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2 **Supplementary Methods**

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4 *Historical Background*

5           Beyond the important role of the phytochemical landscape driving insect herbivore diet breadth,  
6 herbivorous insects are subject to a list of general factors that affect the diet breadth of foragers.  
7 Originally broadly conceptualized for hunting animals by MacArthur & Pianka<sup>7</sup>, this list was adapted for  
8 application to a pollinator diet by Wasser et al<sup>8</sup>. These factors are listed in Table S1 with common factors  
9 between the two treatments.

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11 **Table S1:** Factors favoring specialization in foraging as detailed in MacArthur & Pianka<sup>7</sup> and their  
12 corresponding construction in Wasser et al's<sup>8</sup> study on pollinator specialization. The third column  
13 describes the common factor in each treatment. The factor noted in green highlights the work which  
14 helped inspire our study.

Factors favouring specialisation of diet for hunting animals (MacArthur and Pianka 1966)	Factors favouring generalisation of diet for pollinators (Waser et al. 1996)	Common factor
Greater food density	Pollinator lifespan is long relative to the flowering of individual plant species	The density of resources, as measured relative to the foraging range/period of the animal
Increased mobility of animal, or decreased environmental resistance to movement	Travel is costly	The cost associated with travelling to many or few resources
Increased differences between prey types, or increased specialisation of pursuing behaviour	Floral rewards are similar across plant species	The inherent differences in resource quality
Increased mobility of prey, or greater difficulty in pursuit	Constraints of behaviour and morphology are minor	The inherent difficulty involved in accessing different resources

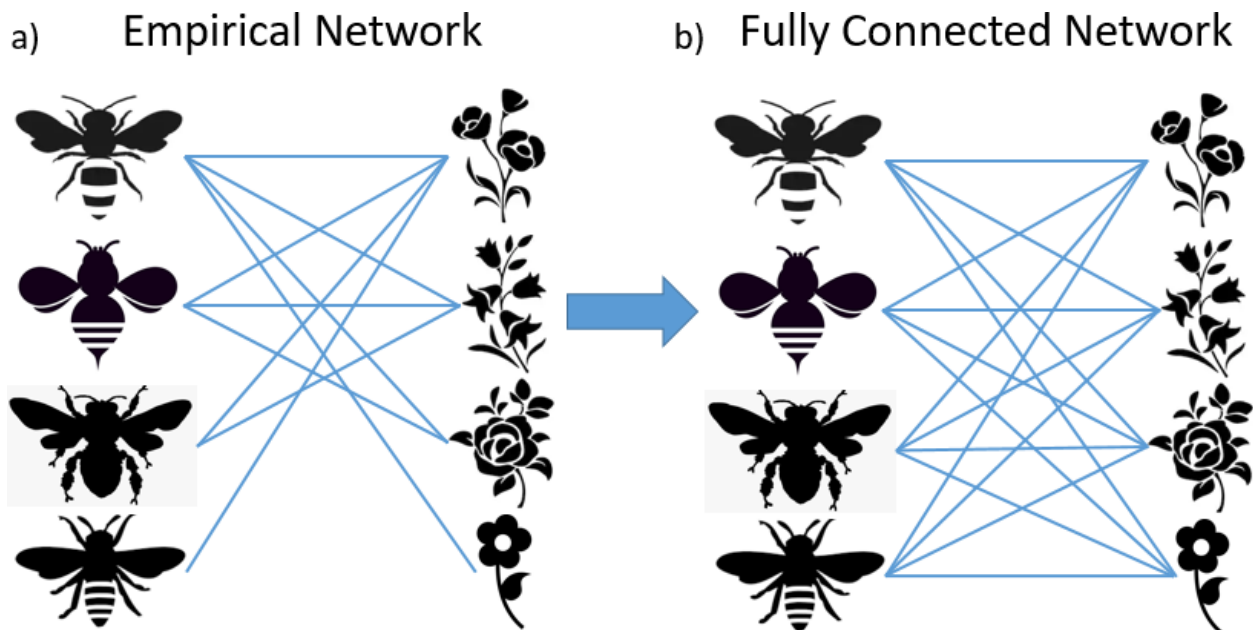
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17 *Baseline model*

18           As with recent studies of ecological networks<sup>10,31</sup>, the makeup of the overall network model used  
19 here has two major fundamental components: the structure of the pollination networks themselves and the  
20 dynamics occurring on the networks.

21           The structure of a network describes which links (representing species interactions) between  
22 plants (*p*) and animal pollinators (*a*) are present or absent, regardless of the strength of the link. Typical  
23 ecological network studies have a collection of unique topological connections across different networks,  
24 meaning only certain links of the possible links between plants and pollinators can potentially be realized

25 (Fig S1a). However, the networks we used in the models/simulations here were fully connected, meaning  
26 all connections are possible (Fig S1b). The baseline of these networks in our study are sourced from an  
27 empirical pollination network<sup>32</sup>. Using a real-world pollination network as a basis ensured a plausible  
28 ratio of flowering plant populations to pollinator populations, which in this case was 58 plant species to  
29 100 pollinator species. The network was then fully connected (see Figure S1) such that each pollinator  
30 had potential access to all plant species and vis-versa. Fully connecting the plant-pollinator network was  
31 done in order to give each pollinator population the maximum within-model range of dietary options.  
32 Doing so allows us to test the ability of the phenological mechanism to drive plasticity in pollinator  
33 specialization without a priori constraints on pollinator behavior and network structure. The size of this  
34 basic network framework was then modified to test effects of species richness, resulting in 3 network size  
35 classes ( $N_p$ =plant richness,  $N_a$ =animal pollinator richness):  $N_p = 58$  &  $N_a = 100$ ,  $N_p = 48$  &  $N_a = 71$ ,  
36 and  $N_p = 30$  plants &  $N_a = 50$ . While only these 3 network frameworks were used, the exact topology of  
37 each changed with thousands of permutations of phenological parameters (see below).

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40 **Figure S1: Underlying network structure.** Example diagram describing the creation of the baseline  
41 network structure. Pictures of bees represent populations of pollinators and pictures of flowering plants  
42 represent populations of flowering plants. Blue links between them represent a potential pollination  
43 interaction between plants and pollinators. a) Example of a starting empirical network. b) Example of  
44 fully connecting the empirical network to use in simulations.

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46           The dynamics occurring on the networks refer to the internal population demographics (birth and  
47 death) and species interactions taking place amongst the species in the network. In the case of our model,  
48 species interactions refer to competition for resources, consumption of resources, and pollination events.  
49 Dynamics were simulated based on the work of Valdovinos et al<sup>9</sup> which mechanistically modeled  
50 pollination as a consumer-resource interaction by separately accounting for vegetative abundance and  
51 floral rewards consumed by pollinators. The model tracks the adaptive dynamics of each plant species'  
52 population dynamics ( $p_i$ ), each animal pollinator species population dynamics ( $a_j$ ), each plant species'  
53 pool of floral rewards ( $R_i$ ), and the adaptive dynamics of the per-capita foraging effort preferences of  
54 each pollinator species for each plant species ( $\alpha_{ij}$ ). Model parameters are described in Table S2.

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85 **Table S2:** Baseline model state variables and parameters. In Mean Value column, \* indicate initial  
 86 conditions,  $k_{aj}$  is the number of interactions of animal  $j$

Definition	Symbol	Dimension	Mean Value
Density of plant population $i$	$p_i(t)$	individuals area <sup>-1</sup>	0.7*
Density of animal population $j$	$a_j(t)$	individuals area <sup>-1</sup>	0.7*
Density of floral resources of plant population $i$	$R_i(t)$	mass area <sup>-1</sup>	0.7*
Foraging Effort of pollinator $j$ on plant $i$	$\alpha_{ij}(t)$	none	$\frac{1}{k_{aj}}$ *
Visitation Efficiency	$\tau_{ij}$	visits area time <sup>-1</sup> individuals <sup>-1</sup>	1
Expected number of seeds produced per pollination event	$e_{ij}$	individuals visits <sup>-1</sup>	0.8
Per capita mortality rate of plants	$\mu_i^P$	time <sup>-1</sup>	0.002
Conversion efficiency of floral resources to pollinator births	$c_{ij}$	individuals mass <sup>-1</sup>	0.2
Per capita mortality rate for pollinators	$\mu_j^A$	time <sup>-1</sup>	0.003
Pollinator extraction efficiency of resource $R_i$ in each visit	$b_{ij}$	individuals visits <sup>-1</sup>	0.4
Max fraction of total seeds that recruit to plants	$g_i$	none	0.4
Intra-specific competition coefficient for plants	$u_i$	area individuals <sup>-1</sup>	1.2
Inter-specific competition coefficient for plants	$w_i$	area individuals <sup>-1</sup>	0.002
Production rate of floral resources	$\beta_i$	mass individuals <sup>-1</sup> time <sup>-1</sup>	0.2
Self-limitation parameter for resource production	$\phi_i$	time <sup>-1</sup>	0.04
Adaptation rate of pollinator foraging effort	$G_j$	none	2

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 88 Changes in population density of plant species ( $p_i$ ) are calculated through:

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$$\frac{dp_i}{dt} = \gamma_i \sum_{j \in A_j} e_{ij} \sigma_{ij} V_{ij} - \mu_i^P p_i \quad \text{Eq (1)}$$

90 The second term in the equation describes background mortality, where  $\mu_i^P$  is the constant  
 91 density-independent per-capita mortality rate of plant  $i$ . The first term describes plant population growth  
 92 where  $\gamma_i$  describes the realized fraction of seeds that successfully recruit to adults:

93 
$$\gamma_i = g_i (1 - \sum_{l \neq i \in P} u_l p_l - w_i p_i) \quad \text{Eq (2)}$$

94 where  $g_i$  is the maximum fraction of seeds that can potentially recruit to fecund adulthood. The  
 95 recruitment is subject to both interspecific ( $u_l$ ) and intraspecific ( $w_i$ ) competition with  $u_l < w_i$ . The  
 96 parameter  $e_i$  in Equation (1) is the constant max seed set induced by a pollination event between plant

97 and pollinator. The quality of each pollination event is determined by the fraction of pollen from  
 98 conspecific plants on a pollinator compared to other plant species pollen. This fraction is proportional to  
 99 the visits each animal pollinator ( $a_j$ ) makes on each plant species ( $p_i$ ). We label this term,  $\sigma_{ij}$  and define  
 100 it as follows:

$$101 \quad \sigma_{ij} = \frac{V_{ij}}{\sum_{k \in P_j} V_{kj}} \quad \text{Eq (3)}$$

102 where  $V_{ij}$  is the frequency of visits by animal species  $j$  to plant species  $i$  and it defined by:

$$103 \quad V_{ij} = \alpha_{ij} \tau_{ij} T_{a_j}(t) a_j p_i \quad \text{Eq (4)}$$

104 Visits from pollinator  $j$  to plant species  $i$  are zero ( $V_{ij} = 0$ ) if the two do not interact. Pollinator  
 105  $j$ 's visitation efficiency on plant  $i$  is determined by the parameter  $\tau_{ij}$  and is fixed at 1 for this study so as  
 106 not to bias any pollination interaction over others and affect visitation preferences a priori. The function  
 107  $T_{a_j}(t)$  is the phenological determinant of activity of pollinator  $a_j$ , in this case controlling the flight period  
 108 of  $a_j$ . See Phenology section below for more. The dimensionless function  $0 \leq \alpha_{ij} \leq 1$  is the foraging  
 109 preference of pollinator  $j$  on plant  $i$  and changes over time as defined by:

$$110 \quad \frac{d\alpha_{ij}}{dt} = T_{a_j}(t) G_j \alpha_{ij} \left( c_{ij} \tau_{ij} b_{ij} R_i - \sum_{k \in P_j} \alpha_{kj} c_{kj} \tau_{kj} b_{kj} R_k \right) \quad \text{Eq (5)}$$

111 where  $G_j$  is the basal adaptation rate of foraging preference. Higher or lower rates of  $G_j$  produce faster or  
 112 slower rates of adaptation based on changes seen inside the parentheses of Eq (5).  $c_{ij}$  represents the  
 113 constant per-capita conversion efficiency of pollinator  $j$  converting plant  $i$ 's floral resources into  $j$ 's  
 114 births.  $b_{ij}$  is the constant efficiency of pollinator  $j$  extracting plant  $i$ 's floral resources ( $R_i$ ). Pollinator  $j$   
 115 allocates more foraging effort to plant species  $i$  whenever such reallocation increases  $j$ 's food intake.  
 116 Such reallocation causes a commensurate reduce in foraging effort from other plant species. For every  
 117 animal pollinator species  $j$ ,  $\sum \alpha_{ij} = 1$  for all plant species. Finally, the function  $T_{a_j}(t)$  appears here to  
 118 limit the adaptation of foraging preference only to periods when pollinators are actively flying.

119 Each plant  $i$ 's floral resources,  $R_i$ , changes over time as defined by:

120 
$$\frac{dR_i}{dt} = T_{p_i}(t)\beta_i p_i - \phi_i R_i - \sum_{j \in A} V_{ij} b_{ij} \left(\frac{R_i}{p_i}\right) \quad \text{Eq (6)}$$

121 where  $\beta_i$  is plant  $i$ 's per-capita resource production rate and  $\phi_i$  is a constant self-limitation parameter.

122 Rewards of plant  $i$  are removed with an efficiency  $b_{ij}$  by pollinator  $j$  in proportion to the amount of visits,

123  $V_{ij}$ . The function  $T_{p_i}(t)$  controls the phenological expression of resource production in each flowering

124 plant  $i$ . Further details are provided below in Phenology section. The population dynamics of the animal

125 pollinators are then defined by:

126 
$$\frac{da_j}{dt} = \sum_{i \in P} c_{ij} V_{ij} b_{ij} \left(\frac{R_i}{p_i}\right) - \mu_j^A a_j \quad \text{Eq (7)}$$

127 where  $c_{ij}$ ,  $V_{ij}$ , and  $b_{ij}$  are as defined above. Pollinator population growth is driven by the sum of

128 resources gathered from pollination visits while death occurs at a constant rate  $\mu_j^A$ .

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### 130 *Incorporating phenology into baseline model*

131 Creating temporal plasticity in network connectivity is implemented by modifying the rates

132 controlling interactions between plants and pollinators in the network. In other words, the expression of

133 certain species' rates/behaviors are modified by time dependent functions which activate and deactivate

134 said rates across time. In flowering plant species, this is implemented by modifying the production of

135 floral rewards ( $R_i$ ) that drive pollinator foraging preference ( $\alpha_{ij}$ ) and reproductive benefit for both plants

136 and pollinators. In Eq (6), the rate of floral reward production ( $\beta_i$ ) is regulated across time steps by the

137 phenology function  $T_{p_i}(t)$ , Eq (8). Parameter definitions are given in Table S3.

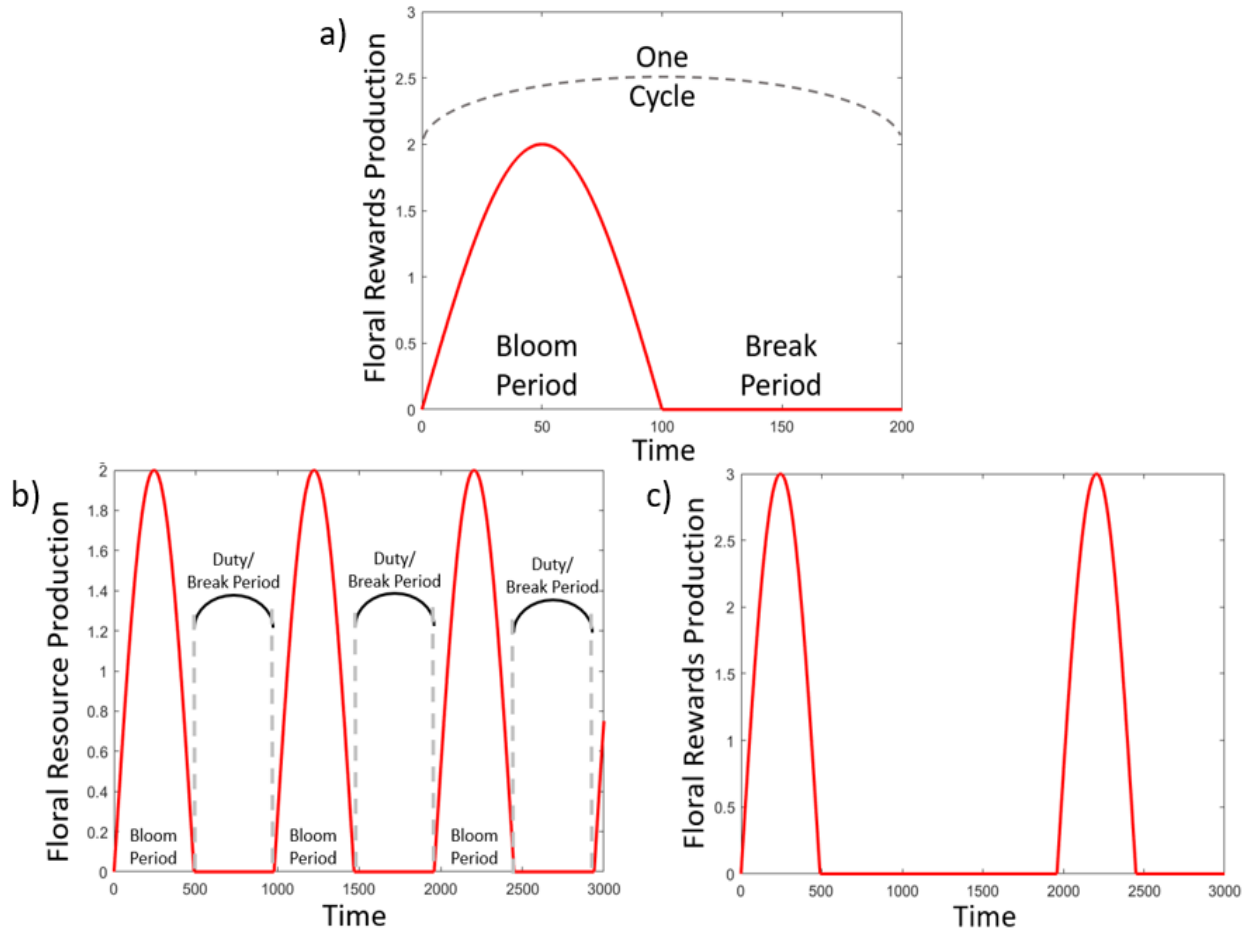
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139 
$$T_{p_i}(t) = \left| f(b_{bv}) * \sin(b_{pt}\pi t - b_{ws}) * \frac{\left(1 + \text{square}\left(\frac{b_{pt}\pi t - b_{ws}}{b_{wa}'}\right)\right)}{2} \right| \quad \text{Eq (8)}$$

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**Table S3:** Phenology parameter definitions for  $T_{p_i}(t)$ 

Phenology Parameter	Description	Definition
Bloom Period ( $b_p$ )	No. of time steps with floral resource production ( $\beta > 0$ )	Defined by user
Bloom Period translated ( $b_{pt}$ )	Transforming $b_p$ into useable form for $T_{p_i}$	$\frac{1}{b_p}$
Bloom break value ( $b_{bv}$ )	No. of cycles between subsequent blooms	Defined by user
Bloom Break Translated ( $b_{bt}$ )	Transforming $b_{bv}$ into useable form for $T_{p_i}$	$\frac{b_{bv}}{2} + 0.5$
( $d$ )	% of maximum separation between $T_{p_i}$	1
Separation distance ( $p_{s_d}$ )	Distance on the timeline between consecutive $T_{p_i}$ , here $N_p$ is the number of plant species	$\frac{\left(\frac{2\pi b_{bv}}{N_p}\right)}{d}$
Wave Shift ( $b_{w_s}$ )	Separation distance assigned to each plant species in sequence.	$\{p_{s_d} * n\}_{n=0}^{N_p-1}$
Wave Augment ( $b_{w_a}$ )	Augment to save shift in the square wave	$b_{bv} + 1$
$f(b_{bv})$	Function mitigating lost resources with higher break value by increasing floral reward production	$b_{bv} + 2$

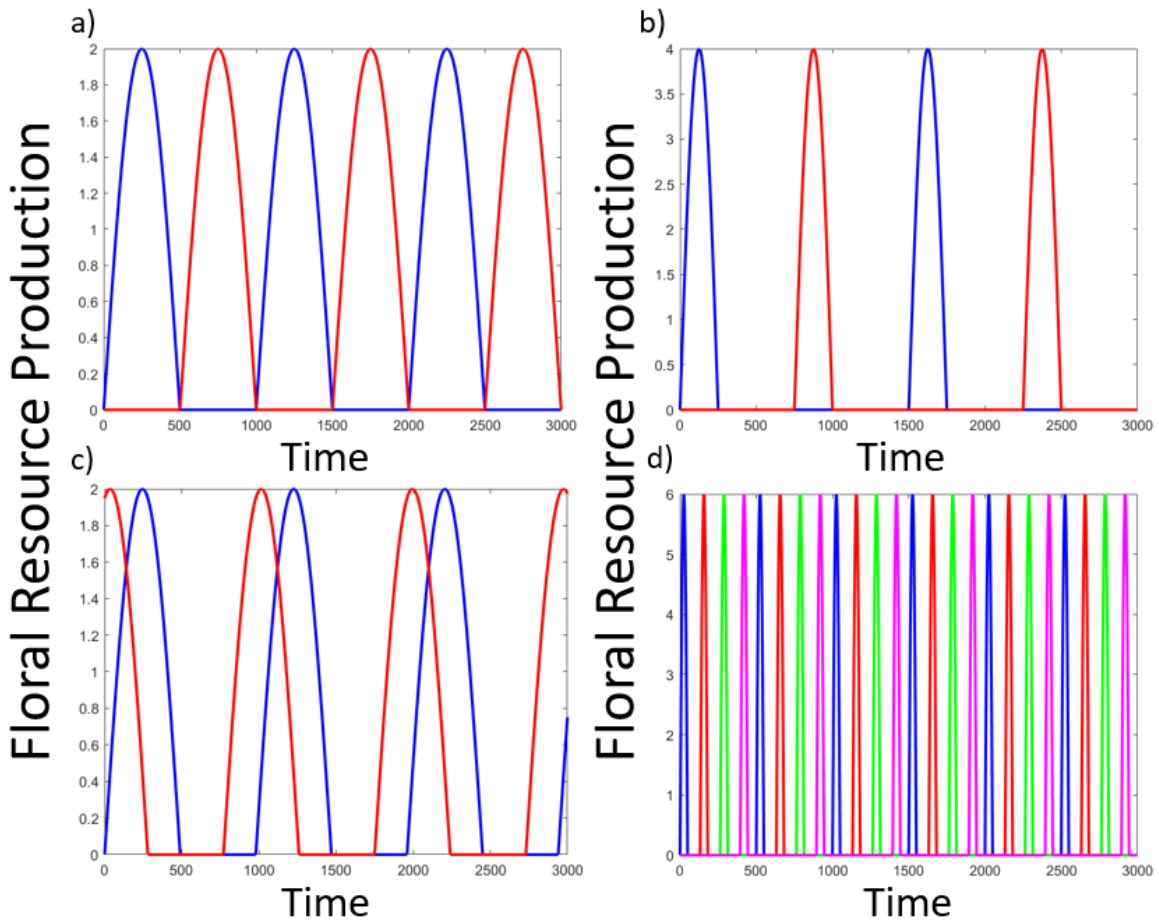


144 **Figure S2: Example  $T_{p_i}$  figures.** A) Detail of the components of each  $T_{p_i}$ . B) Example of  $T_{p_i}$  run across  
 145 time. Bloom Period = 490, Break Period = 0. C) Example of  $T_{p_i}$  run across time. Bloom Period = 490,  
 146 Break Period = 1.  
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149 The form of  $T_{p_i}(t)$  is a composite of sine and square waves which produce a continuous bounded  
 150 function (always  $\geq 0$ ), with both active and inactive periods in one "cycle," the bloom period and break  
 151 period respectively. Bloom and break periods are controlled through the two parameters "bloom period"  
 152 and "bloom break value" respectively (Fig S2a). The bloom period corresponds to the number of time  
 153 steps that a plant will produce floral rewards from start to finish. Floral resource production follows a  
 154 sinusoidal growth and decay during the bloom period, with peak production occurring during the middle  
 155 of the bloom period (Fig S2a). Each bloom period is accompanied by a corresponding break period or  
 156 "off period" where the value of  $T_{p_i} = 0$ . This is similar to the "duty" of a traditional square wave  
 157 function. This break period is of equal length to the bloom period such that there is an even split between



158 active and inactive parts of a single cycle when the break value is 0. In this default formulation,  $T_{p_i}$  will  
 159 cycle through active and inactive periods (Fig S2b), thereby modifying the production of floral rewards.  
 160 When break value  $> 0$ , then  $T_{p_i}$  will skip the number of cycles assigned to the break value before the  
 161 ensuing bloom period (Fig S2c). For the purpose of parity in comparing across different bloom periods,  
 162 the length of a cycle's break period scales with its bloom period. This facilitates normalizing available  
 163 resource quantities between bloom period.



164 **Figure S3: Examples of multiple  $T_{p_i}$ .** a) An example of two plant species'  $T_{p_i}$  functions with bloom  
 165 period of 500 and break values of 0. b) An example of two plant species'  $T_{p_i}$  functions with bloom  
 166 periods of 250 and break values of 2. c) An example of two overlapping plant species'  $T_{p_i}$  functions with  
 167 bloom periods of 500 and break values of 0. d) Example of multiple  $T_{p_i}$  for  $i \in (1,4)$  with bloom periods  
 168 of 125 and break value of 4.  
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171 Every  $p_i$  is assigned its own  $T_{p_i}(t)$  and their separation along the time of a simulation is put at a  
 172 maximum (Fig S3a) in simulations, depending upon the break value (Fig S3b). Though the model does

173 allow for more direct overlap (Fig S3c). This all then scales with the number of plant species,  $p_i$ , in the  
174 system (Fig S3d).

175 Phenology in bee species,  $T_{a_i}$ , is formulated similarly across visits ( $V_{ij}$ ) in Eq (4) and  $G_j$ , the  
176 basal adaptation rate of foraging preference ( $\alpha_{ij}$ ), in Eq (5). Both visitation and adaptation are modified  
177 by  $T_{a_i}$  because foraging preference should not change when there is no active foraging. The formulation  
178 of  $T_{a_i}$  is given in Eq (9) and its parameter definitions are given in Table S4. Similar to  $T_{p_i}(t)$ , overall  
179 control of the specific form of  $T_{a_i}$  is governed by two parameters, “flight period” and “flight break value.”  
180 The general form of  $T_{p_i}(t)$  and  $T_{a_i}(t)$  was chosen heuristically based on its ability to interface with the  
181 baseline model and the ability to maintain sufficient control over the specific form of the function with  
182 only two parameters. This makes it both readily applicable from a research stand point and relatively user  
183 friendly for other interested researchers.

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$$185 \quad T_{a_i}(t) = \left| f(f_{bv}) * \sin(f_{pt}\pi t - f_{ws}) * \frac{\left(1 + \text{square}\left(\frac{f_{pt}\pi t - f_{ws}}{2f_{bt}} - \frac{f_{ws}}{f_{wa}f_{bt}}\right)\right)}{2} \right| \quad \text{Eq (9)}$$

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**Table S4:** Phenology parameter definitions for  $T_{a_i}(t)$ 

Phenology Parameter	Description	Definition
Flight Period ( $f_p$ )	No. of time steps with active flight ( $V > 0$ & $G_j > 0$ )	Defined by user
Flight Period translated ( $f_{pt}$ )	Transforming $f_p$ into useable form for $T_{a_i}$	$\frac{1}{f_p}$
Flight break value ( $f_{bv}$ )	No. of cycles between subsequent flights	Defined by user
Flight Break Translated ( $b_{bt}$ )	Transforming $f_{bv}$ into useable form for $T_{a_i}$	$\frac{f_{bv}}{2} + 0.5$
( $d$ )	% of maximum separation between $T_{a_i}$	1
Separation distance for animal phenology ( $a_{sd}$ )	Distance on the timeline between consecutive $T_{a_i}$ , here $N_a$ is the number of animal pollinator species	$\frac{\left(\frac{2\pi f_{bv}}{N_a}\right)}{d}$
Wave Shift ( $f_{ws}$ )	Separation distance assigned to each animal species in sequence.	$\{a_{sd} * n\}_{n=0}^{N_a-1}$
Wave Augment ( $f_{wa}$ )	Augment to save shift in the square wave	$f_{bv} + 1$
$f(f_{bv})$	Function mitigating lost flight time with higher break value by increasing peak flight activity	$f_{bv} + 2$

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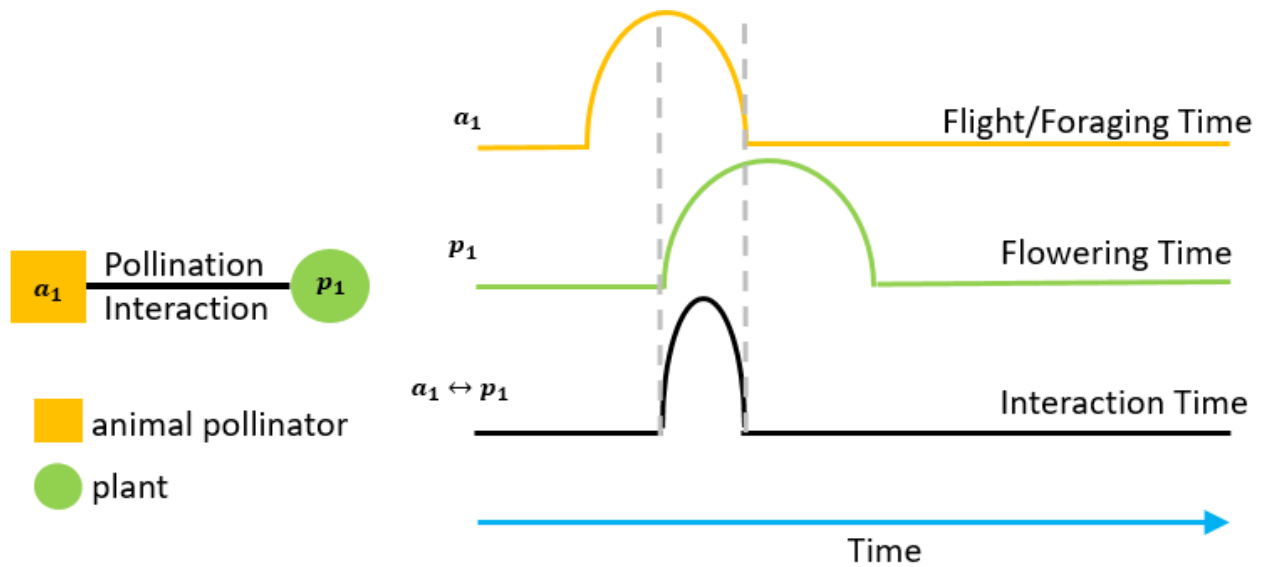
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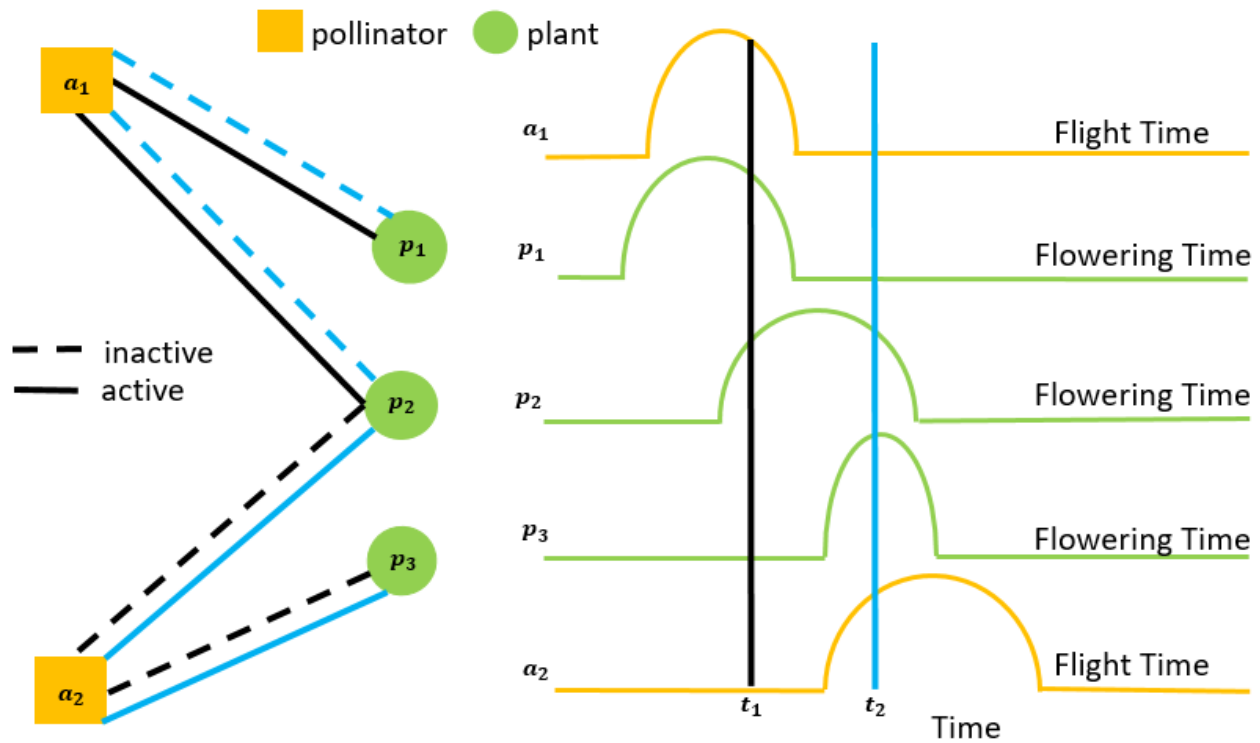
With both plant and animal phenology integrated into the model, the temporal plasticity of pollination interactions and network topology can be realized. When a pollinator  $j$ 's flight/foraging time overlaps with a plant  $i$ 's flowering time, the pollination interaction is potentially active (depending on foraging preference  $\alpha_{ij}$ ) and counted as a "link" in the network for the duration of the overlap (Fig S4). Otherwise, the link is inactive and interactions between the plant and pollinator do not occur.



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 217 **Figure S4: Phenology controlled interaction.** Diagram of an example pollination interaction in time due  
 218 to phenology of pollinator and plant. Note, while only one active period is shown for the pollinator and  
 219 plant, this is only for readability in the diagram. In model simulations, all phenology functions cycle as  
 220 shown in Fig S2&S3.  
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222 This framework scales up to multiple interactions and ultimately the network level as network  
 223 topology changes dynamically as potential interactions activate and deactivate in the network across time.  
 224 A diagram of this is provided in a small example plant-pollinator network is provided in Fig S5. Given  
 225 foraging preference ( $\alpha$ ), even a potentially active interaction may not be particularly active, but only  
 226 during phenological overlap can the interaction potentially occur.

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 229 **Figure S5: Diagram of example network with phenology.** Example diagram of interacting phenologies  
 230 changing the active topology of a small example network. At different times, as indicated by the black  
 231 ( $t_1$ ) and blue bars ( $t_2$ ), different links in the network are active. This scales up to the networks used in  
 232 simulations and analysis here. Note, while only one active period is shown for each pollinator and plant,  
 233 this is only for readability in the diagram. In model simulations, all phenology functions cycle as shown  
 234 in Fig S2&S3.  
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236 *Experimental simulation design*

237 Without phenology induced oscillations, baseline model simulations generally achieve reach  
 238 asymptotic dynamic behavior in approximately 3000 time steps. In order to ensure that transient dynamics  
 239 minimally affect measured model output, models here were run for 6000 time steps to reach asymptotic  
 240 dynamics. No burn in period without phenology is used in simulations as that would produce preceding  
 241 bias to foraging preference before phenology functions are activated. All plant and pollinator species  
 242 experience their phenological changes in rates from the beginning of simulations.

243 Baseline parameters for plants (non-phenological), including competition coefficients, floral  
 244 reward productivity, reward self-limitation, and mortality differ among plant species by assigning unique  
 245 values stochastically varied within 0.1% of a mean value (Table S2). Competitive coefficients of plants  
 246 are kept low ( $e^{-3}$ ) in order to reduce effects on pollinator diet breadth through abundance loss and

247 potential species loss in plants (Table S1). Our simulations intentionally produced no extinctions in plants  
248 or animals. Baseline parameters for animal pollinators (non-phenological, Table S2), including extraction  
249 efficiency, conversion efficiency, and mortality differ among pollinator species by assigning unique  
250 values stochastically varied within 0.5% of a mean value (Table S2). Similar to using fully connected  
251 networks, limiting variability in baseline parameter values across species and pollination interactions  
252 within single simulations allows us to focus analysis on the effect of phenology and temporal resource  
253 overlap on specialization. Distinct differences in productivity between plants or efficiencies in pollinators  
254 through more varied parameter values would bias foraging preferences towards certain interactions more  
255 than others. For example, a highly productive plant or a pollinator with uniquely high fundamental  
256 efficiency towards one plant species over others would drive specialization by assumption alone. Keeping  
257 parameter values closely centered around the mean for all possible interactions limits this bias while still  
258 allowing for moderate distinction in pollinator and plant traits. Our parameter set up best allows us to test  
259 the ability of phenological mechanisms to drive plasticity in pollinator specialization without a priori  
260 constraints on pollinator behavior though underlying baseline model parameters.

261 Baseline model sensitivity analysis has been thoroughly investigated by past studies<sup>9,10,31</sup> allowing  
262 us to focus analysis on effects of phenology. Parameter sweeps across phenological parameters were done  
263 with 37 combinations of bloom period and bloom break values for plant species. This created a  
264 distribution of temporal overlap in floral resources across plant species (see Metrics) that was then tested  
265 on bee phenologies composed of 56 combinations of flight period and flight break value. Each simulation  
266 of the 2072 possible combinations of the plant and animal phenologies was replicated 10 times using  
267 varied baseline (non-phenological) parameters (see paragraph above). While baseline model parameters  
268 vary across both plant and pollinator species within single simulations, all flowering and flight phenology  
269 parameters are shared across all plant and pollinator species respectively. This allows us to test the  
270 phenological mechanism against numerous baseline parameters per pollination interaction per simulation.  
271 Across all 2072 unique phenology parameter combinations simulated in each of our 3 network

272 frameworks, each replicated 10 times, we simulated 62160 plant-pollinator networks representing over 22  
273 million distinct pollination interactions.

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275 *Choice of model bee genera & regions for empirical study*

276 *Andrena* (Hymenoptera: Andrenidae) and *Lasioglossum* (Hymenoptera: Halictidae) were selected  
277 as two contrasting model bee genera for this analysis. These two genera are the largest bee genera in the  
278 world<sup>33</sup>, and both are well represented in Northern Hemisphere bee communities. *Andrena* contains  
279 around 1,500 species<sup>34</sup> and is distributed principally across the Holarctic with only a small number of  
280 species extending south to the Neotropics, sub-Saharan Africa and south-east Asia. *Lasioglossum* is a  
281 larger genus, containing nearly 1,800 species<sup>35</sup>, and has a more cosmopolitan distribution being found in  
282 every continent except for Antarctica. The use of these large, widely distributed genera allows for  
283 comparisons across different biogeographical regions within two distinct bee lineages, each with a shared  
284 evolutionary history amongst its constituent species.

285 *Andrena* and *Lasioglossum* have notably different life history strategies. *Andrena* are  
286 protandrous, with males emerging in advance of the females but at the same time of the year. Females  
287 mate and then build nests and collect pollen and provision their offspring before dying. The pollen  
288 foraging period is short, typically lasting only a few weeks<sup>36,37</sup>. In contrast, already mated *Lasioglossum*  
289 females emerge in the spring and found nests. They collect pollen and rear offspring that often emerge  
290 and overlap with their activity period. Some species are eusocial, and will produce a brood of workers  
291 before producing reproductives<sup>38</sup>. *Lasioglossum* species display a range of social behaviors from solitary  
292 to eusocial<sup>39-41</sup>, sometimes even within the same species across different parts of its range<sup>42</sup>. However,  
293 importantly, both social and solitary species of *Lasioglossum* have longer foraging periods than *Andrena*,  
294 typically spanning several months<sup>36,37,42</sup>. *Andrena* can consequently be considered a genus comprised of  
295 species with a ‘short’ foraging period, and *Lasioglossum* can be considered a genus of species with a  
296 ‘long’ foraging period, relative to one another (see also *Selection and Standardization of pollen load*  
297 *data*).

298 Both genera are found within the major clade of short-tongued bees within Apoidea<sup>35</sup>. Though  
299 many species of short-tongued bees from across this clade have independently evolved elongate  
300 proboscides to access nectar<sup>43</sup>, morphological adaptations in *Andrena* or *Lasioglossum* bees for harvesting  
301 pollen are almost unknown. *Andrena* (*Scoliandrena*) and *Andrena* (*Hamandrena*) possess hooked hairs on  
302 the galea to pull pollen from the anthers of *Cryptantha* (Boraginaceae) and *Anchusa* (Boraginaceae)  
303 respectively, but these members of these subgenera are restricted to Western North America<sup>44</sup> and  
304 southern and eastern Europe<sup>34,45</sup> outside of our selected study regions of Britain and Michigan. In  
305 *Lasioglossum*, members of the subgenus *Sphecodogastra* s.s. are specialists on Onagraceae, and possess a  
306 scopa comprised of unbranched and sparse hairs and bristles rather than the typical scopa of branched or  
307 dense hairs<sup>39</sup>. These species are restricted to North America<sup>39</sup>. Although some species of *Andrena* and  
308 *Lasioglossum* preferentially forage from more morphologically complex flowers (e.g. Fabaceae, *Andrena*  
309 *wilkella* and *Lasioglossum lativentre*, ref 36), both genera as a whole favor shallow, open, and radially  
310 symmetrical flowers<sup>36,43,46</sup>.

311 Plant species can have pollen that is difficult to digest by non-specialized bees<sup>47</sup>, leading to  
312 patterns of specialization or avoidance<sup>48</sup>. Some plant species protect pollen physically by hiding it in deep  
313 tubes (Boraginaceae), or in poricidal anthers (Ericaceae, Solanaceae), or nototribic anthers (Lamiaceae)  
314 that deposit pollen on the bodies of bees<sup>49</sup>. There is therefore considerable variation in the rewards offered  
315 by different plant species. Conducting the analysis in Britain and Michigan, both of which are found in  
316 the Holarctic biogeographic region, means that whilst the constituent species of the respective floras  
317 differ, the botanical families present are very similar<sup>50,51</sup> and therefore likely to present rewards of a  
318 similar composition and availability. Furthermore, the two regions provide suitable extremes in their  
319 temporal resource overlap, making them ideal for addressing our hypothesis. The highly seasonal  
320 continental climate of Michigan<sup>20</sup> produces lower degrees of overlap and highly seasonal flowering  
321 communities, while the more mild oceanic climate of the British Isles<sup>20</sup> and its consistent temperatures  
322 produces longer, overlapping flowering times among plant species<sup>21</sup>.



323 Restricting the analysis to the same genera across two regions also controls for possible impacts  
324 of differing travel costs when gathering resources. In broad terms, bee species foraging range is  
325 influenced by body size, with larger species able to travel greater distances to forage<sup>52</sup>. As *Andrena* and  
326 *Lasioglossum* communities contain species of the same size across both regions, potentially interacting  
327 effects of travel costs are minimized.

328 The use of both *Andrena* and *Lasioglossum* within two Holarctic regions therefore controls as  
329 much as possible for the possible effects of phylogenetic structuring that may affect the cost of travel,  
330 constraints of morphology, and unequal rewards between plant families. By comparing within and  
331 between these genera across the two regions of Britain and Michigan, the relative importance of foraging  
332 period and environmental seasonality in structuring a generalized foraging response in wild bees can be  
333 determined.

334

#### 335 *Selection and standardization of pollen load data*

336 *Andrena* are characterized as short-season bees, collecting pollen over only a period of a few  
337 weeks. However, some species of *Andrena* express bivoltine behavior, having two reproductive  
338 generations in a single year. Although not unknown<sup>53</sup>, bivoltinism is extremely rare in Nearctic *Andrena*  
339 and is not displayed by any of *Andrena* species in Michigan<sup>54</sup>. In contrast, bivoltinism is displayed by 13  
340 (13/60, 22%) of extant British *Andrena* species and nine (9/29, 31%) of species included in our British  
341 dataset<sup>37</sup>. In order to prevent bivoltinism affecting our categorization of *Andrena* as bees with a short  
342 pollen foraging period, British *Andrena* with multiple generations were analyzed with each generation  
343 considered a separate species.

344 Data on British *Andrena* and *Lasioglossum* pollen collection come from the datasets compiled in  
345 Wood *et al.*<sup>55</sup> and Wood and Roberts<sup>56</sup>. Data on Michigan *Andrena* come from Wood and Roberts<sup>46</sup>.  
346 These were combined with new data on Michigan *Lasioglossum*, and additional new pollen load data for  
347 British *Lasioglossum*. Pollen was removed from these specimens and identified using light microscopy  
348 following the same method across all specimens following the methodology of Wood and Roberts<sup>46</sup>. The

349 size of pollen loads on individual bees was estimated, ranging from a full load to a one-eighth load. Pollen  
350 grains were removed from the scopa using an entomological pin and transferred to a drop of water on a  
351 microscope slide. Grains were left to absorb water for a few minutes and then the slides were gently  
352 heated to allow evaporation. Molten glycerine jelly stained with fuchsin was added, and the slide was  
353 sealed with a coverslip. Following Müller and Kuhlmann<sup>48</sup>, the percentage of the load composed of  
354 different plant species was estimated along three randomly selected lines across the cover slip at a  
355 magnification of  $\times 400$ . The percentage of the load was estimated by the relative area of the slide occupied  
356 by each plant species, rather than the absolute number of grains<sup>57</sup>. Pollen species representing  $< 2\%$  of the  
357 load were excluded from further analysis because their presence might have arisen from contamination.  
358 The percentages of pollen collected were corrected according to the overall size of each load to give a  
359 final weighting. Pollen loads were identified to the lowest taxonomic level possible using a reference  
360 collection assembled during the project, in most cases to genus.

361         Though pollen was identified to genus, the analyses were conducted at the botanical family level.  
362 Specialist bees, or oligoleges, collect all their pollen from a single botanical family<sup>48</sup>, and this is the level  
363 at which most dietary specialization occurs in bees<sup>8</sup>. A minimum sample size of five pollen loads per  
364 species was selected as the cut-off for inclusion in this study in order to maximize the number of species  
365 included in the analysis. This sample size restriction meant that the first generation data for four British  
366 bivoltine *Andrena* was excluded, resulting in an effective sample size of 34 species in the British *Andrena*  
367 analysis (20 univoltine species, 5 species with data from both the spring and the summer generations, 4  
368 species with data from the summer generation only).

369         All together, these criteria produced a final dataset of 2,561 pollen loads from 120 species,  
370 specifically 671 pollen loads from 51 Michigan *Andrena* species (63% of the *Andrena* fauna, ref 54), 355  
371 pollen loads from 24 Michigan *Lasioglossum* species (30% of the *Lasioglossum* fauna), 815 pollen loads  
372 from 29 British *Andrena* species (49% of the *Andrena* fauna, ref 37), and 731 pollen loads from 16  
373 British *Lasioglossum* species (50% of the *Lasioglossum* fauna).

374 Only one species was shared between the British and Michigan datasets, the Holarctic *Andrena*  
375 *barbilabris*. Because the British *Andrena* dataset compiled by Wood and Roberts<sup>56</sup> focused on polylectic  
376 species (species collecting pollen from multiple plant families), only two of the 29 species are oligoleges  
377 (2/29, 7%), a significantly smaller proportion than the extant British fauna (20/59, 34%, Chi squared,  
378  $\chi^2=7.3$ ,  $p=0.007$ ). Following Wood and Roberts<sup>46</sup>, 10 species of oligolectic *Andrena* were added to this  
379 dataset to bring this proportion in to line with the whole fauna (12/39, 31%,  $\chi^2=0.1$ ,  $p=0.790$ ). Because  
380 these are well-characterized oligolectic bees<sup>36</sup>, no pollen load analysis was conducted for these species.  
381 There were no differences in the proportion of specialists in the *Lasioglossum* datasets and the entire  
382 regional fauna for Michigan ( $\chi^2=0.3$ ,  $p=0.790$ ) or Britain ( $\chi^2=0.0$ ,  $p=1.000$ ). Full details on the overall  
383 *Andrena* and *Lasioglossum* faunas of Britain and Michigan, their dietary status, and species with pollen  
384 load sample sizes included in this study can be found in Tables S6, S7, and S8.

385

### 386 *Metrics*

387 In model simulations, temporal resource overlap between any two plant species is defined as the  
388 shared area under each  $R_i(t)$  curve (Fig S6a). The shared area can be found by:

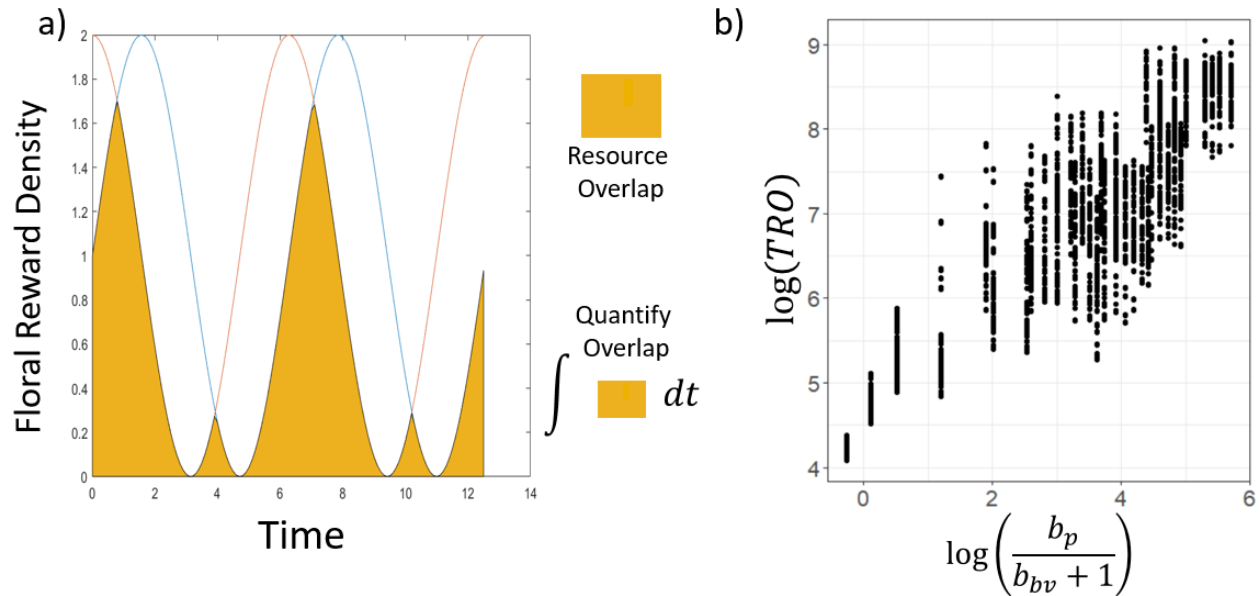
- 389 1. Taking the minimum of any two  $R_1$  and  $R_2$ .
- 390 2. This will give you a new curve,  $\min(R_1, R_2)$ .
- 391 3. The area underneath this new curve  $\min(R_1, R_2)$  is the resource overlap between  $R_1$  and  $R_2$   
392 (shaded region in Fig S6a).
- 393 4. This resource overlap can be quantified by taking the integral of  $\min(R_1, R_2)$ . Integrals were  
394 taken using the trapezoidal method with unit spacing through the trapz function in Matlab.

395

396 Overlap per simulation was quantified as 1) total resource overlap summed across all  $p_i$  (labeled  
397 *TRO*) and 2) average resource overlap experienced by each individual  $p_i$  (labeled *ARO*). Simply counting  
398 overlapping shared time steps where  $R_i > 0$  for two  $R_i$  would be an insufficient metric because it would

399 miss the quantity of resources that overlap in time. Our intuitive metric algorithm accounts for both  
 400 shared time and quantity of overlapping resources. Modifying the bloom period ( $b_p$ ) of plants with  
 401 different bloom break values  $b_{bv}$  provided a suitably even coverage of overlap values, whether measured  
 402 as total overlap (Fig S6b) or average individual plant overlap. The exact overlap of a simulation at any  
 403 given value of  $\log(bs/bbv+1)$  will vary depending on the pollinator community.

404



405 **Figure S6: Details of overlap metrics.** a) Diagram of overlap defined by two  $R_i(t)$  curves. Two example  
 406 plant species rewards production curves across time ( $R_i(t)$ ) are shown in red and blue. Shared area  
 407 under the curve is considered the overlapping resources and is shaded orange. Quantifying this area is done by  
 408 taking the integral of the shared area. b) Example from 58p x 100a web simulations of range in total  
 409 resource overlap ( $TRO$ ) provided by separating bloom period ( $b_p$ ) values by bloom break values ( $b_{bv}$ ).  
 410 The denominator adds 1 to  $b_{bv}$  avoid dividing by 0 when  $b_{bv} = 0$ . Each dot represents overlap per  
 411 simulation at different  $b_p$  and  $b_{bv}$  values. The range in overlap per combination of  $b_p$  and  $b_{bv}$  comes  
 412 from the different phenology metrics tested for the pollinators.

413  
 414  
 415 Defining the confines of a specialist or generalist has been a long-running debate in ecology and  
 416 evolutionary biology, with different sub-fields often using different metrics. For example, phylogenetic  
 417 studies have found strong evidence of herbivorous insects specializing on plants at the family level<sup>13</sup>,  
 418 while in other fields, such as network ecology, specialists and generalists have been defined by the  
 419 number of species interactions through the degree distribution of links in the network<sup>58</sup>. In order to  
 420 consider the range of ideas used in defining specialists and generalists, we have employed multiple

421 metrics to measured specialization that can be applied to both the foraging effort ( $\alpha$ ) based metrics of the  
 422 model and the pollen loads from our empirical data.

423 We label the first metric as “Deviation from Generalism” or DFG. For a single pollinator species,  
 424 DFG is defined as the degree away from completely even foraging efforts or pollen loads across all  
 425 possible resources. Specifically, DFG for a pollinator species  $j$  is defined as the sum of pairwise  
 426 differences of foraging effort across all plant species divided the number of plant species minus 1.  
 427 Parametrically, we can write:

$$428 \quad DFG_{\alpha_j} = \frac{\sum_{i,k \in p} |\alpha_{ij} - \alpha_{kj}|}{N_p - 1} \quad \text{Eq (10)}$$

429 where DFG ranges from [0,1] with a perfect generalist scoring 0 and a complete specialist scoring 1. An  
 430 example is provided in Table S5.

431 **Table S5:** Example foraging preference matrix used to calculate DFG for pollinators from simulations  
 432 (using  $\alpha$ ) or pollen load data. In the case of empirical pollen load data, the percent of pollen load is either  
 433 grouped by plant family or plant genus.  
 434

Pollinators (model)	Effort on Plant 1	Effort on Plant 2	Effort on Plant 3	Effort on Plant 4	DFG
Pollinators (pollen)	Plant 1 Pollen %	Plant 2 Pollen %	Plant 3 Pollen %	Plant 4 Pollen %	DFG
Bee sp. 1	1.0	0	0	0	1
Bee sp. 2	0.5	0.5	0	0	0.667
Bee sp. 3	0.2	0.4	0.2	0.2	0.2
Bee sp. 4	0.25	0.25	0.25	0.25	0

435 In this example, the DFG scores would be calculated as follows:  
 436

$$437 \quad DFG_1 = \frac{|1 - 0| + |1 - 0| + |1 - 0| + |0 - 0| + |0 - 0| + |0 + 0|}{3} = \frac{3}{3} = 1$$

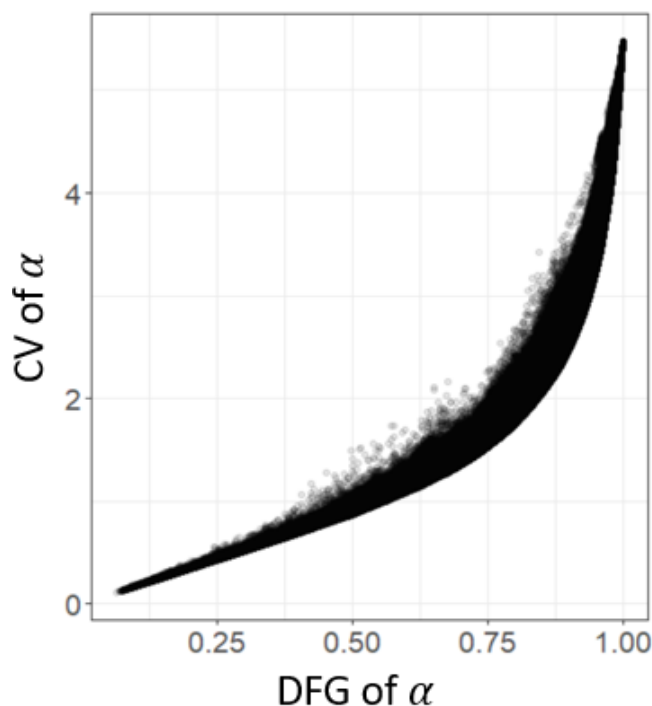
$$438 \quad DFG_2 = \frac{|0.5 - 0.5| + |0.5 - 0| + |0.5 - 0| + |0.5 - 0| + |0.5 - 0| + |0 - 0|}{3} = \frac{2}{3} = 0.667$$

$$439 \quad DFG_3 = \frac{|0.2 - 0.4| + |0.2 - 0.2| + |0.2 - 0.2| + |0.4 - 0.2| + |0.4 - 0.2| + |0.2 - 0.2|}{3} = \frac{0.6}{3} = 0.2$$

$$440 \quad DFG_4 = \frac{|0.25 - 0.25| + |0.25 - 0.25| + |0.25 - 0.25| + |0.25 - 0.25| + |0.25 - 0.25| + |0.25 - 0.25|}{3} = \frac{0}{3} = 0$$

441

442 When the DFG metric is used with pollen load data, the pollen amounts from each plant group in  
443 a bee species' overall pollen load is broken into percentages and substituted for the model's foraging  
444 effort (Table S5), under the assumption that higher pollen loads of any particular plant group generally  
445 correspond to higher foraging effort on that group. The term group is used here because pollen data was  
446 evaluated against both family and genus level plant data. The algorithm used to calculate our DFG score  
447 is a holistic accounting for every possible interaction and compares all possible interactions amongst each  
448 other to accumulate a score. However, it may not be the best option in all circumstances. While not  
449 necessarily requiring a complete accounting of all available resources, DFG's [0,1] range and attempt to  
450 calculate specialization while considering all potential foraging options means DFG functions best when  
451 available data can convincingly represent all possible foraging options. This is not necessarily guaranteed  
452 in empirical surveys.



453 **Figure S7: Comparison of specialization metrics.** Comparison of DFG and CV from all model  
454 simulations in the 2<sup>nd</sup> largest network tested. Each dot represents a measurement from a single pollinator  
455 taken at the end of the simulation which in this case represents 7,061,376 data points.  
456

457 In light of the above, we also employed the coefficient of variance (CV) as our second metric of  
458 specialization. With model simulations, we consider the CV of pollinators'  $\alpha$  values whereas in the  
459

460 empirical data we take CV of the percent of pollen load across plant groups. As a metric of specialization,  
461 the CV will increase as when there are a limited number of extreme values. It performs the same whether  
462 or not the full range of possible resource options for foraging pollinators is known. The relationship  
463 between the two metrics is positive monotonic but non-linear (Fig S7) showing that the two metrics relate  
464 to the measurement of specialization differently as desired.

465 In measuring model output, both DFG and CV metrics are measured in two ways. First each  
466 metric is taken on the  $\alpha$  values at the end of each simulation ( $DFG_{End}$  &  $CV_{End}$  taken at  $t=6000$ ). Second,  
467 each metric is run on the  $\alpha$  values averaged across the last 1000 time steps of each simulation ( $DFG_{Avg}$  &  
468  $CV_{Avg}$ ). This is done to provide multiple points of comparison to our empirical pollen load data. One  
469 could argue that pollen loads taken over multiple years would be better compared to model data taken  
470 across an extended period of time steps. On the other hand, it could also be argued that foraging bees  
471 collected for data are exhibiting an innate search pattern that is the end result of generations of evolved  
472 behavior, better compared with the end state of simulations. Either way, the two methods are intuitively  
473 correlated and using either supports our qualitative conclusions.

474 In measuring empirical pollen load data, we measured DFG and CV of bee species by grouping  
475 plants by either family level or genus level. Network studies in pollination ecology, including our model,  
476 tend to group plants at the species level. While, identifying pollen to species level is prohibitively  
477 difficult, genus level identifications allow for a closer approximation. However, studies focused on  
478 specialization in herbivores (particularly insects) have centered around grouping plants at the family  
479 level<sup>13,48,57</sup>. Given the range, we decided to use both taxonomic levels and found that results were  
480 qualitatively similar regardless of grouping.

481

#### 482 *Statistics*

483 Statistical analysis was done using R version 3.3.2<sup>59</sup>. Differences in CV and DFG scores between  
484 bee genera and geographic regions were tested using Kruskal-Wallis one-way analysis of variance tests.

485 Because both the CV and DFG scores were calculated from deeply non-normal underlying data  
486 (necessarily so since patterns of diet breadth are decidedly non-normal at the botanical family level,  
487 Forister *et al.* ref 13), it was not possible to transform them sufficiently to allow for parametric statistical  
488 assessment. Regression analysis on model diet breadth results was done using the `lm` function and  
489 measured with traditional  $R^2$  metric when working with  $DFG_{End}$  results or with beta regressions (betareg  
490 package in R) and the pseudo  $R^2$  metric when working with  $DFG_{Avg}$ . When measuring diet breadth  
491 results with  $CV_{End}$  or  $CV_{Avg}$ , log-linked gamma regressions were completed with the `mgcv` package and  
492 measured with the for the amount of deviance accounted for by the regression model with the  $D^2$  metric<sup>60</sup>.

493

#### 494 *Code availability & simulation information*

495 Simulation code, metric code, and simulation data are available at the repository

496 <https://github.com/fsvaldovinos/Phenology>.

497

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- 572

573 **Supplementary Discussion**

574           When considering the factors that drive specialization in insect herbivores, it is impossible not to  
575 consider the role of plant chemistry. Phytochemical diversity, the diversity of plant compounds including  
576 anti-herbivory defense compounds, has been strongly associated with both insect herbivore diversity and  
577 dietary specialization<sup>19,22,23</sup>. For many insect herbivores, their diversity is much greater in tropical  
578 environments. This is particularly well studied in Lepidoptera where both their species richness and  
579 degree of specialization increases from temperate to tropical regions<sup>22,24</sup>. However, a completely different  
580 pattern is seen in the bees where tropical diversity and specialization is mediocre compared to diversity in  
581 Mediterranean and xeric environments where it is high<sup>8,25,26</sup>. Indeed, tropical environments are dominated  
582 by highly generalized and often social species that visit a huge variety of botanical families (e.g. ref 27,  
583 28, 61).

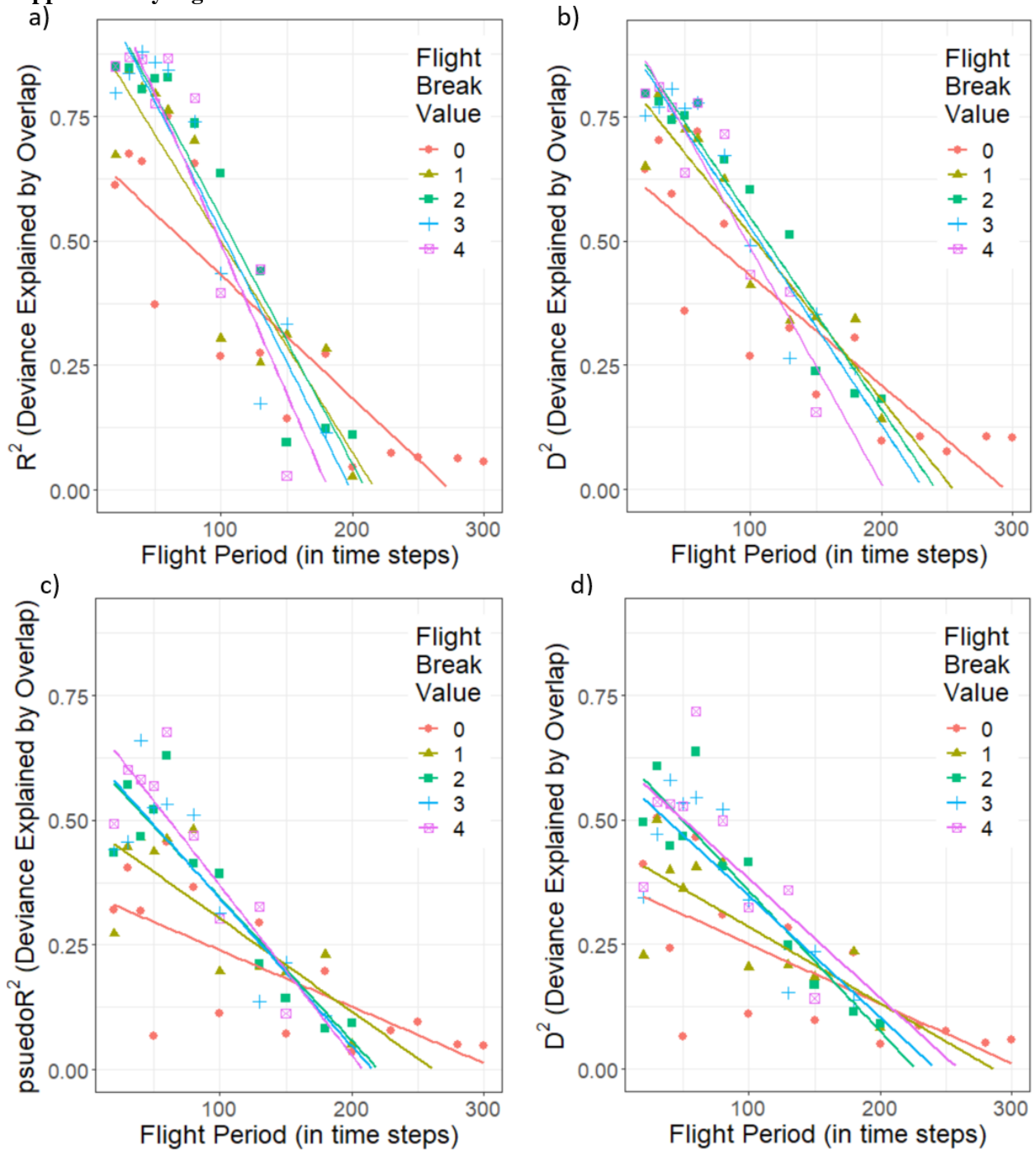
584           Though the theoretical impact of variable quality between different resources is clear<sup>7,8</sup>, bees have  
585 an ecology that fundamentally differs from most insect herbivores. They are nest makers, and they collect  
586 pollen as adults before feeding it to their offspring. Therefore, even though their larvae are immobile, they  
587 are effectively mobile because they have the potential to feed on pollen collected from many botanical  
588 families in a way that most larvae which must feed themselves are not, due to their limited mobility  
589 during this stage of their development. In this regard bee larvae are functionally closer to those insects  
590 that are herbivorous during their adult stages such as Chrysomelid beetles<sup>62</sup>, and indeed these groups  
591 show higher levels of generalization<sup>13</sup>.

592           The ability to feed their offspring from multiple combined sources has led to the suggestion that  
593 bees may adaptively pollen mix to negate the harmful properties of a particular pollen type that would be  
594 lethal if consumed as the sole source of larval nutrition<sup>63</sup>. This mixing of different resources is however  
595 ultimately also affected by resource overlap, as it does not matter how much mobility an organism has if  
596 there are still limited different resources available to it during the course of its lifespan. Indeed, pollen  
597 mixing of botanical families identified as having negative pollen properties as a behavior is found in the  
598 *Andrena* of the UK but not those in Michigan<sup>46</sup>. This is not to say that plant chemistry is unimportant for

599 bees, and indeed there are many examples from within this group of plant chemistry driving and indeed  
600 restricting host plant choice<sup>47,64</sup>. Instead, we argue that the fundamental difference in the life stage at  
601 which herbivory occurs means that for bees, inherent resource quality is relatively less important than  
602 resource availability, as defined by the balance between their inherent flight period and local flowering  
603 patterns. Clearly, despite existing in the same extremely phytochemically diverse landscapes, tropical  
604 bees have not evolved anything approaching the same high degree of dietary specialization as seen in the  
605 tropical Lepidoptera.

606         This weaker relationship in dietary specialization in bees compared to other insect herbivores is  
607 illustrated by directly comparing the overall pattern of specialization at the botanical family level. Species  
608 in Michigan adhere more closely to a power law relationship, see Supplementary Figure S11a,c, similar to  
609 Forister et al<sup>13</sup>, but the pattern is much looser and closer to a zero-inflated Poisson distribution  
610 (Supplementary Figure S11b, d). Constraining the number of dietary choices available to a mobile species  
611 within its lifespan by reducing flowering overlap is directly analogous to reducing its mobility. Even if it  
612 can fly, if there is only one flowering plant available then it is functionally the same as being an egg laid  
613 on a plant; their choices are limited. We would therefore expect that phytochemical diversity and other  
614 factors that influence resource quality would show the greatest impact on bee diets in environments where  
615 their choices are limited by flowering patterns. More studies on patterns of pollen collection in bees from  
616 a wider variety of global environments are needed, but it would seem that the biggest driver of the  
617 divergent patterns of herbivory seen in bees is their highly mobile period of pollen foraging as adults.

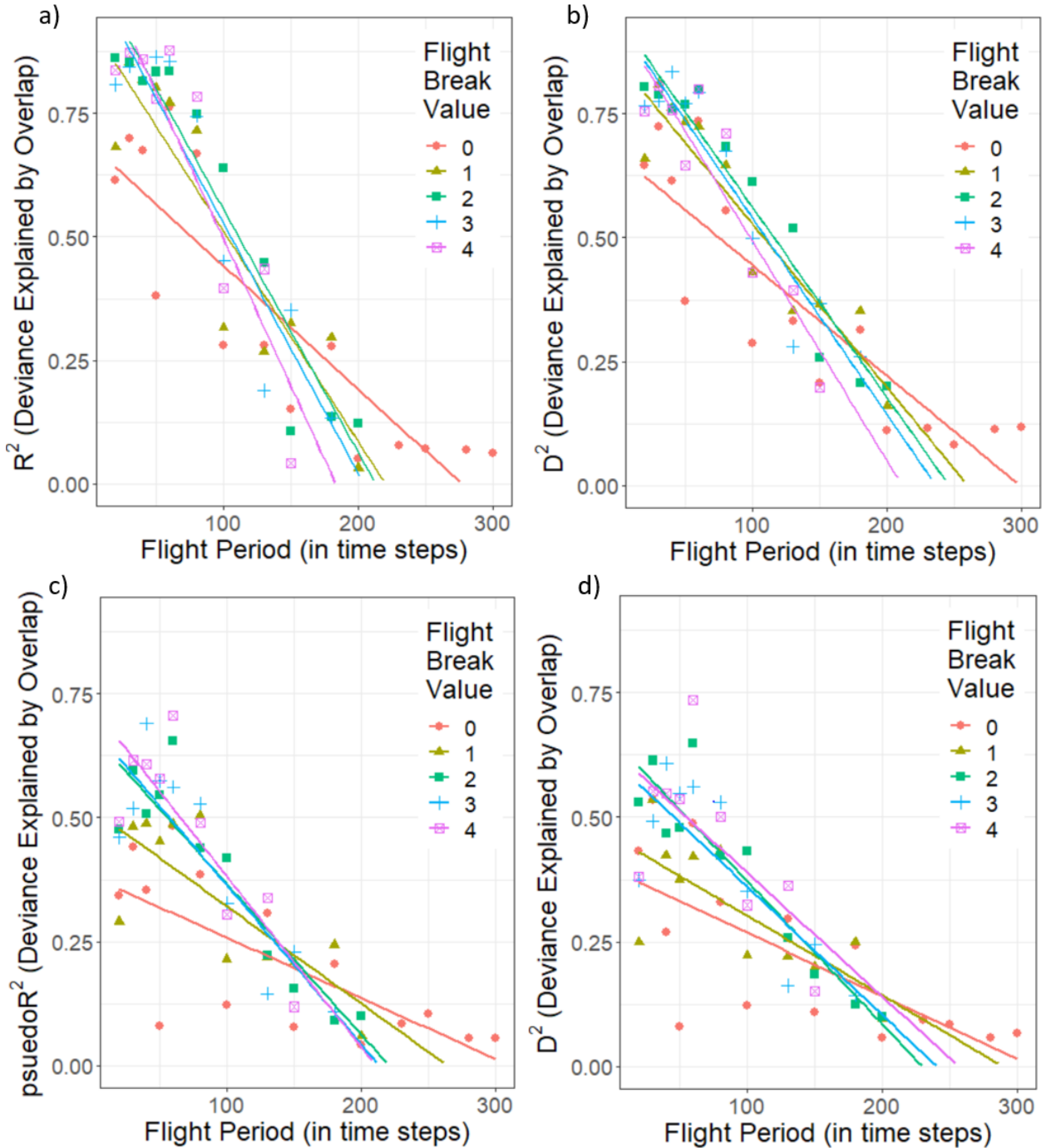
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632 **Figure S8: Results summary in  $N_p = 30$  plants &  $N_a = 50$  framework.** Diet breadth deviance  
 633 explained by average resource overlap ( $ARO$ ) across flight periods ( $f_p$ ) and flight break values ( $f_{bv}$ ). a)  
 634 The  $R^2$  values of diet breadth measured through  $DFG_{End}$  regressed against  $ARO$  in linear models across  
 635 different flight period ( $f_p$ ) and flight break values ( $f_{bv}$ ). Regression lines plotted for visual aid. b) The  $D^2$   
 636 values of diet breadth measured through  $CV_{End}$  regressed against  $ARO$  in generalized linear models  
 637 (Gamma distribution w/ log link) across different flight period ( $f_p$ ) and flight break vales ( $f_{bv}$ ).  
 638 Regression lines plotted for visual aid. c) The pseudo  $R^2$  values of diet breadth measured through  
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640  $DFG_{Avg}$  regressed against  $ARO$  in beta regression models across different flight period ( $f_p$ ) and flight  
641 break values ( $f_{bv}$ ). Regression lines plotted for visual aid. b) The  $D^2$  values of diet breadth measured  
642 through  $CV_{Avg}$  regressed against  $ARO$  in generalized linear models (Gamma distribution w/ log link)  
643 across different flight period ( $f_p$ ) and flight break vales ( $f_{bv}$ ). Regression lines plotted for visual aid.  
644 Overall, regardless of  $f_{bv}$ , there is a decrease in the effect of temporal resource overlap on diet breadth as  
645 the  $f_s$  of pollinators increases. Data taken from network framework w/  $N_p = 30$  plants &  $N_a = 50$ .

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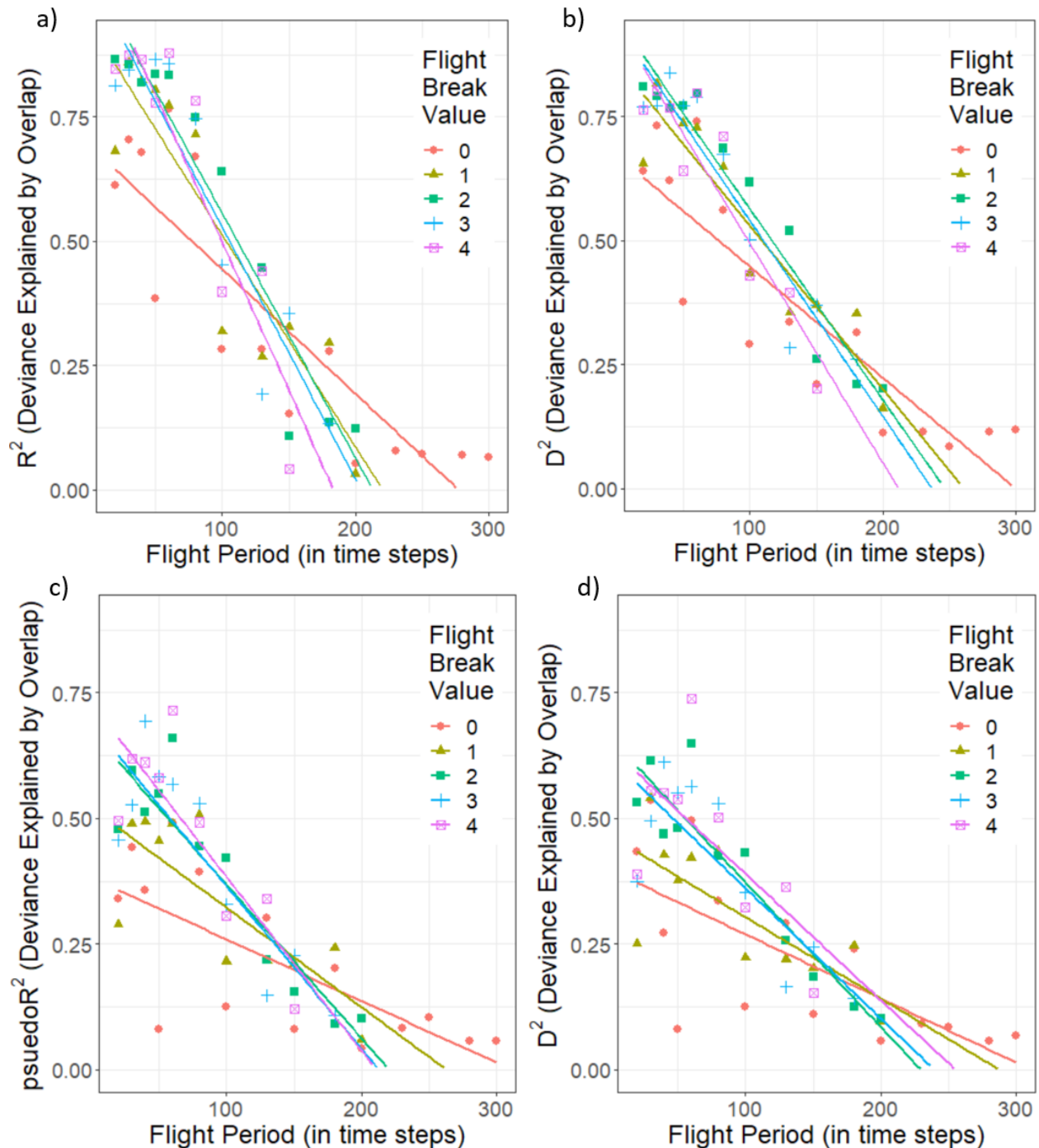
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**Figure S9: Results summary in  $N_p = 48$  plants &  $N_a = 71$  framework.** Diet breadth deviance explained by average resource overlap ( $ARO$ ) across flight periods ( $f_p$ ) and flight break values ( $f_{bv}$ ). a) The  $R^2$  values of diet breadth measured through  $DFG_{End}$  regressed against  $ARO$  in linear models across different flight period ( $f_p$ ) and flight break values ( $f_{bv}$ ). Regression lines plotted for visual aid. b) The  $D^2$  values of diet breadth measured through  $CV_{End}$  regressed against  $ARO$  in generalized linear models (Gamma distribution w/ log link) across different flight period ( $f_p$ ) and flight break values ( $f_{bv}$ ). Regression lines plotted for visual aid. c) The pseudo  $R^2$  values of diet breadth measured through

681  $DFG_{Avg}$  regressed against  $ARO$  in beta regression models across different flight period ( $f_p$ ) and flight  
682 break values ( $f_{bv}$ ). Regression lines plotted for visual aid. b) The  $D^2$  values of diet breadth measured  
683 through  $CV_{Avg}$  regressed against  $ARO$  in generalized linear models (Gamma distribution w/ log link)  
684 across different flight period ( $f_p$ ) and flight break vales ( $f_{bv}$ ). Regression lines plotted for visual aid.  
685 Overall, regardless of  $f_{bv}$ , there is a decrease in the effect of temporal resource overlap on diet breadth as  
686 the  $f_s$  of pollinators increases. Data taken from network framework w/  $N_p = 48$  plants &  $N_a = 71$ .

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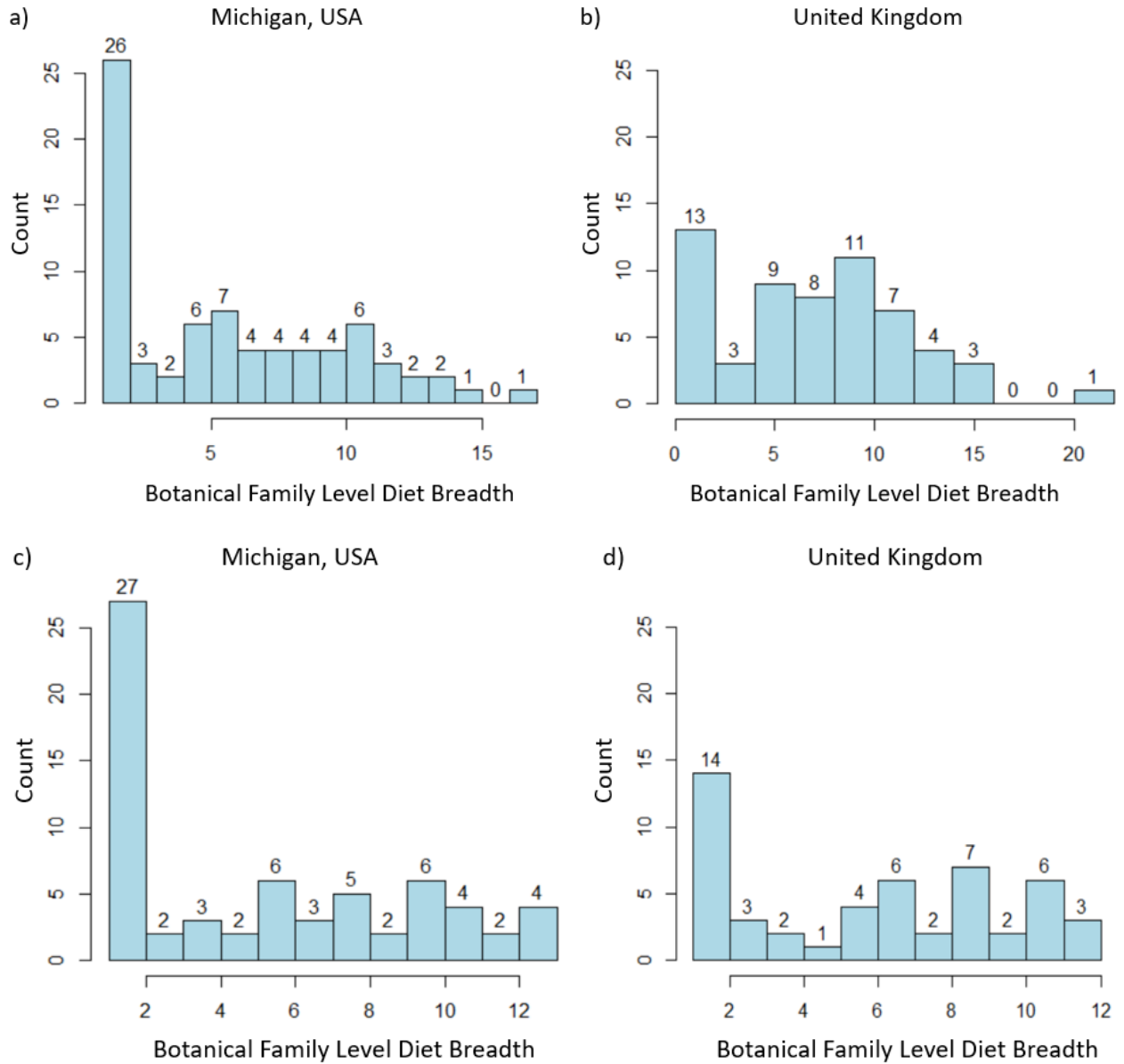
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**Figure S10: Results summary in  $N_p = 58$  plants &  $N_a = 100$  framework.** Diet breadth deviance explained by average resource overlap ( $ARO$ ) across flight periods ( $f_p$ ) and flight break values ( $f_{bv}$ ). a) The  $R^2$  values of diet breadth measured through  $DFG_{End}$  regressed against  $ARO$  in linear models across different flight period ( $f_p$ ) and flight break values ( $f_{bv}$ ). Regression lines plotted for visual aid. b) The  $D^2$  values of diet breadth measured through  $CV_{End}$  regressed against  $ARO$  in generalized linear models (Gamma distribution w/ log link) across different flight period ( $f_p$ ) and flight break values ( $f_{bv}$ ). Regression lines plotted for visual aid. c) The pseudo  $R^2$  values of diet breadth measured through  $DFG_{Avg}$  regressed against  $ARO$  in beta regression models across different flight period ( $f_p$ ) and flight

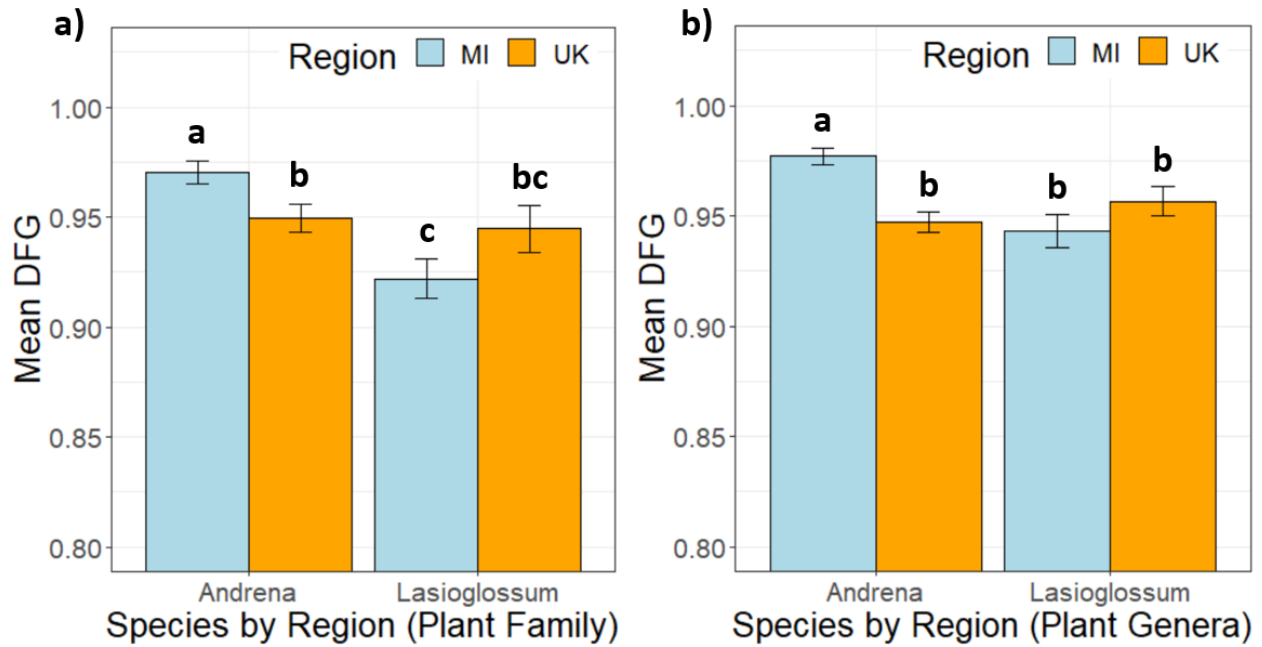


721 break values ( $f_{bv}$ ). Regression lines plotted for visual aid. b) The  $D^2$  values of diet breadth measured  
 722 through  $CV_{Avg}$  regressed against  $ARO$  in generalized linear models (Gamma distribution w/ log link)  
 723 across different flight period ( $f_p$ ) and flight break vales ( $f_{bv}$ ). Regression lines plotted for visual aid.  
 724 Overall, regardless of  $f_{bv}$ , there is a decrease in the effect of temporal resource overlap on diet breadth as  
 725 the  $f_s$  of pollinators increases. Data taken from network framework w/  $N_p = 58$  plants &  $N_a = 100$ .  
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 731 **Figure S11: Diet breadth distributions.** Botanical family level diet breadth for studied bee species  
 732 following the format of Forister *et al*<sup>13</sup>. Data are from a) raw Michigan, USA data, b) raw United  
 733 Kingdom data, c) rarefied Michigan, USA data, d) rarefied United Kingdom data. Data rarefaction  
 734 followed Wood and Roberts<sup>56</sup>, and samples were rarefied to the minimum sample size of 10 pollen loads.  
 735 Bivoltine *Andrena* generations were treated as separate species. This resulted in a dataset of 2,524 pollen  
 736 loads from 113 species (functionally 116 species).  
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**Figure S12: Specialization across regions using Departure from Generalism (DFG).** Difference in dietary specialization of *Andrena* and *Lasioglossum* bees between Michigan and the UK at (a) the botanical family and (b) botanical genus level, with higher DFG score indicating greater average specialization per bee species. Bars headed by different letters are significantly different ( $p < 0.05$ ) error bars show standard error.

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**Table S6.** Extant *Andrena* species of Michigan and Britain and their dietary status. Species are ordered by subgenus. Species without a listed host range are polylectic.

Subgenus	Michigan species	Host range	British species	Host range
<i>Andrena s. str.</i>	<i>carolina</i> Viereck	<i>Vaccinium</i>	<i>apicata</i> Smith	<i>Salix</i>
	<i>clarkella</i> Kirby	<i>Salix</i>	<i>clarkella</i> Kirby	<i>Salix</i>
	<i>frigida</i> Smith	<i>Salix</i>	<i>fucata</i> Smith	
	<i>mandibularis</i> Robertson		<i>fulva</i> Müller	
	<i>milwaukeeensis</i> Graenicher		<i>helvola</i> L.	
	<i>rufosignata</i> Cockerell		<i>lapponica</i> Zetterstedt	
	<i>thaspis</i> Graenicher <i>tridens</i> Robertson		<i>praecox</i> Scopoli <i>synadelpha</i> Perkins <i>varians</i> Rossi	<i>Salix</i>
<i>Callandrena s.l.</i>	<i>aliciae</i> Robertson	Asteraceae		
	<i>asteris</i> Robertson	<i>Solidago</i>		
	<i>gardineri</i> Cockerell	<i>Packera</i>		
	<i>helianthi</i> Robertson	<i>Helianthus</i>		
	<i>krigiana</i> Robertson	<i>Krigia</i>		
	<i>placata</i> Mitchell	<i>Solidago</i>		
	<i>rudbeckiae</i> Robertson <i>simplex</i> Smith	<i>Rudbeckia</i> <i>Solidago</i>		
<i>Charitandrena</i>		<i>hatterfiana</i> Fabricius	Dipsacaceae	
<i>Chlorandrena</i>		<i>humilis</i> Imhoff	Asteraceae	
<i>Chrysandrena</i>		<i>fulvago</i> Christ	Asteraceae	
<i>Cnemidandrena</i>	<i>canadensis</i> Dalla Torre	<i>Solidago</i>	<i>denticulata</i> Kirby	Asteraceae
	<i>chromotricha</i> Cockerell	Asteraceae	<i>fuscipes</i> Kirby	Ericaceae
	<i>hirticineta</i> Provancher	<i>Solidago</i>	<i>nigriceps</i> Kirby	
	<i>nubecula</i> Smith	<i>Solidago</i>	<i>simillima</i> Smith	
	<i>parnassiae</i> Cockerell	<i>Parnassia</i>		
	<i>peckhami</i> Cockerell	<i>Helianthus</i>		
	<i>robervalensis</i> Mitchell	<i>Solidago</i>		
<i>Conandrena</i>	<i>bradleyi</i> Viereck	<i>Vaccinium</i>		
<i>Euandrena</i>	<i>algida</i> Smith	<i>Salix</i>	<i>bicolor</i> Fabricius	
	<i>geranii</i> Robertson	<i>Hydrophyllum</i>	<i>ruficrus</i> Nylander	<i>Salix</i>
	<i>nigrihirta</i> Ashmead			
	<i>polemonii</i> Robertson	<i>Polemonium</i>		
<i>Gonandrena</i>	<i>fragilis</i> Smith	<i>Cornus</i>		
	<i>integra</i> Smith	<i>Cornus</i>		
	<i>persimulata</i> Viereck	<i>Cornus</i>		
	<i>platyparia</i> Robertson	<i>Cornus</i>		
<i>Holandrena</i>	<i>cressonii</i> Robertson		<i>labialis</i> Kirby	
<i>Hoplandrena</i>			<i>bucephala</i> Stephens	
			<i>ferox</i> Smith	<i>Quercus</i>
			<i>rosae</i> Panzer	
			<i>scotica</i> Perkins <i>trimmerana</i> Kirby	
<i>Iomelissa</i>	<i>violae</i> Robertson	<i>Viola</i>		
<i>Larandrena</i>	<i>miserabilis</i> Cresson			
<i>Leucandrena</i>	<i>barbilabris</i> Kirby		<i>argentata</i> Smith	
	<i>erythronii</i> Robertson	<i>Erythronium</i>	<i>barbilabris</i> Kirby	
<i>Margandrena</i>			<i>marginata</i> Fabricius	Dipsacaceae
<i>Melandrena</i>	<i>carlini</i> Cockerell		<i>cineraria</i> L.	
	<i>commoda</i> Smith		<i>nigroaenea</i> Kirby	
	<i>dunningi</i> Cockerell		<i>nitida</i> Müller	
	<i>hilaris</i> Smith		<i>thoracica</i> Fabricius	
	<i>nivalis</i> Smith		<i>vaga</i> Panzer	<i>Salix</i>

	<i>pruni</i> Robertson				
	<i>regularis</i> Malloch				
	<i>vicina</i> Smith				
<i>Micrandrena</i>	<i>illinoensis</i> Robertson	<i>Salix</i>	<i>alfkenella</i> Perkins		
	<i>melanochroa</i> Cockerell		<i>falsifica</i> Perkins		
	<i>neonana</i> Viereck		<i>minutula</i> Kirby		
	<i>nigrae</i> Robertson		<i>minutuloides</i> Perkins		
	<i>personata</i> Robertson		<i>niveata</i> Friese	Brassicaceae	
	<i>salictaria</i> Robertson	<i>Salix</i>	<i>semilaevis</i> Pérez		
	<i>ziziae</i> Robertson	Apiaceae	<i>subopaca</i> Nylander		
<i>Notandrena</i>			<i>chrysoseles</i> Kirby		
			<i>nitidiuscula</i> Schenck	Apiaceae	
<i>Oreomelissa</i>			<i>coitana</i> Kirby		
<i>Parandrena</i>	<i>andrenoides</i> Cresson	<i>Salix</i>			
	<i>wellesleyana</i> Robertson	<i>Salix</i>			
<i>Plastandrena</i>	<i>crataegi</i> Robertson		<i>bimaculata</i> Kirby		
			<i>nigrospina</i> Thompson	Brassicaceae	
			<i>pilipes</i> Fabricius		
			<i>tibialis</i> Kirby		
<i>Poecilandrena</i>			<i>labiata</i> Fabricius		
<i>Poliandrena</i>			<i>florea</i> Fabricius	Bryonia	
<i>Proxiandrena</i>			<i>proxima</i> Kirby	Apiaceae	
<i>Ptilandrena</i>	<i>distans</i> Provancher	<i>Geranium</i>	<i>angustior</i> Kirby		
	<i>erigeniae</i> Robertson	<i>Claytonia</i>			
<i>Rhacandrena</i>	<i>brevipalpis</i> Cockerell	<i>Rhus</i>			
	<i>robertsonii</i> Dalla Torre				
<i>Scaphandrena</i>	<i>arabis</i> Robertson	Brassicaceae			
<i>Scrapteropsis</i>	<i>alleghaniensis</i> Viereck				
	<i>imitatrix</i> Cresson				
<i>Simandrena</i>	<i>nasonii</i> Robertson		<i>congruens</i> Schmiedeknecht		
	<i>wheeleri</i> Graenicher		<i>dorsata</i> Kirby		
<i>Taeniandrena</i>			<i>ovatula</i> Kirby		
			<i>similis</i> Smith	Fabaceae	
<i>Tarsandrena</i>			<i>wilkella</i> Kirby	Fabaceae	
<i>Thysandrena</i>	<i>bisalicis</i> Viereck	<i>Salix</i>	<i>tarsata</i> Nylander	<i>Potentilla</i>	
	<i>w-scripta</i> Viereck				
<i>Trachandrena</i>	<i>ceanothi</i> Viereck		<i>haemorrhoea</i> Fabricius		
	<i>forbesii</i> Robertson				
	<i>heraclei</i> Robertson				
	<i>hippotes</i> Robertson				
	<i>mariae</i> Robertson	<i>Salix</i>			
	<i>mirandra</i> Smith				
	<i>nuda</i> Robertson				
	<i>rehni</i> Viereck				
	<i>rugosa</i> Cockerell				
	<i>sigmundi</i> Cockerell	<i>Salix</i>			
	<i>spiraeana</i> Robertson				
<i>Tylandrena</i>	<i>virginiana</i> Mitchell				
	<i>erythrogaster</i> Ashmead	<i>Salix</i>			
	<i>perplexa</i> Smith				
	<i>wilmattiae</i> Cockerell				
<i>Zonandrena</i>			<i>flavipes</i> Panzer		
			<i>gravida</i> Imhoff		
Total:		81	42	59	20
Proportion oligolectic:			51.9		33.9

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754 **Table S6 Notes.** Wood and Roberts<sup>46</sup> added 11 oligolectic species to their analysis, including *Andrena*  
755 *lapponica* Zetterstedt. However, Müller<sup>65</sup> demonstrated that this species is polylectic, and so it was not  
756 used in the analysis presented in the current paper.  
757 Gibbs *et al.*<sup>54</sup> listed *Andrena barbara* Bouseman & LaBerge, *A. morrisonella* Viereck, *A. confederata*  
758 Viereck and *A. wilkella* Kirby as part of the Michigan fauna. Examination of material at the University of  
759 Michigan Museum of Zoology (Ann Arbor, Michigan) has shown that the record of *A. barbara* is based  
760 on a misidentification (TJW, *unpublished data*). The status of *Andrena morrisonella* is still taxonomically  
761 uncertain and females cannot be reliably separated from *A. imitatrix*<sup>66</sup>. *Andrena confederata* was recorded  
762 from Michigan on the basis of a single male that cannot be found<sup>54</sup>, and repeated searching at the locality  
763 has not produced any more records of this species. *Andrena wilkella* is introduced to North America<sup>67</sup>.  
764 These species have therefore been excluded from the Michigan fauna for the purposes of this study.  
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767 **Table S7.** Extant pollen-collecting *Lasioglossum* species of Michigan and Britain and their dietary status.  
 768 Species are ordered by subgenus. Species without a listed host range are polylectic.

Subgenus	Michigan species	Host range	British species	Host range
<i>Dialictus</i>	<i>abanci</i> Crawford		<i>cupromicans</i> Pérez	
	<i>achilleae</i> Mitchell		<i>leucopus</i> Kirby	
	<i>admirandum</i> Sandhouse		<i>morio</i> Fabricius	
	<i>albipenne</i> Robertson		<i>smeathmanellum</i> Kirby	
	<i>anomalum</i> Robertson			
	<i>atwoodi</i> Gibbs			
	<i>bruneri</i> Crawford			
	<i>callidum</i> Sandhouse			
	<i>cattellae</i> Ellis			
	<i>ceanothi</i> Mitchell			
	<i>coeruleum</i> Robertson			
	<i>coreopsis</i> Robertson			
	<i>cressonii</i> Robertson			
	<i>dreisbachi</i> Mitchell			
	<i>ellisae</i> Sandhouse			
	<i>ephialtum</i> Gibbs			
	<i>fattigi</i> Mitchell			
	<i>floridanum</i> Robertson			
	<i>foveolatum</i> Robertson			
	<i>gotham</i> Gibbs			
	<i>hartii</i> Robertson			
	<i>heterognathum</i> Mitchell			
	<i>hitchensi</i> Gibbs			
	<i>illinoense</i> Robertson			
	<i>imitatum</i> Smith			
	<i>laevissimum</i> Smith			
	<i>leucocomum</i> Lovell			
	<i>lineatulum</i> Crawford			
	<i>nigroviride</i> Graenicher			
	<i>novascotiae</i> Mitchell			
	<i>oblongum</i> Lovell			
	<i>obscurum</i> Robertson			
	<i>oceanicum</i> Cockerell			
	<i>paradmirandum</i> Knerer & Atwood			
	<i>perpunctatum</i> Ellis			
	<i>pictum</i> Crawford			
	<i>pilosum</i> Smith			
	<i>planatum</i> Lovell			
	<i>pruinatum</i> Robertson			
	<i>rufipes</i> Cockerell			
	<i>sagax</i> Sandhouse			
	<i>sheffieldsi</i> Gibbs			
	<i>smilacinae</i> Robertson			
	<i>subversans</i> Mitchell			
	<i>subviridatum</i> Cockerell			
<i>taylorae</i> Gibbs				
<i>tegulare</i> Robertson				
<i>tenax</i> Sandhouse				
<i>timothyi</i> Gibbs				
<i>trigeminum</i> Gibbs				
<i>versans</i> Lovell				

	<i>versatum</i> Robertson			
	<i>vierecki</i> Crawford			
	<i>viridatum</i> Lovell			
	<i>weemsi</i> Mitchell			
	<i>zephyrum</i> Smith			
<i>Evylaeus</i> s.s.	<i>cinctipes</i> Provancher			
<i>Hemihalictus</i>	<i>birkmanni</i> Crawford		<i>angusticeps</i> Perkins	
	<i>fedorensis</i> Crawford		<i>brevicorne</i> Schenck	Asteraceae
	<i>foxii</i> Robertson		<i>minutissimum</i> Kirby	
	<i>inconditum</i> Cockerell	Asteraceae	<i>nitidiusculum</i> Kirby	
	<i>lustrans</i> Cockerell		<i>parvulum</i> Schenck	
	<i>macoupinense</i> Robertson	Nymphaceae	<i>pauperatum</i> Brullé	
	<i>nelumbonis</i> Robertson		<i>punctatissimum</i> Schenck	
	<i>pectorale</i> Smith		<i>puncticolle</i> Morawitz	
	<i>swenki</i> Crawford		<i>rufitarse</i> Zetterstedt	
			<i>semilucens</i> Alfken	
			<i>sexstrigatum</i> Kirby	
			<i>villosulum</i> Kirby	Asteraceae
<i>Lasioglossum</i>	<i>acuminatum</i> McGinley		<i>laevigatum</i> Kirby	
<i>s. str.</i>	<i>athabascense</i> Sandhouse		<i>lativentris</i> Schenck	
	<i>coriaceum</i> Smith		<i>prasinum</i> Smith	
	<i>forbesii</i> Robertson		<i>quadrinotatum</i> Kirby	
	<i>fuscipenne</i> Smith		<i>xanthopus</i> Kirby	
	<i>paraforbesii</i> McGinley			
<i>Leuchalictus</i>			<i>leucozonium</i> Schrank	
			<i>zonulum</i> Smith	
<i>Sphecodogastra</i>	<i>comagenense</i> Knerer & Atwood		<i>albipes</i> Fabricius	
	<i>oenothera</i> Stevens	<i>Oenothera</i>	<i>calceatum</i> Scopoli	
	<i>quebecense</i> Crawford		<i>fratellum</i> Pérez	
	<i>seillean</i> Gibbs & Packer		<i>fulvicorne</i> Kirby	
	<i>texanum</i> Cresson	<i>Oenothera</i>	<i>laticeps</i> Schenck	
	<i>truncatum</i> Robertson		<i>malachurum</i> Kirby	
			<i>pauillum</i> Schenck	
Total:	77	4	32	2
Proportion oligolectic:		5.2		6.3

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770 **Table S7 Notes.** The parasitic *L. lionotum* Sandhouse, *L. michiganense* Mitchell, and *L. platyparium*  
771 Robertson<sup>54</sup> do not collect pollen and so were excluded from the faunal list for this study. *Lasioglossum*  
772 *leucozonium* and *Lasioglossum zonulum* are introduced to North America<sup>54,67</sup> and so were also excluded.

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**Table S8.** Summary of the species included in this study and the number of analyzed pollen loads per species.

Michigan dataset		British dataset	
Species	Sample size	Species	Sample size
<i>Andrena algida</i>	11	<i>Andrena alfenella</i>	23
<i>Andrena aliciae</i>	5	<i>Andrena angustior</i>	18
<i>Andrena alleghaniensis</i>	13	<i>Andrena argentata</i>	11
<i>Andrena andrenoides</i>	15	<i>Andrena barbilabris</i>	7
<i>Andrena arabis</i>	10	<i>Andrena bicolor</i>	41
<i>Andrena barbilabris</i>	23	<i>Andrena bimaculata</i>	13
<i>Andrena bradleyi</i>	9	<i>Andrena chrysoceles</i>	39
<i>Andrena brevipalpis</i>	25	<i>Andrena cineraria</i>	16
<i>Andrena canadensis</i>	6	<i>Andrena denticulata</i>	16
<i>Andrena carlini</i>	21	<i>Andrena dorsata</i>	55
<i>Andrena carolina</i>	5	<i>Andrena flavipes</i>	74
<i>Andrena ceanothi</i>	16	<i>Andrena fucata</i>	15
<i>Andrena chromotricha</i>	6	<i>Andrena fulva</i>	6
<i>Andrena commoda</i>	12	<i>Andrena haemorrhoea</i>	49
<i>Andrena crataegi</i>	28	<i>Andrena helvola</i>	12
<i>Andrena cressonii</i>	21	<i>Andrena labialis</i>	12
<i>Andrena distans</i>	5	<i>Andrena labiata</i>	10
<i>Andrena erigeniae</i>	7	<i>Andrena minutula</i>	74
<i>Andrena erythrogaster</i>	14	<i>Andrena minutuloides</i>	53
<i>Andrena forbesii</i>	25	<i>Andrena nigriceps</i>	5
<i>Andrena frigida</i>	11	<i>Andrena nigroaenea</i>	22
<i>Andrena gardineri</i>	5	<i>Andrena nitida</i>	28
<i>Andrena geranii</i>	5	<i>Andrena scotica</i>	39
<i>Andrena helianthi</i>	6	<i>Andrena semilaevis</i>	98
<i>Andrena hippotes</i>	22	<i>Andrena subopaca</i>	16
<i>Andrena hirticincta</i>	13	<i>Andrena synadelpha</i>	9
<i>Andrena illinoiense</i>	8	<i>Andrena thoracica</i>	10
<i>Andrena imitatrix</i>	15	<i>Andrena trimmerana</i>	18
<i>Andrena integra</i>	10	<i>Andrena wilkella</i>	24
<i>Andrena mandibularis</i>	13		
<i>Andrena miranda</i>	19	plus 10 oligolectic species	
<i>Andrena miserabilis</i>	23		
<i>Andrena nasonii</i>	20	<i>Andrena ferox</i>	
<i>Andrena nigrihirta</i>	6	<i>Andrena florea</i>	
<i>Andrena nivalis</i>	13	<i>Andrena fuscipes</i>	
<i>Andrena nubecula</i>	7	<i>Andrena hattorfiana</i>	
<i>Andrena nuda</i>	10	<i>Andrena marginata</i>	
<i>Andrena perplexa</i>	10	<i>Andrena nigrospina</i>	
<i>Andrena placata</i>	9	<i>Andrena nitidiuscula</i>	
<i>Andrena platyparia</i>	7	<i>Andrena niveata</i>	
<i>Andrena robertsonii</i>	10	<i>Andrena proxima</i>	
<i>Andrena rudbeckiae</i>	8	<i>Andrena tarsata</i>	
<i>Andrena rufosignata</i>	19		
<i>Andrena rugosa</i>	17		
<i>Andrena spiraeana</i>	13		
<i>Andrena thaspiae</i>	9		
<i>Andrena vicina</i>	37		
<i>Andrena virginiana</i>	13		
<i>Andrena wellesleyana</i>	9		
<i>Andrena w-scripta</i>	16		
<i>Andrena ziziae</i>	11		



Total	671	Total	804
<i>Lasioglossum acuminatum</i>	20	<i>Lasioglossum albipes</i>	8
<i>Lasioglossum anomalum</i>	12	<i>Lasioglossum calceatum</i>	38
<i>Lasioglossum cattellae</i>	8	<i>Lasioglossum fulvicorne</i>	12
<i>Lasioglossum cinctipes</i>	12	<i>Lasioglossum laevigatum</i>	11
<i>Lasioglossum coriaceum</i>	24	<i>Lasioglossum lativentre</i>	18
<i>Lasioglossum cressonii</i>	28	<i>Lasioglossum leucopus</i>	11
<i>Lasioglossum foxii</i>	11	<i>Lasioglossum leucozonium</i>	26
<i>Lasioglossum hitchensi</i>	18	<i>Lasioglossum malachurum</i>	437
<i>Lasioglossum imitatum</i>	23	<i>Lasioglossum morio</i>	15
<i>Lasioglossum laevisimum</i>	19	<i>Lasioglossum parvulum</i>	12
<i>Lasioglossum leucomum</i>	18	<i>Lasioglossum pauxillum</i>	70
<i>Lasioglossum lineatulum</i>	17	<i>Lasioglossum prasinum</i>	8
<i>Lasioglossum lustrans</i>	7	<i>Lasioglossum puncticolle</i>	13
<i>Lasioglossum macoupinense</i>	6	<i>Lasioglossum villosulum</i>	29
<i>Lasioglossum nigroviride</i>	7	<i>Lasioglossum xanthopus</i>	11
<i>Lasioglossum oenothera</i>	5	<i>Lasioglossum zonulum</i>	12
<i>Lasioglossum paradmirationum</i>	8		
<i>Lasioglossum paraforbesii</i>	15		
<i>Lasioglossum pectorale</i>	24		
<i>Lasioglossum pilosum</i>	25		
<i>Lasioglossum quebecense</i>	6		
<i>Lasioglossum subviridatum</i>	8		
<i>Lasioglossum versans</i>	7		
<i>Lasioglossum versatum</i>	27		
Total	355	Total	731
Grand total	1026	Grand total	1535

778

779

780 **Table S9: Pollen load data.** The pollen load percentages and botanical family counts of sampled  
781 *Andrena* and *Lasioglossum* bees from both the U.K. and Michigan, USA. Please find the data attached as  
782 an .xls file separated by location and botanical taxonomic level.

783

784 **Table S10: Simulation phenology parameters.** The phenology parameters for both pollinators and  
785 plants used in simulations. All potential combinations of the listed parameters were used to give 2072  
786 unique phenological bases per network framework. Please find the data attached as an .xls file.

787

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