1 FRAIR: AN R PACKAGE FOR FITTING AND COMPARING CONSUMER

- 2 FUNCTIONAL RESPONSES
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SUMMARY

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- 1. Consumer-resource interactions (i.e. the functional response) underpin decades of ecological advancements. However, selecting, fitting and comparing functional response models using appropriate methods remains a non-trivial endeavour.
- 2. The R package *FRAIR* provides tools for selecting and differentiating various forms of consumer functional response models, a consistent interface for fitting and visualising response curves, and a selection of statistically robust methods for comparing fitted parameters.
 - 3. Using real data from crustacean predator-prey systems, we demonstrate the utility of *FRAIR*, highlighting best practice and common analytical mistakes.
- 25 Keywords: consumer-resource interactions; predator-prey; resource use; non-linear curve
- 26 fitting; bootstrapping; maximum likelihood

INTRODUCTION

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Consumer-resource interactions are at the heart of ecology because all organisms must consume resources of some kind. Functional responses describe how the per capita feeding rates of consumers change systematically with resource availability as a result of the consumer's search for, capture, and handling of resources (Holling 1959, 1966). The ubiquity and simplicity of principles underpinning the functional response continues to resonate with ecologists working at scales ranging from the behaviour of individuals (Toscano & Griffen 2014) to entire food webs (Brose 2010). Across fields—from theoretical explorations of stability and coexistence (Williams & Martinez 2004) to applications in biocontrol, invasions and conservation—functional responses remain central to much ecological research.

THE ANATOMY OF A FUNCTIONAL RESPONSE

- 39 Despite decades of refinements (e.g. Real 1977; Hassell 1978; Arditi & Ginzburg 1989;
- 40 Skalski & Gilliam 2001; Okuyama 2012), the essential components of search, capture and
- 41 handling outlined by Holling (1959) have remained largely unchanged. A generalised version
- 42 of the Holling disc equation is (Real 1977):

43
$$N_e = \frac{aTN^{(q+1)}}{1 + ahN^{(q+1)}}$$
 (1)

where N is the resource density or number of prey; T is experimental time (typically hours or days); a is the instantaneous resource capture rate of the consumer, per unit area/volume per unit time; h in practice represents the time spent subjugating, ingesting and digesting each prey item, with the same units as T (Jeschke et al. 2002; Sentis et al. 2013); and q is a scaling exponent defining the extent to which the functional response changes from a decelerating hyperbola (Type II: q = 0 and Fig. 1a purple) to a sigmoidal form (Type III: q > 0 and Fig. 1a green).

51 When q is 0, capture rates are constant with resource density, whereas where q > 0, capture 52 rates follow a power-law relationship with resource density, often implying that consumers 53 learn as they forage (Real 1977). Type I (linear rather than saturating sensu Holling; Fig. 1a 54 orange) functional responses can be described where q = 0 and h = 0. Since handling time 55 determines the maximum consumption rate (1/h), doubling h suppresses the asymptote for 56 consumers with identical capture rates (Fig. 1c: dashed versus solid blue curve). In contrast, 57 for consumers with identical handling times, doubling capture rates (a) increases 58 consumption at low resource densities (Fig. 1c: dashed *versus* solid purple curves).

An important assumption of equation 1 is that local resource density does not decline.

60 However, in many experiments, consumers deplete resources, rendering models in the

61 equation 1 family inappropriate (e.g. Bollache et al. 2008). The family of models introduced

by Royama (1971) and popularised by Rogers (1972) provide a solution to this problem by

integrating instantaneous consumption over time. The modification of equation 1 assuming

64 depletion is:

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$$N_e = N_0(1 - exp(aN_0^q(hN_e - T)))$$
 (2)

where N_0 is the initial prey density, and other parameters are as in equation 1. Although the number of prey eaten (N_e) appears on both sides of equation 2, it can often be solved using the Lambert-W function (W). The derivation and definition of W is beyond the scope of this manuscript but it is described in detail in Corless *et al.* (1996) and with respect to ecological applications in Lehtonen (2016).

APPLICATIONS OF FUNCTIONAL RESPONSES

Ecologists often seek objective comparisons between one or more groups; with functional responses this usually necessitates comparisons of fitted model parameters, though the

particular methods employed remain a subject of confusion and debate (Houck & Strauss 1985; Juliano 2001). Renewed interest in consumer functional response models has driven several innovative analytical solutions, at least two of which have been widely adopted. The first involves explicitly modelling the difference fitted parameters between two (or more) groups. This approach – described in Juliano (2001) – whilst computationally simple, requires reparameterisation of the underlying model. It provides a coefficient (the difference between groups of interest) that can be interpreted within a regression-modelling framework, and with proper formulation and sufficient data, can be extended to moderately complex hypotheses (e.g. Paterson et al. 2015). A second approach involves bootstrapping (resampling with replacement) of either raw data (e.g. Bovy et al. 2015) or modelled residuals (e.g. Médoc et al. 2015). This computationally intensive approach explores the likely range of fitted coefficients, and allows for direct comparison of the range of these values (e.g. via confidence intervals). Not all analytical approaches in the recent literature are as well advised. For example, some have applied null-hypothesis significance tests to bootstrapped parameter estimates from functional response models (e.g. Dodd et al. 2014; Bunke et al. 2015) – an approach that is clearly flawed (White et al. 2014). We suspect that the lack of a common toolset for nonspecialists to fit and examine consumer functional response models has contributed to the propagation of these methods. With research output increasing, it is critical that ecologists working on functional responses can make robust analyses: we anticipate that FRAIR can meet this need.

THE FRAIR PACKAGE

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FRAIR is a package in the R statistical environment for selection, fitting and comparisons among common functional response models and constituent parameters. FRAIR is available

- on CRAN and development is undertaken openly on GitHub
- 99 (http://github.com/dpritchard/frair).
- This tutorial is based on FRAIR version 0.5 (the most recent version available on CRAN) and
- outlines key functionalities whilst providing a general introduction to these analyses. The
- tutorial is based on two experimentally derived datasets included with the package:
- gammarus, a subset of data from Paterson et al. (2015) and bythotrephes, a previously
- unpublished dataset.
- The gammarus dataset describes consumption of dipteran larvae (Simulium spp.) by two
- amphipod species (Gammarus duebeni celticus and Gammarus pulex). The bythotrephes
- dataset describes consumption of three size classes of the cladoceran *Polyphemus pediculus*
- by the cladoceran *Bythotrephes longimanus*. Both datasets concern experimental designs
- incorporating prey depletion. For further examples, readers are directed to other published
- studies utilising FRAIR (https://github.com/dpritchard/frair/wiki/FRAIR-in-use).

```
111
     # Gammarus
112
     data("gammarus")
113
     str(gammarus)
                         224 obs. of 4 variables:
114
     ## 'data.frame':
115
     ## $ density: int 2 2 2 2 2 2 2 2 2 2 ...
116
     ## $ eaten : int 0 2 2 2 2 2 2 2 2 2 ...
117
     ##
         $ alive : int
                         20000000000...
118
                  : Factor w/ 2 levels
         $ spp
119
     levels(gammarus$spp)
120
     ## [1] "G.d.celticus" "G.pulex"
```

```
121
122
     # Bythotrephes
123
     data("bythotrephes")
124
     str(bythotrephes)
125
     ## 'data.frame':
                        72 obs. of 4 variables:
126
     ##
        $ density: int 1 1 1 3 3 3 2 2 2 4 ...
127
     ##
         $ eaten : int 1 1 0 3 2 3 2 2 2 4 ...
128
     ## $ alive : int 0010100000...
129
     ## $ size : Factor w/ 3 levels
```

130 levels(bythotrephes\$size) 131 ## [1] "small" "medium" "large" 132 133 The FRAIR workflow involves a three-step process: (1) model selection; (2) model fitting 134 and; (3) comparison of fits and coefficients. An essential step in this process is to visually 135 inspect the raw plotted data (Fig. 2). 136 **MODEL SELECTION** 137 FRAIR offers a range of commonly used functional response models that can be viewed using 138 frair responses(). Basic models assume constant resource density throughout 139 experimental trials (resources are replaced). For experiments where resources are depleted 140 (so-called non-replacement experiments), models are provided (suffixed with nr) with 141 Rogers (1972) modifications and solved using the 'lambertW' function (Bolker 2008). 142 Although equations 1 and 2 imply consumer functional responses can be described on a 143 linear (Type I) to sigmoidal (Type III) continuum, the original categorical descriptions of 144 Holling remain prominent (e.g. Denny 2014). This is likely because deviations from Type II 145 towards Type III functional responses can stabilise otherwise chaotic consumer-resource 146 dynamics (Williams & Martinez 2004; Barrios-O'Neill et al. 2016). 147 Juliano (2001) advocates fitting polynomial logistic functions to proportional consumption 148 data to determine functional response Type. Type II is characterised by a negative first-order 149 term (declining proportional consumption with increasing resource density; Fig. 1b), in 150 contrast to a positive first-order term of Type III (initial increase and subsequent decrease in 151 proportional consumption; Fig. 1b). Using this logic, the frair test function uses forward 152 selection based on the sign and significance of first-order (density) and second-order 153 (density^2) terms in logistic regressions.

```
154
      # Gammarus
155
      frair_test(formula = eaten~density, data = gammarus)
156
      ## FUNCTIONAL RESPONSE TEST
157
158
      ## Evidence for type-II response:
                                              Yes
159
      ## Evidence for type-III response:
160
161
      ## Type-II logistic regression output:
162
                    Estimate Std. Error z value Pr(>|z|)
163
      ## density -0.0792704 0.0044298 -17.895 < 2.2e-16 ***
164
      ## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
165
166
167
      # Bythotrephes
168
      frair test(formula = eaten~density, data = bythotrephes)
169
      ## FUNCTIONAL RESPONSE TEST
170
      ##
171
      ## Evidence for type-II response:
172
      ## Evidence for type-III response:
173
      ##
174
      ## Type-III logistic regression output:
175
      ##
                          Estimate Std. Error z value Pr(>|z|)
                         0.3646093 0.1009794 3.6107 0.0003053 ***
176
      ## density
177
      ## I(density^2) -0.0206557  0.0051263 -4.0293 5.593e-05 ***
178
179
      ## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
180
181
      Although this approach provides a statistical test to distinguish between Type II and Type III,
182
      it is considered phenomenological in that describes only the general shape of the response,
183
      without determining whether a particular mechanistic model is appropriate. An alternative
      approach involves fitting a generalised form of the functional response model with a scaling
184
      exponent (q) parameterised such that q = 0 represents a Type II response (equation 1 or 2),
185
186
      thus exposing a useful null-hypothesis test (i.e. q \neq 0) via a regression output and allowing
187
      for comparison of models using information criteria (e.g. AIC, BIC, AICc). For example,
188
      with the bythotrephes dataset:
189
      # Bythotrephes
190
      # Fit a model where q can vary:
191
      b_flex <- frair_fit(eaten~density, data=bythotrephes,</pre>
192
                            response='flexpnr',
```

```
193
                           start=list(b = 1, q = 0, h = 0.08),
194
                           fixed=list(T = 12/24))
195
      # Fit a model where q is fixed to zero:
196
      b_II <- frair_fit(eaten~density, data=bythotrephes,</pre>
                         response='flexpnr',
197
198
                         start=list(b = 1, h = 0.08),
199
                         fixed=list(T = 12/24, q = 0))
      summary(b_flex$fit) # q != 0 : Type III preferred
200
      AIC(b flex$fit, b II$fit) # The model including g is preferred
201
```

- 203 The usefulness of these tests depends on the quality of data at low resource densities
- 204 (Barrios-O'Neill et al. 2015) and some authors recommend that proportional relationships are
- visually inspected with locally weighted regression (Juliano 2001).
- The experimental designs of our datasets indicate that depletion models are required as prey
- are not replaced during the experiment. Plots of the raw data and these analyses suggest that
- for the gammarus dataset, a Type II model is sufficient, however a Type III—or flexible
- 209 model—may be most appropriate for the bythotrephes data.

210 MODEL FITTING

- 211 Essential to the optimisation of non-linear models is the provision of reasonable starting
- values for free parameters. There are some rules of thumb, for example, for Type II models, h
- 213 can be approximated as the inverse of the maximum number eaten where T is set to 1 (Bolker
- 214 2008). An equally reliable method is a visual assessment of the data, plotting of putative
- starting values and trial and error (Fig. 2).

```
216
      # Gammarus
      with(gammarus, plot(density, eaten, xlab="Prey Density",
217
                           ylab="No. Prey Eaten"))
218
      x \leftarrow with(gammarus, seq(from = min(density), to = max(density),
219
220
                               by = (0.1)
221
      lines(x, rogersII(X = x, a = 1.2, h = 0.08, T = 40/24),
222
            col='grey50', lty=2)
223
      lines(x, rogersII(X = x, a = 0.6, h = 0.16, T = 40/24),
224
           col='grey50', lty=2)
```

```
225
226
      # Bythotrephes
227
      with(bythotrephes, plot(density, eaten, xlab="Prey Density",
                              ylab="No. Prey Eaten"))
228
229
      x <- with(bythotrephes, seq(from = min(density), to = max(density),</pre>
230
                                   by = (0.1)
      lines(x, flexpnr(X = x, b = 1, h = 0.04, q = 1, T = 12/24),
231
232
            col='grey50', lty=2)
233
      lines(x, flexpnr(X = x, b = 2.4, h = 0.04, q = 0, T = 12/24),
234
            col='grey50', lty=2)
```

Note that all *FRAIR* functional response models take at least one fixed parameter (*T*), which is experimental time. Although not optimised, this value will change the units of the fitted coefficients. For example, with the gammarus dataset:

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```
239
      # The role of T in modifying fitted coefficients.
240
      g_T1 <- frair_fit(formula = eaten~density, data = gammarus,</pre>
                         response = "rogersII",
241
                         start = list(a = 2, h = 0.1), fixed = <math>list(T = 1)
242
243
      g Td <- frair fit(formula = eaten~density, data = gammarus,
244
                         response = "rogersII",
245
                         start = list(a = 1, h = 0.1), fixed = list(T = 40/24))
246
      g_Th <- frair_fit(formula = eaten~density, data = gammarus,</pre>
247
                         response = "rogersII",
248
                         start = list(a = 0.05, h = 4), fixed = <math>list(T = 40)
249
      diff_t <- round(rbind(coef(g_T1), coef(g_Td), coef(g_Th)), 2)</pre>
250
      row.names(diff_t) <- c("g_T1 (Time)", "g_Td (Days)", "g_Th (Hours)")</pre>
251
      print(diff_t)
252
      ##
                                      Τ
                               h
                          а
253
      ## g_T1 (Time) 2.37 0.11 1.00
254
      ## g_Td (Days) 1.42 0.18 1.67
255
      ## g_Th (Hours) 0.06 4.33 40.00
```

Many authors implicitly accept units of experimental time" by setting T=1. Unless the raw data is made available this limits the use of parameter estimates in subsequent studies (e.g. meta-analyses, food-web models). Therefore, we recommend users adopt units of either hour or day and have adopted units of day in this manuscript. Once starting estimates and fixed values are provided, the model is optimised using maximum likelihood estimation (MLE).

This robust approach to fitting non-linear models (Bolker 2008) allows for optimisation on the basis of arbitrary probability distributions. Internally, all *FRAIR* models use a binomial likelihood function, which imposes an upper (all prey eaten) and lower (no prey eaten) limit on the response. A practical limitation of this likelihood specification is that *FRAIR* can only fit curves when the density (x-axis) is specified as whole integer values (the most common situation for individual prey items).

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In *FRAIR*, optimisation by MLE is provided by frair_fit and is implemented using bbmle::mle2 (Bolker 2008). The resulting output (of class frair_fit) provides information on the fit and the maximum likelihood estimators (fitted coefficients) and a lines method to plot the fitted curve (Fig. 2). frair_fit also returns the raw output from the maximum likelihood optimisation, which provides typical regression output including asymptotic standard errors, *z*-statistics and *p*-values.

```
274
      # A fit to the entire gammarus dataset
275
      g fit <- frair fit(formula = eaten~density, data = gammarus,</pre>
276
                         response = "rogersII",
277
                         start = list(a = 1, h = 0.1),
278
                         fixed = list(T = 40/24))
279
      with(gammarus, plot(density, eaten, xlab="Prey Density",
280
                          ylab="No. Prey Eaten"))
281
      lines(g_fit, lty = 1, col = "grey25")
282
      print(g_fit)
283
     ## FUNCTIONAL RESPONSE FIT
284
     ##
285
     ## Response:
                              rogersII
286
     ## Description:
                              Roger's type II decreasing prey function
287
      ## Optimised variables: a, h
288
     ## Fixed variables:
289
      ##
290
     ## Coefficients:
291
     ##
                         Т
             а
292
      ## 1.423 0.180 1.667
293
294
      ## NOTE: It is recommended you inspect the raw fit too (see: ?frair fit)
295
      summary(g fit$fit)
296
      ## Coefficients:
297
            Estimate Std. Error z value Pr(z)
```

```
298
     ## a 1.4228013 0.1314562 10.823 < 2.2e-16
299
     ## h 0.1802657 0.0098583 18.286 < 2.2e-16
300
301
     ## -2 log L: 1129.631
302
303
      # A fit to the entire bythotrephes dataset
304
      b_fit <- frair_fit(formula = eaten~density, data = bythotrephes,</pre>
                         response = "flexpnr",
305
306
                         start = list(b = 1.5, h = 0.04, q = 1),
307
                         fixed = list(T = 12/24))
308
     with(bythotrephes, plot(density, eaten, xlab="Prey Density",
309
                              ylab="No. Prey Eaten"))
310
      lines(b_fit, lty = 1, col = "grey25")
311
      print(b_fit)
312
     ## FUNCTIONAL RESPONSE FIT
313
     ##
314
     ## Response:
                              flexpnr
315
     ## Description:
                              Flexible exponent, not assuming replacement
     ## Optimised variables: b, h, q
316
317
     ## Fixed variables:
318
     ##
319
     ## Coefficients:
320
     ##
             b
                         h
321
     ## 0.652 1.215 0.053 0.500
322
     ##
323
     ## NOTE: It is recommended you inspect the raw fit too (see: ?frair fit)
324
      summary(b fit$fit)
     ## Coefficients:
325
326
           Estimate Std. Error z value
                                            Pr(z)
327
     ## b 0.651730
                      0.258996
                               2.5164
                                          0.01186
328
     ## q 1.215357
                      0.296077 4.1049 4.045e-05
329
     ## h 0.052912
                      0.005112 10.3509 < 2.2e-16
330
     ##
331
     ## -2 log L: 241.1805
```

MODEL COMPARISON

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The third step in the *FRAIR* workflow includes comparisons of fitted coefficients. The two approaches currently implemented are the delta or difference method of Juliano (2001), provided by frair_compare and non-parametric bootstrapping of the raw data, provided by frair_boot. Both functions operating on objects produced by frair_fit (i.e. class frfit).

Comparisons between constituent parameters require that those parameters are equivalent.

Comparisons of handling times, h, and maximum feeding rates (1/hT) are possible between all models in FRAIR (assuming consumers are handling limited), but comparisons of capture rates are often problematic. For example, there is no equivalence between capture rates as defined in hassIIInr and rogersII, which respectively describe Type III and Type II responses (e.g. Alexander $et\ al.\ 2012$). Indeed, a Type II model assumes a prey density-independent capture rate, whilst for a Type III model capture rates typically follow a power law with prey density. Where comparing Type II and Type III models it is common to resort to comparisons of maximal capture rates, usually the steepest part of the curve (Englund $et\ al.\ 2011$). Often, however, responses in a dataset are of the same categorical form, making comparisons straightforward.

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```
349
      # Compare two species in the gammarus dataset
350
      pulex <- gammarus[gammarus$spp=='G.pulex', ]</pre>
      celt <- gammarus[gammarus$spp=='G.d.celticus', ]</pre>
351
352
      st < -list(a = 1, h = 0.1)
353
      fx < - list(T = 40/24)
354
      p fit <- frair fit(eaten~density, data = pulex, response = 'rogersII',</pre>
355
                          start = st, fixed = fx)
356
      c_fit <- frair_fit(eaten~density, data=celt, response='rogersII',</pre>
357
                          start = st, fixed = fx)
358
      frair_compare(p_fit, c_fit)
359
      ## FUNCTIONAL RESPONSE COEFFICIENT TEST
360
      ##
361
      ## Response:
                               rogersII
362
      ## Optimised variables: a,h
363
      ## Fixed variables:
364
      ##
365
      ## Original coefficients:
366
      ##
367
      ## p fit 1.47748 0.14268
368
      ## c_fit 1.41745 0.23381
369
370
      ## Test: p_fit - c_fit
371
      ##
372
      ##
            Estimate Std. Error z value Pr(z)
373
      ## Da 0.05961
                         0.27132 0.2197 0.8261
374
      ## Dh -0.09115
                        0.02087 -4.3681 1e-05
```

```
frair_compare implements a difference test with the null hypothesis that fitted parameters
do not differ. The fitted parameters Da and Dh estimate the differences between the capture
rates and handling times of the two predators respectively. Here, we have evidence that
capture rates do not differ (Da = 0.06, z = 0.22, p = 0.826), but that the handling time of
G. pulex is shorter than that of G. d. celticus (Dh = -0.02, z = -4.36, p < 0.001).
Unfortunately the difference method does not allow for direct comparisons between predicted
consumption a across the range of resource densities and because consumers can switch
between Type II and Type III responses (Barrios-O'Neill et al. 2016) objective comparisons
using this approach are often impossible. Therefore, FRAIR also provides frair_boot,
which implements non-parametric bootstrapping and leverages boot::boot (Canty & Ripley
2016). This method generates multiple estimates of curves and constituent parameters (based
on a default minimum of 999 samples; Dixon 2001) and reports 95% confidence intervals
(CIs) by default. We recommend using bias corrected and accelerated intervals – BCa – to
account for bias, skew and bounded parameters (a and h > 0). It is expected that the
underlying maximum likelihood estimation will sometimes fail, even with reasonable starting
values, therefore frair_boot warns if > 10% of all bootstrapped fits fail and returns an error
if >50% of the fits fail. Because bootstrapping generates population metrics, the equivalent of
a null hypothesis test is simply a lack of overlap between the CIs of model parameters.
```

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```
394
      # Bootstrap the Gammarus pulex fit
395
      p fitb <- frair boot(p fit)</pre>
396
      confint(p_fitb, citypes = 'bca')
397
      ## Coefficient CI Type
                                       Lower
                                                Upper
398
      ## a
                       BCa
                                       0.998
                                                2.295
399
      ## h
                       BCa
                                       0.102
                                                0.203
400
401
      # Bootstrap the Gammarus duebeni celticus fit
402
      c_fitb <- frair_boot(c_fit)</pre>
403
      confint(c_fitb, citypes = 'bca')
```

404	## Coefficient	CI Type	Lower	Upper	
405	## a	BCa	0.94	2.133	
406	## h	BCa	0.183	0.286	

Bootstrapping outputs for the gammarus dataset concur with the difference method for capture rates: the 95% CIs clearly overlap. In contrast to the difference method frair_boot suggests no difference between consumer handling times (95% CIs for h fractionally overlap). While both methods are sensitive to underlying data quality and quantity, the difference method makes assumptions about the error structure of the fitted parameters, whilst bootstrapping reflects the likely range of values given the data provided, whilst accounting for the bounded (e.g. non-negative) nature of handling times.

Based on the output from bootstrapped fits, FRAIR provides visual comparisons of entire functional response curves using drawpoly (Fig. 3). This function plots empirical approximations of the confidence intervals using the desired quantile predictions (0.025 and 0.975 for 95% CIs). Even where estimates of 95% CIs for all fitted parameters overlap (as in this example), parameters can combine to yield differences in predicted consumption as a function of prey density (Fig. 3). Such differences cannot be addressed using the delta method, and drawpoly provides a means to identify where predicted consumption may differ

LIMITATIONS

along an axis of resource density.

Fitting non-linear models to ecological data can be a challenging and frustrating process (Bolker *et al.* 2013), resulting from highly variable data, low replication, use of an overly complex model, a desire to test many hypotheses, or a combination of these. Although there have been computational improvements, the challenges are as real now as they were in 1988, when Trexler *et al.* noted that it may be impossible to fit a curve to data, even with 11

resource densities and 10 replicates per resource density – a quantity of data rarely attained in experimental functional response analyses (Trexler *et al.* 1988). Even after many days of laboratory work, it may be impossible to fit the desired functional response model, or distinguish between the subtleties of a Type II and Type III response. This may be an unavoidable problem that no software can solve, but accessible tools for analysis will improve understanding of the strengths and limitations of consumer functional responses.

Nevertheless, even with these tools, it seems clear that there is nothing straightforward about application or interpretation.

FRAIR has been designed with the non-specialist in mind. However, for those seeking advanced analyses, FRAIR has some practical limitations. For example, currently FRAIR does not provide ratio- or predator-dependent models (e.g. Hassell & Varley 1969; Beddington 1975) or body size-dependent models (e.g. Kalinkat *et al.* 2013) and FRAIR does not include some convenience functions (e.g. to explore and avoid local optima) or the

capacity specify user defined models (e.g. those with arbitrary probability distributions). We

package development (https://github.com/dpritchard/frair). Those seeking to work outside the

structure provided by FRAIR should consider the details provided by Bolker (2008) and can

find some guidance in the *FRAIR* help manual (e.g. ?frair fit).

aim to add these features to FRAIR in the future and welcome third party participation in

CONCLUSION

We have presented the *FRAIR* package and demonstrated how it provides a reproducible framework for the selection, fitting and comparison of functional response models. We anticipate that *FRAIR* will help to consolidate functional response analysis methods for non-specialists by ensuring that common mistakes are not perpetuated, and by exemplifying the

current best practice for non-linear curve fitting and comparison. Consumer-resource interactions are fundamental to many aspects of contemporary ecological research and thus, we anticipate that in providing an accessible open source package for functional response analysis, *FRAIR* will provide a useful tool for many ecologists.

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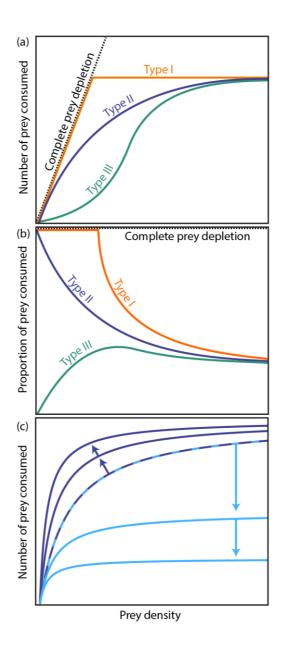


Figure 1. Categorical forms of functional response curves (Holling 1959) describe relationships between prey density and prey consumption (a), differentiated by corresponding relationships between prey density and proportional consumption (b). For a Type II functional response (c, dashed curve), doubling capture rates (a in equation 1, purple curves) primarily increases consumption at lower prey densities, whilst doubling handling time (h equation 1, blue curves) reduces asymptotic consumption.

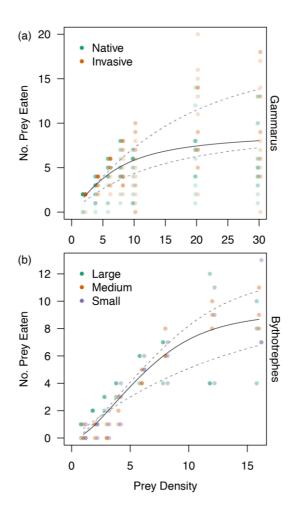


Figure 2. Visualisation of the datasets included with the *FRAIR* package. (a) Consumption of dipteran larvae (*Simulium* spp.) by native *Gammarus duebeni celticus* and invasive *G. pulex* and (b) The consumption of three size classes of *Polyphemus pediculus* by *Bythotrephes longimanus*. Dashed lines represent plausible starting values for MLE optimisation and solid lines represent optimised fits for Rogers (Type II, Gammarus) or Flexible Exponent (Bythotrephes) models.

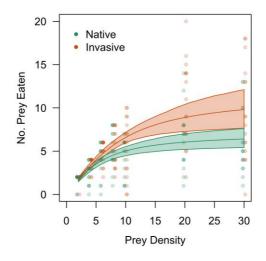


Figure 3. Empirical approximations of 95% confidence intervals based on bootstrapped model fits for the number of prey eaten by native *Gammarus duebeni celticus* and invasive *G. pulex* (Gammarus dataset).