

Inference and model determination for Temperature-Driven non-linear Ecological Models: supplemental document

S1. TABLES WITH SUMMARIES AND POSTERIOR ESTIMATES OF THE STATISTICAL METHODS USED

A. *Propylea quatuordecimpunctata* dataset

Table S1. Algorithmic working time in seconds, for two datasets.

| <i>Tetranychus urticae</i> | | | | |
|--------------------------------------|-------|--------|----------|--------|
| Gaussian | | | | |
| | Bieri | Briere | Analytis | Lactin |
| HMC | 2011 | 476 | 9852 | 5672 |
| ADVI-meanfield | 8 | 1 | 52 | 1 |
| ADVI-fullrank | 45 | 6 | 38 | 44 |
| Inverse Gamma | | | | |
| HMC | 1375 | 761 | 3231 | 4917 |
| ADVI-meanfield | 2 | 4 | 15 | 27 |
| ADVI-fullrank | 2 | 34 | 14 | 44 |
| <i>Propylea quatuordecimpunctata</i> | | | | |
| Gaussian | | | | |
| | Bieri | Briere | Analytis | Lactin |
| HMC | 4335 | 20218 | 4913 | 1426 |
| ADVI-meanfield | 13 | 7 | 3 | 16 |
| ADVI-fullrank | 48 | 11 | 12 | 16 |
| Zero Inflated Inverse Gamma | | | | |
| HMC | 1078 | 321 | 15291 | 3073 |
| ADVI-meanfield | 41 | 5 | 9 | 10 |
| ADVI-fullrank | 52 | 5 | 39 | 18 |

Table S2. BMA weights for the *Tetranychus urticae* data

| Gaussian distribution | | | | | | | |
|----------------------------|---------|---------|---------|---------|---------|---------|----------|
| | aic_w | dic_w | loocv_w | waic_w | bic_w | elbo_mf | elbo_fr |
| Bieri | 4.9E-17 | 9.4E-16 | 2.3E-16 | 2.4E-16 | 8.1E-18 | 3.1E-53 | 7.3E-45 |
| Briere | 1.9E-32 | 2.3E-31 | 6.6E-33 | 6.9E-33 | 1.1E-31 | 2.9E-27 | 1.5E-18 |
| Analytis | 1 | 1 | 1 | 1 | 1 | 0.001 | 1 |
| Lactin | 1.0E-14 | 4.9E-14 | 1.2E-12 | 1.2E-12 | 9.0E-18 | 0.999 | 3.5E-39 |
| Inverse Gamma distribution | | | | | | | |
| Bieri | 3.0E-43 | 4.5E-43 | 1.1E-42 | 1.0E-42 | 3.0E-43 | 1.6E-20 | 1.0E-200 |
| Briere | 6.6E-36 | 8.1E-36 | 2.2E-36 | 2.1E-36 | 3.8E-35 | 8.9E-19 | 1.0E-171 |
| Analytis | 1.4E-5 | 7.1E-6 | 2.1E-5 | 2.1E-5 | 1.9E-6 | 1 | 1 |
| Lactin | 0.999 | 0.999 | 0.999 | 0.999 | 1 | 1.0E-36 | 2.7E-58 |

Table S3. BMA weights for the *Propylea quatuordecimpunctata* data

| Gaussian distribution | | | | | | | |
|--|---------|---------|---------|---------|---------|----------|----------|
| | aic_w | dic_w | loocv_w | waic_w | bic_w | elbo_mf | elbo_fr |
| Bieri | 0.999 | 0.968 | 0.991 | 0.991 | 1 | 1 | 1 |
| Briere | 3.3E-34 | 7.3E-30 | 5.5E-35 | 5.5E-35 | 4.8E-33 | 5E-203 | 3E-218 |
| Analytis | 1.1E-31 | 1.5E-32 | 3.8E-32 | 3.8E-32 | 4.0E-31 | 9.0E-269 | 1.0E-210 |
| Lactin | 5.9E-04 | 0.032 | 0.009 | 0.009 | 1.1E-05 | 5.0E-159 | 3.0E-162 |
| Zero Inflated Inverse Gamma distribution | | | | | | | |
| Bieri | 9.3E-5 | 0.001 | 0.001 | 0.001 | 3.5E-4 | 5.1E-53 | 3.4E-72 |
| Briere | 1.7E-38 | 3.9E-38 | 7.3E-38 | 7.2E-38 | 2.4E-37 | 1 | 1.1E-23 |
| Analytis | 1 | 0.999 | 0.999 | 0.999 | 1 | 3.3E-35 | 1 |
| Lactin | 1.7E-8 | 2.1E-8 | 5.8E-8 | 5.8E-8 | 6.4E-8 | 3.0E-114 | 2.0E-140 |

Table S4. The mean and 95% Cr.I. limits of the BMA estimates of parameters of interest calculated with the use of information criteria score weights assuming the Gaussian and Inverse Gamma distributions respectively for *Tetranychus urticae* data.

| Gaussian Model | | | | | | | | |
|---------------------|------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|
| | | aic_w | dic_w | loocv_w | waic_w | bic_w | elbo_mf | elbo_fr |
| T_{min} | Mean | 4.4 | 4.4 | 4.4 | 4.4 | 4.4 | 4.4 | 4.4 |
| | 95% Cr.I. | (4.0, 5.3) | (4.0, 5.3) | (4.0, 5.3) | (4.0, 5.3) | (4.0, 5.3) | (4.0, 5.3) | (4.0, 5.3) |
| T_{opt} | Mean | 32.9 | 32.9 | 32.9 | 32.9 | 32.9 | 32.6 | 32.9 |
| | 95% Cr.I. | (32.7, 33.3) | (32.7, 33.3) | (32.7, 33.3) | (32.7, 33.3) | (32.7, 33.3) | (32.4, 32.8) | (32.7, 33.3) |
| T_{max} | Mean | 35.3 | 35.3 | 35.3 | 35.3 | 35.3 | 36.9 | 35.3 |
| | 95% Cr.I. | (35.1, 35.5) | (35.1, 35.5) | (35.1, 35.5) | (35.1, 35.5) | (35.1, 35.5) | (36.5, 37.3) | (35.1, 35.5) |
| dev [†] | Mean | -1750.3 | -1750.3 | -1750.3 | -1750.3 | -1750.3 | -1693.9 | -1750.3 |
| | 95% Cr.I. | (-1758.0,-1738.3) | (-1758.0,-1738.3) | (-1758.0,-1738.3) | (-1758.0,-1738.3) | (-1758.0,-1738.3) | (-1703.1,-1679.7) | (-1758.0,-1738.3) |
| Inverse Gamma Model | | | | | | | | |
| T_{min} | Mean | 4.2 | 4.2 | 4.2 | 4.2 | 4.2 | 4.2 | 4.2 |
| | 95% Cr.I. | (4.0, 4.6) | (4.0, 4.6) | (4.0, 4.6) | (4.0, 4.6) | (4.0, 4.6) | (4.0, 4.6) | (4.0, 4.6) |
| T_{opt} | Mean T_opt | 32.0 | 32.0 | 32.0 | 32.0 | 32.0 | 33.6 | 33.6 |
| | 95% Cr.I. | (31.8, 32.2) | (31.8, 32.2) | (31.8, 32.2) | (31.8, 32.2) | (31.8, 32.2) | (33.3, 33.9) | (33.3, 33.9) |
| T_{max} | Mean | 38.4 | 38.4 | 38.4 | 38.4 | 38.4 | 35.0 | 35.0 |
| | 95% Cr.I. | (38.1, 38.9) | (38.1, 38.9) | (38.1, 38.9) | (38.1, 38.9) | (38.1, 38.9) | (35.0, 35.1) | (35.0, 35.1) |
| dev [†] | Mean | -1916.3 | -1916.3 | -1916.3 | -1916.3 | -1916.3 | -1894.0 | -1894.0 |
| | 95% Cr.I. | (-1920.6,-1908.3) | (-1920.6,-1908.3) | (-1920.6,-1908.3) | (-1920.6,-1908.3) | (-1920.6,-1908.3) | (-1899.2,-1885.2) | (-1899.2,-1885.2) |

† deviance of the model given the data.

Table S5. The mean and 95% Cr.I. limits of the BMA estimates of parameters of interest calculated with the use of information criteria score weights assuming the Gaussian and Inverse Gamma distributions respectively for the *Propylea quatuordecimpunctata* data.

| Gaussian distribution | | | | | | | | |
|----------------------------|-----------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|
| | | aic_w | dic_w | loocv_w | waic_w | bic_w | elbo_mf | elbo_fr |
| T_{min} | Mean | 10.6 | 10.6 | 10.6 | 10.6 | 10.6 | 10.6 | 10.6 |
| | 95% Cr.I. | (9.7, 11.4) | (9.7, 11.4) | (9.7, 11.4) | (9.7, 11.4) | (9.7, 11.4) | (9.7, 11.4) | (9.7, 11.4) |
| T_{opt} | Mean | 32.6 | 32.5 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 |
| | 95% Cr.I. | (32.0, 33.5) | (31.9, 33.4) | (32.0, 33.5) | (32.0, 33.5) | (32.0, 33.5) | (32.0, 33.5) | (32.0, 33.5) |
| T_{max} | Mean | 35.0 | 35.0 | 35.0 | 35.0 | 35.0 | 35.0 | 35.0 |
| | 95% Cr.I. | (34.98, 35.0) | (34.98, 35.0) | (34.98, 35.0) | (34.98, 35.0) | (34.98, 35.0) | (34.98, 35.0) | (34.98, 35.0) |
| dev [†] | Mean | -818.8 | -818.5 | -818.7 | -818.7 | -818.8 | -818.8 | -818.8 |
| | 95% Cr.I. | (-833.1, -800.8) | (-832.4, -801.1) | (-832.9, -800.9) | (-832.9, -800.9) | (-833.1, -800.8) | (-833.1, -800.8) | (-833.1, -800.8) |
| Inverse Gamma distribution | | | | | | | | |
| T_{min} | Mean | 5.0 | 5.0 | 5.0 | 5.0 | 5.0 | 11.1 | 5.0 |
| | 95% Cr.I. | (4.0, 7.0) | (4.0, 7.0) | (4.0, 7.0) | (4.0, 7.0) | (4.0, 7.0) | (10.3, 11.9) | (4.0, 7.0) |
| T_{opt} | Mean | 33.5 | 33.5 | 33.5 | 33.5 | 33.5 | 29.3 | 33.5 |
| | 95% Cr.I. | (32.3, 34.9) | (32.3, 34.9) | (32.3, 34.9) | (32.3, 34.9) | (32.3, 34.9) | (29.2, 29.5) | (32.3, 34.9) |
| T_{max} | Mean | 33.6 | 33.6 | 33.6 | 33.6 | 33.6 | 35.0 | 33.6 |
| | 95% Cr.I. | (32.5, 34.9) | (32.5, 34.9) | (32.5, 34.9) | (32.5, 34.9) | (32.5, 34.9) | (34.8, 35.0) | (32.5, 34.9) |
| dev [†] | Mean | -736.2 | -736.2 | -736.2 | -736.2 | -736.2 | -563.8 | -736.2 |
| | 95% Cr.I. | (-742.1, -729.1) | (-742.1, -729.1) | (-742.0, -729.1) | (-742.0, -729.1) | (-742.1, -729.1) | (-568.0, -555.9) | (-742.1, -729.1) |

† deviance of the model given the data.

Table S6. Posterior summaries for the four models using the Gaussian distribution for the *Tetranychus urticae* data. In each column we report the HMC, the ADVI-Mean field and ADVI-Full rank estimates respectively.

| | T_{min} | | | neff [†] | T_{opt} | | | neff [‡] |
|----------|----------------------|----------------------|----------------------|-------------------|-------------------------------|-------------------------------|-------------------------------|-------------------|
| Bieri | 10.5 (10.2, 10.8) | 9.8 (9.5, 10.2) | 9.8 (9.2, 10.3) | 15089 | 33.0 (32.7, 33.4) | 158.6 (144.4, 165.4) | 183.8 (76.4, 368.5) | 8164 |
| Briere | 9.3 (8.6, 9.9) | 9.3 (9.1, 9.5) | 9.3 (8.6, 9.9) | 8690 | 33.1 (32.5, 33.7) | 33.0 (32.8, 33.2) | 33.1 (32.4, 33.7) | 8028 |
| Analytis | 4.4 (4.0, 5.3) | 4.3 (4.2, 4.4) | 5.3 (4.8, 6.1) | 8757 | 32.9 (32.7, 33.3) | 33.0 (32.9, 33.1) | 33.2 (32.6, 33.7) | 41 |
| Lactin | 10.4 (10.1, 10.7) | -3.9 (-5.8, -1.9) | -0.7 (-4.0, 3.0) | 11526 | 32.6 (32.4, 32.8) | 32.2 (32.0, 32.3) | 32.0 (31.8, 32.2) | 9884 |
| | T_{max} | | | neff [†] | dev [†] | | | neff [‡] |
| Bieri | 36.3 (35.9, 36.8) | 164.9 (161, 169) | 190.6 (80, 376.1) | 7561 | -1677.1 (-1683.2, -1666.6) | -1461.0 (-1467.7, -1443.6) | -1461.7 (-1467.7, -1456.3) | 10087 |
| Briere | 40.0 (39.3, 40.9) | 39.9 (39.6, 40.1) | 40.0 (39.1, 40.9) | 7562 | -1602.2 (-1606.8, -1593.4) | -1593.2 (-1605.7, -1569.1) | -1598.5 (-1606.3, -1583.6) | 9618 |
| Analytis | 35.3 (35.1, 35.5) | 35.2 (35.2, 35.3) | 35.2 (35.1, 35.4) | 8246 | -1750.3 (-1758.0, -1738.3) | -1744.7 (-1755.6, -1724) | -1709.1 (-1741.9, -1606.9) | 10954 |
| Lactin | 36.9 (36.6, 37.3) | 38.3 (38.1, 38.5) | 38.2 (37.9, 38.5) | 7797 | -1693.9 (-1703, -1679.6) | -1764.0 (-1780.3, -1738.1) | -1776.2 (-1784.9, -1762) | 8227 |

[†] deviance of the model given the data,

[‡] effective sample size.

Table S7. Posterior summaries for the four models using the Gaussian distribution for the Propylea Coccinellidae data. In each column we report the HMC, the ADVI-Mean field and ADVI-Full rank estimates respectively.

| | | T_{min} | | | neff [†] | T_{opt} | | | neff [‡] |
|-----------------------|----------|----------------------------|----------------------------|----------------------------|-------------------|----------------------------|----------------------------|----------------------------|-------------------|
| Mean 95% Cr. I. | Bieri | 10.6 (9.7, 11.4) | 10.7 (10.6, 10.8) | 10.7 (10, 11.4) | 7906 | 32.6 (32, 33.5) | 32.2 (32, 32.5) | 32.2 (31.8, 32.5) | 7620 |
| | Briere | 13.1 (12.4, 13.8) | 13.3 (12.9, 13.8) | 8.2 (1.8, 15.6) | 4 | 29.7 (29.6, 29.8) | 29.7 (29.5, 29.8) | 27.3 (11.7, 30.1) | 4 |
| | Analytis | 6.3 (4.1, 10.6) | 21.5 (7.7, 55.2) | 6.9 (5.4, 9.3) | 3742 | 33.2 (32.1, 34.8) | 39.2 (18.1, 89.1) | 33.2 (31.7, 37.7) | 4435 |
| | Lactin | -154.4 (-234.7, -119.3) | -146.2 (-154.3, -138.1) | -159.2 (-243.1, -119.0) | 7560 | 31.2 (30.9, 31.3) | 31.1 (31.1, 31.2) | 31.1 (30.9, 31.3) | 8024 |
| | | T_{max} | | | neff [†] | dev [†] | | | neff [‡] |
| Mean 95% Cr. I. | Bieri | 35.0 (34.98, 35.02) | 33.8 (33.6, 33.9) | 33.7 (33.5, 33.9) | 7194 | -818.7 (-833.1, -800.6) | -672.7 (-685.1, -657.4) | -672.5 (-686.2, -657.1) | 11673 |
| | Briere | 35.0 (35.0, 35.01) | 35.0 (34.8, 35) | 32.9 (14.3, 35) | 113 | -660.5 (-667.0, -649.7) | -535.8 (-543.2, -520.5) | -429.7 (-535.0, -402.1) | 14478 |
| | Analytis | 33.6 (32.5, 34.9) | 42.5 (32.7, 94.5) | 36.1 (4.6, 133.2) | 9370 | -674.1 (-690.2, -666.3) | -160.0 (-261.3, -98.2) | -491.9 (-595.9, -293.6) | 5164 |
| | Lactin | 35.0 (35, 35.04) | 35.0 (35.0, 35.1) | 35.0 (35.0, 35.1) | 21622 | -809.8 (-823.7, -792.2) | -804.7 (-820.5, -784.8) | -778.5 (-807.5, -702.6) | 12147 |

[†] deviance of the model given the data,

[‡] effective sample size.

Table S8. Model selection criteria for the eight models applied to the *Propylea Coccinellidae* data

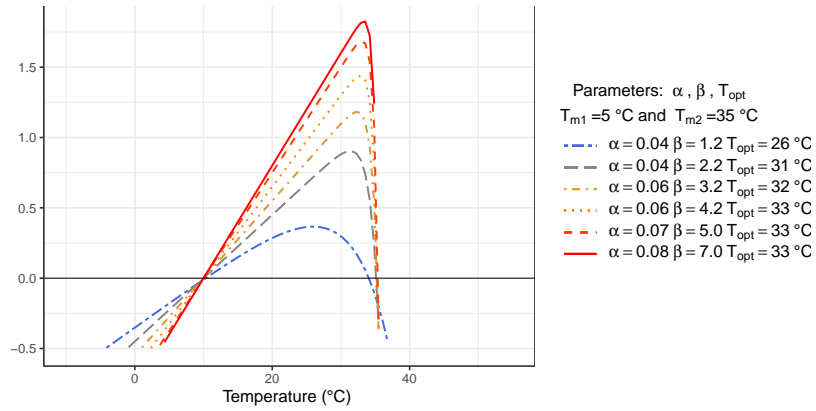
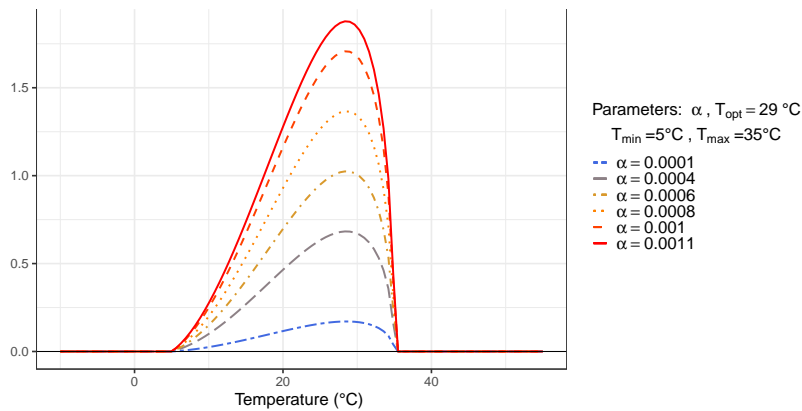
| | | AIC | DIC | LooCV | WAIC | BIC | $\log(P_{yIS})^{\dagger}$ (se) | $\log(P_{yPP})^{\ddagger}$ (se) | $\log(P_{yBS})^{\S}$ (se) |
|---------------------|----------|--------|--------|--------|--------|--------|--------------------------------|---------------------------------|---------------------------|
| Gaussian model | Bieri | -804.7 | -783.6 | -816.1 | -816.1 | -786.1 | 419.9 (19.6) | 433.4 (18.0) | 462.4 (9.2) |
| | Briere | -650.5 | -649.5 | -658.3 | -658.3 | -637.3 | 299.2 (24.6) | 235.4 (6.7) | 231.4 (1.2) |
| | Analytis | -662.1 | -637.1 | -671.4 | -671.4 | -646.1 | 283.7 (24.0) | 312.2 (10.0) | 274.2 (33.7) |
| | Lactin | -789.8 | -776.8 | -806.7 | -806.7 | -763.3 | 390.1 (33.5) | 328.1 (23.0) | 334.7 (1.7) |
| Inverse Gamma model | Bieri | -716.1 | -719.3 | -719.3 | -719.3 | -702.8 | 334.5 (25.9) | 342.9 (31.5) | 333.2 (5.0) |
| | Briere | -560.8 | -561.4 | -561.4 | -561.4 | -550.2 | 268.2 (23.2) | 265.7 (4.6) | 251.7 (1.9) |
| | Analytis | -734.7 | -732.4 | -732.4 | -732.4 | -718.8 | 340.8 (26.7) | 371.3 (14.5) | 335 (31.2) |
| | Lactin | -698.9 | -699.1 | -699.1 | -699.1 | -685.6 | 329.2 (19.5) | 329.3 (11.8) | 313.7 (18.8) |

$\dagger \log(P_{yIS})$ denotes the logarithm of estimated marginal likelihood via Importance sampling,

$\ddagger \log(P_{yPP})$ denotes the logarithm of estimated marginal likelihood via Power posterior,

$\S \log(P_{yBS})$ denotes the logarithm of estimated marginal likelihood via Bridge sampling.

S2. ECOLOGICAL MODELS CURVES AND POSTERIOR PREDICTION GRAPHS FOR BOTH DATASETS

**Fig. S1.** Bieri developmental rates**Fig. S2.** Briere developmental rates

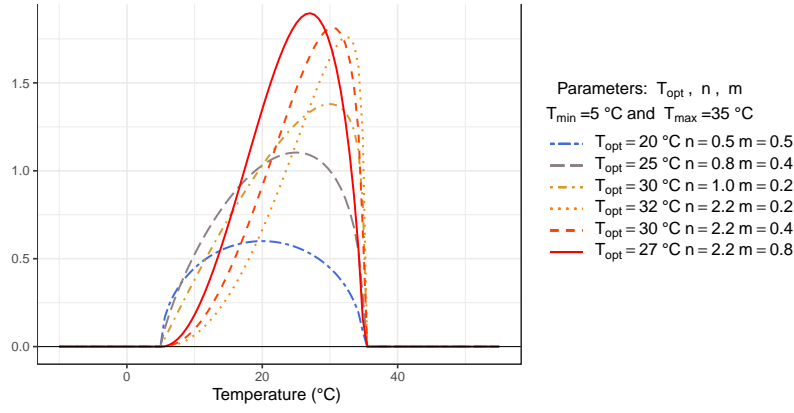


Fig. S3. Analytis developmental rates

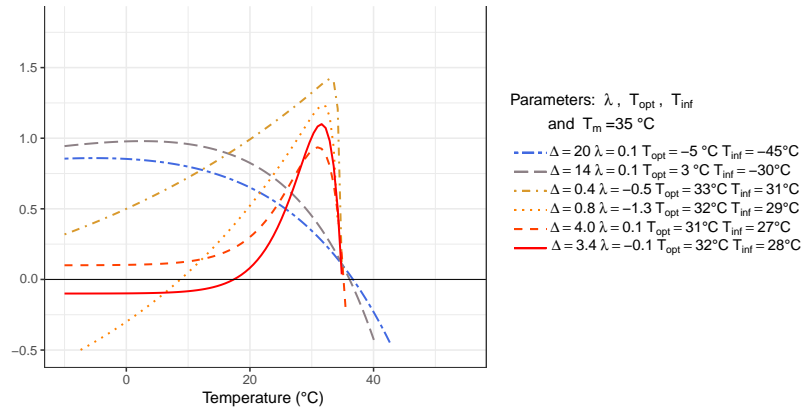


Fig. S4. Lactin developmental rates

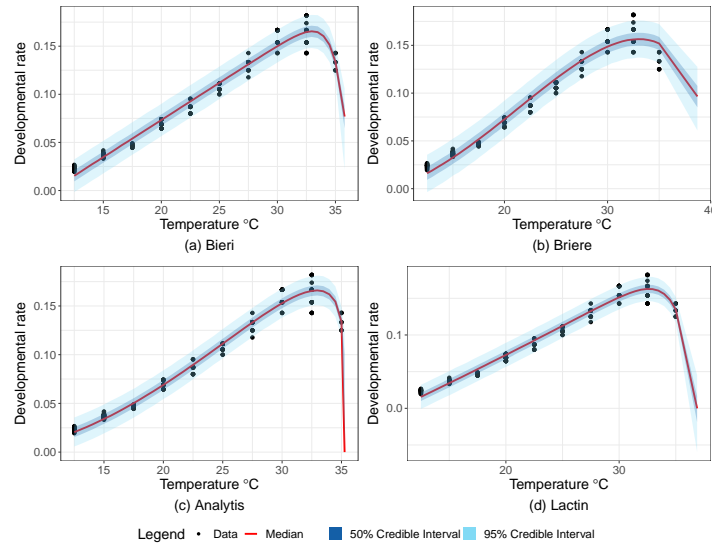


Fig. S5. Predicted posteriors versus *Tetranychus urticae* data using Gaussian distribution

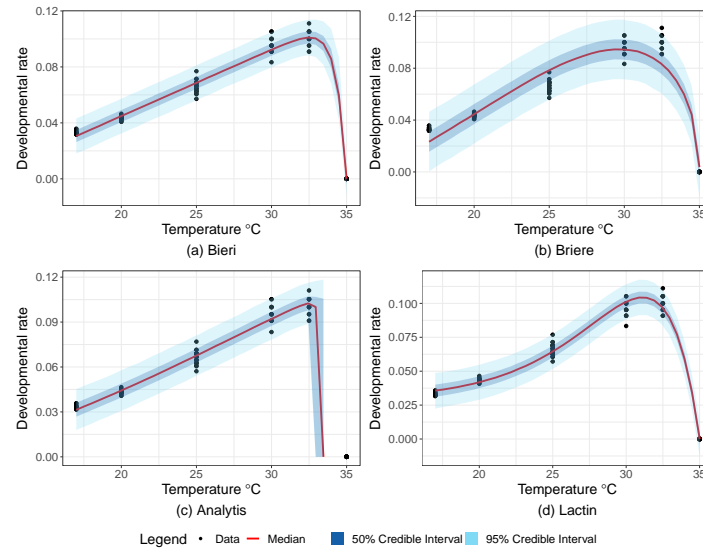


Fig. S6. Predicted posteriors versus *Propylea Coccinellidae* data using Gaussian distribution

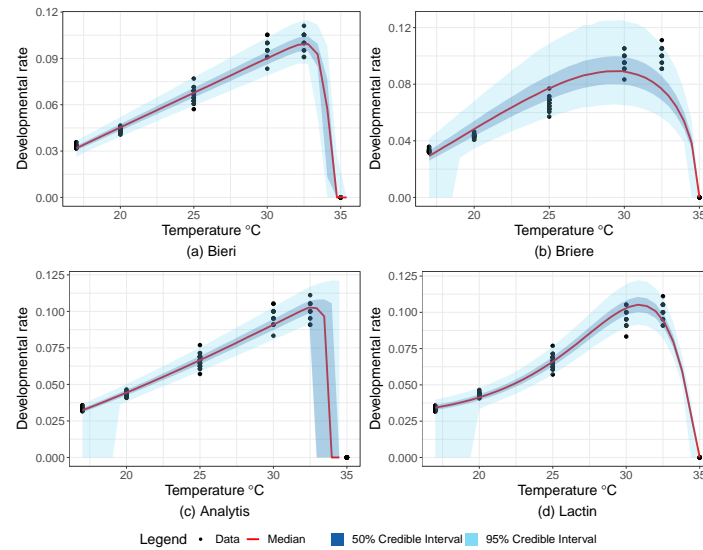


Fig. S7. Predicted posteriors versus *Propylea Coccinellidae* data using Zero Inflated Inverse Gamma distribution

S3. BAYESIAN INFERENCE

In the current section, we provide details of statistical model specifications in the Bayesian framework. Specifically, we provide a brief description of the most important features of Stan’s implementation of HMC and VB so the reader can get familiar with the tools that Stan is based on. We then provide model selection and model averaging techniques in order to compare the different ecological models and to explore and interpret the parameters of interest combining predictions from all the four of them.

A. HMC and VB techniques

The HMC method is a Monte Carlo technique that uses Hamiltonian dynamics in order not only to explore efficiently the target distribution but also to propose distant samples in the parameter space that do not exclusively depend on the current state of the Markov chain like considered in previous MCMC methodology [Steve et al \(2011\)](#). In this way, many performance challenges are tackled like either the low convergence due to the fact that the parameter space with high posterior support is not reached or the poor exploration of the target distribution due to its multi-modality or its shape irregularities. The existence of Hamiltonian dynamics in the system of the joint density mass function allows the preservation of volume and hence adequate trajectories can be used to define complex mappings of the parameter state space without the need to account for cumbersome Jacobian calculations [Barber et al \(2003\)](#). Thus, by carefully designing automated trajectory realizations in the Hamiltonian dynamics system, the Stan team managed to create an augmented software called STAN [Carpenter et al \(2017\)](#), which materializes HMC sampling for the parameters of interest.

Moreover, independently, Automatic Differentiation Variational Inference (ADVI) technique is referred to the machine learning field [Blei et al \(2017\)](#). The latter is a VB method and posterior target distributions are approximated by choosing the closest distribution to a parametric family of tractable distributions like the exponential family via optimization. In order to achieve this point-wise estimations of the parameters of the family distribution are estimated so that the Kullback–Leibler ‘KL’ divergence function is minimized. Specifically, since the KL divergence is intractable the Evidence Lower Bound is maximized instead [Blei et al \(2017\)](#).

B. Model selection and model averaging

In case there are m models $(\mathcal{M}_1, \dots, \mathcal{M}_m)$ under consideration, the posterior probability of the suitability of the i^{th} model given the data \mathbf{y} , is given by

$$p(\mathcal{M}_i|\mathbf{y}) = \frac{p(\mathbf{y}|\mathcal{M}_i)p(\mathcal{M}_i)}{\sum_{k=1}^m p(\mathbf{y}|\mathcal{M}_k)p(\mathcal{M}_k)} \quad (S1)$$

where $p(\mathcal{M}_i)$ expresses the prior belief for the i^{th} model, while the $p(\mathbf{y}|\mathcal{M}_i)$ is the model evidence also called ‘marginal likelihood’ and it can be interpreted as the likelihood over the space of models, marginalizing out the parameters of the i^{th} model. The ratio of the marginal likelihoods between two models $p(\mathbf{y}|\mathcal{M}_i)/p(\mathbf{y}|\mathcal{M}_j)$ is called Bayes factor and is the posterior odds of the null hypothesis that the i_{th} model fits better the data than the j_{th} model does when the prior probability of the null is one-half [Kass et al \(1995\)](#). The Bayes factor is used in order to give evidence for the most probable model given the data, when comparing two alternative models [Kass et al \(1995\)](#).

In the case of Bayesian model averaging, the model selection uncertainty is taking into account in statistical inference. The joint posterior $p(\mathcal{M}_i, \boldsymbol{\theta}_i|\mathbf{y})$ of the i^{th} model with vector of parameters $\boldsymbol{\theta}_i$, using the Baye’s rule, is proportional to the product of the likelihood of the i^{th} model times the prior distribution of the parameters $p(\boldsymbol{\theta}_i)$ times the prior distribution $p(\mathcal{M}_i)$ (that expresses our uncertainty of the i^{th} model)

$$p(\mathcal{M}_i, \boldsymbol{\theta}_i|\mathbf{y}) \propto p(\mathbf{y}|\boldsymbol{\theta}_i, \mathcal{M}_i) \cdot p(\boldsymbol{\theta}_i) \cdot p(\mathcal{M}_i). \quad (S2)$$

The uncertainty of the i^{th} model given the data can then be re-expressed via the posterior probability $p(\mathcal{M}_i|y)$ defined by the ratio in (S1), in case of existence of multiple models. The posteriors of the models can be thought as weights that are critical to the Bayesian model averaging as they can be used to extract useful weighted statistics from the data distribution while at the same time taking into account model uncertainties. Estimation of model parameters and model uncertainties can be achieved either by directly sampling from the joint posterior (S2) or by approximating the marginal likelihood of each model independently and, accordingly, by controlling the outcomes with a view to formulating proper weights and proceeding with the calculation of the averaged statistics. For the former case, techniques like the reversible jump MCMC (Green, 1995; George and McCulloch, 1997) and variable selection samples (Carlin and Chib, 1995; Kuo and Mallick, 1998; Dellaportas et al, 2000) are used. On the other hand, for the later case, techniques of marginal likelihood approximations via thermodynamic integration Friel and Pettitt (2008), bridge sampling Meng and Wong (1996), importance sampling Perrakis et al (2014) or via information- criteria perspective like in Kass et al (1995) are used.

B.1. Information criteria

The criteria used in the current work are the Akaike information criterion ‘AIC’, the Bayesian information criterion ‘BIC’, the Deviance information criterion ‘DIC’, the Watanabe–Akaike information criterion ‘WAIC’ and the Leave-one-out cross-validation criterion ‘Loocv’. Briefly, these criteria provide an approximation of the expected log predictive density for new-coming data while correcting bias from data usage. In particular AIC Akaike (1974) is defined as the difference

$$AIC(\mathcal{M}_i) = -2 \log p(y|\hat{\theta}_i) + 2k_i$$

where $\hat{\theta}_i$ is the maximum likelihood estimate ‘MLE’ of the k_i parameters of the i^{th} model. Similarly, BIC Schwarz (1978) is defined as the difference

$$BIC(\mathcal{M}_i) = -2 \log p(y|\hat{\theta}_i) + k_i \cdot \log(n)$$

where n is the sample size. In addition, DIC Spiegelhalter et al (2002) is defined as the following difference:

$$DIC(\mathcal{M}_i) = -2 \log p(y|\hat{\theta}_i) + 2p_{DIC}$$

where $\hat{\theta}_i$ is the posterior mean of the parameters of the i^{th} model, whereas p_{DIC} is the effective number of parameters and it is evaluated following (Spiegelhalter et al, 2002; Gelman et al, 2013) by either

$$p_{DIC_1} = E_{\theta_i|y} \{-2 \log p(y|\theta_i)\} + 2 \log \{p(y|\hat{\theta}_i)\},$$

or

$$p_{DIC_2} = \frac{Var_{\theta_i|y} \{\log p(y|\theta_i)\}}{2},$$

where $E_{\theta_i|y} \{\log p(y|\theta_i)\}$ is an expectation over the posterior density of θ_i , whereas $Var_{\theta_i|y} \{\log p(y|\theta_i)\}$ is the variance of the log likelihood of observed data y , over the posterior density of θ_i . Furthermore, WAIC Watanabe (2010) is defined as the following difference:

$$WAIC(\mathcal{M}_i) = -2 \sum_{j=1}^N \log E_{\theta_i} \{p(y_j|\theta_i)\} + 2p_{WAIC}$$

where $E_{\theta_i} \{p(y_j|\theta_i)\}$ is the expectation of the probability at y_j data point over the posterior distribution of the parameters of the i^{th} model, whereas p_{WAIC} is the effective number of parameters and it is evaluated following Gelman et al (2013) by either

$$p_{WAIC_1} = 2 \sum_{j=1}^N \left[\log E_{p(\theta_i|y)} \{p(y_j|\theta_i)\} - E_{p(\theta_i|y)} \{\log p(y_j|\theta_i)\} \right]$$

or

$$p_{WAIC_2} = \sum_{j=1}^N \text{var}_{p(\theta_i|y)} \{\log p(y_j|\theta_i)\}$$

where $E_{p(\theta_i|y)} \{\log p(y_j|\theta_i)\}$ is the expectation of the logarithm at value y_j over the posterior density of θ_i , whereas $\text{var}_{p(\theta_i|y)} \{\log p(y_j|\theta_i)\}$ is the variance of the log posterior density of the observed data y_j , over the posterior density of θ_i .

Furthermore, LooCV [Gelman et al \(2013\)](#) is defined as the following difference:

$$\text{LooCV}(\mathcal{M}_i) = -2 \sum_{j=1}^N \log E_{\theta_i^{-j}} \{p(y_j|\theta_i^{-j})\} - 2\beta_{\text{LooCV}}$$

where $E_{\theta_i^{-j}} \{p(y_j|\theta_i^{-j})\}$ is the expectation of the probability at y_j data point over the posterior distribution of the parameters of the i^{th} model. The posterior distribution $p(\theta_i^{-j}|\mathbf{y}_{-j})$ is sampled considering a partition of the data, leaving one data value (y_j) out of the original sample. The β_{LooCV} is a bias correction of the measure and it is evaluated following [Gelman et al \(2013\)](#) by

$$\beta_{\text{LooCV}} = \sum_{j=1}^N \log E_{\theta_i} \{p(y_j|\theta_i)\} - \frac{1}{N} \sum_{\kappa=1}^N \sum_{j=1}^N \log E_{\theta_i^{-\kappa}} \{p(y_j|\theta_i^{-\kappa})\}$$

where $E_{\theta_i^{-\kappa}} \{p(y_j|\theta_i^{-\kappa})\}$ is the expectation of the probability at y_j data point over the posterior distribution of the parameters of the i^{th} model leaving out the κ^{th} observation.

B.2. Marginal likelihood estimation techniques

The marginal likelihood can be viewed as a normalizing constant $z_i = p(\mathbf{y}|\mathcal{M}_i)$ of the density $q(\theta_i|\mathbf{y}) = p(\mathbf{y}|\theta_i) \cdot p(\theta_i)$ within the i^{th} ecological model that includes parameters θ_i . In the general scheme of comparing the two densities q_0 and q_1 of interest, as in the case of the Bayes factor of two models or in the case model's prior and posterior, a general path from q_0 to q_1 can be created according to [Gelman and Meng \(1998\)](#) using a class of densities $p(\theta_i|\mathbf{y}, t)$ on the same space indexed by the continuous auxiliary variable say $t \in [0, 1]$. A key formula that links the corresponding normalizing constant $z(t)$ and the unnormalized density $q(\theta_i|\mathbf{y}, t)$ that correspond to the sampling distribution $p(\theta_i|\mathbf{y}, t)$ is given by:

$$\frac{d}{dt} \log z(t) = \int \frac{1}{z(t)} \frac{d}{dt} q(\theta_i|\mathbf{y}, t) p(\theta_i|\mathbf{y}, t) d\theta_i = E_t \left\{ \frac{d}{dt} \log q(\theta_i|\mathbf{y}, t) \right\}, \quad (\text{S3})$$

where the expectation is with respect to the sampling distribution $p(\theta_i|\mathbf{y}, t)$.

In addition, another key formula of estimating a ratio of normalizing constants has been of great interest such as in computing likelihood ratios in hypothesis testing or in computational physics in estimating free energy differences, or in computing the Bayes factor in Bayesian framework [Meng and Wong \(1996\)](#). The general formula is as follows:

$$\frac{z_1}{z_0} = \frac{p(\mathbf{y}|\theta, t=1)}{p(\mathbf{y}|\theta, t=0)} = \frac{E_0 \{h(\theta) \cdot q(\theta|\mathbf{y}, t=1)\}}{E_1 \{h(\theta) \cdot q(\theta|\mathbf{y}, t=0)\}} \quad (\text{S4})$$

where E_0 and E_1 expectations are with respect to posterior distribution densities $p(\theta|\mathbf{y}, t=0)$ and $p(\theta|\mathbf{y}, t=1)$ respectively, whereas the bridge function $h(\theta)$ is defined and overlapped by the common support of the former densities.

Using general formulas (S3) and (S4), several marginal probability evaluation schemes of the i^{th} model are derived Gelman and Meng (1998). The power posterior sampling Friel and Pettitt (2008), the importance sampling Perrakis et al (2014) and the bridge sampling (Meng and Wong, 1996; Overstall and Forster, 2010) techniques are used for the current work.

In the power posterior case, formula (S3) is integrated with respect to variable t and $q(\theta_i|y, t)$ is substituted with density $p(\theta_i|y)^t p(\theta_i)$. The marginal likelihood $z_i = p(y|\mathcal{M}_i)$ is derived from logarithmic scale by the equation:

$$\log \{p(y|\mathcal{M}_i)\} = \int_0^1 E_{\theta_i|y,t} \{\log p(y|\theta_i)\} dt \quad (S5)$$

where expectation $E_{\theta_i|y,t}$ is taken with respect to the density $p(\theta_i|y)^t p(\theta_i)$ which is defined as the power posterior at temperature t Friel and Pettitt (2008).

Additionally, the standard error se_i for the i th model estimator (S5), as shown in section S5 of the appendix is approximated by:

$$\hat{se}_i = \sqrt{\frac{(t_2 - t_1)^2}{2} s_1^2 + \sum_{k=2}^{n-1} \frac{(t_k - t_{k-1})^2}{2} s_k^2 + \frac{(t_n - t_{n-1})^2}{2} s_n^2},$$

where t_k is the time after discretization $0 = t_0 < t_1 < t_k < t_n = 1$ and s_k is the standard error of the corresponding estimation $\log \{p(y|\mathcal{M}_i)\}$ given in (S5).

In the case of importance sampling, the marginal likelihood is assessed by introducing the proper density function g . After sampling from the proposed density function g , the marginal likelihood is calculated as with respect to g as:

$$p(y|\mathcal{M}_i) = E_g \left\{ \frac{q(\theta_i|y)}{g(\theta_i)} \right\}$$

Following Perrakis et al (2014), we use the density $q(\theta_i|y)$ equal to $p(y|\theta_i, \phi_i) \cdot p(\theta_i, \phi_i)$ and the auxiliary importance function g used is as follows:

$$g(\theta_i) = g(\theta_i, \phi_i) = p(\theta_i|y)p(\phi_i|y), \quad (S6)$$

where (θ_i, ϕ_i) are the parameters of the i^{th} model divided into two blocks θ_i and ϕ_i which may or may not be independent. The right hand side of (S6) is the product of the marginal posterior distributions of the block. Thus, the marginal probability which gives the target value is given as follows:

$$p(y|\mathcal{M}_i) = \iint \frac{p(y, \theta_i, \phi_i)}{g(\theta_i, \phi_i)} g(\theta_i, \phi_i) d(\theta_i, \phi_i) = E_g \left\{ \frac{p(y, \theta_i, \phi_i)}{g(\theta_i, \phi_i)} \right\} \quad (S7)$$

The standard error se_i of (S7) as shown in section S6 of the appendix is:

$$\hat{se}_i = \sqrt{\frac{1}{K} \sum_{j=1}^K \left\{ \frac{p(y|\theta^j, \phi^j) \cdot p(\theta^j, \phi^j)}{g(\theta^j)} - \hat{z}_i \right\}^2},$$

where \hat{z}_i is the estimation of the corresponding marginal probability (in the same form of (S7)), while (θ^j, ϕ^j) are draws $j = 1, 2, \dots, K$ from the importance function in (S6).

Additionally, using an alternative version of (S4) in (Meng and Wong, 1996; Frühwirth-Schnatter, 2004; Overstall and Forster, 2010) the marginal likelihood of a single model is evaluated using bridge sampling by the formula:

$$z_i = p(y|\mathcal{M}_i) = \frac{E_g \{h(\theta_i) \cdot q(\theta_i|y)\}}{E_p \{h(\theta_i) \cdot g(\theta_i)\}}, \quad (S8)$$

where E_g and E_p are the expectations with respect to $g(\theta_i)$ a so-called proposal distribution and to $p(\theta_i|\mathbf{y})$ the i^{th} model posterior distribution respectively.

The bridge function $h(\theta_i)$ is selected to minimize the relative mean-squared error of (S4). Following Meng and Wong (1996) the bridge function is specified by:

$$h(\theta_i) = \mathcal{C} \cdot \frac{1}{s_1 \cdot q(\theta_i|\mathbf{y}) + s_2 \cdot p(\mathbf{y}) \cdot g(\theta_i)}, \quad (\text{S9})$$

where $s_1 = N_1/N_1 + N_2$, $s_2 = N_2/N_1 + N_2$ and \mathcal{C} is a constant. N_1 is the sample size from the posterior and N_2 is the sample size from $g(\theta_i)$.

The optimal bridge function in (S9) includes the marginal likelihood under-assessment so that it cannot be evaluated directly. For this purpose the iterative method suggested by Meng and Wong (1996) and applied in Gronau et al (2020) in R software R Core Team (2020) is used. The alternatives used in place of distribution g is either a multivariate normal distribution with mean vector and covariance matrix that match the respective posterior samples quantities or a standard multivariate normal distribution in combination with a warped posterior distribution of which the first three moments correspond to Gronau et al (2020).

Moreover, following Frühwirth-Schnatter (2004) the relative mean square error $RE_i^2 = \frac{E\{\hat{z}_i - z_i\}^2}{z_i^2}$ of (S8) is evaluated by the formula:

$$\widehat{RE}_i^2 = \frac{1}{N_2} \frac{V_g\{f_1(\theta_i)\}}{E_g^2\{f_1(\theta_i)\}} + \frac{\rho_{f_2}(0)}{N_1} \frac{V_p\{f_2(\theta_i)\}}{E_p^2\{f_2(\theta_i)\}}, \quad (\text{S10})$$

where $f_1(\theta_i) = \frac{q(\theta_i|\mathbf{y})}{s_1 \cdot q(\theta_i|\mathbf{y}) + s_2 \cdot g(\theta_i)}$, $f_2(\theta_i) = \frac{g(\theta_i)}{s_1 \cdot q(\theta_i|\mathbf{y}) + s_2 \cdot g(\theta_i)}$, $V_g(f_1(\theta_i)) = \int \{f_1(\theta_i) - E(f_1(\theta_i))\}^2 g(\theta_i) d\theta$ is the variance of $f_1(\theta_i)$ with respect to $g(\theta_i)$. The term $\rho_{f_2}(0)$ in (S10) corresponds to the normalized spectral density of the auto-correlated process $f_2(\theta_i)$ at the frequency 0.

Following Gronau et al (2020) the square root of RE^2 can be interpreted as coefficient of variation provided that the bridge sampling estimator \hat{z}_i is unbiased. Then the standard error se_i of the bridge estimator is evaluated by the product $\widehat{se}_i = \widehat{RE} \cdot E(\hat{z}_i)$

B.3. BMA weights

We can derive a weighted prediction \tilde{y} over the m different models $\mathcal{M}_1, \mathcal{M}_2, \dots, \mathcal{M}_m$ predictions $\hat{y}_1, \hat{y}_2, \dots, \hat{y}_m$ by imposing appropriate weights w_1, w_2, \dots, w_m .

$$\tilde{y} = \sum_{i=1}^m \hat{y}_i \cdot w_i \quad \text{and} \quad \sum_{i=1}^m w_i = 1.$$

In the Bayesian framework, model weights definition is straightforward. The model weights used are the posterior model weights $w_i = p(\mathcal{M}_i|\mathbf{y})$ given in (S1) that represent the relative probability of each model given the data. So a major challenge is to estimate these Bayesian weights. Except for using the marginal likelihood estimations mentioned in previous section, we also investigate approximations of the weights by using the BIC for each model. In particular, model weights can be estimated through the following equations (Kass et al, 1995; Buckland et al, 1997):

$$w_i = \frac{e^{-0.5 \cdot (BIC(\mathcal{M}_i))}}{\sum_{j=1}^m e^{-0.5 \cdot (BIC(\mathcal{M}_j))}}. \quad (\text{S11})$$

Instead of BIC, the AIC, DIC, WAIC and LooCV are also used in (S11). We investigate both approaches in insect observed rates and compare the results taking into account model complexity, data scarcity and Biological interpretation.

S4. POWER POSTERIOR FOR GAUSSIAN AND INVERSE GAMMA DISTRIBUTION

Following [Friel and Pettitt \(2008\)](#) the power posterior in (S5) includes the likelihood raised to the power of t $p(\theta_i|\mathbf{y})^t$.

In the the Gaussian case, the likelihood involved becomes:

$$p(\mathbf{y}|\theta)^t = p^t(\mathbf{y}|\mu, \sigma^2) = \frac{e^{-\frac{1}{2}(\sqrt{t} \cdot \frac{\mathbf{y}-\mu}{\sigma})^2}}{\sqrt{2\pi\sigma^2}} = p\left(\mathbf{y}|\mu, \frac{\sigma^2}{t}\right) \cdot \frac{\sqrt{t}}{t}.$$

Inserting the current ecological model $r(T; \theta)$, the log of the power posterior is given by:

$$\log(p(\mathbf{y}|\theta)^t) = -\frac{1}{2} \log(2\pi\sigma^2) - \frac{1}{2} \left(\sqrt{t} \cdot \frac{\mathbf{y} - r(T; \theta)}{\sigma} \right)^2. \quad (S1)$$

In the Inverse Gamma case, the likelihood involved becomes:

$$\begin{aligned} p(\mathbf{y}|\theta)^t &= p(\mathbf{y}|\alpha, \beta)^t = \frac{\beta^{\alpha \cdot t}}{\Gamma^t(\alpha)} \mathbf{y}^{-\alpha \cdot t - t} \exp\left(-\frac{\beta \cdot t}{\mathbf{y}}\right) = \\ &= \frac{(\beta \cdot t)^{\alpha \cdot t}}{\Gamma(\alpha \cdot t)} \frac{\Gamma(\alpha \cdot t)}{\Gamma^t(\alpha) \cdot (t)^{\alpha \cdot t}} \mathbf{y}^{-\alpha \cdot t - 1} \mathbf{y}^{1-t} \exp\left(-\frac{\beta \cdot t}{\mathbf{y}}\right) = \\ &= \text{InG}(\alpha \cdot t, \beta \cdot t) \cdot \frac{\Gamma(\alpha \cdot t)}{\Gamma^t(\alpha) \cdot (t)^{\alpha \cdot t}} \cdot \mathbf{y}^{1-t}. \end{aligned} \quad (S2)$$

Inserting the current ecological model $r(T; \theta)$, the log of the power posterior is given by:

$$\begin{aligned} \log(p(\mathbf{y}|\theta)^t) &= \alpha \cdot t \cdot (\log(\alpha - 1) + \log(r(T; \theta))) - \\ &= t \cdot \log(\Gamma(\alpha)) - t \cdot (\alpha + 1) \cdot \log(\mathbf{y}) - \frac{(\alpha - 1) \cdot (r(T; \theta)) \cdot t}{\mathbf{y}}. \end{aligned} \quad (S3)$$

S5. ESTIMATION OF VARIANCE OF POWER POSTERIOR METHOD

$$\begin{aligned} \hat{\sigma}_y^2 &= \text{Var}\{\log P(\mathbf{y}|\theta)\} = \text{Var}\left\{\int_0^1 E\{\log P(\mathbf{y}|\theta)\} dt\right\} \simeq \\ &= \sum_{i=1}^{n-1} \frac{1}{4} \text{Var}\left\{E_{\theta|y, t_i}\{\log P(\mathbf{y}|\theta)\} + E_{\theta|y, t_{i+1}}\{\log P(\mathbf{y}|\theta)\}\right\} (t_{i+1} - t_i)^2 \simeq \\ &= \sum_{i=1}^{n-1} \left[\frac{sd_{\theta|y, t_i}^2}{2} \right] \cdot (t_{i+1} - t_i)^2 \end{aligned} \quad (S1)$$

where $sd_{\theta|y, t_i}$ is the std error estimated at the t_i temperature

S6. ESTIMATION OF VARIANCE OF IMPORTANCE SAMPLING METHOD

The marginal likelihood estimate for the i th model is given by $m = p(\mathbf{y}|M_i) = E_g\left\{\frac{q(\theta_i|\mathbf{y})}{g(\theta_i)}\right\} = \int \frac{q(\theta_i|\mathbf{y})}{g(\theta_i)} g(\theta_i) d\theta_i$ provided $g(\theta_i) > 0$ whenever $q(\theta_i|\mathbf{y}) \neq 0$ where the density $q(\theta_i|\mathbf{y})$ is equal to $p(\mathbf{y}|\theta_i, \phi_i) \cdot p(\theta_i, \phi_i)$ and the auxiliary importance function g used is the following: $g(\theta_i) = g(\theta_i, \phi_i) = p(\theta_i|\mathbf{y}) p(\phi_i|\mathbf{y})$. Removing the i th model index we can evaluate the marginal likelihood via MC integration which gives the formula below:

$$\hat{z}_y = \hat{p}(\mathbf{y}) = \frac{1}{M} \sum_{j=1}^M \frac{q(\theta^j|\mathbf{y})}{g(\theta^j)}$$

where $\theta^j, j = 1, 2, 3, \dots, M$ are obtained from density: $g(\theta_i)$.

$$E_g(\hat{z}_y) = \frac{1}{M} \sum_{j=1}^M E_g \left\{ \frac{q(\theta^j|y)}{g(\theta^j)} \right\} = p(y) = m.$$

Assuming that $Cov \left\{ \frac{q(\theta^i|y)}{g(\theta^i)}, \frac{q(\theta^j|y)}{g(\theta^j)} \right\} = 0$, for $i \neq j$

$$\begin{aligned} V_g(\hat{z}_y) &= V_g \left(\frac{1}{M} \sum_{j=1}^M \left\{ \frac{q(\theta^j|y)}{g(\theta^j)} \right\} \right) = \frac{1}{M^2} \sum_{j=1}^M V_g \left\{ \frac{q(\theta^j|y)}{g(\theta^j)} \right\} + \\ &\frac{1}{M^2} \sum_{k,j=1}^M Cov_g \left\{ \frac{q(\theta^k|y)}{g(\theta^k)}, \frac{q(\theta^j|y)}{g(\theta^j)} \right\} = \\ &\frac{1}{M^2} \sum_{j=1}^M V_g \left\{ \frac{q(\theta^j|y)}{g(\theta^j)} \right\} = \frac{1}{M} V_g \left\{ \frac{q(\theta|y)}{g(\theta)} \right\} = \frac{1}{M} \left\{ E_g \left\{ \frac{q(\theta|y)}{g(\theta)} \right\}^2 - E_g^2 \left\{ \frac{q(\theta|y)}{g(\theta)} \right\} \right\} = \\ &\frac{1}{M} \int_G \left\{ \frac{q(\theta|y)}{g(\theta)} \right\}^2 g(\theta) d\theta - \frac{1}{M} m^2 \Rightarrow \end{aligned}$$

Also, using properties of expectation and the fact that $g(\theta)$ is proper

$V_g(\hat{z}_y) = \frac{1}{M} \int_G \left\{ \frac{q(\theta|y) - m \cdot g(\theta)}{g(\theta)} \right\}^2 g(\theta) d\theta = \frac{\sigma_y^2}{M}$ The latest can be used to estimate the std error of the estimator \hat{z}_y via the formula:

$$\hat{\sigma}_y = \sqrt{\frac{1}{K} \sum_{j=1}^K \left\{ \frac{q(\theta^j|y)}{g(\theta^j)} - \hat{z}_y \right\}^2} \quad (S1)$$

where $\theta^j, j = 1, 2, 3, \dots, K$ are obtained from density $g(\theta_i)$.

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