Pollinator size and its consequences: Predictive allometry for pollinating insects

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**Abstract**

Allometric scaling laws have key implications for the conservation and management of pollinating insects. Body size (BS) can predict influential ecological traits yet available predictive models are outdated, rely upon geographically restricted sampling and have limited applicability for non-bee taxa. More accurate predictions of pollinator body size require dynamic models that consider biogeography, intraspecific variation and phylogenetic relatedness within an iterative, updatable framework. We catalogued existing predictive allometries for pollinating insects (Hymenoptera (BS: 38), Diptera (BS: 26) and Lepidoptera (BS: 21)) and improved upon pre-existing equations for estimating body size in two key pollinating taxa (bees and hoverflies).We measured dry weight and intertegular distance (ITD) of bees (species total: 298) and hoverflies (species total: 103) across three biogeographic regions: Australia, Europe and USA.We then used linear mixed effect (LME) and phylogenetic generalised least squares (PGLS) models to construct a suite of state-of-the-art equations for estimating interspecific pollinator body size. We used OLS linear regression to assess intraspecific ITD - body size predictions. Interspecific model validation was assessed using k-fold cross validation. Overall differences between these models were minimal with PGLS models performing similarly to LME models. Intraspecific models found ITD a reliable predictor of body size for bees and hoverflies. These highly applicable models form the R package '*pollimetry*’ and provide an updated resource for allometric research concerning wild and managed pollinators globally.

**Keywords**: allometry, Apoidea, body size, pollination, Syrphidae

**Introduction**

Body size is an intrinsic trait of all organisms that influences key patterns across all levels of biological organisation. Adult body size variation (both intra- and interspecific) in insects is the outcome of natural selection affecting physiological and biochemical processes during ontogeny (see Chown & Gaston 2010’s review on body size variation). Therefore, body size is central to physiological (e.g. metabolic and growth rates (Angilletta et al. 2004; Ehnes et al. 2011; Harrison et al. 2014)), life history (e.g. life span, reproductive rate and type (i.e. capital or income breeders) (Speakman 2005; Teder et al. 2008)) and ecological attributes (e.g. species abundance and richness, trophic interactions, geographic range size and dispersal ability) (Brown et al. 2004; White et al. 2007; Chown & Gaston 2010, Rall et al. 2011; Stevens et al. 2012; Velghe & Gregory-Eaves 2013; DeLong et al. 2015). These effects lead to differing spatial and temporal size-frequency distributions within populations and communities as well as drive key ecosystem functions and services such as decomposition, carbon cycling, primary productivity and pollination (Greenleaf et al. 2007; Rudolf & Rasmussen 2013; Schramski et al. 2015).

Studies of body size variation utilise allometric theory. Gould (1966) defined allometry as the ‘study of size and its consequences.’ Allometric scaling laws refer to how traits, which can be morphological, physiological or chemical, co-vary with an organism’s body size, often with important ecological and evolutionary implications (Gould 1966; Huxley 1993). However, direct measurements of body size, traits and inferred allometric relationships can be impractical for a number of reasons. First, direct measurements can be time consuming and require destructive methods, which are unfeasible for museum specimens and threatened species (Rogers et al. 1977; Henschel & Seely 1997). Secondly, in diet/food web studies, body size estimates come from digested prey items (e.g. Hodar 1997). Thirdly, a lack of life-history information, especially for ecologically cryptic and rare species, may not be known. As such, predictive allometry, which attempts to estimate body size or a hypothesised allometric characteristic using a co-varying trait, has emerged across many biological disciplines.

Most commonly, body length has been used extensively to predict body size, such as in fish (e.g. Karachle & Stergiou 2012), mammals (e.g. Trites & Pauly 1998) and both aquatic (e.g. Burgherr & Meyer 1997; Benke et al. 1999) and terrestrial invertebrates (e.g. Rogers et al. 1977; Sample et al. 1993; Sabo et al. 2002). These models often show considerable support (*R2* > 0.9), which has led to the proliferation of multiple models for a wide range of taxa worldwide, especially insects. However, when compared, these models show significantly different coefficients both within- and between insect orders (Schoener 1980; Sample et al. 1993; Ganihar 1997; Benke et al. 1999; Brady & Noske 2006), often due to biogeography (i.e. latitude, see Martin et al. 2014), and/or methodological influences such as sampling biases and model choice.

These differences highlight a need for consolidation and improvement in predictive allometric theory and practice. Predictive models require a robust and iterative framework in model choice, development and validation. Ordinary least squares (OLS) or Major-axis/Standardized Major Axis regression have been seen as ideal for allometric prediction (Warton et al. 2006; Legendre & Legendre 2012). This has led to a lack of incorporation of mixed effects and/or phylogenetic model structures (e.g. phylogenetic generalized least squares (PGLS) (Harvey & Pagel 1991)) despite their importance in explaining key ecological and evolutionary processes (e.g. Bolker et al. 2009, Duncan et al. 2007). Further, model validation techniques, such as cross-validation, which are common-place in statistics (Stone 1974), have been overlooked in predictive ecology, with the exception of species distribution and resource selection modelling (e.g. Boyce et al. 2002; Wenger & Olden 2012; Boria et al 2014). It is becoming clear these methods, in model building and testing, are necessary given the increasing burden of proof in biological prediction. Further, ‘iterative model-building’, whereby equations can be periodically updated rather than differentiated and replaced, represents an as-yet untested avenue for greater accuracy and wider applicability of predictive allometry.

A number of key pollination traits exhibit allometric scaling. In bees, body size affects insect activity rates/periods (Streinzer et al. 2016), pollen load (e.g. Ramalho et al. 1998), foraging distance (e.g. Greenleaf et al. 2007; van Nieuwstadt & Iraheta 1996), proboscis length (Cariveau et al. 2016) and plant-pollinator trait matching (Stang et al 2009; Olesen et al., 2010). Despite the ubiquity of pollination-related allometric traits, few predictive models exist for pollinating insects, with one notable exception. Cane (1987) established a predictive allometric model for bee body size as a function of the intertegular distance (ITD) (the distance between the wing-attachment points on either side of the thorax). Cane (1987)’s model was developed with a sample of single females from 20 solitary bee species in North America that represented six major bee families. It is now the most commonly used metric for estimating bee body size and has used in ecological (e.g. Williams et al. 2010), sensory (e.g. Spaethe & Chittka 2003; Kapustjanskij et al. 2007) and behavioural studies (e.g. Oliveira & Schlindwein 2010). It also firmly developed ITD as an important body size proxy for establishing other ecologically important allometric relationships (e.g. foraging distances and bee proboscis length; Greenleaf et al. 2007; Cariveau et al. 2016).

The utility of Cane’s equation has not previously been tested beyond North American solitary bee species except in bumblebees (Hagen & Dupont 2013). Further, it hasn’t been tested in conjunction with biogeography, within more complex model structures or in other key pollinating taxa, such as hoverflies (Diptera: Syrphidae). Therefore, we aimed to develop predictive allometric equations within our prescribed iterative framework that take into account these factors and place them alongside a catalogue of pre-existing equations for key pollinating insect taxa within the unified resource of an *R* package, entitled “*pollimetry*”.

**Methodology**

*Existing equations*

We selected three key pollinating insect orders: Diptera, Hymenoptera and Lepidoptera and collated all known predictive allometric models using a systematic literature search. Additional predictive equations were garnered from Martin et al. (2014).

*Specimen collection and measurements*

Only recently curated (<5 years)- or fresh- undamaged specimens were included. For every included specimen, we obtained preservative time, sample location (latitude and longitude), collection method (pan trap, sweeping, malaise trap) and taxonomic designation. Cane’s (1987) original data was obtained using Engauge Digitizer version 10.6 (Mitchell et al. 2018).

*Body size and intertegular distance*

Dry weight (mg) was measured on an analytical balance to an accuracy to 0.001g. Both fresh and curated specimens were dehydrated at 70 °C for 24 - 48hrs prior to weighing to remove residual humidity. Specimen pins were not removed prior to weighing. Instead, we identified the pin type and weighed a sample of 10-50 pins per type. The mean weight was then subtracted off total weight. Intertegular distance was measured in millimetres using a stereo-microscope, either mounted with a calibrated scale or microscope camera.

*Data analysis: Model structure*

All analyses were undertaken in *R* v3.5.0 (R Core Team , 2018). For each taxon, we constructed species mean datasets stratified for measurer and country of origin. We used a power function in model formulation which is typical of predictive allometry:

Ln(Y) = ln(a) + b\*ln(IT) + c\*ln(IT)

We extended this formula to include multiple interactions with IT: sex, biogeographic region and taxonomic family. We constructed linear mixed effect models using *lme4* (Bates et al. 2014) to predict body size, over linear regression as species overlap between measurers and within biogeographic regions required a more-complex model structure. Both measurer and species were included as random terms.

*Data analysis: Incorporating phylogeny*

We explored the influence of phylogenetic relatedness in predicting pollinator body size using a simplified mean dataset, with a single species mean per region. Sex was not considered in these models. The European honeybee (*Apis mellifera*) and the sweat bee, *Halictus rubicundus*, were present in multiple regions so specimens were removed from their introduced regions, Australia and North America respectively, prior to analysis. For bees, we used a genera tree (Hedtke et al. 2013). Non-represented genera were pruned, using *ape* (Paradis et al., 2004) and species added to genera tips as pure-birth subtrees using *phytools* (Revell et al. 2012). As such, we made the explicit assumption that phylogenetic patterns in body size were assessed at and above the genera level.

We assessed the significance of phylogenetic signal of both body size and ITD using Pagel’s λ (Pagel 1999) with *phytools* (Revell et al. 2017). To assess if incorporating phylogeny improved body size predictions, we then determined the relationship between dry weight and ITD and biogeographic region using phylogenetic generalized least squares (PGLS) regression using *nlme* (Pinheiro et al. 2017). λ was fitted at an initial value of 0.5 and optimized by maximum likelihood using *ape* (Paradis et al. 2004).

*Data analysis: Model selection and cross-validation*

We first fitted the full model with all predicted explanatory variables, for LME: ITD in interaction with family, region and sex. For PGLS: IT in interaction with region. We then performed model selection assessing all subset models using the ‘dredge’ function within *MuMIn* (Barton 2018). The best fitting models were then ranked by Akaike Information Criterion (AIC). Given our predictive framework, we iteratively removed terms region and sex from LME models for both taxa for wider utility. Lastly, we considered ITD in isolation.

*Data analysis: Cross-validation*

We implemented k-fold cross validation to test overall model performance and compare prediction error (Stone 1974; Kohavi 1995). Species mean datasets were divided into five equal sets containing a random subset of species. Each model was then evaluated iteratively upon each k-1 set (training set), and then actual-predicted values were compared within the 5-k set (test set). This was done repeatedly so each set was both the test set and contained within the training sets. New levels of random terms were allowed within each predicted set. We then assessed model performance on the basis of average root-mean square error (RMSE), cross-validated *R2* and AIC across the five sets. For PGLS models, λ for each model was fixed at the optimised value from the full dataset. Simplified cross validation was used to test the predictive accuracy of Cane’s (1987) original equation. We compared actual-predicted values of each test set individually and derived a mean RMSE.

*Data analysis: Intraspecific predictions*

We assessed the utility of ITD in predicting intraspecific body size variation. For the five most abundant species of both bees and hoverflies we tested the utility of ITD in predicting intraspecific female body size variation using species-level OLS regression.

*Data availability*

All data and R code is freely available here: <https://github.com/liamkendall/pollimetry>/data

**Results**

*Species and specimen distribution*

In total, we measured 298 bee species from Australia, North America and Europe, including Cane’s (1987) original 20 species and 103 hoverfly species from Australia and Europe. Five out of six bee families and both syrphid subfamilies were represented.

*Interspecific model selection and performance*

For bees, LME analyses found that models which considered region, family and sex in interaction with ITD best-predicted body size on the basis of AIC (Table 1A). In particular, family and region in interaction with ITD were most informative, however for hoverflies, region and sex were important than subfamily across the best fitting models.

Phylogenetic signal was highly significant (*p* <0.001) for bee ln body size (λ: 0.71) and ln ITD (λ: 0.75) (Figure 1). Larger body size was most pronounced within Apidae, the largest bee in our dataset being female *Xylocopa (Koptortosoma) lieftincki* (mean weight: 260.25g), whereas Halictid (i.e. *Lasioglossum* species)and Colletid bees (in particular, *Euhesma* and *Hylaeus* species) were smaller than average. PGLS models exhibited similar trends to LME models with regional models best-explaining the body size ~ ITD relationship (Table 1). Further, PGLS models showed considerable decrease in AIC relative to standard GLS models (ITD \* Region: Δ 25.47, λ 0.54; ITD + Region: Δ 25.89, λ 0.54; ITD Δ 43.28, λ: 0.6).

Cross-validation indicated that high predictive accuracy persisted across all tested models for both bees and hoverflies. Overall model precision was higher in bee models than hoverfly models (bees: RMSE: 0.381 – 0.432, *R*2: 0.858 – 0.89, AIC 394.85-446.23; hoverflies: RMSE: 0.417 – 0.438, *R*2 =0.815 – 0.832, AIC: 167.31 – 173.64 (Table 2, Figure 2). In hoverflies, there was less overall dispersion in prediction error. Interestingly, the top-ranked LME models differed on the basis of RMSE, *R2* and AIC in both data sets. Incorporating phylogeny into model-fitting resulted in a marginal increase in predictive precision for bees when considered in interaction with biogeographic region. Minimal differences in model precision were observed between phylogenetic- and non-phylogenetic models which considered only ITD or in addition to region. All new bee models out-performed Cane’s (1987) original equation.

*Intra-specific predictions*

Across the five most abundant species of bees and hoverflies (females only), the strength of intraspecific predictions of body size using ITD was varied (Table 3; Figure 3). All bee species exhibited a significant relationship between ITD and dry weight, however *R2*differed considerably from 0.02 in *Homalictus urbanus* to 0.46 for *Lasioglossum lanarium* (Table 3, Figure 3). In contrast to bees, three of five hoverfly species, *Austrosyrphus* sp., *Helophilus parallelus and Melanostoma scalare* exhibited significant trends.

*Summary of R package functions*

The accompanying R package, ‘pollimetry’, includes a total of X functions for estimation of pollinator body size using pre-existing equations (see Table S1) or our new equations (Table 1). Also included are Greenleaf et al.’s (2007) and van Nieuwstadt and Iraheta’s (1996) allometric equations for estimating foraging distance in bees using ITD or head width respectively, as well as Cariveau et al’s (2016) allometric equations for estimating bee tongue length.

**Discussion**

Herein, we defined a novel iterative framework in which we developed and tested a suite of dynamic predictive allometric models for two key pollinating taxa, bees and hoverflies. The hoverflies models represent the first predictive allometric models for this important insect group and the most comprehensive examination of both bee hoverfly body variation to date. We demonstrated clear and unequivocal proof of the utility of the intertegular distance (ITD) in predicting intra- and interspecific body size variation, as was first demonstrated by Cane (1987). Overall, both LME and PGLS model structures exhibited high predictive precision, resulting in a suite of highly applicable models for researchers worldwide. By incorporating biogeography, gender and/or taxonomy/phylogeny we improved model performance and overcame the limitations of traditional predictive allometry. These three predictors represent fundamentally related causes of body size variation in pollinating insects.

Terrestrial invertebrates show considerable geographic variation in shape and biogeographical differences in predictive allometry are well-established. We found subtle yet significant body size variation in interaction with ITD between all three regions. The most pronounced differences in our study were between Australia and North America or Europe: both North American and European bees were heavier per unit ITD and exhibited reduced slopes. Martin et al (2014) assessed biogeographical patterns of order-level insect body-length allometric coefficients and contributed differences between geographic regions to a latitudinal gradient, suggesting comparable geographic regions should exhibit similar allometric coefficients. Our results conform to this prediction, although latitude wasn’t explicitly tested due to poor overall coverage within regions. However, previous studies have found both similarities (Gowing & Recher 1984 and Rogers et al. 1977) and differences in allometric coefficients between comparable regions (Schoener 1980 and Rogers et al. 1977) and only one prior predictive allometric study examined multiple biogeographic regions in concert, albeit as individual models (Schoener 1980).

The key difference between these studies and our own, is that this study demonstrated that the influence of different biogeographic regions appears in conjunction with species evolutionary histories and sexual dimorphism. Observed biogeographical differences can arise from differing diversification patterns and as well as from sampling biases, such as random variation among species and the ranges of body size measured. Extrapolating estimates for specimens beyond the range of sizes/lengths used for model creation can lead to imprecise estimation of larger insects’ body mass because of the non-linear nature of allometric models (Sage 1982). Yet in both taxa, we sampled systematically across a wide range of body sizes (see Figure 1 for bees) and incorporated far more species than the majority of prior allometric studies that formulated predictive models at either the superfamily or family level. Therefore, differing diversification patterns and random variation in species sampled appear central to biogeographic differences in allometric coefficient patterns in this study. As a result, predictive allometric model development requires large-scale efforts incorporating multiple regions, biomes and ecosystems for greater accuracy in order to develop biological hypotheses and reasoning driving observed trends.

Sex was retained as an integral predictor either in addition or in interaction with ITD for both taxa. This suggests that although ITD is a robust predictive trait, other morphological aspects must differ between the sexes resulting in sexual size dimorphism (SSD) in absence of ITD differences.SSD is common among insects. In both Diptera and Hymenoptera, SSD is predominantly (>80%) female-biased, including in Apoidea and Syrphidae (Shreeves and Field 2008; Francuski et al. 2011; Milankov et al. 2013). Female-biased SSD is hypothesised to be a result of the greater fitness and increased fecundity inferred by larger female body size (Teder and Tammaru 2005: Stillwell 2010). In bees, SSD is attributed to the physical requirements of nest provisioning and construction. As such, female-biased SSD is more pronounced in ground nesting and/or provisioning taxa than non-provisioning and/or cavity nesting taxa (Shreeves and Field 2008). SSD is also smaller in eusocial species (Medina et al. 2016). Furthermore, female bees exhibit specialised morphological structures for resource collection (i.e. scopal hairs and corbiculae) as well as self-preservation (i.e. a stinging ovipositor). In hoverflies, there exist few examples of specialised morphological sexual dimorphism, other than eye shape. How these traits co-vary with ITD is at present unknown. However, our results demonstrate that ITD as a predictive trait is sensitive to sexual dimorphism making sex an important consideration in prediction, especially as ecologically relevant allometric traits are gender-related (e.g. foraging distance).

Few previous studies have assessed the utility of predictive models in describing intrageneric or intraspecific allometric traits (e.g. Hagen & Dupont 2013; Cariveau et al. 2016). Our results provide reasonable proof that intraspecific body variation can be predicted using ITD. However, the large variation in predictive power suggests that it is potentially sensitive to environmental conditions and small sample sizes. Adult body size variation in holometabolous insects is a direct result of diet and environment during ontogeny and larval development (Davidowitz et al. 2004). Sampled specimens in many cases, came from differing environments and likely developed in disjunct conditions, potentially leading to prediction error. Despite this, our results suggest there are reasonable constraints upon the overall influence of ontogeny and larval development on adult body size, resulting in adequate predictive power in intraspecific models. Sample size is also an important consideration for intraspecific predictions. The two hoverfly species which showed no-trend had small sample sizes. Although *Melanostoma scalare* exhibited a significant trend with the same sample size, we caution the development of intra-specific predictive allometric models with a sample size < 10. In any case, the interspecific model should provide adequate estimations of body size distributions within a given population.

Our prescribed iterative framework provides a new and much needed re-invigoration of the field of predictive allometry. A key principle of this is the incorporation of complex model structures. Traditional predictive allometry have typically utilised ordinary least squares or major axis regression. Although both have some attractive statistical properties for allometric prediction (Warton et al. 2006; Legendre & Legendre 2012), both fail to statistically incorporate the non-independence, pseudo-replication and random variation that are part and parcel of biological research. LME structures allowed us to accurately account for species overlap within regions and potential differences in equipment measurement error to assess macro-ecological trends.

Phylogenetic signal in body size variation has been inferred in a number of vertebrate and invertebrate groups (see Ashton 2004). Failing to account for dependent phylogenetic patterns heightens the risk of inaccurate predictions (Martins 1991; Martins et al. 2002; Garland et al. 2005). Incorporating phylogeny considerably decreased AIC in our predictive PGLS models relative to GLS models. This suggests that PGLS methods are more informative than non-phylogenetic allometric models. Where phylogenetic information is unavailable, incorporating taxonomy represents an adequate compromise. Including taxonomic family within our LME bee models improved predictive accuracy however in hoverflies, including subfamily was less informative in describing body size variation. Of interest from a predictive sense, incorporating taxonomy can aid in elucidating dependent patterns within a phylogeny, such as the disproportionately larger body sizes observed in Apid bees such as inthe genera *Bombus* and *Xylocopa*. Taxonomy has been used successfully before as a phylogenetic proxy (Cariveau et al. 2016). As such, our results suggest both phylogenetic and taxonomic models can improve model predictions.

An important yet underutilised aspect of predictive ecology is estimating model performance on untested data. As independent data is most-often unavailable to researchers, k-fold cross validation is an attractive alternative (Stone 1974; Kohavi 1995). By dividing our data into sequential validation and testing sets, we were able to assess how accuracy differs between test sets, each comprising a different random subset of our entire dataset. Such an approach has garnered interest in validating species distribution models, in particular, to address spatial auto-correlation (Hijmans 2012; Wenger & Olden 2012). However, despite its utility here, it remains largely unused in other fields of predictive ecology. The function of cross-validation is most apparent herein given the differential results, in terms of model performance metrics: AIC, CV *R2* and RMSE between k datasets and the full dataset used in model selection. Each in isolation lead to differing selections of the ‘best’ LME models for both bees and hoverflies. The PGLS ITD \* Region model was the only model congruent in both full-model selection and cross-validation. By considering multiple metrics (AIC, RMSE and CV *R2*) a better predictive picture is produced and disseminating the best model becomes a hypothesis-driven formula. It was also for this reason that we selectively removed predictors (i.e. region or sex). In essence, predictive allometry requires acceptance of multiple models as equal-best or ‘most accurate’, with model choice and usage becoming the decision of the end-user and based on the aims of the proposed study.

The accompanying R package, “pollimetry”, provides a user-friendly interface to estimate pollinator body size and some allometric traits (bee foraging distance and proboscis length). Sampling regimes and research questions may not garner investigation of sex-related allometric differences and will occur outside the included biogeographic regions. It was for these reasons we chose not to average models. More useful predictive allometries require multiple reduced models. These models will continue to be updated as new body size data becomes available, including from other biogeographic regions (South America and Africa), and will enable investigation and re-evaluation of other allometric traits at both intra- or inter-specific levels. The consequence of size is ubiquitous within pollination research yet few have utilised allometric theory in studying pollinating taxa beyond bees. The prescribed framework heralds a dynamic new direction for predictive allometry and should provide greater prediction through hypothesis-led model choice, testing and investigation in allometric research.

Table 1. AIC and delta for interspecific models. Model types: i) LME: linear mixed effect models and ii) PGLS: phylogenetic generalised least squared models. As these two model types used different datasets, AIC values are not directly comparable.

1. Bees

|  |  |  |  |
| --- | --- | --- | --- |
| Model | Explanatory variables | AIC | Δ |
| LME | 1. ITD \* Family + ITD \* Region + ITD \* Sex | **430.1** | 0 |
|  | 2. ITD \* Family + ITD \* Region + Sex | 433.0 | 2.9 |
|  | 3. ITD \* Family + ITD \* Region | 445.9 | 15.8 |
|  | 4. ITD \* Family + ITD \* Sex | 493.3 | 63.1 |
|  | 5. ITD \* Family | 509.2 | 79.1 |
|  | 6. ITD | 546.6 | 116.5 |
| PGLS | ITD \* Region | **195.1** | 0 |
|  | ITD + Region | 215.7 | 20.6 |
|  | ITD | 233.2 | 38.1 |

1. Hoverflies

|  |  |  |  |
| --- | --- | --- | --- |
| Model | Explanatory variables | AIC | Δ |
| LME | 1. ITD + Sex | **194.7** | 0 |
|  | 2. ITD + Region + Sex | 194.8 | 0.1 |
|  | 3. ITD + Region + Sex + Subfamily | 195.2 | 0.5 |
|  | 4. ITD + Sex + Subfamily | 195.3 | 0.6 |
|  | 5. ITD \* Sex | 195.4 | 0.7 |
|  | 6. ITD \* Sex + Region | 195.5 | 0.8 |
|  | 7. ITD + Subfamily | 199.6 | 4.9 |
|  | 8. ITD | 199.6 | 4.9 |

Table 2. Full k-fold cross validation results. MSE: Mean standard error, RMSE: Root mean square error, *R2*: Cross-validated *R2* and AIC: Akaike Information Criterion. Values are the mean across five folds.

1. Bees

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Model | | Explanatory variables | RMSE | *R2* | AIC |
| LME | 1. ITD \* Family + ITD \* Region + ITD \* Sex | | **0.3816629** | **0.8903881** | 396.205 |
|  | 2. ITD \* Family + ITD \* Region + Sex | | 0.383455 | 0.8893434 | **394.8568** |
|  | 3. ITD \* Family + ITD \* Region | | 0.3877454 | 0.8865717 | 400.3984 |
|  | 4. ITD \* Family + ITD \* Sex | | 0.4154217 | 0.8708062 | 431.536 |
|  | 5. ITD \* Family | | 0.4221665 | 0.8663327 | 436.4804 |
|  | 6. ITD | | 0.4317461 | 0.8588888 | 446.232 |
| PGLS | 1. ITD \* Region | | **0.3776816** | **0.894051** | **157.675** |
|  | 2. ITD + Region | | 0.3900165 | 0.886211 | 175.5921 |
|  | 3. ITD | | 0.3892253 | 0.886775 | 174.6972 |

1. Hoverflies

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Model | Explanatory variables | RMSE | *R2* | AIC |
| LME | 1. ITD + Sex | 0.4187792 | 0.8176169 | 167.9012 |
|  | 2. ITD + Region + Sex | **0.417564** | 0.8179376 | 169.993 |
|  | 3. ITD + Region + Sex + Subfamily | 0.4303686 | 0.8214873 | 173.6362 |
|  | 4. ITD + Sex + Subfamily | 0.4300453 | 0.8211913 | 171.2439 |
|  | 5. ITD \* Sex | 0.4212705 | 0.8154102 | 169.9698 |
|  | 6. ITD \* Sex + Region | 0.4208831 | 0.8158122 | 172.054 |
|  | 7. ITD + Subfamily | 0.4379373 | **0.8325788** | 171.2974 |
|  | 8. ITD | 0.4381055 | 0.8271961 | **167.3067** |

Table 3. Model parameters of intraspecific ln(body size)~ln(IT) size relationships. F: F-statistic and degrees of freedom for each model. A and B: intercept and IT co-efficient, *R2*: Adjusted R-squared and P: p-value of full model. Only females were used in both analyses.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Taxa | Species | F(df) | A | B | *R2* | P |
| Bees | *Andrena flavipes* | 21.07 (1,57) | 1.308 | 2.029 | 0.257 | <0.001 |
|  | *Bombus lucorum* | 81.15 (1,101) | 1.412 | 1.966 | 0.44 | <0.001 |
|  | *Homalictus urbanus* | 6.055 (1,209) | -0.164 | 1.166 | 0.024 | 0.014 |
|  | *Lasioglossum lanarium* | 53.87 (1,61) | 0.702 | 2.13 | 0.46 | <0.001 |
|  | *Lasioglossum pauxillum* | 43.92 (1,110) | 0.402 | 3.112 | 0.279 | <0.001 |
| Hoverflies | *Austrosyrphus spp.* | 12.7 (1,30) | 0.087 | 2.032 | 0.274 | 0.001 |
|  | *Helophilus parallelus* | 14.84 (1,17) | 0.286 | 2.485 | 0.435 | 0.001 |
|  | *Sphaerophoria macrogaster* | 0.04 (1,8) | 0.361 | 0.195 | -0.11 | N.S. |
|  | *Episyrphus balteatus* | 0.08 (1,8) | 1.334 | 0.885 | -0.11 | N.S. |
|  | *Melanostoma scalare* | 6.38 (1,7) | -2.172 | 7.619 | 0.4 | 0.03 |

Figure 1. Bee genera tree from Hedtke et al. (2013) with species subtrees added. Colour denotes ln(body size) of each bee species included in analyses.

Fig 2. Root mean square error (RMSE) across k-fold training and test sets for each model. Model numbers refer to these described in Table 2.



**Figure 3.** Intraspecific predictions of female body size with intertegular distance. Lines denote line of best fit from OLS regression.

SUPPLEMENTARY; Description of *pre-existing equations*

Diptera: 26 allometric models for Diptera were collated (Table S1A). 11 models were reported for the entire order, including nine without any taxonomic breakdown of samples used. 12 for the three main suborders Nematocera (6), Brachycera (4) and Cycllorapha (2) and two for specific families; Asilidae and Bombyliidae.

Hymenoptera: 38 allometric models for Hymenoptera were collated (Table S1B). These included eight combined, seven excluding ants (Formicidae) as well as ten for Formicidae. There are three equations for Vespidae and two equations for Apidae (Cane 1987 & Sabo et al. (2002). Sample et al’s (1993) body length (BL) and body length\*width (BW) equations are provided for Braconidae, Ichneumonidae, Halictidae and Pompilidae.

Lepidoptera: 21 allometric models for Lepidoptera were collated (Table S1C). This includes 13 with varying taxa and without lower classifications. Hodar (1997) provides specific models for Heterocera (moths) and Ropalocera (butterflies). Sample et al. (1993) provide BL and BL\*BW models for Microlepidoptera and two moth families: Geometridae and Arctiidae.

Foraging distance and proboscis length: We collated six bee foraging distance models from van Nieuwstadt and Iraheta (1996) and Greenleaf et al. (2007) and three models for bee proboscis length from Cariveau et al. (2016) (Table S2 – maybe doesn’t need to be tabulated??).

Table S1. Allometric equations for pollinating taxa. BL = Body length, BW = Body width, IT = intertegular distance. OLS = Ordinary Least Squares regression. MA = Major axis regression, MU = Multivariate regression. Equations are present in the form of y = ln(B0) + ln(B1), which is equivalent to y = b0Xb1. \* = Included body width as well as length

1. **Diptera**.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Source** | | **Taxa** | | **Families** | | **Sample size** | | **Biogeographical region** | | | **Measure** | **Range in body length** | **Reg. Type** | **Type** | **Equation** | | | |
|  |  | |  | |  | | **(Families: species)** | |  |  | | **(mm)** |  | | ***B*0 ± S.E.** | ***B*1 ± S.E.** | **Resi. SE** | ***R2*** |
| Rogers et al. (1977) | |  | |  | | (#:84) | | Washington, USA | | | BL | 0.9-34 | OLS | PF | -3.298 ± 0.115 | 2.366 ± 0.078 | 0.57 | **0.96** |
| Schoener (1980) | |  | |  | |  | | Dry forest, CR | | | BL | N.P | OLS | PF | A=-2.603 ± 0.0688 | B = 1.64 ± 0.1224 | NA | 0.795 |
| Schoener (1980) | |  | |  | |  | | Rain forest, CR | | | BL | N.P. | OLS | PF | A = -2.688 ± 0.051 | B = 1.59 ± 0.1173 | NA | 0.775 |
| Schoener (1980) | |  | |  | | (#:171) | | Massachusetts | | | BL | N.P. | OLS | PF | A=-3.816 ± 0.561 | B=2.42 ± 0.0969 | NA | 0.89 |
| Gowing and Recher (1984) | |  | |  | | (100) | | NSW, Australia | | | BL | 2-11 | OLS | PF | 3.653 ± 0.129 | 2.546 ± 0.071 | 0.37 | **0.93** |
| Sample et al. (1993) | |  | | Combined | | (15:257) | | West Virginia, USA | | | BL | 2.9-23.65 | OLS | PF | -3.184 ± 0.184 | 2.213 ± 0.085 | NA | 0.85 |
| “ | |  | |  | |  | | “ | | | BL\*BW | “ | OLS | PF | -2.197 ± 0.089 | 1.309 ± 0.03 | NA | **0.94** |
| “ | | NEM | | BIB,SCI,TIP | | (3:46) | | “ | | | BL | 3.55-23.65 | OLS | PF | -3.675 ± 0.23 | 2.212 ± 0.141 | NA | **0.92** |
| “ | |  | |  | |  | | “ | | | BL\*BW | “ | OLS | PF | -2.217 ± 0.205 | 1.288 ± 0.071 | NA | **0.94** |
| “ | | BRA | | ASI, DOL, EMP, RHA, STR, THE | | (6:80) | | “ | | | BL | 2.9-17.99 | OLS | PF | -3.374 ± 0.230 | 2.158 ± 0.101 | NA | **0.92** |
| “ | |  | |  | |  | | “ | | | BL\*BW | “ | OLS | PF | -2.2 ± 0.147 | 1.259 ± 0.049 | NA | **0.95** |
| “ | | CYC | | CAL, LAU, MUS, OTI, SYR, TAC | | (6:119) | | “ | | | BL | 2.9-15.65 | OLS | PF | -3.619 ± 0.212 | 2.632 ± 0.101 | NA | **0.92** |
| “ | |  | |  | |  | | “ | | | BL\*BW | “ | OLS | PF | -2.02 ± 0.131 | 1.298 ± 0.042 | NA | **0.94** |
| Hodar (1997) | | BRA | |  | | (26) | | Gaudix-Baza, Spain | | | HW | NA | OLS | PF | A=0.655 ± 0.105 | B=2.526 ± 0.139 | 0.47 | **0.933** |
|  | | NEM | |  | | (10) | | “ | | | HW | NA | OLS | PF | A=3.942 ± 0.259 | B=3.106 ± 0.278 | 0.55 | **0.94** |
| Ganihar (1997) | |  | | NA | | (#:20) | | Goa, India | | | BL |  | OLS | PF | -3.4294 ± 0.01994 | 2.5943 ± 0.0334 | 0.03 | **0.99** |
| Johnson and Strong (2000) | | ALL | | NA | | (75) | | Jamaica | | | BL | 1-12.5 |  | PF | -2.462 ± 0.196 | 1.881 ± 0.146 |  | 0.83 |
| “ | | NEM | | NA | | (21) | | “ | | | BL | 1-4.8 |  | PF | -2.562 ± 0.244 | 1.373 ± 0.207 |  | 0.836 |
| “ | | NEM exc. | | NA | | (54 | | “ | | | BL | 1.2-12.5 |  | PF | -2.105 ± 0.178 | 1.805 ± 0.124 |  | 0.895 |
| *Sabo et al. (2002)* | | *BRA* | |  | |  | | *California, USA* | | | *BL* | *N.P.* |  | *PF* | *A = 0.006 ± 0.007* | *B = 3.05 ± 0.36* |  | *0.85* |
| *“* | | *NEM* | |  | |  | | *“* | | | *BL* | *N.P.* |  | *PF* | *A = 0.1 ± 0.06* | *B = 1.57 ±0.2* |  | ***0.9*** |
| *“* | |  | | *Asilidae* | | *(1:9)* | | *“* | | | *BL* | *N.P.* |  | *PF* | *A = 0.38 ± 2.625* | *B = 1.5 ± 2.469* |  | *0.74* |
| *“* | |  | | *Bombyliidae* | | *(1:10)* | | *“* | | | *BL* | *N.P.* |  | *PF* | *A = 0.007 ± 0.011* | *B = 3.337 ±0.676* |  | ***0.95*** |
| *Brady and Noske (2006)* | | *NA* | | *NA* | | *(9 sp:78 spe)* | | *NT, AUS* | | | *B:* | *2-28* | *OLS* | *L* | *A= -0.041 ± 0.004* | *B = 0.010 ± 0.001* | *0.02* | *0.838* |
| Wardhaugh (2013) | |  | |  | | (#:16) | | QLD, AUS | | | BL |  | MA | PF | -3.29 ± 0.45 | 2.65 ± 0.36 | NA | 0.72 |
| Wardhaugh (2013) | |  | |  | | (#:16) | | QLD, AUS | | | BL \* BW |  | MA | PF | -1.91 ± 0.19 | 1.22 ± 0.11 | NA | 0.87 |

BIB =Bibionidae, SCI = Sciaridae, TIP = Tipulidae, ASI= Asilidae, DOL = Dolichopodidae, EMP = Empidae, RHA = Rhagionidae, STR = Stratiomyidae, THE = Therevidae, CAL = Calliphoridae, LAU = Lauxaniidae, MUS = Muscidae, OTI = Otitidae, SYR = Syrphidae, TAC = Tachinidae.NEM = Nematocera, BRA= Brachycera, CYC = Cyclorrapha

1. **Hymenoptera.**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Source** | | **Taxa** | | **Families** | | **Sample size** | | | **Biogeographical region** | | **Measure** | **Range in body length** | | **Reg. Type** | **Type** | **Equation** | | | |
|  |  | |  | |  | | **(Families: species)** |  | |  | | | **(mm)** |  | | ***B*0 ± S.E.** | ***B*1 ± S.E.** | **Resi. SE** | ***R2*** |
| Rogers et al. (1977) | |  | | \*\* | | (#:97) | | | Washington, USA | | BL | 0.7-27 | | OLS | PF | -3.871 ± 0.108 | 2.407 ± 0.06 | 0.55 | **0.97** |
| “ | |  | | FOR | | (#:34) | | | “ | | BL | 1.2-13.5 | | OLS | PF | -4.029 ± 0.171 | 2.572 ± 0.097 | 0.40 | **0.98** |
| Cane (1987) | |  | | Apidae | | (6:20) | | | USA | | ITD | 1-6 | | NL | EXP | A=0.77 | B=0.405 |  | **0.96** |
| *Schoener (1980)* | | *ALL* | | *\*\** | | *(#:174)* | | | *Dry forest, C. Rica* | | *BL* | *N.P* | | *OLS* | *PF* | *A = 0.043 ± 0.05* | *B = 2.07 ± 0.091* | *NA* | *0.87* |
| *“* | | *“* | | *“* | | *(#:122)* | | | *Rain forest, C. Rica* | | *BL* | *N.P.* | | *OLS* | *PF* | *A = 0.022 ± 0.056* | *B = 2.29 ± 0.137* | *NA* | *0.835* |
| *“* | | *“* | | *“* | | *(#:82)* | | | *Massachusetts* | | *BL* | *N.P.* | | *OLS* | *PF* | *A = 0.016 ± 0.072* | *B = 2.55 ± 0.107* | *NA* | *0.937* |
| *“* | | *“* | | *FOR* | | *(#:25)* | | | *Dry forest, C. Rica* | | *BL* | *N.P* | | *OLS* | *PF* | *A = 0.012 ± 0.113* | *B = 2.72 ± 0.26* | *NA* | ***0.907*** |
| *“* | | *“* | | *“* | | *(#:20)* | | | *Rainforest, C. Rica* | | *BL* | *N.P.* | | *OLS* | *PF* | *A = 0.21 ± 0.127* | *B = 2.31 ± 0.224* | *NA* | ***0.934*** |
| *“* | | *“* | | *“* | | *(#:13)* | | | *Massachusetts* | | *BL* | *N.P.* | | *OLS* | *PF* | *A = 0.034 ± 0.155* | *B = 2.19 ± 0.342* | *NA* | ***0.908*** |
| Gowing and Recher (1984) | |  | | \*\* | | (86) | | | NSW, Australia | | BL | 1-12 | | OLS | EXP | -2.860 ± 0.099 | 0.478 ± 0.016 | 0.48 | **0.918** |
| “ | |  | | FOR | | (68) | | | “ | | BL | 2-18 | | OLS | PF | -3.306 ± 0.258 | 2.489 ± 0.051 | 0.32 | **0.973** |
| Sample et al. (1993) | | ALL | | - | | (7:274) | | | West Virginia, USA | | BL | 2.81-34.91 | | OLS | PF | -4.284 ± 0.183 | 2.696 ± 0.083 | NA | 0.89 |
| “ | |  | | “ | | “ | | | “ | | BL \* BW | “ | |  | “ | -2.375 ± 0.08 | 1.456 ± 0.028 | NA | **0.95** |
| “ | |  | | Ichneumonidae | | (1: 106) | | | “ | | BL | 3.65-34.91 | |  | “ | -4.149 ± 0.262 | 2.464 ± 0.116 | NA | **0.9** |
| “ | |  | | “ | | “ | | | “ | | BL \* BW | “ | |  | “ | -2.497 ± 0.147 | 1.445 ± 0.053 | NA | **0.94** |
| “ | |  | | Braconidae | | (1:41) | | | “ | | BL | 2.81-15.42 | |  | “ | -3.854 ± 0.273 | 2.441 ± 0.147 | NA | **0.94** |
| “ | |  | | “ | | “ | | | “ | | BL \* BW | “ | |  | “ | -2.19 ± 0.142 | 1.445 ± 0.069 | NA | **0.96** |
| “ | |  | | Vespidae | | (1:19) | | | “ | | BL | 8.14-20.58 | |  | “ | -3.540 ± 0.544 | 2.782 ± 0.195 | NA | **0.96** |
| “ | |  | | “ | | “ | | | “ | | BL \* BW | “ | |  | “ | -1.537 ± 0.307 | 1.319 ± 0.07 | NA | **0.98** |
| “ | |  | | Formicidae | | (1:45) | | | “ | | BL | 3.62-17.41 | |  | “ | -4.727 ± 0.350 | 2.919 ± 0.11 | NA | **0.93** |
| “ | |  | | “ | | “ | | | “ | | BL \* BW | “ | |  | “ | -2.378 ± 0.265 | 1.473 ± 0.106 | NA | **0.9** |
| “ | |  | | Halictidae | | (1:21) | | | “ | | BL | 6-12.76 | |  | “ | -2.891 ± 0.386 | 2.302 ± 0.182 | NA | **0.95** |
| “ | |  | | “ | | “ | | | “ | | BL \* BW | “ | |  | “ | -2.758 ± 0.357 | 1.590 ± 0.119 | NA | **0.95** |
| “ | |  | | Pompilidae | | (1:15) | | | “ | | BL | 5.55-14.32 | |  | “ | -2.341 ± 0.873 | 2.006 ± 0.396 | NA | 0.81 |
| “ | |  | | “ | | “ | | | “ | | BL \* BW | “ | |  | “ | -1.946 ± 0.431 | 1.444 ± 0.154 | NA | **0.93** |
| Hodar (1997) | | ALL | |  | |  | | | Gaudix-Baza, Spain | | HW |  | | OLS | PF | A= 1.999 ± 0.112 | B= 2.09 ± 0.132 | 0.51 | **0.919** |
| “ | |  | | FOR – Workers | |  | | | “ | | HW |  | |  | “ | A= 0.552 ± 0.068 | B= 2.550 ± 0.116 | 0.19 | **0.982** |
| “ | |  | | FOR –Winged | |  | | | “ | | HW |  | |  | “ | A= 1.607 ± 0.127 | B= 2.752 ± 0.25 | 0.31 | **0.938** |
| Ganihar (1997) | |  | | NA \*\* | | (#:26) | | | Goa, India | | BL |  | | OLS | PF | -3.5917 ± 0.1646 | 2.6429 ± 0.1127 | 0.24 | **0.94** |
| Johnson and Strong (2000) | | ALL | |  | |  | | | Jamaica | | BL | 1.4-24.3 | | OLS | PF | -3.556 ± 0.183 | 2.193 ± 0.110 | NA | **0.923** |
|  | | FOR | |  | |  | | | “ | | BL | 1.6-9.9 | | OLS | PF | -3.730 ± 0.298 | 2.103 ± 0.238 | NA | **0.901** |
|  | | \*\* | |  | |  | | | “ | | BL | 1.4-24.3 | | OLS | PF | -3.295 ± 0.241 | 2.102 ± 0.132 | NA | **0.917** |
| *Sabo et al. (2002)* | | *ALL* | | *7\*\*\*\** | | *(7:54)* | | | *California, USA* | | *BL* | *N.P.* | | *NLL* | *PF* | *A= 0.56 ± 0.64* | *B= 1.56 ± 0.4* |  | *0.75* |
| *“* | |  | | *API* | | *(1:10)* | | | *“* | | *BL* | *N.P.* | | *NLL* | *PF* | *A= 0.006 ± 0.041* | *B= 3.407 ± 2.471* |  | *0.81* |
| *“* | |  | | *VES* | | *(1:19)* | | | *“* | | *BL* | *N.P.* | | *NLL* | *PF* | *A= 0.001 ± 0.002* | *B= 3.723 ± 0.798* |  | *0.95* |
| *Brady and Noske (2006)* | |  | | *FOR* | | *(8 sp:100)* | | | *NT, AUS* | | *BL* | *2-10* | | *OLS* | *P* | *0.001* | *2.330 ± 0.0151* | *0.49* | *0.708/0.956* |
| *“* | |  | | *\*\** | | *(9 sp:28)* | | | *NT, AUS* | | *BL* | *4-29* | | *OLS* | *P* | *6.783 ± 0.001* | *2.544 ± 0.26* | *0.57* | *0.786/0.905* |
| Wardhaugh (2013) | |  | |  | | (#:26) | | | Daintree QL AUS | | BL |  | | MA | PF | -4.3 ± 0.38 | 3 ± 0.24 | NA | 0.83 |
| Wardhaugh (2013) | |  | |  | | (#:26) | | | Daintree QL AUS | | BL \* BW |  | | MA | PF | -2.1 ± 0.09 | 1.34 ± 0.05 | NA | **0.97** |

ANT = Anthophoridae, API = Apidae, CHR = Chrysididae, FOR = Formicidae, ICH = Ichneumonidae, SPH = Sphecidae, VES = Vespidae. \*\* = excluded ants. \*\*\*\*Seven families = ANT, API, CHR, FOR, ICH, SPH, VES

1. **Lepidoptera**. \*\*\* = Multivariate regression using multiple length measures: length, width, wing area and wing length. See Garcia-Barros (2015) for parameters.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Source** | | **Taxa** | | **Families** | | | **Sample size** | **Biogeographical region** | | | **Measure** | **Range in body length** | **Reg. Type** | | **Type** | **Equation** | | | |
|  |  | |  | |  | **(Families: species)** | | |  |  | | **(mm)** | |  | | ***B*0 ± S.E.** | ***B*1 ± S.E.** | **Resi. SE** | ***R2*** |
| Rogers et al. (1977) | |  | |  | | | (#:22) | Washington, USA | | | BL | 1.6-17 | OLS | | PF | -4.037 ± 0.133 | 2.903 ± 0.08 | 0.31 | **0.99** |
| Sample et al. (1993) | | ALL | |  | | | (#:384) | West Virginia, USA | | | BL | 2.76-40.73 |  | | PF | -5.036 ± 0.157 | 3.122 ± 0.064 |  | **0.93** |
| “ | | “ | |  | | | “ | “ | | | BL \* BW | “ |  | | “ | -2.607 ± 0.088 | 1.457 ± 0.024 |  | **0.95** |
| “ | |  | | MIC. | | | (#:46) | “ | | | BL | 2.76-10.6 |  | | “ | -4.913 ± 0.325 | 2.918 ± 0.169 |  | **0.93** |
| “ | |  | |  | | |  | “ | | | BL \* BW |  |  | | “ | -2.715 ± 0.199 | 1.395 ± 0.08 |  | **0.93** |
| “ | |  | | GEO | | | (1:58) | “ | | | BL | 6.45-21.70 |  | | “ | -4.172 ± 0.411 | 2.628 ± 0.167 |  | **0.9** |
| “ | |  | |  | | |  | “ | | | BL \* BW | “ |  | | “ | -2.343 ± 0.283 | 1.387 ± 0.084 |  | **0.91** |
| “ | |  | | ARC | | | (1:60) | “ | | | BL | 5.05-20.06 |  | | “ | -3.755 ± 0.242 | 2.658 ± 0.105 |  | **0.96** |
| “ | |  | |  | | |  | “ | | | BL \* BW | “ |  | | “ | -1.658 ± 0.148 | 1.222 ± 0.044 |  | **0.96** |
| Sage et al. (1982) | |  | |  | | | (#:25) | Texas, USA | | | BL | 4.9-22.9 |  | | PF |  |  |  | **0.92** |
| Hodar (1996) | | HET | |  | | | (10) | Gaudix-Baza, Spain | | | HW |  |  | | PF | A=2.053 ± 0.25 | B=2.804 ± 0.236 | 0.493 | 0.946 |
| “ | | ROP | |  | | | (10) | “ | | | HW |  |  | | “ | A=1.634 ± 0.46 | B=2.793 ± 0.446 | 0.485 | 0.831 |
| Ganihar et al. (1997) | |  | | NA | | | (#:10) | Goa, India | | | BL |  |  | | PF | -4.7915 ± 0.7507 | 2.8585 ± 0.2567 | 0.4568 | **0.93** |
| Johnson and Strong (2000) | |  | | NA | | | (40) | Jamaica | | | BL | 2.2-18.6 | OLS | | PF | -3.268 ± 0.255 | 2.243 ± 0.130 | NA | **0.942** |
| *Schoener (1980)* | |  | | *NA* | | | *(#:29)* | *Dry forest, Canas, Costa Rica* | | | *BL* | *N.P.* |  | | *PF* | *A= 0.026 ± 0.186735* | *B= 2.55 ± 0.571429* |  | ***0.958*** |
| *“* | |  | | *NA* | | | *(#:7)* | *Rainforest, Guipiles, Costa Rica* | | | *BL* | *N.P.* |  | | *“* | *A= 0.078 ± 0.139796* | *B= 1.32 ± 0.683673* |  | *0.749* |
| *“* | |  | | *NA* | | | *(#:18)* | *Massachusetts* | | | *BL* | *N.P.* |  | | *“* | *A= 0.014 ± 0.18673* | *B= 2.55 ± 0.571429* |  | *0.77* |
| *Brady and Noske (2006)* | |  | |  | | | *((6 sp: 28)* | *NT, AUS* | | | *BL* | *7-34* | *OLS* | | *PF* | *0.001* | *2.313 ± 0.223* | *0.396* | *0.805/0.938* |
| Wardhaugh (2013) | |  | | NA | | | (#:11) | Daintree QL AUS | | | BL |  | MA | | PF | -3.83 ± 0.41 | 2.77 ± 0.27 | NA | 0.83 |
| Wardhaugh (2013) | |  | | NA | | | (#:11) | Daintree QL AUS | | | BL \* BW |  | MA | | “ | -2.1 ± 0.21 | 1.37 ± 0.11 | NA | 0.88 |

HET = Heterocera, ROP = Ropalocera, MIC = Microlepidoptera, GEO = Geometridae, ARC = Arctiidae

Table S2. Predictive allometries for bee foraging distance and proboscis length (to be added). HW: Head width, IT: Intertegular distance.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Source** | **Metric** | **Taxa** | **Measure** | **Equation** |
| van Nieuwstadt & Iraheta (1996) | Foraging distance | Stingless bees (Apidae:Meliponini) | Artificial nectar source |  |
|  |  |  | “ |  |
| Greenleaf et al. (2007) |  | Apidae | Max |  |
|  |  |  | Typical |  |
|  |  |  | Feeder |  |
|  |  |  | Comm |  |

**#SUPP# Preservative time**

**Method**

A key confounding factor which can affect predictive allometric models for insects is the time specimens spend within preservative (i.e. ethanol Leuven et al. 1985). As a trade-off between including greater species diversity and those that had been preserved, we assessed the impact of preservative time using Australian and German specimens (species n = 20), where there was considerable overlap in preserved and unpreserved specimens in species.

We fitted a linear-mixed effect model with y = Specimen weight ~ IT + Sex + preservative time with two random terms: country and species.

We also fitted a linear-mixed effect model with y = log(Specimen weight) ~ IT + Sex + preservative time with two random terms: country and species.

**Result**

Depending on model choice, there was a insignificant or significant effect of preservative time on specimen weight. Not logged: t-value 0.53, logged: t-value 4.1, - loss of 0.0001 per day

**##SUPP## Sample size variation**

Furthermore, we plotted species trait means independently against increasing sample size to estimate the adequate sample size whereby variance stabilised within confidence intervals of the actual sample size. ANY IDEAS FOR A TEST FOR THIS OR IF A TEST IS NEEDED? – I THINK PERHAPS WE LEAVE THIS PART OUT COMPLETELY

Sample size exhibited an interesting trend in relation to both ITD and dry weight. In bees, mean ITD and dry weight stabilised within the confidence intervals of the total sample size with >20 specimens per species (Figure S1A). For hoverflies, the lower overall sample sizes of each species limited inference of sample-size / mean stabilisation (FIGURE S1B).



Fig 4A. Intraspecific variation in IT and dry weight in relation to sample size in bees. Red line denotes the total trait mean and green lines represent 95% confidence intervals.



Fig 4B. Intraspecific variation in IT and dry weight in relation to sample size in hoverflies. Red line denotes the total trait mean and green lines represent 95% confidence intervals.

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