possible models for *Notonecta glauca*.

Model (AIC)	df	dAIC	Model (BIC)	df	dBIC
Model 15h	7	0.000	Model 15h	7	0.000
Model 16h	10	1.274	Model 9r	3	1.004
Model 16r	10	1.274	Model 11h	4	1.485
Model 15r	7	1.990	Model 11r	4	1.485
Model 14r	7	4.189	Model 13r	6	1.507
Model 13r	6	4.854	Model 15r	7	1.990
Model 12h	7	8.352	Model 7h	4	2.516
Model 12r	7	8.352	Model 14r	7	4.189
Model 8h	7	8.459	Model 10r	4	4.478
Model 8r	7	8.459	Model 7r	4	5.947
Model 14h	7	9.938	Model 12h	7	8.352
Model 11h	4	11.526	Model 12r	7	8.352
Model 11r	4	11.526	Model 8h	7	8.459
Model 7h	4	12.557	Model 8r	7	8.459
Model 9r	3	14.392	Model 14h	7	9.938
Model 10r	4	14.519	Model 3h	3	10.853
Model 7r	4	15.988	Model 3r	3	10.853
Model 4h	6	20.141	Model 16h	10	11.316
Model 4r	6	20.141	Model 16r	10	11.316
Model 10h	4	21.456	Model 10h	4	11.415
Model 3h	3	24.241	Model 5r	3	16.378
Model 3r	3	24.241	Model 4h	6	16.794
Model 6h	4	28.922	Model 4r	6	16.794
Model 6r	4	28.922	Model 6h	4	18.880
Model 5r	3	29.767	Model 6r	4	18.880
Model 13h	6	33.151	Model 13h	6	29.804
Model 2h	3	43.253	Model 2h	3	29.864
Model 2r	3	43.253	Model 2r	3	29.864
Model 9h	3	44.833	Model 9h	3	31.445
Model 5h	3	53.840	Model 5h	3	40.451
Model 1h	2	125.439	Model 1h	2	108.704
Model 1r	2	125.439	Model 1r	2	108.704

All summary including original `bbmle::summary` outputs

The tables below are build using the function `bbmle::summary` from the `bbmle` package (Bolker et al., 2023). This means that all values *except the slopes* are displayed on \log_{10} scale in the column **Orig. Est.** (original estimate). The column **Estimate.** displays the values on normal scale. The significance values are all tested against “0”, in the case of the \log_{10} -transformed parameters they are tested against a value of 1 on normal scale. As example, the maximum feeding rate value is tested if it differs significantly from 1 $\frac{\text{items}_{\text{prey}}}{\text{day}}$ eaten, not if F_{max} differs between treatments. Therefore, the significance for the \log_{10} -transformed parameters are not relevant. Only the significance for the slopes is of interest as it tells if the model finds a significant effect of the amount of habitat in the experimental trial (0, 2, or 3 ring structures).

Ischnura elegans

Table 20: All 32 summary tables from *Ischnura elegans* model fits.

Name	Orig. Est.	SE	z	p	Estimate	CI low	CI up
Model 1h							
t_h_log10	-1.204	0.065	-18.648	0.0000	0.063	0.046	0.084
a_log10	-0.510	0.054	-9.505	0.0000	0.309	0.242	0.393
Model 1r							
f_max_log10	1.204	0.065	18.648	0.0000	15.996	11.945	21.262
n_half_log10	1.714	0.107	16.036	0.0000	51.718	32.004	83.081
Model 2h							
t_h_log10	-1.277	0.077	-16.592	0.0000	0.053	0.037	0.075
a_hab0_log10	-0.257	0.085	-3.038	0.0024	0.553	0.376	0.809
a_hab1_log10	-0.643	0.061	-10.541	0.0000	0.228	0.173	0.300
Model 2r							
f_max_log10	1.277	0.077	16.592	0.0000	18.906	13.430	26.744
n_half_hab0_log10	1.534	0.134	11.424	0.0000	34.166	18.773	62.092
n_half_hab1_log10	1.920	0.126	15.274	0.0000	83.088	47.343	147.006
Model 3h							
t_h_log10	-1.254	0.073	-17.191	0.0000	0.056	0.040	0.078
a_intercept_log10	-0.307	0.082	-3.746	0.0002	0.493	0.338	0.712
a_slope	-0.121	0.034	-3.509	0.0005	-0.121	-0.189	-0.053
Model 3r							
f_max_log10	1.254	0.073	17.191	0.0000	17.957	12.976	24.899
n_half_intercept_log10	1.562	0.129	12.102	0.0000	36.451	20.659	65.407
n_half_slope	0.121	0.034	3.509	0.0005	0.121	0.052	0.187
Model 4h							
t_h_log10	-1.277	0.075	-16.930	0.0000	0.053	0.038	0.074
a_0_log10	-0.257	0.084	-3.047	0.0023	0.553	0.376	0.812
a_1_log10	-0.813	0.099	-8.248	0.0000	0.154	0.099	0.242
a_2_log10	-0.554	0.104	-5.319	0.0000	0.279	0.174	0.445
a_3_log10	-0.612	0.094	-6.534	0.0000	0.244	0.161	0.375
a_4_log10	-0.589	0.105	-5.636	0.0000	0.257	0.162	0.411
Model 4r							
f_max_log10	1.277	0.075	16.930	0.0000	18.907	13.516	26.626
n_half_0_log10	1.534	0.132	11.576	0.0000	34.168	18.797	61.835
n_half_1_log10	2.089	0.142	14.724	0.0000	122.880	64.746	233.211
n_half_2_log10	1.831	0.152	12.023	0.0000	67.712	34.208	133.078
n_half_3_log10	1.889	0.140	13.493	0.0000	77.424	41.498	147.115
n_half_4_log10	1.866	0.154	12.150	0.0000	73.468	37.491	146.453
Model 5h							
t_h_hab0_log10	-1.792	0.237	-7.545	0.0000	0.016	0.006	0.046
t_h_hab1_log10	-1.084	0.064	-16.928	0.0000	0.082	0.062	0.110
a_log10	-0.499	0.054	-9.273	0.0000	0.317	0.250	0.402

(continued on next page...)

Table 20: All 32 summary tables from *Ischnura elegans* model fits.
(continued)

Name	Orig. Est.	SE	z	p	Estimate	CI low	CI up
Model 5r							
f_max_hab0_log10	1.448	0.083	17.543	0.0000	28.081	19.460	40.684
f_max_hab1_log10	1.164	0.069	16.839	0.0000	14.578	10.744	19.878
n_half_log10	1.756	0.111	15.797	0.0000	57.000	34.600	93.757
Model 6h							
t_h_hab0_log10	-1.578	0.176	-8.959	0.0000	0.026	0.012	0.058
t_h_hab1_log10	-1.126	0.074	-15.163	0.0000	0.075	0.053	0.104
a_hab0_log10	-0.378	0.092	-4.091	0.0000	0.419	0.275	0.636
a_hab1_log10	-0.561	0.065	-8.607	0.0000	0.275	0.205	0.366
Model 6r							
f_max_hab0_log10	1.578	0.176	8.959	0.0000	37.807	17.073	84.917
f_max_hab1_log10	1.126	0.074	15.163	0.0000	13.361	9.561	18.668
n_half_hab0_log10	1.955	0.250	7.837	0.0000	90.245	29.098	283.205
n_half_hab1_log10	1.687	0.126	13.389	0.0000	48.647	27.284	86.065
Model 7h							
t_h_hab0_log10	-1.639	0.198	-8.274	0.0000	0.023	0.009	0.056
t_h_hab1_log10	-1.107	0.070	-15.876	0.0000	0.078	0.057	0.107
a_intercept_log10	-0.420	0.087	-4.817	0.0000	0.380	0.257	0.562
a_slope	-0.047	0.040	-1.157	0.2471	-0.047	-0.127	0.033
Model 7r							
f_max_hab0_log10	1.563	0.133	11.770	0.0000	36.596	19.873	66.952
f_max_hab1_log10	1.132	0.071	15.910	0.0000	13.563	9.810	18.747
n_half_intercept_log10	1.935	0.185	10.474	0.0000	86.008	36.761	199.815
n_half_slope	-0.094	0.074	-1.272	0.2035	-0.094	-0.238	0.055
Model 8h							
t_h_hab0_log10	-1.578	0.176	-8.959	0.0000	0.026	0.012	0.058
t_h_hab1_log10	-1.133	0.074	-15.380	0.0000	0.074	0.053	0.103
a_0_log10	-0.378	0.092	-4.091	0.0000	0.419	0.277	0.634
a_1_log10	-0.748	0.108	-6.904	0.0000	0.179	0.109	0.288
a_2_log10	-0.468	0.111	-4.201	0.0000	0.341	0.205	0.556
a_3_log10	-0.541	0.104	-5.219	0.0000	0.288	0.179	0.463
a_4_log10	-0.504	0.110	-4.585	0.0000	0.313	0.191	0.519
Model 8r							
f_max_hab0_log10	1.578	0.176	8.959	0.0000	37.807	16.859	83.762
f_max_hab1_log10	1.133	0.074	15.380	0.0000	13.569	9.735	18.938
n_half_0_log10	1.955	0.250	7.837	0.0000	90.243	28.852	280.525
n_half_1_log10	1.880	0.150	12.570	0.0000	75.896	37.975	149.796
n_half_2_log10	1.600	0.156	10.243	0.0000	39.837	19.642	80.261
n_half_3_log10	1.674	0.148	11.291	0.0000	47.174	24.214	92.181
n_half_4_log10	1.637	0.153	10.687	0.0000	43.351	21.408	85.946
Model 9h							
t_h_intercept_log10	-1.528	0.132	-11.571	0.0000	0.030	0.016	0.054
t_h_slope	0.162	0.050	3.261	0.0011	0.162	0.066	0.258
a_log10	-0.495	0.053	-9.382	0.0000	0.320	0.252	0.404
Model 9r							
f_max_intercept_log10	1.402	0.082	17.130	0.0000	25.244	17.490	36.671
f_max_slope	-0.091	0.022	-4.179	0.0000	-0.091	-0.133	-0.047
n_half_log10	1.750	0.110	15.840	0.0000	56.226	34.184	92.142
Model 10h							
t_h_intercept_log10	-1.428	0.120	-11.919	0.0000	0.037	0.022	0.064
t_h_slope	0.096	0.051	1.887	0.0592	0.096	-0.004	0.197
a_hab0_log10	-0.320	0.087	-3.692	0.0002	0.479	0.322	0.708

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Table 20: All 32 summary tables from *Ischnura elegans* model fits.
(continued)

Name	Orig. Est.	SE	z	p	Estimate	CI low	CI up
a_hab1_log10	-0.598	0.064	-9.422	0.0000	0.252	0.189	0.334
Model 10r							
f_max_intercept_log10	1.339	0.094	14.301	0.0000	21.827	14.351	33.331
f_max_slope	-0.048	0.041	-1.160	0.2461	-0.048	-0.130	0.032
n_half_hab0_log10	1.622	0.153	10.633	0.0000	41.882	21.301	83.526
n_half_hab1_log10	1.834	0.136	13.524	0.0000	68.270	37.131	125.088
Model 11h							
t_h_intercept_log10	-1.440	0.124	-11.641	0.0000	0.036	0.021	0.063
t_h_slope	0.111	0.052	2.135	0.0327	0.111	0.009	0.212
a_intercept_log10	-0.372	0.084	-4.453	0.0000	0.425	0.292	0.618
a_slope	-0.077	0.039	-2.001	0.0454	-0.077	-0.152	-0.002
Model 11r							
f_max_intercept_log10	1.440	0.124	11.640	0.0000	27.542	15.663	48.729
f_max_slope	-0.111	0.052	-2.136	0.0327	-0.111	-0.214	-0.007
n_half_intercept_log10	1.812	0.184	9.852	0.0000	64.841	27.856	150.111
n_half_slope	-0.034	0.079	-0.430	0.6669	-0.034	-0.190	0.125
Model 12h							
t_h_intercept_log10	-1.476	0.134	-11.024	0.0000	0.033	0.018	0.062
t_h_slope	0.117	0.055	2.132	0.0330	0.117	0.007	0.224
a_0_log10	-0.339	0.088	-3.863	0.0001	0.458	0.312	0.681
a_1_log10	-0.798	0.100	-7.961	0.0000	0.159	0.102	0.250
a_2_log10	-0.533	0.105	-5.093	0.0000	0.293	0.184	0.475
a_3_log10	-0.536	0.107	-5.010	0.0000	0.291	0.178	0.473
a_4_log10	-0.500	0.113	-4.429	0.0000	0.316	0.191	0.524
Model 12r							
f_max_intercept_log10	1.476	0.134	11.024	0.0000	29.898	16.275	55.286
f_max_slope	-0.117	0.055	-2.132	0.0330	-0.117	-0.225	-0.010
n_half_0_log10	1.815	0.200	9.092	0.0000	65.239	26.557	162.288
n_half_1_log10	2.039	0.138	14.746	0.0000	109.348	59.075	206.432
n_half_2_log10	1.774	0.147	12.083	0.0000	59.458	30.437	116.870
n_half_3_log10	1.660	0.164	10.137	0.0000	45.741	21.643	96.379
n_half_4_log10	1.624	0.168	9.686	0.0000	42.029	19.635	90.289
Model 13h							
t_h_0_log10	-1.765	0.224	-7.883	0.0000	0.017	0.006	0.047
t_h_1_log10	-0.944	0.111	-8.513	0.0000	0.114	0.069	0.187
t_h_2_log10	-1.044	0.117	-8.904	0.0000	0.090	0.054	0.153
t_h_3_log10	-1.056	0.126	-8.379	0.0000	0.088	0.050	0.155
t_h_4_log10	-1.203	0.097	-12.358	0.0000	0.063	0.040	0.097
a_log10	-0.488	0.055	-8.902	0.0000	0.325	0.254	0.413
Model 13r							
f_max_0_log10	1.442	0.082	17.509	0.0000	27.663	19.079	40.515
f_max_1_log10	1.056	0.090	11.759	0.0000	11.369	7.543	16.919
f_max_2_log10	1.185	0.088	13.388	0.0000	15.298	10.321	22.706
f_max_3_log10	1.169	0.091	12.886	0.0000	14.750	9.776	22.173
f_max_4_log10	1.213	0.077	15.704	0.0000	16.325	11.451	23.244
n_half_log10	1.745	0.111	15.673	0.0000	55.625	33.815	92.282
Model 14h							
t_h_0_log10	-1.578	0.176	-8.959	0.0000	0.026	0.012	0.059
t_h_1_log10	-0.981	0.119	-8.209	0.0000	0.104	0.061	0.179
t_h_2_log10	-1.079	0.127	-8.508	0.0000	0.083	0.047	0.148
t_h_3_log10	-1.107	0.142	-7.810	0.0000	0.078	0.041	0.147
t_h_4_log10	-1.240	0.109	-11.393	0.0000	0.058	0.035	0.095
a_hab0_log10	-0.378	0.092	-4.091	0.0000	0.419	0.276	0.633

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Table 20: All 32 summary tables from *Ischnura elegans* model fits.
(continued)

Name	Orig. Est.	SE	z	p	Estimate	CI low	CI up
a_hab1_log10	-0.547	0.067	-8.164	0.0000	0.284	0.211	0.386
Model 14r							
f_max_0_log10	1.578	0.176	8.959	0.0000	37.807	17.335	82.854
f_max_1_log10	1.016	0.093	10.869	0.0000	10.364	6.799	15.768
f_max_2_log10	1.143	0.093	12.336	0.0000	13.903	9.133	21.185
f_max_3_log10	1.125	0.095	11.827	0.0000	13.324	8.697	20.549
f_max_4_log10	1.177	0.080	14.628	0.0000	15.038	10.496	21.907
n_half_hab0_log10	1.955	0.250	7.837	0.0000	90.243	29.660	274.483
n_half_hab1_log10	1.672	0.126	13.262	0.0000	46.939	26.342	83.141
Model 15h							
t_h_0_log10	-1.592	0.179	-8.886	0.0000	0.026	0.011	0.058
t_h_1_log10	-0.957	0.113	-8.457	0.0000	0.110	0.066	0.185
t_h_2_log10	-1.057	0.120	-8.806	0.0000	0.088	0.051	0.150
t_h_3_log10	-1.127	0.152	-7.403	0.0000	0.075	0.038	0.147
t_h_4_log10	-1.256	0.117	-10.729	0.0000	0.055	0.033	0.094
a_intercept_log10	-0.389	0.089	-4.357	0.0000	0.409	0.276	0.611
a_slope	-0.060	0.043	-1.411	0.1582	-0.060	-0.144	0.023
Model 15r							
f_max_0_log10	1.526	0.148	10.322	0.0000	33.565	17.366	66.217
f_max_1_log10	1.050	0.090	11.707	0.0000	11.214	7.548	16.928
f_max_2_log10	1.178	0.088	13.332	0.0000	15.083	10.308	22.562
f_max_3_log10	1.120	0.106	10.611	0.0000	13.168	8.247	21.101
f_max_4_log10	1.173	0.089	13.253	0.0000	14.896	10.014	22.163
n_half_intercept_log10	1.878	0.214	8.759	0.0000	75.506	29.433	202.826
n_half_slope	-0.072	0.094	-0.764	0.4447	-0.072	-0.258	0.112
Model 16h							
t_h_0_log10	-1.578	0.176	-8.959	0.0000	0.026	0.012	0.058
t_h_1_log10	-1.145	0.205	-5.593	0.0000	0.072	0.028	0.181
t_h_2_log10	-0.984	0.125	-7.859	0.0000	0.104	0.059	0.180
t_h_3_log10	-1.074	0.167	-6.416	0.0000	0.084	0.040	0.178
t_h_4_log10	-1.266	0.142	-8.913	0.0000	0.054	0.029	0.102
a_0_log10	-0.378	0.092	-4.091	0.0000	0.419	0.274	0.633
a_1_log10	-0.754	0.141	-5.346	0.0000	0.176	0.092	0.332
a_2_log10	-0.377	0.135	-2.790	0.0053	0.420	0.227	0.760
a_3_log10	-0.509	0.138	-3.689	0.0002	0.310	0.167	0.576
a_4_log10	-0.583	0.128	-4.537	0.0000	0.261	0.148	0.463
Model 16r							
f_max_0_log10	1.578	0.176	8.959	0.0000	37.806	17.201	84.553
f_max_1_log10	1.145	0.205	5.593	0.0000	13.955	5.585	34.170
f_max_2_log10	0.984	0.125	7.859	0.0000	9.638	5.519	16.984
f_max_3_log10	1.074	0.167	6.416	0.0000	11.850	5.600	25.789
f_max_4_log10	1.266	0.142	8.913	0.0000	18.439	9.802	35.173
n_half_0_log10	1.955	0.250	7.837	0.0000	90.242	29.714	282.040
n_half_1_log10	1.898	0.319	5.951	0.0000	79.115	19.114	321.310
n_half_2_log10	1.361	0.230	5.906	0.0000	22.968	8.189	65.282
n_half_3_log10	1.582	0.281	5.639	0.0000	38.234	10.922	138.140
n_half_4_log10	1.849	0.248	7.462	0.0000	70.559	23.679	215.708

Table 21: All 32 summary tables from *Ischnura elegans* model fits.

Name	Orig. Est.	SE	z	p	Estimate	CI low	CI up
Model 1h							
t_h_log10	-1.372	0.020	-67.929	0.0000	0.042	0.039	0.046
a_log10	-0.177	0.028	-6.309	0.0000	0.665	0.585	0.756
Model 1r							
f_max_log10	1.372	0.020	67.929	0.0000	23.560	21.489	25.796
n_half_log10	1.550	0.044	35.545	0.0000	35.447	29.129	43.218
Model 2h							
t_h_log10	-1.397	0.021	-65.700	0.0000	0.040	0.037	0.044
a_hab0_log10	0.180	0.050	3.567	0.0004	1.513	1.204	1.888
a_hab1_log10	-0.308	0.031	-10.011	0.0000	0.493	0.429	0.566
Model 2r							
f_max_log10	1.397	0.021	65.701	0.0000	24.927	22.644	27.417
n_half_hab0_log10	1.217	0.062	19.709	0.0000	16.473	12.421	21.708
n_half_hab1_log10	1.704	0.047	36.543	0.0000	50.605	41.143	62.513
Model 3h							
t_h_log10	-1.398	0.021	-66.503	0.0000	0.040	0.036	0.044
a_intercept_log10	0.185	0.048	3.861	0.0001	1.532	1.234	1.902
a_slope	-0.198	0.019	-10.239	0.0000	-0.199	-0.237	-0.160
Model 3r							
f_max_log10	1.398	0.021	66.503	0.0000	24.980	22.749	27.442
n_half_intercept_log10	1.212	0.060	20.267	0.0000	16.306	12.343	21.316
n_half_slope	0.198	0.019	10.239	0.0000	0.198	0.160	0.236
Model 4h							
t_h_log10	-1.405	0.021	-65.883	0.0000	0.039	0.036	0.043
a_0_log10	0.172	0.050	3.426	0.0006	1.487	1.188	1.859
a_1_log10	-0.329	0.056	-5.873	0.0000	0.469	0.365	0.601
a_2_log10	-0.111	0.050	-2.227	0.0259	0.775	0.619	0.967
a_3_log10	-0.440	0.050	-8.781	0.0000	0.363	0.288	0.454
a_4_log10	-0.404	0.053	-7.639	0.0000	0.395	0.309	0.500
Model 4r							
f_max_log10	1.405	0.021	65.883	0.0000	25.418	23.085	27.980
n_half_0_log10	1.233	0.062	19.975	0.0000	17.098	12.952	22.618
n_half_1_log10	1.734	0.067	25.749	0.0000	54.184	40.069	73.606
n_half_2_log10	1.516	0.060	25.109	0.0000	32.788	24.904	43.114
n_half_3_log10	1.845	0.060	30.740	0.0000	70.047	53.255	91.844
n_half_4_log10	1.809	0.063	28.531	0.0000	64.392	48.444	85.980
Model 5h							
t_h_hab0_log10	-1.616	0.038	-42.110	0.0000	0.024	0.020	0.029
t_h_hab1_log10	-1.291	0.021	-60.565	0.0000	0.051	0.046	0.056
a_log10	-0.162	0.028	-5.689	0.0000	0.689	0.605	0.782
Model 5r							
f_max_hab0_log10	1.543	0.025	61.397	0.0000	34.907	31.164	39.118
f_max_hab1_log10	1.311	0.021	61.828	0.0000	20.471	18.639	22.542
n_half_log10	1.535	0.044	35.142	0.0000	34.239	28.046	41.700
Model 6h							
t_h_hab0_log10	-1.498	0.035	-43.204	0.0000	0.032	0.027	0.037
t_h_hab1_log10	-1.329	0.024	-54.437	0.0000	0.047	0.042	0.052
a_hab0_log10	0.084	0.055	1.510	0.1310	1.212	0.949	1.556
a_hab1_log10	-0.250	0.033	-7.580	0.0000	0.562	0.485	0.651
Model 6r							
f_max_hab0_log10	1.498	0.035	43.204	0.0000	31.487	26.960	36.847

(continued on next page...)

Table 21: All 32 summary tables from *Ischnura elegans* model fits.
(continued)

Name	Orig. Est.	SE	z	p	Estimate	CI low	CI up
f_max_hab1_log10	1.329	0.024	54.437	0.0000	21.335	19.089	23.771
n_half_hab0_log10	1.414	0.082	17.338	0.0000	25.971	17.951	37.382
n_half_hab1_log10	1.579	0.052	30.513	0.0000	37.942	30.024	48.050
Model 7h							
t_h_hab0_log10	-1.486	0.033	-45.247	0.0000	0.033	0.028	0.038
t_h_hab1_log10	-1.338	0.024	-54.753	0.0000	0.046	0.041	0.051
a_intercept_log10	0.116	0.051	2.273	0.0230	1.307	1.039	1.646
a_slope	-0.153	0.023	-6.625	0.0000	-0.153	-0.197	-0.108
Model 7r							
f_max_hab0_log10	1.464	0.030	49.125	0.0000	29.114	25.423	33.345
f_max_hab1_log10	1.350	0.024	55.297	0.0000	22.380	20.020	24.936
n_half_intercept_log10	1.318	0.069	19.192	0.0000	20.773	15.274	28.430
n_half_slope	0.124	0.031	4.048	0.0001	0.124	0.064	0.183
Model 8h							
t_h_hab0_log10	-1.498	0.035	-43.204	0.0000	0.032	0.027	0.037
t_h_hab1_log10	-1.342	0.025	-53.876	0.0000	0.045	0.041	0.051
a_0_log10	0.084	0.055	1.510	0.1310	1.212	0.944	1.562
a_1_log10	-0.263	0.060	-4.351	0.0000	0.546	0.415	0.722
a_2_log10	-0.063	0.051	-1.224	0.2209	0.865	0.685	1.091
a_3_log10	-0.396	0.053	-7.411	0.0000	0.402	0.314	0.511
a_4_log10	-0.350	0.056	-6.209	0.0000	0.447	0.346	0.577
Model 8r							
f_max_hab0_log10	1.498	0.035	43.204	0.0000	31.487	26.874	36.873
f_max_hab1_log10	1.342	0.025	53.876	0.0000	21.986	19.648	24.623
n_half_0_log10	1.414	0.082	17.338	0.0000	25.971	17.980	37.791
n_half_1_log10	1.605	0.075	21.508	0.0000	40.242	28.727	56.082
n_half_2_log10	1.405	0.064	21.810	0.0000	25.415	18.962	34.113
n_half_3_log10	1.738	0.066	26.357	0.0000	54.714	40.542	73.798
n_half_4_log10	1.692	0.070	24.294	0.0000	49.227	36.033	67.242
Model 9h							
t_h_intercept_log10	-1.607	0.036	-44.903	0.0000	0.025	0.021	0.029
t_h_slope	0.128	0.014	8.866	0.0000	0.127	0.099	0.155
a_log10	-0.157	0.029	-5.486	0.0000	0.697	0.612	0.794
Model 9r							
f_max_intercept_log10	1.542	0.024	62.993	0.0000	34.831	31.166	38.841
f_max_slope	-0.094	0.009	-11.012	0.0000	-0.094	-0.110	-0.077
n_half_log10	1.531	0.044	35.031	0.0000	33.937	28.016	41.154
Model 10h							
t_h_intercept_log10	-1.510	0.033	-45.322	0.0000	0.031	0.026	0.036
t_h_slope	0.076	0.016	4.826	0.0000	0.076	0.046	0.108
a_hab0_log10	0.072	0.054	1.314	0.1887	1.179	0.921	1.511
a_hab1_log10	-0.241	0.033	-7.353	0.0000	0.574	0.496	0.667
Model 10r							
f_max_intercept_log10	1.513	0.031	48.459	0.0000	32.600	28.348	37.620
f_max_slope	-0.078	0.014	-5.425	0.0000	-0.078	-0.106	-0.049
n_half_hab0_log10	1.445	0.076	19.038	0.0000	27.839	19.753	39.275
n_half_hab1_log10	1.562	0.049	31.601	0.0000	36.444	29.204	45.314
Model 11h							
t_h_intercept_log10	-1.488	0.033	-45.420	0.0000	0.033	0.028	0.038
t_h_slope	0.063	0.016	3.856	0.0001	0.063	0.030	0.094
a_intercept_log10	0.102	0.052	1.947	0.0515	1.265	1.001	1.606
a_slope	-0.144	0.024	-5.956	0.0000	-0.144	-0.191	-0.097

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Table 21: All 32 summary tables from *Ischnura elegans* model fits.
(continued)

Name	Orig. Est.	SE	z	p	Estimate	CI low	CI up
Model 11r							
f_max_intercept_log10	1.488	0.033	45.420	0.0000	30.745	26.417	35.617
f_max_slope	-0.063	0.016	-3.857	0.0001	-0.062	-0.095	-0.031
n_half_intercept_log10	1.386	0.077	17.998	0.0000	24.304	17.251	34.374
n_half_slope	0.081	0.036	2.225	0.0261	0.081	0.009	0.153
Model 12h							
t_h_intercept_log10	-1.493	0.033	-45.054	0.0000	0.032	0.028	0.037
t_h_slope	0.062	0.017	3.734	0.0002	0.061	0.030	0.094
a_0_log10	0.089	0.054	1.632	0.1026	1.227	0.955	1.559
a_1_log10	-0.291	0.058	-5.054	0.0000	0.511	0.394	0.659
a_2_log10	-0.083	0.050	-1.654	0.0981	0.826	0.657	1.040
a_3_log10	-0.372	0.056	-6.624	0.0000	0.425	0.331	0.548
a_4_log10	-0.321	0.059	-5.402	0.0000	0.477	0.365	0.623
Model 12r							
f_max_intercept_log10	1.493	0.033	45.054	0.0000	31.101	26.763	36.219
f_max_slope	-0.062	0.017	-3.735	0.0002	-0.061	-0.094	-0.029
n_half_0_log10	1.404	0.079	17.776	0.0000	25.342	17.668	36.458
n_half_1_log10	1.661	0.069	24.147	0.0000	45.803	33.678	62.505
n_half_2_log10	1.452	0.060	24.043	0.0000	28.346	21.591	37.289
n_half_3_log10	1.680	0.074	22.813	0.0000	47.842	34.316	67.135
n_half_4_log10	1.629	0.078	20.921	0.0000	42.570	30.240	60.890
Model 13h							
t_h_0_log10	-1.611	0.038	-42.479	0.0000	0.024	0.021	0.029
t_h_1_log10	-1.233	0.038	-32.446	0.0000	0.059	0.049	0.070
t_h_2_log10	-1.435	0.036	-39.612	0.0000	0.037	0.031	0.043
t_h_3_log10	-1.253	0.039	-32.161	0.0000	0.056	0.047	0.067
t_h_4_log10	-1.208	0.039	-31.368	0.0000	0.062	0.052	0.074
a_log10	-0.153	0.029	-5.358	0.0000	0.703	0.620	0.800
Model 13r							
f_max_0_log10	1.541	0.025	61.458	0.0000	34.784	31.163	38.972
f_max_1_log10	1.287	0.030	42.422	0.0000	19.350	16.841	22.146
f_max_2_log10	1.416	0.028	51.411	0.0000	26.070	23.043	29.561
f_max_3_log10	1.264	0.031	40.568	0.0000	18.371	15.937	21.128
f_max_4_log10	1.255	0.031	40.067	0.0000	17.969	15.602	20.735
n_half_log10	1.531	0.044	35.103	0.0000	33.928	27.896	41.332
Model 14h							
t_h_0_log10	-1.498	0.035	-43.204	0.0000	0.032	0.027	0.037
t_h_1_log10	-1.267	0.041	-30.789	0.0000	0.054	0.045	0.065
t_h_2_log10	-1.477	0.041	-35.995	0.0000	0.033	0.028	0.040
t_h_3_log10	-1.292	0.042	-30.706	0.0000	0.051	0.042	0.062
t_h_4_log10	-1.241	0.041	-30.172	0.0000	0.057	0.048	0.069
a_hab0_log10	0.084	0.055	1.510	0.1310	1.212	0.942	1.548
a_hab1_log10	-0.240	0.033	-7.217	0.0000	0.575	0.493	0.666
Model 14r							
f_max_0_log10	1.498	0.035	43.204	0.0000	31.487	26.945	36.786
f_max_1_log10	1.304	0.033	39.997	0.0000	20.122	17.342	23.285
f_max_2_log10	1.433	0.030	47.723	0.0000	27.122	23.683	31.009
f_max_3_log10	1.282	0.033	38.276	0.0000	19.133	16.415	22.312
f_max_4_log10	1.272	0.034	37.905	0.0000	18.699	16.120	21.760
n_half_hab0_log10	1.414	0.082	17.338	0.0000	25.971	18.035	37.419
n_half_hab1_log10	1.574	0.052	30.458	0.0000	37.468	29.465	47.409
Model 15h							
t_h_0_log10	-1.489	0.033	-44.613	0.0000	0.032	0.028	0.038

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Table 21: All 32 summary tables from *Ischnura elegans* model fits.
(continued)

Name	Orig. Est.	SE	z	p	Estimate	CI low	CI up
t_h_1_log10	-1.243	0.039	-32.106	0.0000	0.057	0.048	0.068
t_h_2_log10	-1.448	0.037	-38.812	0.0000	0.036	0.030	0.042
t_h_3_log10	-1.335	0.047	-28.329	0.0000	0.046	0.037	0.057
t_h_4_log10	-1.276	0.045	-28.270	0.0000	0.053	0.043	0.065
a_intercept_log10	0.107	0.053	2.036	0.0418	1.280	1.009	1.624
a_slope	-0.144	0.024	-5.938	0.0000	-0.144	-0.192	-0.097
Model 15r							
f_max_0_log10	1.488	0.033	45.165	0.0000	30.741	26.538	35.737
f_max_1_log10	1.293	0.031	42.179	0.0000	19.646	17.166	22.554
f_max_2_log10	1.423	0.028	50.988	0.0000	26.474	23.365	30.057
f_max_3_log10	1.305	0.037	34.849	0.0000	20.181	17.040	23.922
f_max_4_log10	1.295	0.037	34.622	0.0000	19.703	16.726	23.341
n_half_intercept_log10	1.385	0.077	17.965	0.0000	24.285	17.185	34.345
n_half_slope	0.081	0.037	2.220	0.0264	0.081	0.010	0.152
Model 16h							
t_h_0_log10	-1.498	0.035	-43.204	0.0000	0.032	0.027	0.037
t_h_1_log10	-1.232	0.045	-27.187	0.0000	0.059	0.048	0.072
t_h_2_log10	-1.423	0.041	-34.733	0.0000	0.038	0.031	0.045
t_h_3_log10	-1.406	0.066	-21.145	0.0000	0.039	0.029	0.053
t_h_4_log10	-1.257	0.049	-25.651	0.0000	0.055	0.044	0.069
a_0_log10	0.084	0.055	1.510	0.1310	1.212	0.947	1.555
a_1_log10	-0.151	0.073	-2.063	0.0391	0.707	0.507	0.985
a_2_log10	-0.125	0.057	-2.193	0.0283	0.750	0.580	0.970
a_3_log10	-0.441	0.067	-6.611	0.0000	0.363	0.268	0.489
a_4_log10	-0.279	0.068	-4.102	0.0000	0.526	0.387	0.717
Model 16r							
f_max_0_log10	1.498	0.035	43.204	0.0000	31.487	26.900	37.002
f_max_1_log10	1.232	0.045	27.187	0.0000	17.046	13.899	20.904
f_max_2_log10	1.423	0.041	34.733	0.0000	26.492	21.959	31.943
f_max_3_log10	1.406	0.066	21.146	0.0000	25.453	18.976	34.438
f_max_4_log10	1.257	0.049	25.651	0.0000	18.057	14.459	22.589
n_half_0_log10	1.414	0.082	17.338	0.0000	25.971	17.864	37.766
n_half_1_log10	1.382	0.106	12.994	0.0000	24.113	14.974	39.065
n_half_2_log10	1.548	0.088	17.666	0.0000	35.334	23.661	52.535
n_half_3_log10	1.846	0.123	15.060	0.0000	70.211	40.660	121.493
n_half_4_log10	1.536	0.104	14.724	0.0000	34.349	21.394	55.261

Project Settings

We created the statistics in this report and the report itself using R version 4.4.3 (2025-02-28) - Trophy Case on a x86_64 computer with Linux Mint 22.1 as operating system. Find the loaded and attached packages that we used in table 22.

Table 22: All loaded R packages that we used in this report, including base packages.

Package Name	Version	Is Package Attached?	Is a Base Package?
base	4.4.3	TRUE	TRUE
datasets	4.4.3	TRUE	TRUE
graphics	4.4.3	TRUE	TRUE
grDevices	4.4.3	TRUE	TRUE
methods	4.4.3	TRUE	TRUE
stats	4.4.3	TRUE	TRUE
utils	4.4.3	TRUE	TRUE
compiler	4.4.3	FALSE	TRUE
grid	4.4.3	FALSE	TRUE
parallel	4.4.3	FALSE	TRUE
stats4	4.4.3	FALSE	TRUE
tools	4.4.3	FALSE	TRUE
dplyr	1.1.4	TRUE	FALSE
foreach	1.5.2	TRUE	FALSE
bbmle	1.0.25.1	FALSE	FALSE
bdsmatrix	1.3-7	FALSE	FALSE
bookdown	0.42	FALSE	FALSE
boot	1.3-31	FALSE	FALSE
cli	3.6.3	FALSE	FALSE
coda	0.19-4.1	FALSE	FALSE
codetools	0.2-20	FALSE	FALSE
colorspace	2.1-1	FALSE	FALSE
curl	6.2.0	FALSE	FALSE
digest	0.6.37	FALSE	FALSE
doParallel	1.0.17	FALSE	FALSE
emdbook	1.3.13	FALSE	FALSE
evaluate	1.0.3	FALSE	FALSE
fastmap	1.2.0	FALSE	FALSE
frair	0.5.100	FALSE	FALSE
generics	0.1.3	FALSE	FALSE
gh	1.4.1	FALSE	FALSE
gitcreds	0.1.2	FALSE	FALSE
glue	1.8.0	FALSE	FALSE
here	1.0.1	FALSE	FALSE
htmltools	0.5.8.1	FALSE	FALSE
httr2	1.1.0	FALSE	FALSE
iterators	1.0.14	FALSE	FALSE
jsonlite	1.8.9	FALSE	FALSE
kableExtra	1.4.0	FALSE	FALSE
knitr	1.49	FALSE	FALSE
lamW	2.2.4	FALSE	FALSE
lattice	0.22-5	FALSE	FALSE
lifecycle	1.0.4	FALSE	FALSE
magrittr	2.0.3	FALSE	FALSE
MASS	7.3-65	FALSE	FALSE
Matrix	1.7-3	FALSE	FALSE
munsell	0.5.1	FALSE	FALSE

mvtnorm	1.3-3	FALSE	FALSE
numDeriv	2016.8-1.1	FALSE	FALSE
pillar	1.10.1	FALSE	FALSE
pkgconfig	2.0.3	FALSE	FALSE
plyr	1.8.9	FALSE	FALSE
purrr	1.0.4	FALSE	FALSE
R6	2.5.1	FALSE	FALSE
rappdirs	0.3.3	FALSE	FALSE
Rcpp	1.0.14	FALSE	FALSE
RcppParallel	5.1.10	FALSE	FALSE
rlang	1.1.5	FALSE	FALSE
rmarkdown	2.29	FALSE	FALSE
rprojroot	2.0.4	FALSE	FALSE
rstudioapi	0.17.1	FALSE	FALSE
scales	1.3.0	FALSE	FALSE
sessioninfo	1.2.3	FALSE	FALSE
stringi	1.8.4	FALSE	FALSE
stringr	1.5.1	FALSE	FALSE
supportR	1.4.0	FALSE	FALSE
svglite	2.1.3	FALSE	FALSE
systemfonts	1.2.1	FALSE	FALSE
tibble	3.2.1	FALSE	FALSE
tidyselect	1.2.1	FALSE	FALSE
vctrs	0.6.5	FALSE	FALSE
viridisLite	0.4.2	FALSE	FALSE
withr	3.0.2	FALSE	FALSE
xfun	0.50	FALSE	FALSE
xml2	1.3.6	FALSE	FALSE
yaml	2.3.10	FALSE	FALSE
