

Supplementary Material for “Spatial phenotypic organization affects the dynamics of metapopulations according to their connectedness”

The Authors (anonymised for submission)

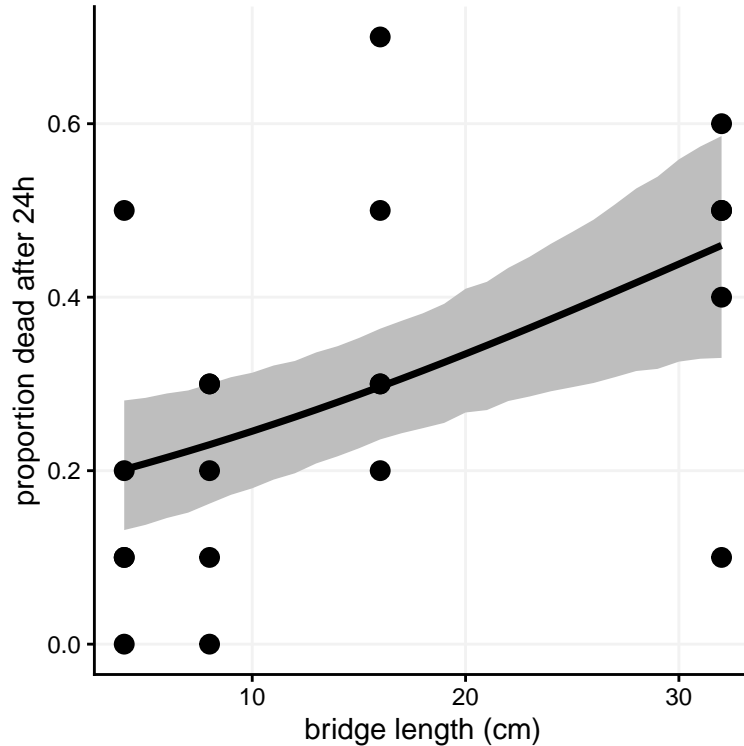
S01 – Quantification of connectedness-dependent dispersal mortality

We tested how dispersal success and individual survival is affected by the length of a Parafilm bridge in a setup similar to the one described in the main text, to empirically demonstrate that the lengths we chose in the main experiment do apply a significant selective pressure onto dispersers.

We tested 4, 8, 16 and 32 cm-long bridges, with five independent replicates per length. The plastic bridges were mounted on a bed of cotton, kept wet using abundant distilled water, and connected on one end only to a fresh bean (*Phaseolus vulgaris* L. cv. Prélude) leaf cut (2.5×1.5 cm² rectangle) to provide secure shelters and food sources to the mites. At the opposite ends of each bridge, we placed 10 adult females from our LS-VL stock population using a thin pen brush. Female age was not controlled for, to better approximate a real, non-synchronized population. Females were placed on a “waiting area”, delimited by a strip of wet paper placed orthogonally onto the bridge approximately 2 cm from the leaf-free end, in order to stop female dispersal until all individuals had been placed. Similar strips were used to lock the leaves in place on the wet cotton and to the bridges, as well as at the open end of the plastic bridge to keep it adherent to the wet cotton. No paper strips were placed along the bridge itself, so dispersing mites were not prevented from falling into wet cotton. All replicates were initialized at the same time, by removing the paper strips that stopped movement; the bridges were then stored into a climatically controlled room for 24 hours ($\simeq 25^{\circ}\text{C}$, L:D 16:8). We then counted the number of live mites on the bridges themselves and the arrival leaves; every unaccounted individual was considered dead and sunken into the wet cotton. We analyzed the effect of bridge length (as a continuous variable) on the proportion of dead individuals using a binomial generalized linear model with weakly informative priors (Normal(0, 1.5) for the intercept and Normal(0, 1) for the slope)(McElreath 2020).

Results

The proportion of dead individuals increased with the length of the plastic bridge the mites were placed upon ($\beta = 0.04$ [0.02, 0.07], **Fig. S01.1**).



27

28 **Figure S01.1** – Mortality rate as a function of bridge length during preliminary trials. Both observed values
 29 (dots) and posterior means with 95% credible band are plotted.

30 **S02 – Experimental metapopulations – practical details and main-** 31 **tenance during experiments**

32 All beans leaves used in the experiment were sourced from bean plants grown without using any pesticide
 33 and under controlled climatic rooms ($21 \pm 1^\circ\text{C}$, L:D 16:8).

34 Each metapopulation was independently mounted on a bed of wet cotton, which was kept soaked with distilled
 35 water to provide hydration to the leaves and to create a barrier to prevent the mites from escaping or moving
 36 between patches outside the designated routes. To ensure constant hydration, automatic gardening pumps
 37 (GARDENA® set 1265-20) were connected to a reserve of distilled water and set to deliver a fixed amount of
 38 water through pipes during 1 minute once every 8 hours. The water flow was monitored to ensure that it
 39 never flooded the leaves or the bridges, to prevent additional stress and ensure that the connection between
 40 patches was always maintained.

41 Landscapes were contained in top-opened plastic crates whose sides were covered in a thick Vaseline layer, to
 42 further ensure that no cross-contamination could happen between different metapopulations. The water pipes
 43 were coated in Vaseline as well, and were positioned so that there was as little direct contact with the cotton
 44 as possible, to reduce the chance of mites climbing on them. To ensure resources remained fresh throughout
 45 the experiment, every leaf in the setup was refreshed with a new one once a week, at the same time counting
 46 was done. First, adult females were counted on the leaf under a stereomicroscope; then they were moved to
 47 the new leaf squares, following the protocol described in the main text. Finally, the old leaves were laid above
 48 the new ones, sustained by short sticks to reduce direct contact (to insure ventilation and prevent the spread
 49 of molds and fungal infestations), and left in place for 48 hours to allow males and juveniles to move on the
 50 new leaves as well. By keeping the old leaves detached from the cotton, we also induced a quick desiccation
 51 and a sudden drop of the food quality, thus stimulating the dispersal of the individuals towards the new leaf.

After 48 hours, all the old leaves were removed along with the sticks to prevent mites from spinning webs around them.

S03 – Stationarity in experimental metapopulations

A key prerequisite to the use of the variability metrics in Wang and Loreau (2014) is stationarity. To check for stationarity in our metapopulations, we fit a negative binomial generalized linear model including metapopulation-specific intercepts and effects of time (priors are the same as for the negative binomial model described **Supplementary Material S04**). In the large majority of the metapopulations (21 out of 24), we find no evidence of deviations from stationarity (no temporal trend) during the experimental run (**Figure S03.1**).

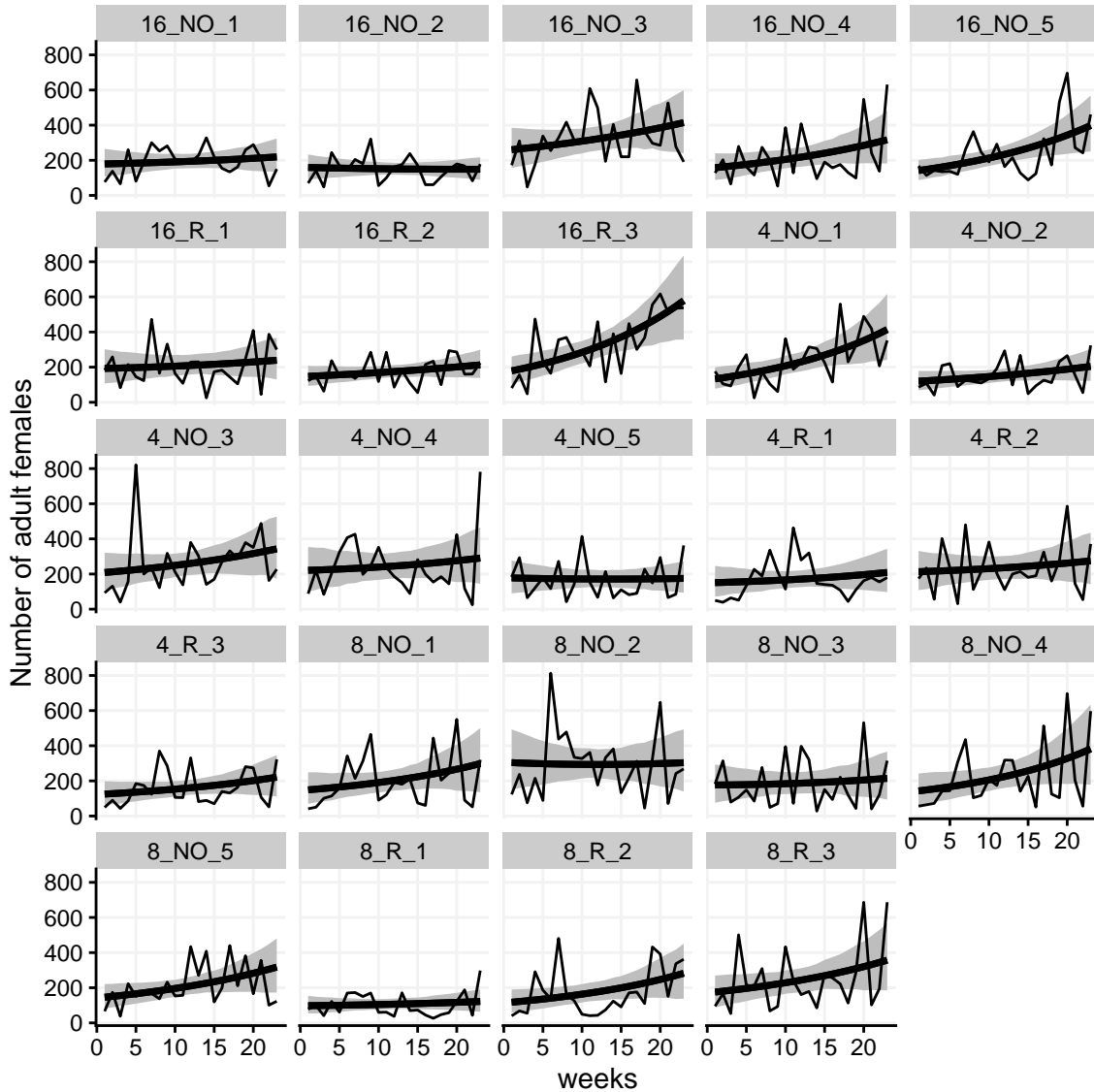


Figure S03.1 – Metapopulation sizes (number of adult females in all 9 patches of a metapopulation) as a function of time. Both observed values (thin lines) and the posterior means with 95% credible band are plotted. Each subplot represents a different replicate metapopulation.

65 S04 – Models description

66 Patch-level model

67 We fit a generalized linear mixed/multilevel model to the abundance data. This Poisson model (because of
 68 count data) includes “random” effects of metapopulation ID (to account for the fact some replicates may
 69 have higher/lower average population sizes) and patch nested in ID (because patches may differ beyond the
 70 effect of treatment, local connectedness and replicate). Importantly, it also includes a time random effect,
 71 to account for temporal patch variance-covariance. You can see below that we are estimating a separate
 72 temporal variance-covariance matrix for each replicate i . This means that (i) each patch has its own temporal
 73 variance, and patches from the same replicate can be correlated. We average everything downstream of the
 74 model as needed, but given the non-linearities everywhere in a GLMM, and the fact patch coordinates are
 75 arbitrary (we could have rotated metapopulations 90, 180 or 270° without changing anything meaningful), it
 76 is better to calculate every metric of interest replicate by replicate first and only average later. It is important
 77 to note that the inclusion of temporal covariance matrices generates what are *de facto* observation-level
 78 random effects (Harrison 2014), so there is no further overdispersion to account for.

79 The intuition behind this formulation (latent residuals via OLRE + specified covariance structure) is the same
 80 as in this comment by Paul Bürkner on the brms R package development page (<https://github.com/paul-buerkner/brms/issues/600#issuecomment-511677732>).
 81

82 The model is *de facto* a multivariate model, with a separate response for each x, y combination. However, it
 83 can just as easily be rewritten as an univariate model for fitting purposes, without changing anything to
 84 the multivariate nature of the underlying model (in particular, the among-patches temporal correlations are
 85 preserved). The univariate re-formulation makes it easier for some packages to estimate some parameters
 86 (here the fixed effects ones); this formulation is the one we provide below.

87 The formula for the model for the number of adult females $N_{i,x,y,t}$ in metapopulation i , in the patch of
 88 coordinates x, y at time t is

$$\begin{aligned}
 & N_{[i,x,y,t]} \sim \text{Poisson}(\lambda_{[i,x,y,t]}), \\
 & \log(\lambda_{[i,x,y,t]}) = B_0 + \sum_{j=1}^J (B_j \times x_{j[i,x,y]}) + a_{[i]} + c_{[i,x,y]} + d_{[i,x,y,t]}, \\
 & a_{[i]} \sim \text{Normal}(0, \sigma_a), \\
 & c_{[i,x,y]} \sim \text{Normal}(0, \sigma_c), \\
 & \begin{bmatrix} d_{[i,1,1,t]} \\ \dots \\ d_{[i,3,3,t]} \end{bmatrix} \sim \text{MVNormal} \left(\begin{bmatrix} 0 \\ \dots \\ 0 \end{bmatrix}, \boldsymbol{\Omega}_{[i]} \right), \\
 & \boldsymbol{\Omega}_{[i]} = \begin{bmatrix} \sigma_{d[i,1,1]} & 0 & \dots \\ 0 & \ddots & \\ \vdots & & \sigma_{d[i,3,3]} \end{bmatrix} \mathbf{R}_{[i]} \begin{bmatrix} \sigma_{d[i,1,1]} & 0 & \dots \\ 0 & \ddots & \\ \vdots & & \sigma_{d[i,3,3]} \end{bmatrix},
 \end{aligned}$$

94 where B_j are the fixed effects (with B_0 the intercept), a are replicate/metapopulation random effects, c
 95 patch-level random effects, and d temporal abundance fluctuations (We use Latin letters here, rather than
 96 the usual Greek script, to avoid confusion with α, β, γ variabilities). $\boldsymbol{\Omega}_{[i]}$ is the temporal covariance matrix
 97 for the replicate i and $\mathbf{R}_{[i]}$ the corresponding correlation matrix. For implementation, we transform the
 98 treatment covariates into dummy centred variables following Schielzeth (2010), this has the added benefit of
 99 making B_0 the intercept of the “average” treatment.

100 All key metrics of interest in the present paper can be derived from this model:

- the mean local population size of the patch x, y in metapopulation i is $\mu_{i,x,y} = \exp(B_0 + \sum_{j=1}^J (B_j \times x_{j[i,x,y]}) + a_{[i]} + c_{[i,x,y]} + \frac{\sigma_{d[i,x,y]}^2}{2})$, i.e. the back-transformed sum of the patch-level latent mean and half the within-patch latent variance [based on the formula for the mean of the log-normal distribution; see also Villemereuil et al. (2016)]. Note that because the observed-scale mean depends on both the latent scale mean and the latent scale within-patch variance, and because our model allows both to vary between treatments, one cannot make inferences about treatment effects on means based on fixed effects alone;
- the observed-scale temporal variances and covariances w (to use the syntax in main text **Table 1**) can be derived from the latent scale patch-level means ($B_0 + \sum_{j=1}^J (B_j \times x_{j[i,x,y]}) + a_{[i]} + c_{[i,x,y]}$) and latent scale within-patch variances ($\sigma_{d[i,x,y]}^2$) using the procedures detailed in Villemereuil et al. (2016);
- α, β_2, φ and γ can be estimated for each metapopulation as outlined in main text **Table 1** once one has all the μ and w corresponding to that metapopulation.

Meta-population model

Similarly, we can write a (much simpler) model for the total metapopulation size (total number of adult females counted in the metapopulation at one time step) M . Because there are here no internal spatial correlations to worry about here, we can use a negative binomial model here to model the within-replicate temporal variation:

$$\begin{aligned}
 M_{[i,t]} &\sim \text{NegBinomial}(\lambda_{[i]}, \phi_{[i]}), \\
 \log(\lambda_{[i]}) &= B_0 + \sum_{j=1}^J (B_j \times x_{j[i]}) + c_{[i]}, \\
 \log(1/\phi_{[i]}) &= a_0 + \sum_{j=1}^J (a_j \times x_{j[i]}) + d_{[i]}, \\
 c_{[i]} &\sim \text{Normal}(0, \sigma_c), \\
 d_{[i]} &\sim \text{Normal}(0, \sigma_d).
 \end{aligned}$$

Here c and d refer to the metapopulation-level random effects, for the mean parameter and for the shape parameter, respectively. Similarly, B and a refer to the fixed effects coefficients for the mean and the shape. We fit the model for the overdispersion parameter on its log-transformed inverse: the inverse transformation (as suggested in the Stan language wiki: <https://github.com/stan-dev/stan/wiki/Prior-Choice-Recommendations>) is used to avoid giving too much prior weight to high overdispersion, the log transformation to keep ϕ estimates > 0 .

Rationale behind priors

Given the models complexity, we combined general weakly informative priors sensu McElreath (2020) with more informative priors based on preexisting density data from a previous study (De Roissart et al. 2015, 2016), which we multiplied as needed to match the total area of a patch/a metapopulation. Ignoring these prior sources of information led to models predicting consistently too high abundances (not shown), although relative differences between treatments remained qualitatively similar.

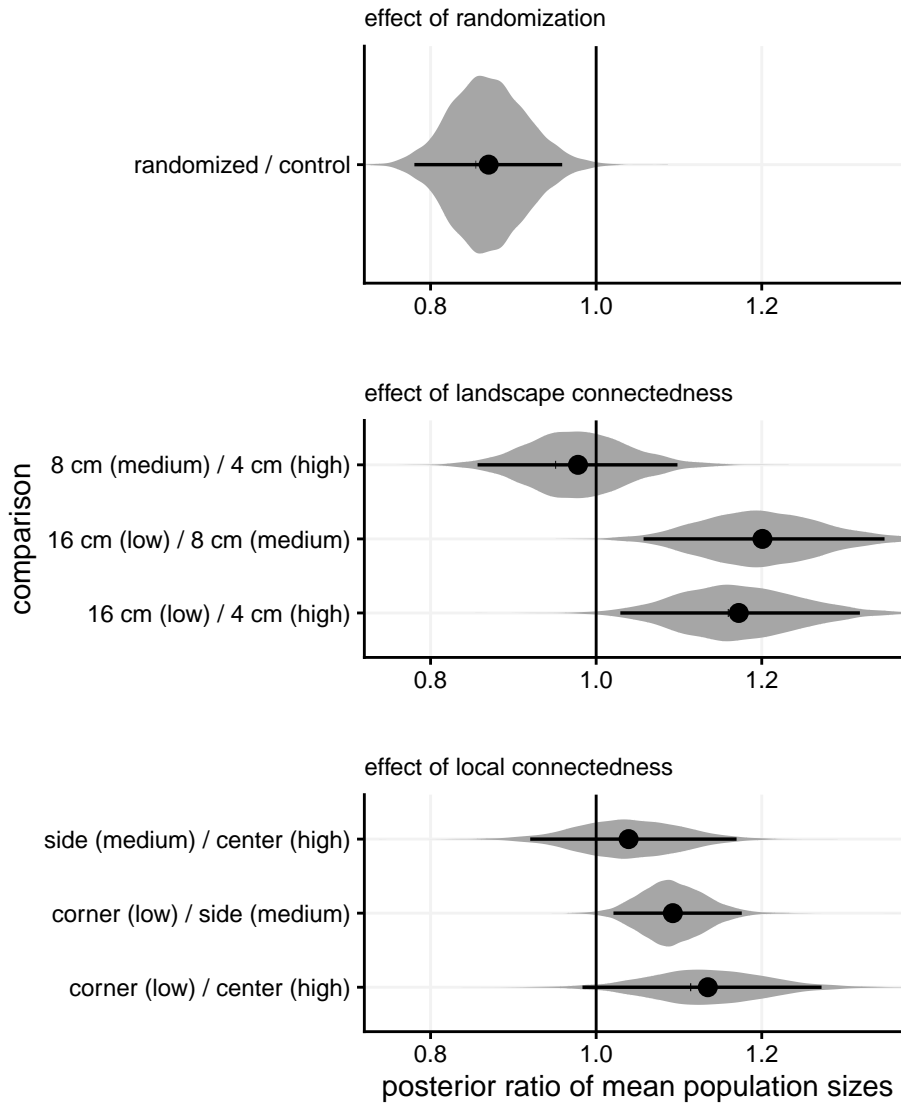
In the patch-level model, priors for the fixed-effects coefficients β_j (except β_0) and for the random effect correlation matrices followed McElreath's suggestions (here $\text{Normal}(0, 1)$ and $\text{LKJCorr}(2)$ respectively). Priors for the intercept β_0 and for the random effect standard deviations were based on the whole distribution of prior abundance data (De Roissart et al. 2015, 2016) and on the variance of that distribution, both on the

log scale. We used a $\text{Normal}(2.8, 1)$ prior for β_0 , and a Half – Normal(0, 0.5) for the σ parameters (when summing across the different random effect levels, this gives an overall prior for log-scale total variance centred on roughly 1, matching prior information).

In the metapopulation-level model, we replaced the prior for β_0 by $\text{Normal}(5, 1)$ in order to match the fact that metapopulations contain 9 patches, and used general purpose $\text{Normal}(0, 1)$ priors for all fixed-effects parameters linked to the shape ϕ .

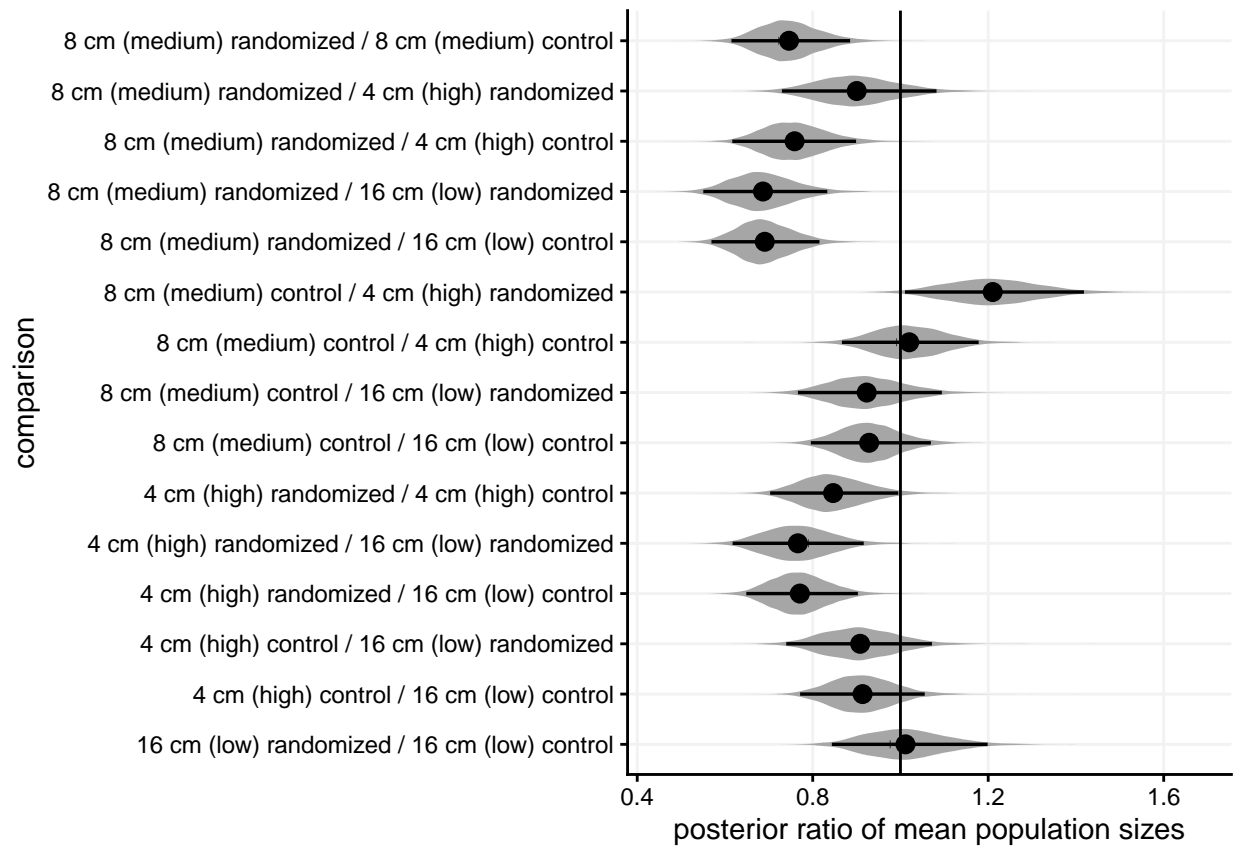
S05 – Posterior pairwise comparisons

The following plots describe the outcome of posterior pairwise comparisons between treatments, regarding local population sizes (Figs S05-1 to S05-3, match with main text Figs 1-2) and variability metrics (Figs S05-4 and S05-5, match with main text Fig. 3). In all cases, comparisons are ratios, and dots and segments represent the posterior mean and 95% Highest Density Interval.



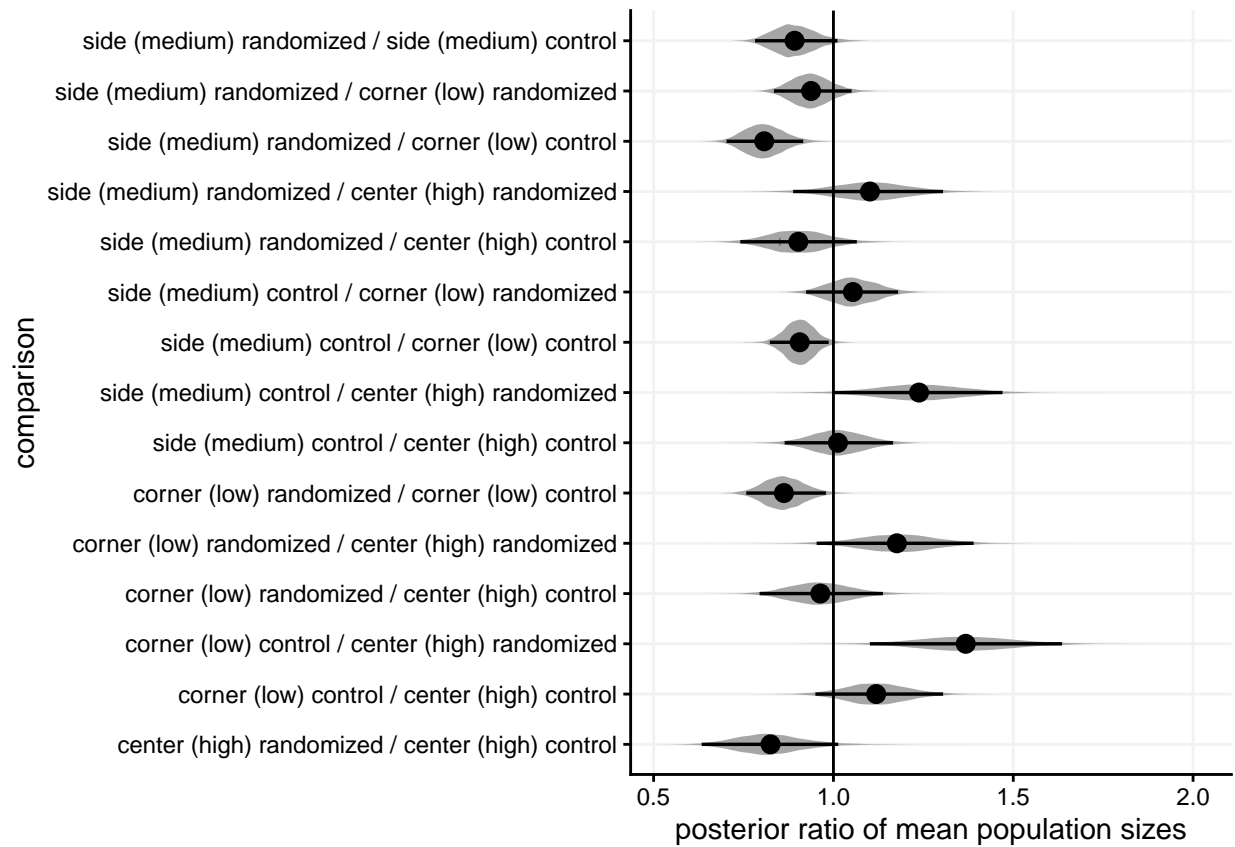
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Figure S05.1 – Additive effects of connectedness and randomization on local population size. For each treatment variable the effects of the others are pooled.



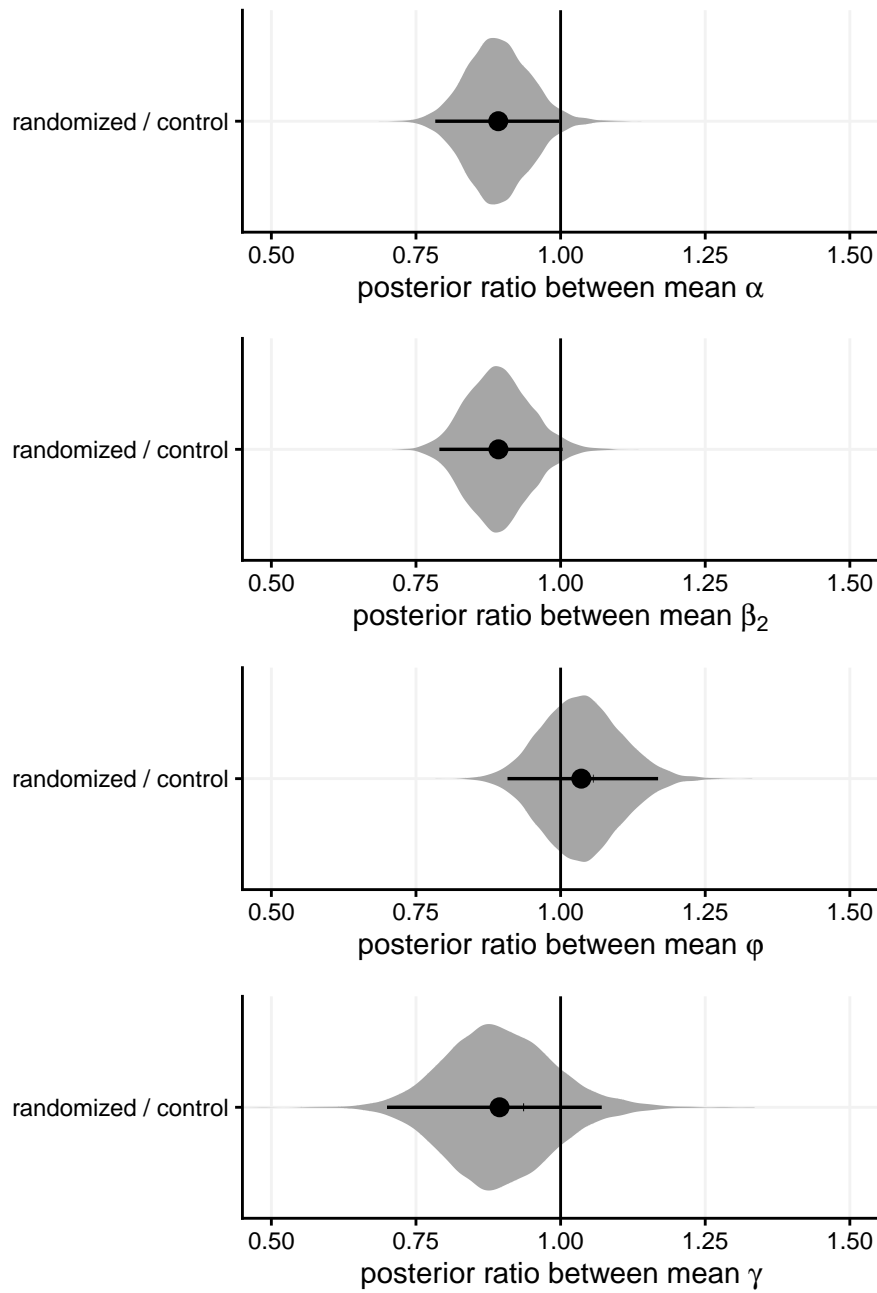
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153 **Figure S05.2** – Combined effects of metapopulation-level connectedness and randomization on local
 154 population size.



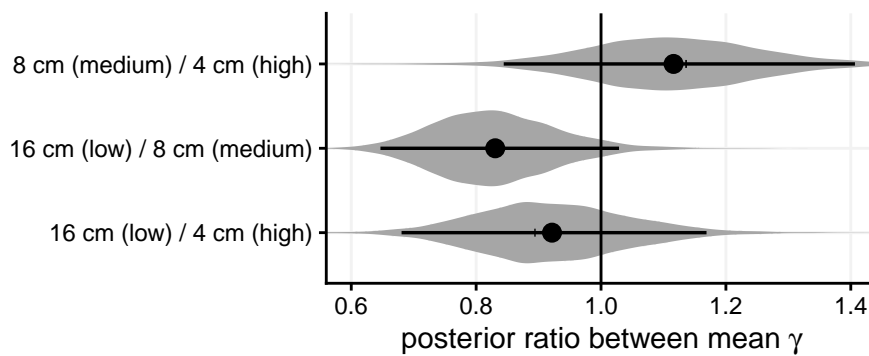
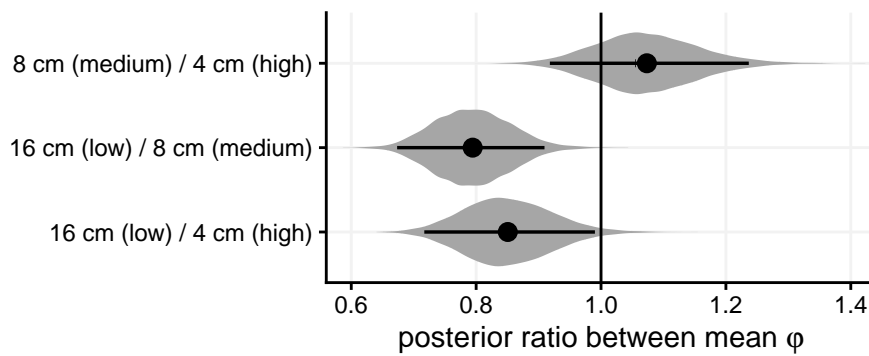
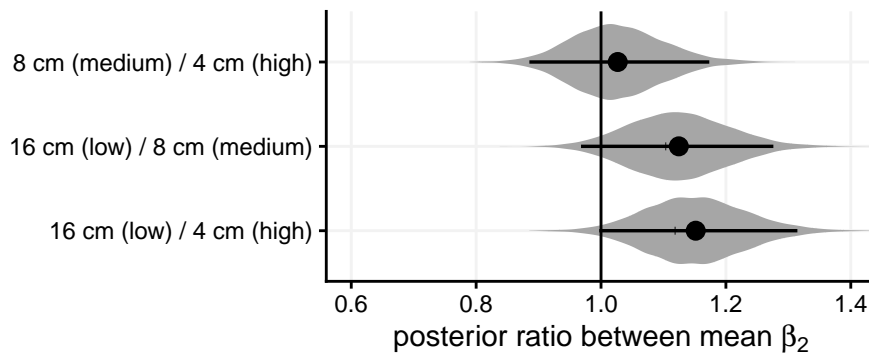
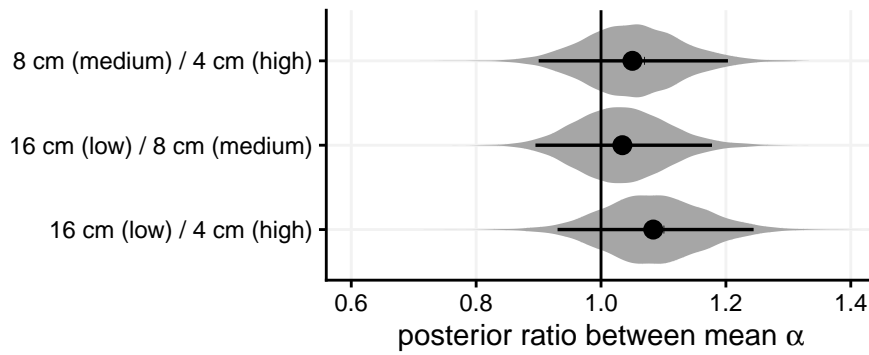
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156 **Figure S05.3** – Combined effects of local connectedness and randomization on local population size.



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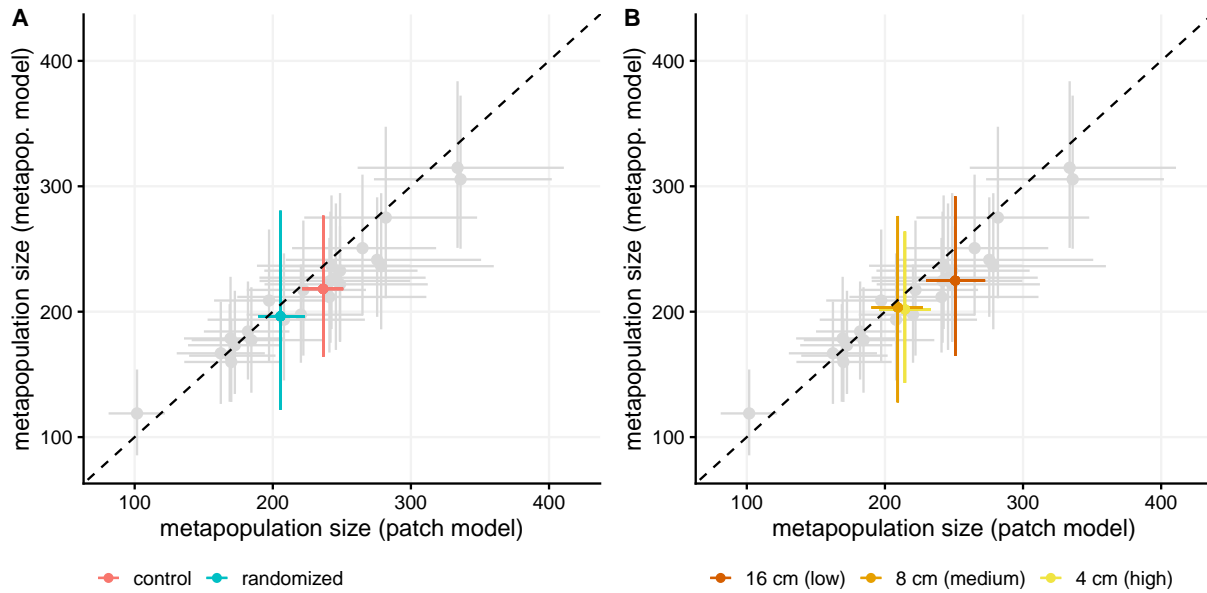
158 **Figure S05.4** – Effect of randomization on variability metrics



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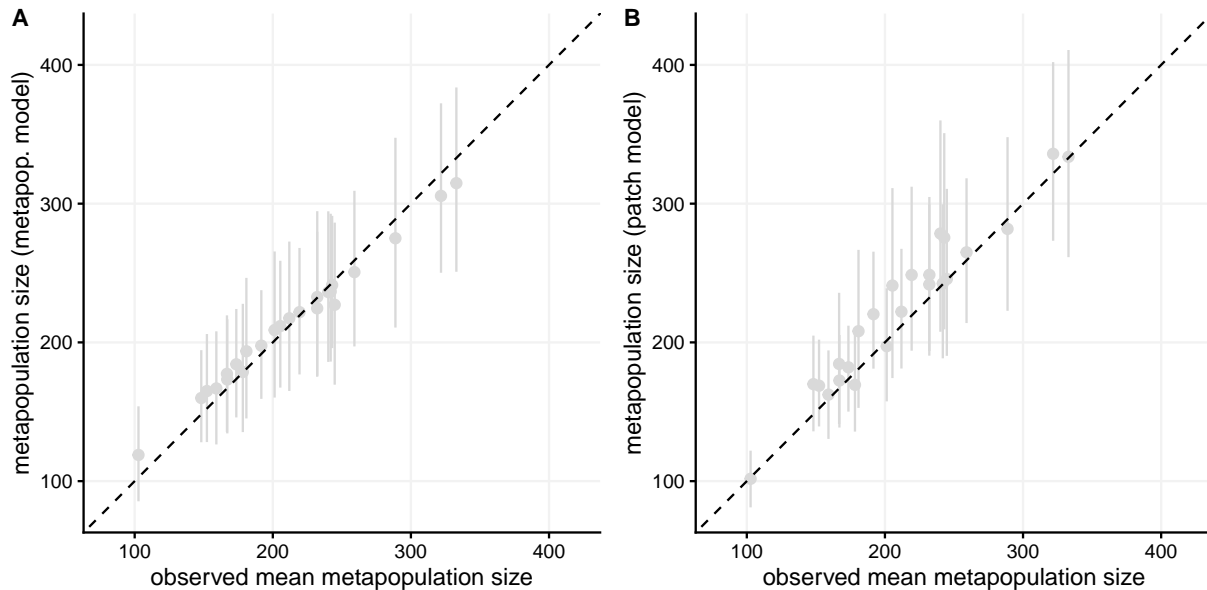
160 **Figure S05.5** – Effect of metapopulation-level connectedness on variability metrics

161 **S06 – Comparisons between patch-level model predictions,**
162 **metapopulation-level model predictions, and observed data**



163

164 **Figure S06.1** – Comparisons between mean metapopulation size predictions (with 95% intervals) from the
165 metapopulation-level model vs. the patch-level model (multiplying mean predictions by the number of patches,
166 implicitly assuming patches are temporally independent). Treatment-level predictions (A: randomization
167 treatment, B: metapopulation connectedness treatment) are added over replicate-level predictions (in grey).
168 Dotted line: $y = x$.



169

170 **Figure S06.2** – Comparisons between observed mean metapopulation sizes and mean metapopulation
171 size predictions (with 95% intervals) from the metapopulation-level model (A) or the patch-level model
172 (B: multiplying mean predictions by the number of patches, implicitly assuming patches are temporally
173 independent). Dotted line: $y = x$.

174 References

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