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Contents

1. Supplementary Methods

1.1. Literature Search

We located papers with data relating plant traits to herbivore performance by conducting keyword searches in ISI Web of Science published up to September 2014 (keywords included insect herbivor* and performance, growth, survival, nutrient, defense, diet, artificial diet, nitrogen, phosphorus, protein, tannin, cardenolide, alkaloid, or secondary metabolit*), by collecting studies from several relevant reviews,[1–3] and by searching papers known to the authors. Studies were included in our analysis only if they met all of the following criteria: 1) a plant defense or nutrient trait was experimentally manipulated and directly related to a measure of insect growth or survival; 2) at least four levels of the plant trait were measured; 3) for all continuous response variables, some estimate of variance in herbivore performance was provided (e.g., SE, SD, or 95% CI) along with the mean and sample size at each treatment level; 4) for binomial survival response variables, studies provided an initial number of individuals at each treatment level and a count, proportion, or percentage that survived; and 5) data on diet traits and herbivore performance could be retrieved from a table, figure, text, or supplement.

We considered only papers that measured herbivore performance and did not consider studies that measured consumption (e.g., leaf area removed, digestive efficiency) or preference (behavioral responses). We excluded studies that examined the relationship between plant traits and insect performance indirectly (e.g., studies that measured effects of fertilization on herbivores).

Our database searches were conducted independently by three of the authors (WW, HK, MR). They identified a total of 1,325 peer-reviewed papers. We found another 101 relevant papers by manually searching the references of relevant reviews, by including peer-reviewed book chapters we knew to be relevant (but absent from database searches), and by including other papers we knew to be relevant. We were able to locate abstracts for all of these papers online or through the University of California Libraries. Screening abstracts based on the five criteria outlined above allowed us to narrow down the pool to 190 papers. We were able to obtain the full text for all but three of these papers, and we again evaluated them based on the eligibility criteria. We rejected 87 papers because they were not controlled experimental manipulations of plant traits; 29 papers because they measured response variables other than growth or survival (e.g., consumption, host preference, plant damage); 24 papers because they lacked measurements on a plant defense or nutrient trait; 14 papers because they had fewer than four levels of the plant trait; 10 papers because they lacked estimates of variance for growth or initial numbers for survival; and 6 papers because the data were not available in a table, figure, text or supplement. Note that many papers were rejected for multiple reasons. In total, 114 papers were disqualified, leaving us with 76 eligible papers, all of which were used in the final analysis.

1.2. Data Collection and Preparation

From each suitable paper, we collected information on plant and herbivore species, plant traits measured in herbivore diets, herbivore growth and survival variables measured, and any transformations applied to plant trait or herbivore performance variables. We categorized plant traits as defenses or nutrients based on the original studies (see Extended Data Fig. 1 for a list of plant traits). For each herbivore species we recorded mobility of feeding stage (single tissue, plant, patch, region) and host breadth (monophagous, oligophagous, or polyphagous as defined by [4]). We collected these data from university and USDA sites and extension resources, species descriptions in the primary literature, and selected online databases maintained by agencies, universities, and/or academic partners (CABI, AgroAtlas, EOL, BAMONA) (see Extended Data Fig. 1 for a graphical summary of the database; see Supplementary Tables 1 and 2 for lists of the herbivore species and studies that met the search criteria).

For growth responses, which were continuously distributed, we collected the mean and variability (e.g., SE, SD, 95% CI) of the herbivore response and sample size at each level of the plant trait. A small minority of studies with continuous responses reported raw data, rather than treatment means and standard errors; to ensure consistency between these and studies reporting means, we reduced raw data to means and standard errors after collection. For survival responses, which were binomially distributed, we collected the initial number of herbivores and the count, proportion, or percent that survived at each level of the plant trait. Some authors provided only the range of sample sizes used; in these cases we assumed the smallest sample size for each level. We excluded studies that measured plant traits on arbitrary scales (e.g., studies that assigned plant hairiness scores). When data were presented in figures, we used the software Plot Digitizer (http://plotdigitizer.sourceforge.net) to assign numeric values.

We adjusted response variables so that more positive values indicated higher insect performance. For example, if authors reported proportions of individuals that died, we subtracted their response from one. We transformed development times into development rates by using the reciprocal. We back-transformed any author transformed plant trait variables to put them on the arithmetic scale.

1.3. Calculation of Jensen's Effect

We used a bootstrapping approach to calculate a distribution of Jensen's effect for each empirical dataset. Bootstrapping allowed us to estimate uncertainty in the strength of Jensen's effects. It was necessary to bootstrap to obtain variances for Jensen's effects because the original studies were conducted for a different purpose and reported neither Jensen's effects nor variance in Jensen's effects. For survival responses, we used nonparametric bootstrapping. We resampled each survival dataset with replacement until we had 10,000 bootstrap datasets. We fit cubic splines with three knots to each bootstrap dataset using the mgcv package in R 3.2.4[5–7]. Limiting splines to three knots somewhat limited the complexity of the shapes that could be fitted, which was done because theory and empirical observation suggest performance curves take relatively simple shapes (although a variety of shapes are possible with three knots, including sigmoidal and nonmonotonic shapes like humps). Further, using three knots for every curve helped maintain consistency in potential shapes across studies. We used binomial errors for survival studies (data were not censored and therefore represent proportional or binary responses rather than requiring formal survival analyses).

For the binomial datasets, we calculated Jensen's effect as the log odds ratio of the mean of the predicted survival probabilities at each plant trait level and the predicted survival probability at the mean plant trait: $\ln\left(\frac{\overline{f(x)}}{1-\overline{f(x)}}\right)-\ln\left(\frac{f(\bar{x})}{1-f(\bar{x})}\right)$, where f is the fitted spline that predicts herbivore survival and x is the vector of plant trait values. This measure is the log odds ratio that is widely used to express effect sizes in meta-analyses of response probabilities[8]. Moreover, the log odds ratio is beneficial because it puts survival probabilities on the logit scale, which accurately represents survival as a multiplicative process both for individual longevity and population dynamics. We adjusted predicted survival probabilities that were less than 0.01 to be 0.01 and greater than 0.99 to be 0.99 before calculating the log odds ratio, both because probabilities this close to zero or one are below the level of detection in all studies in our sample and because log odds ratios cannot be calculated with zero or one probabilities.

For growth data, which were typically reported as means and standard errors at each plant trait level instead of raw data, we used parametric bootstrapping. We assumed growth responses were log-normally distributed[9] because growth is inherently allometric and represents multiplicative or power relationships and results in skewed distributions. We parameterized a log-normal distribution for herbivore growth at each level of the plant trait using the reported herbivore performance means and standard errors. We then drew values from each distribution until the length of our bootstrap response vectors equaled the sample sizes reported at each level of the plant trait. We repeated this procedure to obtain 10,000 bootstrap datasets. We followed the curve fitting methods described above but first log-transformed the responses and then used a Gaussian error distribution.

For growth responses, we calculated Jensen's effect by subtracting the predicted herbivore performance for the mean level of the plant trait (the expected herbivore performance with zero plant trait variance) from the mean of the predicted herbivore performances at each plant trait level (the expected herbivore performance accounting for trait variance and nonlinear averaging): $\overline{f(x)}-f(\bar{x})$, where f is the fitted spline that estimates the performance function and x is the vector of plant trait values. We standardized this difference by dividing it by the standard deviation of the bootstrapped herbivore responses to enable comparison across studies. This

measure thus expresses the effect of nonlinear averaging in terms of standard deviations of herbivore performance and is analogous to Hedges' *d*, one of the most widely used meta-analysis effect sizes[10]. (See Supplementary Discussion for the R scripts used in the analysis).

Because this approach to calculating Jensen's effect involves taking the mean of the predictions at each author-chosen level of the plant trait, it assumes that the values of the plant traits tested by the authors of each study reflect the natural distribution of trait values. We believe this is justified because most authors stated that they chose trait levels representative of those in nature. Moreover, many went as far as reporting natural trait means and variances and showing they reflected experimental trait levels. Regardless, we also repeated the entire analysis assuming two different trait distributions: a uniform distribution between the minimum and maximum of the plant traits tested by the authors, and a Gaussian distribution with a mean equal to the midpoint of the author-chosen doses and a standard deviation that aligned the maximum author-chosen dose with 0.975 of the Gaussian cumulative probability function. We truncated the distribution at the maximum and minimum author-chosen trait levels so as not to extrapolate beyond the empirical data. The results were similar for each of the three trait distributions we tested, so in the main text we present the results based on the analysis that assumes a trait distribution defined by author-chosen trait levels (see Supplementary Discussion for the results of the analyses with uniform and Gaussian distributions).

Our calculation of Jensen's effect applies both to individual herbivores that experience variance in their diet within their lifetime and to populations of herbivores that are distributed across a variable plant population. Individuals that experience diet variance, however, may also experience physiological effects that are separate from the effects of nonlinear averaging. The consequence of this is that while Jensen's effect will influence both individuals and populations, it is most relevant for growth and survival parameters at the population level. This issue has been explored by only one empirical study, which calculated Jensen's effect for one caterpillar species and separately measured performance on variable or constant diets. The study concluded that the effects of diet variance could be explained by Jensen's effect without the need to invoke separate physiological effects of diet variance on an individual's performance[11]. Lastly, herbivore populations as a whole likely experience more plant variance than any one herbivore individual, and therefore the effects of variance at the population level are likely to be more important than the effects of variance at the level of an individual's diet.

These quantitative methods are widely applicable on at least two levels. First, Jensen's inequality is relevant in any nonlinear system; it is not specific to plant-herbivore interactions. Therefore, similar methods can be used to examine the potential influence of Jensen's inequality in other fields of inquiry. Second, our general parametric-bootstrapping procedure can be used to re-analyze any datasets where original authors report means and variances (or SD or SE) of a response variable at multiple levels of a predictor variable (which is commonly all that is available when authors do not share raw data). This allows meta-analysts to use such studies to calculate new statistics, not reported in original studies, and to estimate uncertainty in those statistics. We used this procedure to calculate Jensen's effects, but others could use this procedure to calculate any statistic.

1.4. Statistical Modeling

We addressed our research questions using linear mixed effects models in the metafor package[12] in R 3.2.4[13]. Our response variable was the mean of the Jensen's effect distribution from each empirical dataset. We answered our first question, about differences between variance

in plant defensive and nutritive traits, by fitting a model with plant trait type as an independent variable. We answered our second question, about the effects of herbivore mobility and host-breadth, by including mobility and host-breadth as independent variables. We tested the significance of those independent variables using an omnibus test of the significance of fixed effects based on a χ^2 distribution with degrees of freedom equal to the number of fixed effects parameters excluding the intercept. In the results, we report effect sizes and 95% confidence intervals for each group. Following effect sizes, we also report the results of the omnibus test used to test for the significance of the difference between the groups. We used random intercepts for herbivore family and genus to account for potential correlations due to shared evolutionary history among genera within a family and species within a genus. This approach was necessary because a reliable phylogenetic tree does not exist for this diverse group of insects. We used an additional random intercept to account for the non-independence of multiple Jensen's effects measured on the same species, and we included a random effect for each observation following the standard practice of random effects meta-analysis[10]. Finally, the sampling variance of each observation was set equal to the estimated variance of the distribution of Jensen's effects generated by our bootstrapping procedure for each observation. In the figures, we show empirical best linear unbiased predictions for each herbivore species.

Publication bias[14] was unlikely to be an issue in our analysis because we used data for a different goal than did authors of the original studies—none of the studies in our sample estimated Jensen's effects or curvature. Regardless, we explored the potential for publication bias graphically and found no evidence that suggesting particular curve shapes were more likely to be published than others (Extended Data Figs. 5 and 6; Supplementary Discussion: Analysis of Publication Bias). We explored differences in Jensen's effect among insect orders using models with insect order as a fixed effect (Supplementary Discussion: Results by Insect Order).

Finally, we also used the 95% confidence interval of the bootstrapped effect-size distribution for each observational study to categorize curves as significantly concave-down, linear, or concave-up if the confidence interval fell below zero, overlapped zero, or fell above zero, respectively. This allowed us to indicate the significance of curve shape in figures (Fig. 2, A-B and Fig. 3, E-F).

1.5. Model Specification

Below are the statistical models fit using restricted maximum likelihood in the metafor package[12] within R[6]. Left hand side variables are responses. Fixed effects follow the tilde. Parentheses denote random effects. Forward slashes indicate nestedness. TraitType is a factor with two levels: nutrient or defense.

<u>Comparison between defensive and nutritive traits</u>
Growth effect ~ Intercept + TraitType + (1 | Family / Genus / species / observation)

Survival effect ~ Intercept + TraitType + (1 | Family / Genus / species / observation)

<u>Comparison across herbivore mobility</u>
Growth effect ~ Intercept + Mobility + (1 | Family / Genus / species / observation)

Survival effect ~ Intercept + Mobility + (1 | Family / Genus / species / observation)

Comparison across host-breadth
Growth effect ~ Intercept + HostBreadth + (1 | Family / Genus / species / observation)

Survival effect ~ Intercept + HostBreadth + (1 | Family / Genus / species / observation)

2. Supplementary Tables

2.1. Species List

Acheta domesticas (Orthoptera: Gryllidae)
Acyrthosiphon pisum (Hemiptera: Aphididae) *
Ageneotettix deorum (Orthoptera: Acrididae) *
Anagasta kuehniella (Lepidoptera: Pyralidae) *
Anticarsia gemmatalis (Lepidoptera: Noctuidae) *
Atta sexdens (Hymentoptera: Formicidae) *
Bactrocera cucurbitae (Diptera: Tephritidae) *
Bombyx mori (Lepidoptera: Bombycidae)
Callosobruchus maculatus (Coleoptera: Chrysomelidae) *
Ceratitis capitata (Diptera: Tephritidae) *
Choristoneura freemani (Lepidoptera: Tortricidae) †
Choristoneura fumiferana (Lepidoptera: Tortricidae) †
Chrysomela falsa (Coleoptera: Chrysomelidae)
Drosophila buzzatii (Diptera: Drosophilidae)
Earias insulana (Lepidoptera: Nolidae) *
Frankliniella occidentalis (Thysanoptera: Thripidae) *
Grapholita molesta (Lepidoptera: Tortricidae) *
Helicoverpa armigera (Lepidoptera: Noctuidae) *
Helicoverpa zea (Lepidoptera: Noctuidae) *
Heliothis virescens (Lepidoptera: Noctuidae) *
Hyalophora cecropia (Lepidoptera: Saturniidae)
Hyphantria cunea (Lepidoptera: Arctiidae) †
Junonia coenia (Lepidoptera: Nymphalidae)
Locusta migratoria (Orthoptera: Acrididae) *
Lygus hesperus (Hemiptera: Miridae) *
Lymantria dispar (Lepidoptera: Lymantriidae) †
Malacosoma disstria (Lepidoptera: Lasiocampidae) †
Manduca sexta (Lepidoptera: Sphingidae) *
Melanoplus angustipennis (Orthoptera: Acrididae) *(occasional)
Melanoplus bivittatus (Orthoptera: Acrididae) *
Melanoplus differentialis (Orthoptera: Acrididae) *
Melanoplus femurrubrum (Orthoptera: Acrididae) *
Melanoplus flavidus (Orthoptera: Acrididae) *(occasional)
Melanoplus foedus (Orthoptera: Acrididae)
Melanoplus sanguinipes (Orthoptera: Acrididae) *
Metopolophium dirhodum (Hemiptera: Aphididae) *
Myzus persicae (Hemiptera: Aphididae) *

Operophtera brumata (Lepidoptera: Geometridae) *
Orgyia leucostigma (Lepidoptera: Lymantriidae)
Phoebis philea (Lepidoptera: Pieridae)
Pieris rapae (Lepidoptera: Pieridae) *
Plutella xylostella (Lepidoptera: Plutellidae) *
Popillia japonica (Coleoptera: Scarabaeidae) *
Pyrrhalta luteola (Coleoptera: Chrysomelidae) †
Samia ricini (Lepidoptera: Saturniidae)
Schistocerca gregaria (Orthoptera: Acrididae) *
Spodoptera eridania (Lepidoptera: Noctuidae) *
Spodoptera exigua (Lepidoptera: Noctuidae) *
Spodoptera frugiperda (Lepidoptera: Noctuidae) *
Spodoptera littoralis (Lepidoptera: Noctuidae) *
Spodoptera litura (Lepidoptera: Noctuidae) *
Tribolium castaneum (Coleoptera: Tenebrionidae) *
Trichoplusia ni (Lepidoptera: Noctuidae) *

* Agricultural pest
† Forestry pest

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3. Supplementary Discussion

3.1. Analysis of Publication Bias

Analyses that synthesize results across studies must take into account the potential for publication bias, which is when the probability of publication is a function of the results reported in the study[15]. The most commonly reported publication bias is low rates of publication for studies with non-significant results[10]. This is not a major issue for our analysis because our goal, calculating Jensen's effects and performance curve shapes, differed from the goals of the studies in our sample. This contrasts with typical meta-analyses, in which the meta-analyst is asking the same question as the original studies, using a larger dataset. Indeed, most studies in our sample used an ANOVA approach, in which they tested for differences in herbivore performance between levels of the plant trait. Few studies used a regression approach, which is required for estimating curve shapes. Further nearly all studies using regression fit only one curve shape. Therefore, it is unlikely that the probability of publication varied with the shape of the herbivore performance curve.

As expected our graphical analyses suggest publication bias is not present in our dataset. Funnel plots show no relationship between the sample size of a study and the Jensen's effect we

calculated from that study (Extended Data Fig. 5). Further, in no case was there a significant linear regression between sample size and Jensen's effect (growth: $F_{1,248} = 0.23$, $P = 0.63$, $R^2 = 0.0$; survival: $F_{1,203} = 1.04$, $P = 0.31$, $R^2 = 0.0$). Moreover, Egger bias[16] (the y-axis intercept in a regression of normalized effect size on precision) was low and not significantly different from zero for growth (-0.015 [-0.11, 0.076]) and survival (-0.065 [-0.48, 0.35])[14]. An additional way of examining publication bias is plotting effect size as a function of year of publication. A common result in typical meta-analyses is a decrease in effect size through time. Our calculation of Jensen's effect, however, shows no relationship with time (Extended Data Fig. 6).

3.2. Results by Insect Order

We looked for differences in Jensen's effects among the seven orders of insects in our sample of studies (Coleoptera, Diptera, Hemiptera, Hymenoptera, Lepidoptera, Orthoptera, Thysanoptera). We did this by testing the significance of insect order as a predictor as Jensen's effects in models with the same structure as those described earlier.

Insect order was not a significant predictor of Jensen's effect on plant nutritive traits for herbivore growth ($\chi^2_1 = 0.028$, $P = 0.87$) or survival ($\chi^2_1 = 0.71$, $P = 0.40$). Insect order was not a significant predictor of Jensen's effect on plant defensive traits for herbivore survival ($\chi^2_6 = 3.91$, $P = 0.69$). Insect order was close to being a significant predictor for Jensen's effects on plant defensive traits for herbivore growth ($\chi^2_4 = 8.69$, $P = 0.069$), but this was driven solely by the order Hemiptera, which was represented by only one species. That one hemipteran species had an unusually positive Jensen's effect, whereas Hemiptera in other study types (e.g., manipulative studies of herbivore survival) did not have significantly positive Jensen's effects. When that species was removed, insect order was clearly a poor predictor of Jensen's effect for that group of studies ($\chi^2_3 = 0.70$, $P = 0.87$).

These results indicate that Jensen's effects on plant nutritive or defensive traits do not vary predictably by insect order. This suggests that our conclusions may be general, at least for the seven common insect orders represented in our sample.

3.3. Analysis with Uniform Trait Distribution

We repeated the quantitative analyses assuming a uniform plant trait distribution between the minimum and maximum plant trait levels tested in the original studies. Our main analysis assumes the plant trait distribution follows the distribution of doses tested in the original studies. (See Supplementary Methods for details). Assuming a uniform distribution did not change our conclusions. The results were similar to the results presented in the main text.

How do the Jensen's effects of plant variability on herbivore performance differ between nutritive and defensive plant traits?—The mean Jensen's effect for growth was strongly negative for nutrients (-0.35 [-0.44, -0.26]) and near zero for defenses (0.034 [-0.041, 0.11]), and this difference was significant (-0.38 [-0.46, -0.31]; $\chi^2_1 = 101.8$, $P < 0.0001$). For survival, the mean Jensen's effect was negative for nutrients (-0.73 [-1.18, -0.27]) and potentially slightly positive for defenses (0.29 [0.024, 0.56]), and the difference between Jensen's effects for defenses and nutrients was significant (-1.02 [-1.42 -0.62]; $\chi^2_1 = 24.9$, $P < 0.0001$). This suggests that nutrient variability is predicted to have consistently negative effects on growth and survival across a variety of trait distributions. It also suggests that defense variability is predicted to have consistently zero effects on growth but that the precise effects on survival may depend to some extent on the defense trait distribution, although the difference appears small. This result does

not change our general conclusion that nutrient variability has negative effects, while defense variability has effects close to zero.

How do the Jensen's effects of plant variability on herbivore performance vary with herbivore mobility and host-breadth?—Herbivore mobility was not a significant predictor of Jensen's effect on herbivore growth for nutrients ($\chi^2_1 = 0.41$, $P = 0.52$) or defenses ($\chi^2_1 = 0.034$, $P = 0.85$) or on herbivore survival for defenses ($\chi^2_2 = 0.56$, $P = 0.76$). Herbivore host-breadth also was not a significant predictor of Jensen's effect on growth for nutrients ($\chi^2_1 = 0.72$, $P = 0.39$) or defenses ($\chi^2_1 = 0.13$, $P = 0.72$) or on survival for defenses ($\chi^2_1 = 0.83$, $P = 0.36$). These patterns were consistent for survival and nutrients, but sample size was too small for statistical tests.

3.4. Analysis with Gaussian Trait Distribution

We repeated the quantitative analyses assuming a Gaussian plant trait distribution. (See Supplementary Methods for details). The use of a Gaussian trait distribution did not change our conclusions qualitatively.

How do the Jensen's effects of plant variability on herbivore performance differ between nutritive and defensive plant traits?—The mean Jensen's effect for growth was negative for nutrients (-0.21 [-0.26, -0.16]) and near zero for defenses (0.019 [-0.026, 0.065]), and this difference was significant (-0.23 [-0.27, -0.19]; $\chi^2_1 = 101.12$, $P < 0.0001$). For survival, the mean Jensen's effect was negative for nutrients (-0.37 [-0.65, -0.079]) and close to zero or potentially slightly positive for defenses (0.17 [0.0075, 0.33]), and this difference was significant (-0.54 [-0.79, -0.28]; $\chi^2_1 = 16.67$, $P < 0.0001$). This suggests that nutrient variability has consistently negative effects on growth and survival across a variety of trait distributions. It also suggests that defense variability has consistently zero effects on growth but that the precise effects on survival depend to a small extent on the defense trait distribution. This result does not change our general conclusion that nutrient variability has negative effects, while defense variability has effects close to zero.

How do the Jensen's effects of plant variability on herbivore performance vary with herbivore mobility and host-breadth?—Herbivore mobility was not a significant predictor of Jensen's effect on herbivore growth for nutrients ($\chi^2_1 = 1.23$, $P = 0.27$) or defenses ($\chi^2_1 = 0.033$, $P = 0.86$) or on herbivore survival for defenses ($\chi^2_2 = 0.44$, $P = 0.80$). Herbivore host-breadth also was not a significant predictor of Jensen's effect on growth for nutrients ($\chi^2_1 = 0.45$, $P = 0.50$) or defenses ($\chi^2_1 = 0.03$, $P = 0.86$) or on survival for defenses ($\chi^2_1 = 0.50$, $P = 0.78$). These patterns were consistent for survival and nutrients, but sample size was too small for statistical tests.

3.5. R Script

```
# R script supplement

# Variability in plant nutrients reduces insect herbivore performance
# Wetzel, Kharouba, Robinson, Holyoak, and Karban

# Running this script loads functions for calculating and bootstrapping Jensen's effect.
# After running this script, use function jiterate to run the analysis.

# Description:
# Function jiterate converts data to appropriate format, bootstraps datasets, fits cubic
# splines to each bootstrap, and uses cubic splines to estimate Jensen's effect. It also
# optionally plots bootstraps and cubic splines as it runs. Warning: this function is
```

```
# slow for large datasets.

# Usage:
# jiterate(compFull, dataFull, xdist='auth', prog=TRUE, knots=3, fx=TRUE, ID=FALSE,
#        display = FALSE, nboot=100, method='REML', pause = FALSE)

# Arguments:
# compFull                dataframe of meta-data for each empirical dataset.
# dataFull                dataframe of data.
# xdist                   plant trait distribution. 'auth', 'unif', or 'norm'.
# prog                    display progress bar.
# knots                   number of knots to be used in cubic splines
# fx                      penalization argument. See package mgcv.
# ID                      if specified, analysis will be run only for data with given ID label.
# display                 if TRUE, jiterate will plot each bootstrap and spline as it works.
#                         Warning: this is very slow.
# nboot                   the number of bootstrap replicates per empirical dataset.
# method          fitting method for cubic spline. Recommend restricted maximum likelihood
#                         'REML'. See package mgcv for other options.
# pause                   will pause in between bootstraps to make it easier to see plots.

# Value:
# Returns a list with Jensen's effect sizes and information on the cubic spline fits.


################################################################################

# Contents
# 0. Load required packages
# 1. Functions to generate 1 bootstrap dataset from 1 empirical dataset
                # boot1norm      -- For growth data (normal) summarized as means and SEs
                # boot1bino      -- For survival data (binomial)
                # bootstrap      -- For growth raw data with many levels of x
                # boot1norm.raw  -- For growth raw data with just a few levels of x
# 2. Function jensenGAM to use cubic splines to calculate Jensen's effect from 1 dboot
# 3. Function jiterate, which applies jensenGAM() to each dataset


################################################################################

# 0. Load packages

library(compiler)
library(mgcv)


################################################################################

### 1. Functions to generate 1 boostrap dataset from 1 empirical dataset

# Growth data - log normally distributed y errors:
boot1norm = function(comp1, data1) {

        # Increase length so there is 1 row per rep
        xTemp = rep.int(data1$planttrait1value, data1$nreps)
        yTemp = rep.int(data1$herbvalue, times = data1$nreps)
        herbvarvalueTemp = rep.int(data1$herbvarvalue, times = data1$nreps)
        nrepsTemp = rep.int(data1$nreps, times = data1$nreps)

        # Calculate SD based on herbvarvalue and herbvarunits
        if(comp1$herbvarunits == 'SE')
                sdTemp = sqrt(nrepsTemp) * herbvarvalueTemp else
```

```
        if(comp1$herbvarunits == 'SEx2')
                sdTemp = sqrt(nrepsTemp) * herbvarvalueTemp * 0.5 else
        if(comp1$herbvarunits == 'SD')
                sdTemp = herbvarvalueTemp else
        if(comp1$herbvarunits == '95%CI')
                sdTemp = sqrt(nrepsTemp) * herbvarvalueTemp / 3.92

        # Random draws: no transformation, authors reported y on log scale
        if(comp1$transformation == 'none')
                logY = rnorm(n = length(yTemp), mean = yTemp, sd = sdTemp)

        # Random draws: log normal distribution (log(x) or log(1/x) transformations)
        if(comp1$transformation == 'log(x)' | comp1$transformation == 'log(1/x)') {
                sdTemp = sdTemp[yTemp > 0]
                xTemp = xTemp[yTemp > 0]
                yTemp = yTemp[yTemp > 0]
                meanlog = log(yTemp) - 0.5 * log(1 + sdTemp^2 / yTemp^2)
                sdlog = sqrt( log(1 + sdTemp^2 / yTemp^2) )
                rawY = rlnorm(n = length(meanlog), meanlog = meanlog, sdlog = sdlog)
        }

        # Inverse transform (1/x) waiting times to development rates
        if(comp1$transformation == 'log(1/x)') rawY = 1 / rawY

        # Return message if no transformation specified
        if(comp1$transformation == 'unknown')
                warning('transformation not specified', immediate. = FALSE)

        # Back-transform x's if necessary
        if(comp1$trans.x == 'exp(x)') x = exp(xTemp)
        if(comp1$trans.x == 'x^2') x = xTemp^2
        if(comp1$trans.x == 'none') x = xTemp

        # Calc both logY and rawY
        if(comp1$transformation == 'none')
                rawY = exp(logY)
        if(comp1$transformation == 'log(x)' | comp1$transformation == 'log(1/x)')
                logY = log(rawY)

        # Save x's and bootstrapped y's in a data.frame
        dboot1 = data.frame(x = x, rawY = rawY, logY = logY)
        return(dboot1)
}
boot1norm = cmpfun(boot1norm) # compile boot1norm to speed it up

# Survival data - binomially distributed y errors:
boot1bino = function(comp1, data1) {

        # Calculate survival probabilities for survival data
        if(comp1$herbunits == 'percent' & comp1$fitnessContribution == 1)
                p = data1$herbvalue / 100
        if(comp1$herbunits == 'proportion' & comp1$fitnessContribution == 1)
                p = data1$herbvalue
        if(comp1$herbunits == 'count' & comp1$fitnessContribution == 1)
                p = data1$herbvalue / data1$nherb

        # Convert mortality to survival and calculate survival probabilities
        if(comp1$herbunits == 'percent' & comp1$fitnessContribution == -1)
                p = (100 - data1$herbvalue) / 100
        if(comp1$herbunits == 'proportion' & comp1$fitnessContribution == -1)
                p = 1 - data1$herbvalue
        if(comp1$herbunits == 'count' & comp1$fitnessContribution == -1)
```

```
                p = (data1$nherb - data1$herbvalue) / data1$nherb

        # Give a warning message if p is outside 0-1
        if(max(p) > 1 | min(p) < 0)
                warning('p outside 0-1', immediate. = TRUE)

        # Bootstrap individuals at each level with replacement (same as binom)
        # This is equivalent to nonparametric boostrapping even though it uses rbinom
        survivors = rbinom(nrow(data1), size = data1$nherb, prob = p)
        deaths = data1$nherb - survivors

        # Adjust pseudodata p to stay within 0.01 and 0.99
        PseudoP = survivors / data1$nherb
        PseudoP[PseudoP < 0.01] = 0.01
        PseudoP[PseudoP > 0.99] = 0.99

        # Save logit p
        logitp = log( PseudoP / (1 - PseudoP) )
        # Note PseudoP and logitp are only used for plotting, not analysis

        # Back-transform x's if necessary
        if(comp1$trans.x == 'exp(x)')
                x = exp(data1$planttrait1value)
        if(comp1$trans.x == 'x^2')
                x = data1$planttrait1value^2
        if(comp1$trans.x == 'none')
                x = data1$planttrait1value

        # Save x's and bootstrapped y's in a data.frame
        dboot1 = data.frame(x = x, survivors = survivors, deaths = deaths,
                nherb = data1$nherb, p = PseudoP, logitp = logitp)
        return(dboot1)
}
boot1bino = cmpfun(boot1bino) # compile boot1bino to speed it up

# For raw data from studies with growth responses:
boot1norm.raw = function(comp1, data1) {

        # Sort data1 in order of planttrait1value b/c otherwise by mixes it up
        data1 = data1[order(data1$planttrait1value), ]

        # Calculate means and SDs per level of x
        yMeans = by(data1$herbvalue, data1$planttrait1value, mean)
        ySDs = by(data1$herbvalue, data1$planttrait1value, sd)
        nReps = by(data1$herbvalue, data1$planttrait1value, length)

        # Increase length so there is 1 row per rep
        xTemp = data1$planttrait1value
        yTemp = rep.int(yMeans, times = nReps)
        sdTemp = rep.int(ySDs, times = nReps)

        # Random draws: no transformation
        if(comp1$transformation == 'none')
                logY = rnorm(n = length(yTemp), mean = yTemp, sd = sdTemp)

        # Random draws: log normal distribution (log(x) transformation)
        if(comp1$transformation == 'log(x)') {
                meanlog = log(yTemp) - 0.5 * log(1 + sdTemp^2 / yTemp^2)
                sdlog = sqrt( log(1 + sdTemp^2 / yTemp^2) )
                rawY = rlnorm(n = length(meanlog), meanlog = meanlog, sdlog = sdlog)
        }
```

```
        # Inverse transform (1/x) waiting times to development rates
        if(comp1$transformation == 'log(1/x)') rawY = 1 / rawY

        # Return message if no transformation specified
        if(comp1$transformation == 'unknown')
                warning('transformation not specified', immediate. = FALSE)

        # Back-transform x's if necessary
        if(comp1$trans.x == 'exp(x)')
                x = exp(xTemp)
        if(comp1$trans.x == 'x^2')
                x = xTemp^2
        if(comp1$trans.x == 'none')
                x = xTemp

        # Calc both logY and rawY
        if(comp1$transformation == 'none')
                rawY = exp(logY)
        if(comp1$transformation == 'log(x)' | comp1$transformation == 'log(1/x)')
                logY = log(rawY)

        # Save data in data.frame
        dboot1 = data.frame(x = x, rawY = rawY, logY = logY)
        return(dboot1)
}
boot1norm.raw = cmpfun(boot1norm.raw) # compile to speed up



################################################################################

### 2. Function to fit curves and calculate Jensen's effect from 1 dboot

jensenGAM = function(comp1, data1, display, knots, fx, xdist, sp, gamma, method,
        pause, alpha) {

        # Generate one bootstrap dataset
        if(comp1$dist == 'gaussian' & comp1$plantvariation == 'manipulated' &
                comp1$datatype == 'mean')
                        dboot1 = boot1norm(comp1, data1)
        if(comp1$dist == 'gaussian' & comp1$plantvariation == 'manipulated' &
                comp1$datatype == 'raw')
                        dboot1 = boot1norm.raw(comp1, data1)
        if(comp1$dist == 'binomial' & comp1$plantvariation == 'manipulated')
                dboot1 = boot1bino(comp1, data1)

        # Fit curve with gam
        if(comp1$dist == 'gaussian') {
                mLog = gam(dboot1$logY ~ s(x, bs = 'cr', k = knots, fx = fx), sp = sp,
                        data = dboot1, family = comp1$dist, gamma = gamma, method = method)
                mRaw = gam(dboot1$rawY ~ s(x, bs = 'cr', k = knots, fx = fx), sp = sp,
                        data = dboot1, family = comp1$dist, gamma = gamma, method = method)
        }
        if(comp1$dist == 'binomial') {
                mBin = gam(cbind(dboot1$survivors, dboot1$deaths) ~ s(x, bs = 'cr',
                        k = knots, fx = fx), data = dboot1, weights=dboot1$nherb, sp = sp,
                        family = comp1$dist, gamma = gamma, method = method)
        }

        # Calculate mean in variable world (Mv)
        if(xdist == 'auth') { # Assuming author chosen distribution of doses
                # Take mean of means at each dose level so outcome is not influenced by
```

```
        # number of reps per dose
        if(comp1$dist == 'gaussian' & comp1$datatype != 'raw') {
                MvLog = mean( predict.gam(mLog, newdata=data.frame(x=
                        unique(dboot1$x))) )
                MvRaw = mean( predict.gam(mRaw, newdata=data.frame(x=
                        unique(dboot1$x))) )
        }
        if(comp1$dist == 'binomial') {
                MvP = mean( plogis( predict.gam(mBin, newdata=data.frame(x=
                        unique(dboot1$x))) ) )
                MvLogit = mean( predict.gam(mBin, newdata=data.frame(x=
                        unique(dboot1$x))) )
        }
}
if(xdist == 'unif') { # Assuming uniform distribution of doses
        newx = seq(min(dboot1$x), max(dboot1$x), length=100)
        if(comp1$dist == 'gaussian') {
                MvLog = mean( predict.gam(mLog, newdata = data.frame(x = newx)) )
                MvRaw = mean( predict.gam(mRaw, newdata = data.frame(x = newx)) )
        }
        if(comp1$dist == 'binomial') {
                MvP = mean( plogis( predict.gam(mBin, newdata = data.frame(x =
                        newx)) ) )
                MvLogit = mean( predict.gam(mBin, newdata = data.frame(x =
                        newx)) )
        }
}
if(xdist == 'norm') { # Assuming truncated normal distribution of doses
# Truncate by upper and lower dose levels, so as not to extrapolate beyond
        # data
# Centered on the midpoint of author-chosen trait levels
# With a 0.025 probability mass above the highest author-chosen trait level
        midpoint = (max(dboot1$x, na.rm=TRUE) + min(dboot1$x, na.rm=TRUE)) / 2
        maxDose = max(dboot1$x, na.rm=TRUE)
        # Need SD that will make CDF = 0.975 at maxDose
        SD = (maxDose - midpoint) / 1.96
        newx = seq(min(dboot1$x, na.rm=TRUE), maxDose, length=1000)
        densities = dnorm(newx, mean=midpoint, sd=SD)
        weight = densities / sum(densities)
                if(comp1$dist == 'gaussian') {
                        MvLog = sum( predict.gam(mLog, newdata = data.frame(x = newx)) *
                                weight )
                        MvRaw = sum( predict.gam(mRaw, newdata = data.frame(x = newx)) *
                                weight )
                }
                if(comp1$dist == 'binomial') {
                        MvP = sum( plogis( predict.gam(mBin, newdata = data.frame(x =
                                newx)) ) * weight )
                        MvLogit = sum( predict.gam(mBin, newdata = data.frame(x =
                                newx)) *  weight )
                }
        }


# Predict f(mean(xi)) mean in constant world (Mc)
if(xdist == 'auth') { # Assuming author chosen distribution of doses
        meanDose = mean(unique(dboot1$x)) # mean of means at each dose level
        if(comp1$dist == 'gaussian') {
                McLog = predict.gam(mLog, newdata = data.frame(x = meanDose) )
                McRaw = predict.gam(mRaw, newdata = data.frame(x = meanDose) )
        }
        if(comp1$dist == 'binomial') {
```

```
                McP = plogis(predict.gam(mBin, newdata = data.frame(x = meanDose)))
                McLogit = predict.gam(mBin, newdata = data.frame(x = meanDose))
        }
}
if(xdist == 'unif' | xdist == 'norm') {
# Assuming uniform or normal distribution of doses
# Mc for unif and norm are same because mean of normal is at midpoint
        midpoint = (max(dboot1$x, na.rm=TRUE) + min(dboot1$x, na.rm=TRUE)) / 2
        if(comp1$dist == 'gaussian') {
                McLog = predict.gam(mLog, newdata = data.frame(x = midpoint))
                McRaw = predict.gam(mRaw, newdata = data.frame(x = midpoint))
                }
        if(comp1$dist == 'binomial') {
                McP = plogis(predict.gam(mBin, newdata = data.frame(x = midpoint)))
                McLogit = predict.gam(mBin, newdata = data.frame(x = midpoint))
        }
}

# MvP and McP for binomial are constrained to range from 0.01 - 0.99
if(comp1$dist == 'binomial') {
        if(MvP < 0.01) MvP = 0.01
        if(MvP > 0.99) MvP = 0.99
        if(McP < 0.01) McP = 0.01
        if(McP > 0.99) McP = 0.99
}

# Plotting
if(display == TRUE) {
        # Plot for growth data
        if(comp1$dist == 'gaussian') plot(dboot1$x, dboot1$logY, main=comp1$id2,
                sub = paste("study:",comp1$plantvariation,";","dist:",comp1$dist))
        # Plot for survival data
        if(comp1$dist == 'binomial') plot(dboot1$x, dboot1$logitp,
                main=comp1$id2, sub = paste("study:",comp1$plantvariation,";",
                "dist:",comp1$dist))
        # Add points for Mv and Mc
        if(xdist == 'auth') xpoint = meanDose
        if(xdist == 'unif') xpoint = midpoint
        if(xdist == 'norm') xpoint = midpoint
        if(comp1$dist == 'gaussian') {
                points(xpoint, MvLog, col='red', pch=20)
                points(xpoint, McLog, col='blue', pch=20)
                lines(rep(xpoint, 2), c(MvLog, McLog), col='purple')
        }
        if(comp1$dist == 'binomial') {
                points(xpoint, MvLogit, col='red', pch=20)
                points(xpoint, McLogit, col='blue', pch=20)
                lines(rep(xpoint, 2), c(MvLogit, McLogit), col='purple')
        }
        # Plot cubic spline
        newx = seq(min(dboot1$x), max(dboot1$x), length=100)
        if(comp1$dist == 'gaussian')
                lines(newx, predict.gam(mLog, newdata = data.frame(x = newx)))
        if(comp1$dist == 'binomial')
                lines(newx, predict.gam(mBin, newdata = data.frame(x = newx)))

        # Pause and wait for user to press enter if pause == TRUE
        if(pause) invisible(readline(prompt="Press [enter] to continue"))
}

# Jensen's effect: effect-size calculations
if(comp1$dist == 'gaussian'){
```

```
                jDlog = (MvLog - McLog) / sd(dboot1$logY)
                jRlog = MvLog - McLog
                jDraw = (MvRaw - McRaw) / sd(dboot1$rawY)
                jRraw = log(MvRaw) - log(McRaw)
                logSummary = anova(mLog)
                rawSummary = anova(mRaw)
                dLog = logSummary$dev.expl
                dRaw = rawSummary$dev.expl
                dBin = NA
                pLog = logSummary$s.pv
                pRaw = rawSummary$s.pv
                pBin = NA
        }

        if(comp1$dist == 'binomial') {
                jDlog = MvLogit - McLogit
                # log(odds) ratio from prob scale means:
                jRlog = log(MvP / (1-MvP)) - log(McP / (1-McP))
                jDraw = MvP - McP
                jRraw = log(MvP / McP)
                binSummary = anova(mBin)
                dBin = binSummary$dev.expl
                dLog = NA
                dRaw = NA
                pLog = NA
                pRaw = NA
                pBin = binSummary$s.pv
        }

        # Return a list
        out = list(jDlog = jDlog, jRlog = jRlog, jDraw = jDraw, jRraw = jRraw,
                dBin = dBin, dLog = dLog, dRaw = dRaw, pLog = pLog, pRaw = pRaw,
                pBin = pBin)

        out = lapply(out, as.vector)

        return(out)
}
jensenGAM = cmpfun(jensenGAM) # compile jensen to speed it up


################################################################################

### 3. Function jiterate() to apply jensenGAM() to each curve in dataset

jiterate = function(compFull, dataFull, varSubset=NA, xdist='auth', prog=TRUE,
        dataTypeSubset=NA, knots=3, fx=TRUE, ID=FALSE, display=FALSE, nboot=100,
        sp=NULL, gamma=1.4, method='REML', pause=FALSE, alpha=0.05) {

        # Data prep (decides which comparisons from whole dataset to include)
        if(is.logical(ID)) {

                # Subset by dataTypeSubset if specified
                if(!is.na(dataTypeSubset))
                        comp = comp[comp$datatype == dataTypeSubset, ]

                # Remove mean curves w/o herbvarvalue
                comp = comp[comp$datatype != 'mean' | !is.na(comp$herbvarunits), ]

                # Remove curves with transformation == 'unknown'
                comp = comp[comp$transformation != 'unknown', ]
```

```
        # Remove survival curves where units are "percent relative to control"
        comp = comp[comp$dist != 'binomial' |
                comp$herbunits != 'percent relative to control', ]

        # Update data using newly reduced comp$id2
        data = dataFull[dataFull$id2 %in% comp$id2, ]
}

# If IDs specified, subset by IDs
if(is.character(ID)) {
        comp = compFull[compFull$id2 %in% ID, ]
        data = dataFull[dataFull$id2 %in% ID, ]
}

# Info on curve IDs to be used for the rest of the function
Ncomps = length(unique(comp$id2))
IDs = comp$id2

# Create lists for saving effect sizes, etc.
jDlog = list()
length(jDlog) = Ncomps
names(jDlog) = IDs
jRlog = list()
length(jRlog) = Ncomps
names(jRlog) = IDs
jDraw = list()
length(jDraw) = Ncomps
names(jDraw) = IDs
jRraw = list()
length(jRraw) = Ncomps
names(jRraw) = IDs
dLog = list()
length(dLog) = Ncomps
names(dLog) = IDs
dRaw = list()
length(dRaw) = Ncomps
names(dRaw) = IDs
dBin = list()
length(dBin) = Ncomps
names(dBin) = IDs
pLog = list()
length(pLog) = Ncomps
names(pLog) = IDs
pRaw = list()
length(pRaw) = Ncomps
names(pRaw) = IDs
pBin = list()
length(pBin) = Ncomps
names(pBin) = IDs

# Set up progress bar
if(prog == TRUE) pb = txtProgressBar(min = 0, max = Ncomps, style = 3)

# Loop through comparisons and calculate distribution of Jensen's effect
for(i in 1:Ncomps) {

        idTemp = IDs[i] # Set new comparison ID
        jTemp = NA # Reset jTemp

        # Extract comparison data for idTemp
        comp1 = comp[comp$id2 == idTemp, ]
```

```
# Data prep (decides which rows of data to include)
# Extract data for idTemp and remove rows with NA for herbvalue
data1 = data[data$id2 == idTemp & !is.na(data$herbvalue), ]

# Remove rows with NA for herbvarvalue if gaussian and mean
if(comp1$dist == 'gaussian' & comp1$plantvariation == 'manipulated' &
        comp1$datatype == 'mean')
                data1 = data1[!is.na(data1$herbvarvalue), ]

# Remove rows with NA for nherb and binomial for dist
if(comp1$dist == 'binomial')
        data1 = data1[!is.na(data1$nherb), ]

# Run jensenGAM nboot times for each comparison
# Only run if...
        # nrow(data1) > 3 (want 4 dose levels to estimate nonlinearity)
        # sd(data1$herbvalue) != 0 (need variation in y)
        # sd(data1$planttrait1value) != 0 (need variation in x)
# Use tryCatch() to cope with errors
if(nrow(data1) > 3 & sd(data1$herbvalue) != 0 &
        sd(data1$planttrait1value) != 0) {
                jTemp = replicate( nboot, tryCatch(
                        jensenGAM(comp1 = comp1, data1 = data1, display = display,
                                knots = knots, xdist = xdist, sp = sp, fx = fx,
                                gamma = gamma, method = method, pause = pause,
                                alpha = alpha),
                                        error = function(e) list(
                                                jDlog = NA,
                                                jRlog = NA,
                                                jDraw = NA,
                                                jRraw = NA,
                                                dBin = NA,
                                                dLog = NA,
                                                dRaw = NA,
                                                pLog = NA,
                                                pRaw = NA,
                                                pBin = NA)
                        ) )
}

# Return 'too few dose levels' if nLevels < 4
if(nrow(data1) < 4) jTemp = 'too few dose levels'

# Return 'no variation in response' if response doesn't vary
if(nrow(data1) > 3 & sd(data1$herbvalue) == 0)
        jTemp = 'no variation in response'

# Return 'no variation in X' if X doesn't vary
if(nrow(data1) > 3 & sd(data1$planttrait1value) == 0)
        jTemp = 'no variation in X'

# Save output to lists
if(is.character(jTemp)) {  # If jTemp is a character warning
        jDlog[[i]] = jTemp
        jRlog[[i]] = jTemp
        jDraw[[i]] = jTemp
        jRraw[[i]] = jTemp
        dLog[[i]] = jTemp
        dRaw[[i]] = jTemp
        dBin[[i]] = jTemp
        pLog[[i]] = jTemp
        pRaw[[i]] = jTemp
```

```
                pBin[[i]] = jTemp
            } else {                                    # If jTemp is numeric
                jDlog[[i]] = unlist(jTemp['jDlog',])
                jRlog[[i]] = unlist(jTemp['jRlog',])
                jDraw[[i]] = unlist(jTemp['jDraw',])
                jRraw[[i]] = unlist(jTemp['jRraw',])
                dLog[[i]] = unlist(jTemp['dLog',])
                dRaw[[i]] = unlist(jTemp['dRaw',])
                dBin[[i]] = unlist(jTemp['dBin',])
                pLog[[i]] = unlist(jTemp['pLog',])
                pRaw[[i]] = unlist(jTemp['pRaw',])
                pBin[[i]] = unlist(jTemp['pBin',])
            }

            # Update progress bar
            if(prog == TRUE) setTxtProgressBar(pb, i)
        }
        if(prog == TRUE) close(pb) # Close progress bar

        # Return a list
        out = list(
            jDlog=jDlog, jRlog=jRlog,
            jDraw=jDraw, jRraw=jRraw,
            dLog=dLog,
            dRaw=dRaw, dBin=dBin,
            pLog=pLog, pRaw=pRaw,
            pBin=pBin)

        return(out)
}
jiterate = cmpfun(jiterate)
```

4. Supplementary References

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