Ecography

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Supplementary material

Appendix 1: Details of statistical models

1. Independent analysis of each city

We evaluated the correlation of traits with colonization and extirpation through two separate logistic regressions instead of a single multinomial analysis because 1) an ordinal multinomial model (three responses: extirpated, persistent, colonizer) assumes that the processes of extirpation and colonization are similar (i.e. they select for/against the same traits), thereby preventing us from testing that hypothesis directly, and 2) a multinomial model without ordinal responses does not produce regression coefficients that can be examined in a meta-analysis. The size and complexity of the datasets, and the assumption that cities may show different patterns prevented the use of a single hierarchical model.

We maintained the same model structure throughout all the city-based analyses and did not use any form of variable selection because we are interested in the effect of all ten traits in each of the eleven cities. No quadratic terms were included in the final models because such models did not yield evidence of unimodal behaviour, and their inclusion hampered appropriate model convergence in some cities. Our analyses did not include interactions between the effects. Unlike Duncan *et al.* (2011), we did not incorporate information about the habitat preference of species as a predictor: its effect may be confounded by habitat destruction and/or the fact that species may occupy different habitats when they expand their range.

All the analyses were carried out within a Bayesian inference framework, using Markov Chain Monte Carlo (MCMC) implementation in JAGS software, called from R version 3.1.3 (R Core Team, 2015) through the R2jags package (Su & Yajima, 2014). We specified weakly informative prior distributions for all the estimated parameters and standard deviations (Gelman, 2006; Gelman *et al.*, 2008). Categories within multicategorical traits, and families were treated as random effects and assumed to follow a normal distribution with mean zero and standard deviation estimated from the data.

Data availability varied among traits and species. Missing information ranged from 7% to 40% of the trait records, depending on the particular city and analysis (Table A1). We dealt with missing data by modelling traits as a function of plant family, using all the plant species included in our data sets. We assumed that categorical traits followed a categorical distribution, with the probability of each category depending on the family that a species belongs to, and that standardized quantitative traits followed a normal distribution, where the mean and standard deviation of parameters varied with plant family.

We ran each model for 50,000 iterations, with the first 20,000 discarded as burn-in, which was sufficient to achieve convergence in the estimation of most parameters. Some convergence issues arose due to unbalanced data sets (the proportion of extirpated plants in San Diego, San Francisco and Los Angeles was very low) or traits showing some degree of separation (e.g. no epiphytes were categorized as colonizers). These issues prevented us from using estimates from all cities when comparing colonizers and extirpated plants across urban areas (see *Meta-analysis across cities* section); however, this did not affect the average estimated effects of traits in the subsequent meta-analysis. The Area Under the Curve (AUC) criterion was used to measure model discrimination between groups of plants (Hosmer & Lemeshow, 2000).

a) Traits associated with invasive and persistent plants in urban environments

Table A2 (columns 1-11) shows the estimated values for all the parameters included in the city-levels logistic regressions comparing colonizers and persistent plants. Figures A1(a) to A10(a) represent the predicted probability of being a urban colonizer in each of the eleven cities, along with predictions drawn from the meta-analysis for ease of comparison between estimates. For categorical traits, the probability of occurrence of the reference class has been represented by plotting the estimated intercept value of each city (dashed line). These lines show that Adelaide, Auckland, Melbourne and Singapore have a proportion of colonizers higher than 25% for those plants with reference class categorical traits (Table 1).

The effect of continuous and categorical traits varied among cities. For example, species dispersed by animal external attachment in Adelaide are more often colonizers, while the same trait in Auckland is strongly related to persistent plants (Fig. A10a). Plants with heavier seeds are more prevalent amongst colonizers in Melbourne; however, this trait has no effect on the prevalence of colonizers in Singapore (Fig. A2a).

b) Traits associated with invasive and extirpated plants in urban environments

As for the previous comparison, the estimated effects of traits in the probability of being an urban colonizer in each of the eleven cities are included in Table A3 (columns 1-11). The predicted occurrence of colonizers in each urban flora, along with predictions drawn from the meta-analysis, is represented in Figures A1(b) to A10(b). For all the cities, colonizers represent a proportion of the species larger than for the previous comparison, at least for the reference categories. This is especially noteworthy for Adelaide.

The uncertainty associated with some estimates was high for Los Angeles, San Diego and San Francisco, because relatively few species are recorded as extirpated in those areas (less than 20 species in each city, which stands for less than 10% of the total species in the city-level data set; Fig. 2b). For this reason, these three cities were excluded from the corresponding meta-analysis.

All the city-level models achieved AUC values larger than 0.8; therefore, we assume accurate ability to assign probabilities that correctly discriminate between groups of plant species.

2. Meta-analysis across cities

Like the city-based analyses, the meta-analyses were run through JAGS software using weakly informative prior distributions (Gelman, 2006; Gelman *et al.*, 2008).

Cities were not randomly selected for this work, which may affect our results because some cities can exhibit clustered patterns of extirpation and colonization due to shared biotic and climatic factors. Fig A11 shows the similarity between pairs of cities on their pre-urbanization flora (a) and the introduced flora (b), making clear that some clusters do exist. When the meta-analyses include an extra random effect accounting for non-independence of cities within the same biogeographic regions, the uncertainty associated to the estimated effects of traits highly increases (however, the trends represented by the average values remain more or less similar). The effects of the traits on the log odds of colonizers over persistent and extirpated plants for each of the biogeographic regions have been included in Figs. A12 and A13, respectively.

Despite the large credible intervals shown in the previous two figures, the average effects of some traits seem to vary among regions, including woody forms, several nutrient uptake strategies, photosynthetic pathway and height. Figure 5 shows how the variability among regions appears to be larger (or at least of similar magnitude) than the variability among cities [within regions] for most of the traits we have analyzed. These results point to the fact that regions may have a considerable influence in extirpation and colonization patterns of urban floras. They also suggest that variability can be broken down to quantify accurate effects of different levels of factors (in this case specific features of cities, and biogeographic regional features), if a more comprehensive data set was used to answer questions similar to the ones we present in this paper.

The code used for all the analyses is provided in Appendix 3.

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Table A1. Sources of plant records in each city, and summaries of extirpation and colonization rates.

City	Source for flora surveys	Study length	Extirpation rate / year	Colonization rate / year
Adelaide	Tait et al (2005)	166	0.047	0.241
Auckland	Duncan & Young (2000), Esler (1991)	114	0.191	0.69
Chicago	http://www.vplants.org	147	0.173	0.2
Hong Kong	Corlett et al (2000)	163	0.021	0.082
Los Angeles	M.W.S., unpublished data	145	0.018	0.159
Melbourne	A.K.H. & N.S.G.W., unpublished data	140	0.083	0.309
New York	Moore et al (2004)	207	0.124	0.156
San Diego	M.W.S., unpublished data	145	0.007	0.146
San Francisco	M.W.S., unpublished data	145	0.018	0.138
Singapore	Chong et al (2009)	c. 100	0.275	0.125
Worcester	Bertin (2002)	c. 100	0.213	0.368

Table A2. Sources of trait records.

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ONLINE RESOURCES

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Seed information database (SID), KEW Royal Botanic Gardens. URL: http://data.kew.org/sid/

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Mycorrhizae database, Commonwealth Scientific and Industrial Research Organisation (CSIRO). URL: www.ffp.csiro.au/research/mycorrhiza

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The authors measured some traits from herbarium specimens in the National Herbarium of Victoria (Hahs A & Williams N S G W) and in the wild (Vesk P).

Some information came from unpublished datasets and expert opinion of the members of the "Urbanization and Plant Functional Traits working group of the ARC-NZ Network for Vegetation Function", including Steven Clemants and Mark Schwartz, and other botanists with knowledge of the flora in particular areas, including, but not limited to, Catherine Tait, Monique Hallet, Andrew Hipp and Myla Aronson.

Table A3. Information of the data sets used in the city-level logistic regression models. [a]: each species may have been recorded in more than one city. [b]: species have been categorized as colonizer in at least one city.

	Colonizers and persistent plants data set			**Colonizers and extirpated plants data set**		
	Total	City-level		Total	City-level	
Records	14,800			6,588		
Number of species	9,101[a]	Adelaide	1607	4,020[a]	Adelaide	724
		Auckland	1363		Auckland	1153
		Chicago	1291		Chicago	690
		Hong Kong	1835		Hong Kong	301
		Los Angeles	851		Los Angeles	214
		Melbourne	1559		Melbourne	791
		New York	1711		New York	953
		San Diego	891		San Diego	196
		San Francisco	869		San Francisco	193
		Singapore	1804		Singapore	824
		Worcester	1019		Worcester	549
Species categorized as colonizer	25%[b]	Adelaide	40%	58%[b]	Adelaide	89%
		Auckland	79%		Auckland	93%
		Chicago	29%		Chicago	55%
		Hong Kong	13%		Hong Kong	81%
		Los Angeles	23%		Los Angeles	92%
		Melbourne	43%		Melbourne	85%
		New York	32%		New York	58%
		San Diego	21%		San Diego	96%
		San Francisco	20%		San Francisco	90%
		Singapore	13%		Singapore	27%
		Worcester	37%		Worcester	68%

Missing trait records	19%	Adelaide	21%	27%	Adelaide	40%
		Auckland	37%		Auckland	40%
		Chicago	8%		Chicago	7%
		Hong Kong	14%		Hong Kong	9%
		Los Angeles	11%		Los Angeles	10%
		Melbourne	21%		Melbourne	38%
		New York	8%		New York	8%
		San Diego	11%		San Diego	9%
		San Francisco	10%		San Francisco	8%
		Singapore	20%		Singapore	22%
		Worcester	7%		Worcester	6%

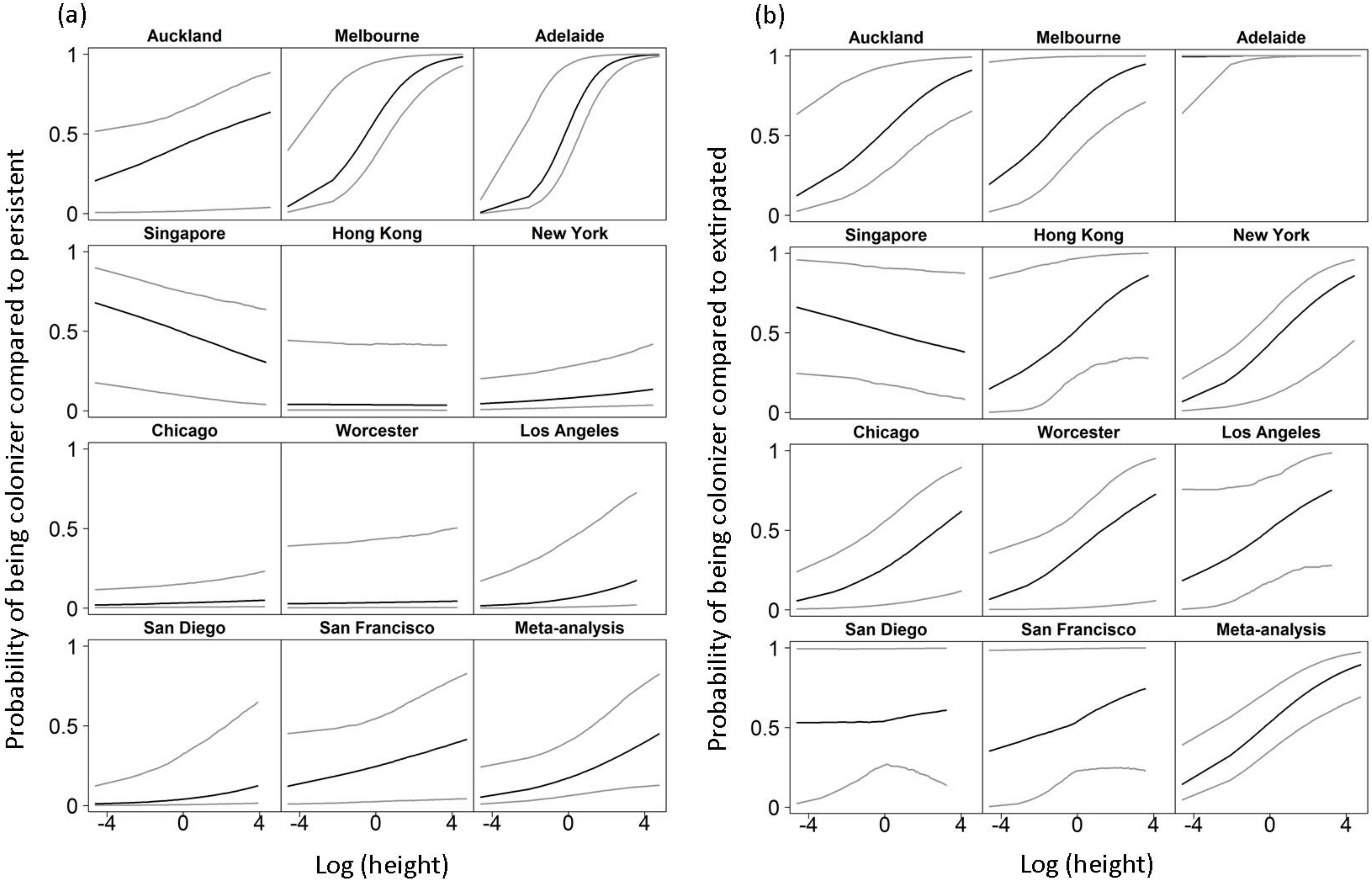
Table A4. Estimated coefficients of city-level logistic regression models (columns 1-11) and meta-analysis across cities (columns 12-13) for the comparison between colonizer and persistent plants.

	ADELAIDE	AUCKLAND	CHICAGO	HONG KONG	LOS ANGELES	MELBOURNE	NEW YORK	SAN DIEGO	SAN FRANCISCO	SINGAPORE	WORCESTER	ACROSS URBAN AREAS [mean]	ACROSS URBAN AREAS [sd]
	mean (sd)	mean (sd)	mean (sd)	mean (sd)	mean (sd)	mean (sd)	mean (sd)	mean (sd)	mean (sd)	mean (sd)	mean (sd)	mean (sd)	mean (sd)
intercept	0.766 (0.909)	-0.586 (1.144)	-3.362 (0.863)	-3.125 (1.315)	-2.635 (1.207)	0.837 (0.945)	-2.408 (0.738)	-3.07 (1.178)	-1.279 (1.103)	-0.177 (0.772)	-3.218 (1.411)		
height	3.948 (0.407)	0.73 (0.387)	0.353 (0.248)	-0.059 (0.285)	1.148 (0.399)	2.705 (0.395)	0.466 (0.241)	1.094 (0.417)	0.603 (0.395)	-0.61 (0.321)	0.189 (0.304)	0.945 (0.457)	2.212 (1.459)
seed mass	1.618 (0.42)	1.21 (0.39)	0.146 (0.239)	-0.189 (0.304)	0.648 (0.365)	1.567 (0.424)	0.743 (0.258)	0.663 (0.372)	0.622 (0.376)	0.002 (0.316)	1.029 (0.376)	0.684 (0.205)	0.346 (0.287)
annual longevity	0.747 (0.25)	0.963 (0.549)	0.823 (0.215)	0.848 (0.26)	0.122 (0.222)	0.906 (0.251)	1.061 (0.194)	0.289 (0.226)	0.132 (0.218)	0.21 (0.388)	0.705 (0.277)	0.61 (0.132)	0.12 (0.115)
spines	0.866 (0.484)	4.09 (1.21)	0.753 (0.32)	0.365 (0.385)	0.498 (0.431)	0.604 (0.416)	0.585 (0.287)	0.527 (0.429)	0.238 (0.412)	0.342 (0.445)	0.58 (0.398)	0.587 (0.14)	0.042 (0.087)
biotic pollination	1.335 (0.408)	0.764 (0.424)	0.824 (0.331)	-0.487 (0.473)	0.259 (0.362)	1.489 (0.432)	0.427 (0.277)	0.359 (0.38)	0.214 (0.389)	-0.074 (0.48)	1.409 (0.581)	0.581 (0.196)	0.254 (0.285)
C4 or CAM photosynthetic pathway	-2.758 (0.378)	-1.109 (0.483)	0.123 (0.31)	0.701 (0.331)	0.313 (0.432)	-2.831 (0.392)	0.036 (0.278)	0.06 (0.387)	-0.529 (0.502)	-0.171 (0.388)	-0.082 (0.363)	-0.561 (0.428)	1.893 (1.276)
Nitrogen fixation	-4.132 (0.998)	-1.301 (1.065)	-3.837 (0.911)	-1.266 (0.563)	-1.824 (0.773)	-4.043 (0.89)	-2.858 (0.58)	-1.781 (0.762)	-2.568 (0.82)	0.488 (1.786)	-4.862 (1.153)	-2.585 (0.451)	1.476 (1.54)
mycorrhizae	-1.546 (0.348)	-0.795 (0.421)	-1.059 (0.233)	0.101 (0.339)	-0.276 (0.41)	-2.224 (0.355)	-1.108 (0.225)	0.151 (0.413)	-0.41 (0.369)	-0.775 (1.324)	-1.217 (0.304)	-0.853 (0.265)	0.603 (0.468)
other nutrient uptake strategy	-25.998 (20.341)	-0.974 (1.002)	-11.711 (11.055)	-6.17 (7.708)	-5.739 (7.546)	-1.94 (1.267)	-12.081 (15.891)	-4.701 (7.23)	-8.806 (10.089)	-8.163 (17.077)	-3.686 (1.454)	-2.858 (1.688)	7.806 (16.461)
tussock	0.092 (0.371)	-1.809 (0.514)	0.039 (0.214)	-0.202 (0.335)	-0.171 (0.342)	0.206 (0.351)	-0.052 (0.264)	-0.386 (0.421)	-0.737 (0.522)	0.875 (0.513)	0.233 (0.357)	-0.117 (0.172)	0.184 (0.269)
woody	-3.978 (0.507)	-2.639 (0.494)	0.134 (0.243)	-0.558 (0.364)	-0.07 (0.258)	-4.023 (0.552)	0.342 (0.302)	-0.212 (0.317)	-0.831 (0.495)	-0.886 (0.375)	0.377 (0.405)	-1.091 (0.579)	3.575 (2.47)
succulent	1.405 (0.665)	1.487 (1.194)	0.073 (0.451)	0.489 (1.4)	-0.285 (0.38)	1.205 (0.708)	-0.781 (1.259)	-0.515 (0.448)	-1.136 (0.519)	-0.099 (2.365)	-0.219 (1.14)	0.041 (0.348)	0.674 (0.83)
epiphyte	3.529 (2.853)	-0.277 (1.115)	0.006 (0.526)	-0.508 (1.181)	-0.066 (0.582)	3.246 (1.838)	0.015 (1.22)	-0.116 (0.822)	-0.325 (1.451)	-2.195 (2.525)	0.016 (1.194)	0.012 (0.342)	0.265 (0.578)
climber	-0.561 (0.563)	-1.236 (0.572)	0.121 (0.27)	-0.238 (0.324)	0.13 (0.343)	-1.137 (0.532)	0.147 (0.298)	0.23 (0.431)	0.339 (0.548)	-0.724 (0.407)	-0.018 (0.406)	-0.171 (0.164)	0.126 (0.182)
aquatic	0.543 (0.769)	0.196 (0.877)	0.084 (0.327)	0.036 (0.632)	0.046 (0.428)	0.045 (0.879)	0.495 (0.52)	0.325 (0.581)	-0.858 (0.964)	0.954 (0.869)	0.062 (0.551)	0.174 (0.194)	0.07 (0.131)
parasite	2.861 (2.504)	2.963 (2.335)	-0.084 (0.486)	-0.352 (1.376)	-0.158 (0.587)	-0.504 (1.574)	-0.368 (1.115)	-0.183 (0.793)	-0.841 (1.388)	-1.563 (3.33)	-0.964 (1.546)	-0.155 (0.353)	0.268 (0.561)
other growth form	0.759 (1.584)	2.82 (2.39)	-0.104 (0.532)	0.03 (1.248)	-0.089 (0.585)	2.107 (1.649)	-0.489 (1.149)	-0.173 (0.823)	-0.486 (1.42)	-0.181 (2.92)	-0.315 (1.156)	0.018 (0.354)	0.26 (0.85)
clonal aboveground	1.35 (0.463)	-1.15 (0.456)	-0.256 (0.256)	0.443 (0.412)	-0.383 (0.476)	0.09 (0.323)	-0.597 (0.283)	-0.09 (0.369)	-0.195 (0.431)	-0.497 (0.613)	-1.191 (0.357)	-0.234 (0.239)	0.467 (0.432)
clonal belowground	-0.24 (0.283)	-0.809 (0.347)	-0.207 (0.194)	-0.222 (0.291)	-0.32 (0.343)	-0.565 (0.297)	-0.16 (0.173)	-0.047 (0.27)	-0.376 (0.338)	-0.751 (0.568)	-0.245 (0.245)	-0.288 (0.093)	0.02 (0.037)
wind dispersal	-0.626 (0.299)	-2.41 (0.413)	-0.302 (0.26)	-1.184 (0.349)	-0.171 (0.256)	-0.378 (0.321)	-0.622 (0.247)	-0.259 (0.3)	0.101 (0.264)	-1.265 (0.408)	-0.819 (0.358)	-0.677 (0.23)	0.479 (0.387)
animal consumption dispersal	1.744 (0.451)	-2.141 (0.442)	-0.107 (0.212)	-1.347 (0.373)	-0.074 (0.29)	1.018 (0.471)	-0.342 (0.25)	-0.072 (0.332)	0.003 (0.304)	-2.02 (0.392)	-0.543 (0.353)	-0.358 (0.406)	1.65 (1.156)
animal external dispersal	-0.03 (0.352)	-0.86 (0.49)	-0.119 (0.243)	0.505 (0.402)	0.042 (0.316)	-0.722 (0.369)	-1.057 (0.288)	-0.189 (0.391)	-0.097 (0.327)	-1.272 (0.821)	-1.158 (0.428)	-0.385 (0.19)	0.248 (0.268)
water dispersal	1.243 (0.727)	0.995 (0.846)	-0.222 (0.32)	0.261 (0.53)	0.118 (0.379)	0.924 (0.779)	-1.755 (0.432)	0.243 (0.434)	0.203 (0.394)	-1.249 (0.56)	-0.587 (0.546)	-0.076 (0.307)	0.757 (0.682)

Table A5. Estimated coefficients of city-level logistic regression models (columns 1-11) and meta-analysis across cities (columns 12-13) for the comparison between colonizer and extirpated plants. For the meta-analysis, estimates of San Diego, San Francisco and Los Angeles were excluded.

	ADELAIDE	AUCKLAND	CHICAGO	HONG KONG	LOS ANGELES	MELBOURNE	NEW YORK	SAN DIEGO	SAN FRANCISCO	SINGAPORE	WORCESTER	ACROSS URBAN AREAS [mean]	ACROSS URBAN AREAS [sd]
	mean (sd)	mean (sd)	mean (sd)	mean (sd)	mean (sd)	mean (sd)	mean (sd)	mean (sd)	mean (sd)	mean (sd)	mean (sd)	mean (sd)	mean (sd)
intercept	9.431 (2.672)	0.278 (0.83)	-1.21 (1.036)	0.28 (1.044)	0.019 (0.734)	1.449 (1.694)	-0.446 (0.66)	0.58 (1.542)	0.546 (1.541)	0.123 (0.887)	-1.023 (1.325)		
height	3.024 (0.811)	1.609 (0.474)	1.32 (0.363)	1.661 (1.391)	1.303 (1.178)	1.863 (0.605)	1.683 (0.388)	0.238 (1.065)	0.949 (1.248)	-0.471 (0.442)	1.436 (0.569)	1.318 (0.354)	0.868 (0.812)
seed mass	0.758 (0.66)	1.163 (0.516)	0.942 (0.397)	-0.048 (0.874)	-1.731 (1.788)	1.785 (0.677)	1.323 (0.44)	-0.266 (1.481)	-0.485 (1.029)	0.557 (0.547)	0.94 (0.532)	0.861 (0.238)	0.158 (0.283)
annual longevity	0.081 (0.368)	1.942 (0.749)	0.612 (0.288)	-0.137 (0.506)	0.415 (0.54)	0.159 (0.336)	1.117 (0.283)	0.531 (0.723)	0.234 (0.56)	-0.104 (0.682)	1.304 (0.472)	0.551 (0.194)	0.213 (0.261)
spines	0.405 (0.639)	1.971 (0.995)	0.187 (0.362)	0.869 (1.359)	0.96 (1.17)	1.488 (0.949)	-0.266 (0.356)	0.031 (0.847)	0.188 (0.751)	0.573 (0.734)	-0.081 (0.471)	0.281 (0.245)	0.183 (0.313)
biotic pollination	-0.399 (0.682)	0.189 (0.436)	0.788 (0.408)	0.088 (0.687)	0.239 (0.569)	1.635 (0.693)	0.338 (0.317)	-0.032 (0.833)	0.197 (0.991)	-0.289 (0.621)	1.115 (0.581)	0.386 (0.203)	0.133 (0.212)
C4 or CAM photosynthetic pathway	-2.228 (0.995)	-0.209 (0.498)	0.028 (0.368)	1.734 (1.215)	0.407 (0.944)	-1.984 (0.642)	0.236 (0.362)	1.429 (1.853)	2.347 (2.621)	0.328 (0.679)	-0.188 (0.51)	-0.131 (0.349)	0.741 (1.012)
Nitrogen fixation	-1.727 (1.646)	0.267 (2.699)	-4.968 (1.158)	-4.509 (2.874)	-0.821 (1.549)	-0.488 (0.998)	-3.946 (0.984)	-1.065 (1.862)	-2.069 (3.137)	2.83 (2.82)	-5.014 (1.616)	-2.271 (0.828)	4.368 (4.739)
mycorrhizae	-2.699 (0.887)	-0.512 (0.507)	-0.982 (0.347)	0.877 (1.118)	1.048 (1.515)	-1.27 (0.544)	-0.896 (0.36)	0.071 (1.442)	0.224 (1.242)	1.852 (1.8)	-1.274 (0.502)	-0.822 (0.292)	0.354 (0.681)
other nutrient uptake strategy	-1.6 (1.684)	-0.416 (1.407)	-13.546 (13.722)	-10.661 (11.683)	1.24 (5.942)	-1.694 (1.189)	-8.511 (9.824)	1.201 (6.489)	-5.233 (10.945)	-4.669 (8.797)	-3.157 (1.545)	-1.786 (1.035)	3.044 (6.883)
tussock	-0.687 (0.717)	-0.242 (0.435)	0.155 (0.312)	3.085 (7.18)	-1.348 (1.691)	-0.293 (0.553)	-0.243 (0.388)	34.763 (84.416)	2.186 (5.954)	1.296 (1.303)	0.2 (0.588)	-0.094 (0.238)	0.144 (0.334)
woody	-1.951 (0.94)	-0.126 (0.409)	0.096 (0.303)	-1.988 (1.373)	4.494 (4.98)	-1.855 (0.8)	0.576 (0.474)	40.27 (78.599)	0.411 (1.543)	-2.348 (0.685)	1.193 (0.735)	-0.504 (0.542)	2.096 (2.084)
succulent	3.006 (3.181)	0.419 (0.871)	0.03 (0.474)	1.698 (6.944)	0.631 (1.643)	1.962 (1.679)	-1.935 (2.666)	39.915 (79.868)	0.898 (2.307)	-1.016 (7.372)	0.041 (2.625)	0.376 (0.585)	0.91 (1.909)
epiphyte	2.156 (3.536)	0.066 (0.535)	0.008 (0.624)	0.149 (8.738)	0.1 (5.977)	0.055 (1.126)	-0.031 (2.931)	1.285 (96.254)	0.043 (5.964)	-8.114 (5.129)	0 (2.364)	-0.015 (0.604)	1.012 (2.727)
climber	3.057 (3.631)	-0.145 (0.447)	0.144 (0.391)	0.511 (2.68)	0.956 (1.481)	-0.186 (0.815)	1.444 (0.853)	39.365 (83.272)	3.067 (5.419)	-2.628 (0.719)	-0.011 (0.677)	-0.028 (0.555)	1.809 (2.4)
aquatic	1.364 (1.239)	0.153 (0.505)	0.129 (0.427)	-5.197 (5.934)	2.624 (5.11)	-0.2 (0.895)	0.615 (0.696)	39.838 (88.888)	1.999 (5.853)	0.121 (1.656)	-0.199 (0.84)	0.212 (0.339)	0.263 (0.627)
parasite	2.083 (3.593)	0.061 (0.522)	-0.112 (0.569)	-2.061 (7.01)	-0.23 (6.139)	-0.501 (1.011)	-1.742 (2.65)	0.05 (88.674)	0.075 (6.077)	-5.637 (5.96)	-1.824 (2.33)	-0.266 (0.592)	0.962 (2.641)
other growth form	0.122 (1.689)	0.347 (0.868)	-0.082 (0.568)	0.014 (7.454)	0.119 (5.796)	0.98 (1.428)	-1.06 (2.394)	-0.356 (109.717)	-0.206 (5.873)	-5.276 (6.195)	0.057 (2.173)	0.081 (0.601)	0.838 (1.928)
clonal aboveground	-0.048 (0.449)	-0.237 (0.433)	-0.126 (0.285)	11.631 (8.575)	0.573 (1.603)	0.123 (0.44)	-0.102 (0.262)	156.958 (574.52)	12.294 (31.026)	0.225 (1.162)	-0.243 (0.378)	-0.095 (0.174)	0.057 (0.127)
clonal belowground	0.242 (0.413)	-0.425 (0.394)	-0.109 (0.217)	-0.879 (1.38)	0.581 (1.109)	-0.23 (0.346)	-0.057 (0.195)	155.342 (535.801)	-0.003 (1.379)	-1.746 (1.142)	0.115 (0.293)	-0.096 (0.148)	0.056 (0.122)
wind dispersal	-0.124 (0.441)	-2.504 (0.482)	-0.552 (0.361)	-0.529 (1.25)	-0.379 (0.984)	-0.636 (0.453)	-0.544 (0.355)	74.991 (198.068)	0.098 (0.897)	-2.424 (0.645)	-0.586 (0.491)	-0.848 (0.353)	0.843 (0.835)
animal consumption dispersal	1.028 (0.962)	-0.549 (0.61)	-0.306 (0.335)	1.171 (1.853)	7.492 (14.335)	2.209 (1.105)	-0.098 (0.323)	86.809 (257.299)	1.072 (1.856)	-2.735 (0.564)	-0.233 (0.432)	-0.102 (0.59)	2.319 (2.519)
animal external dispersal	-0.491 (0.554)	-0.372 (0.613)	0.106 (0.341)	-1.671 (1.547)	2.731 (2.179)	0.514 (0.556)	0.089 (0.344)	70.955 (166.656)	0.691 (2.037)	-1.698 (1.967)	-0.359 (0.525)	-0.054 (0.235)	0.159 (0.352)
water dispersal	-0.402 (0.715)	2.12 (1.177)	-0.082 (0.399)	0.389 (2.268)	6.797 (13.199)	-0.312 (0.745)	-0.334 (0.459)	77.002 (189.659)	1.697 (3.669)	-1.222 (1.201)	-0.336 (0.563)	-0.164 (0.309)	0.278 (0.662)

Figures A1-A10. Predicted prevalence of colonizers over persistent (a) and extirpated (b) urban plants across trait values or categories, based on estimated effects of traits for city-level models and the meta-analysis. Black dots and lines represent mean effects and grey lines represent 95% credible intervals. Horizontal grey dashed lines represent the intercept value estimated for the model in question. Predictions drawn from meta-analysis are based on eleven (a) and eight cities (b). The range of x values over which the predictions of individual cities were made is similar to the range of values covered by species recorded in that particular city. Legend for categorical traits: AN= annual longevity, SP= spines, BP= biotic pollination, C4= C4 or CAM photosynthetic pathway, NF= Nitrogen fixer, MY=mycorrhizae, ON= other nutrient uptake strategy, TU= tussock, WO= woody, SU= succulent, EP= epiphyte, CL= climber, AQ= aquatic, PA= parasite, OG= other growth form, CA= clonal aboveground, CB= clonal belowground, WI= wind dispersal, AI= animal dispersal (consumption), AE= animal dispersal (external), WA= water dispersal.



(a)
Auckland
Melbourne
Adelaide
Singapore
Hong Kong
New York
Chicago
Worcester
Los Angeles
San Diego
San Francisco
Meta-analysis
Probability of being colonizer compared to persistent
Log (height)
(b)
Auckland
Melbourne
Adelaide
Singapore
Hong Kong
New York
Chicago
Worcester
Los Angeles
San Diego
San Francisco
Meta-analysis
Probability of being colonizer compared to extirpated
Log (height)

Figure A1.

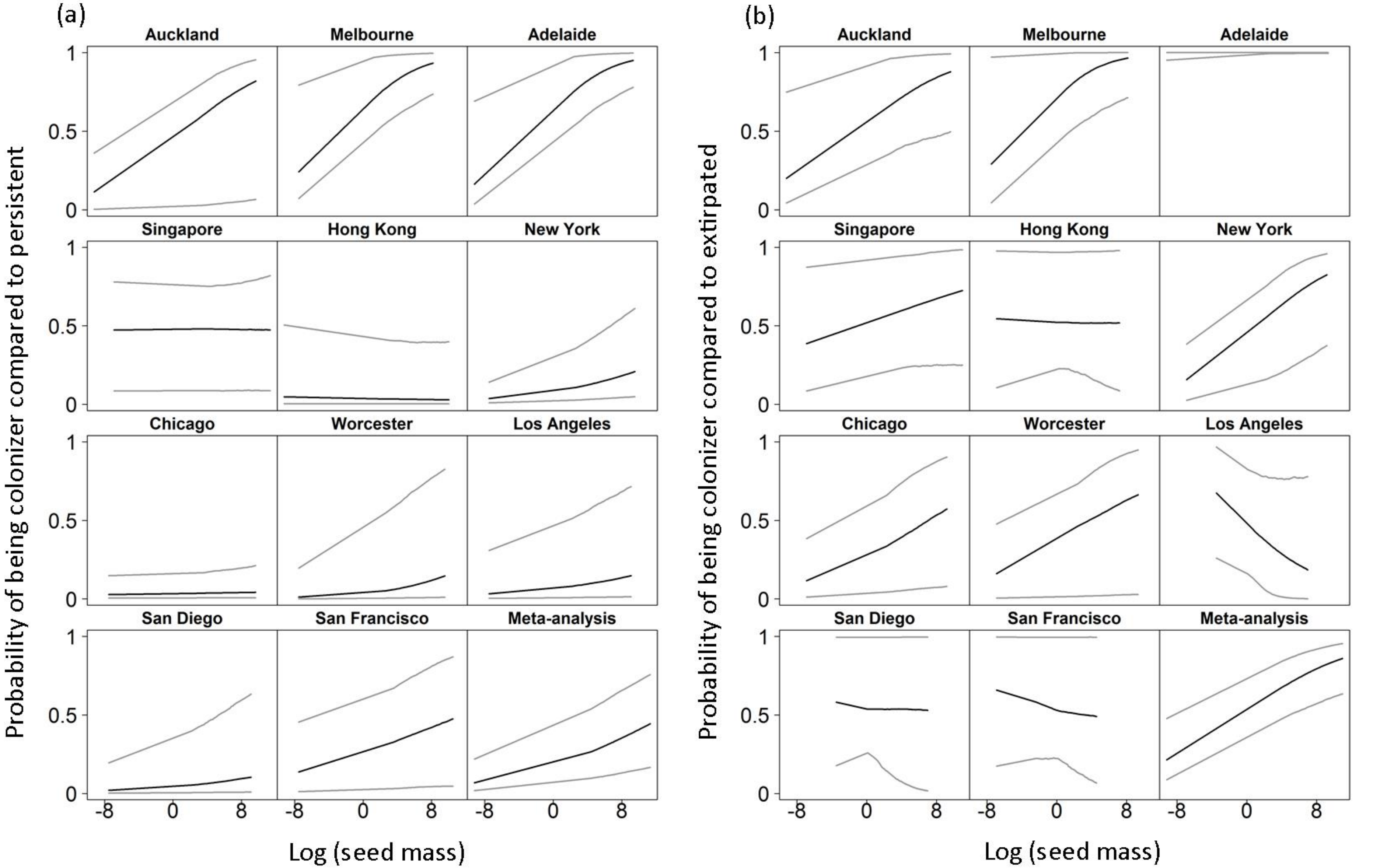

(a)
Auckland
Melbourne
Adelaide
Singapore
Hong Kong
New York
Chicago
Worcester
Los Angeles
San Diego
San Francisco
Meta-analysis
Probability of being colonizer compared to persistent
1
0.5
0
-8
0
8
Log (seed mass)
(b)
Auckland
Melbourne
Adelaide
Singapore
Hong Kong
New York
Chicago
Worcester
Los Angeles
San Diego
San Francisco
Meta-analysis
Probability of being colonizer compared to extirpated
Log (seed mass)

Figure A2.

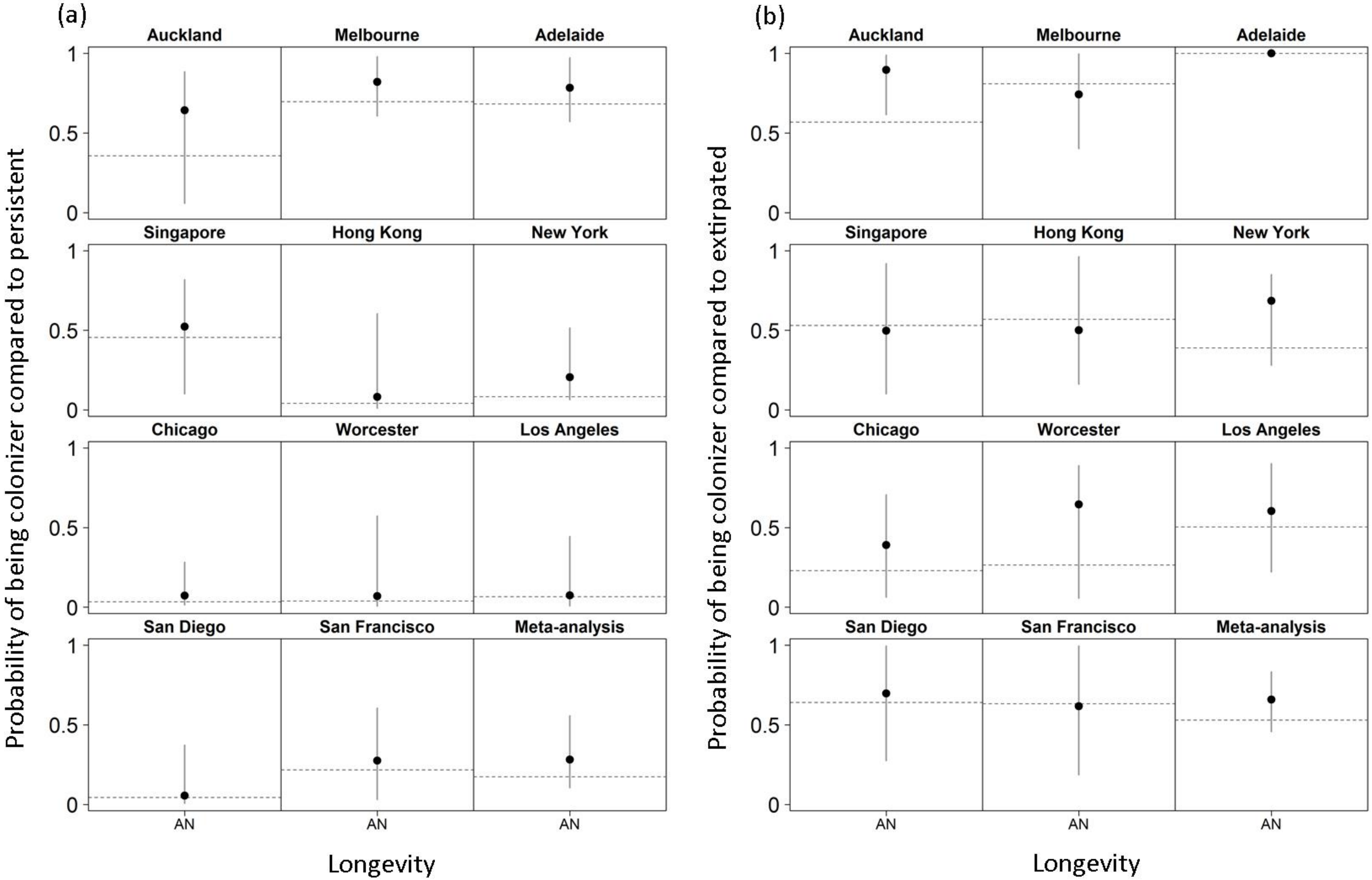

(a)
Auckland
Melbourne
Adelaide
Singapore
Hong Kong
New York
Chicago
Worcester
Los Angeles
San Diego
San Francisco
Meta-analysis
Probability of being colonizer compared to persistent
0
0.5
1
AN
Longevity
(b)
Auckland
Melbourne
Adelaide
Singapore
Hong Kong
New York
Chicago
Worcester
Los Angeles
San Diego
San Francisco
Meta-analysis
Probability of being colonizer compared to extirpated
0
0.5
1
AN
Longevity

Figure A3.

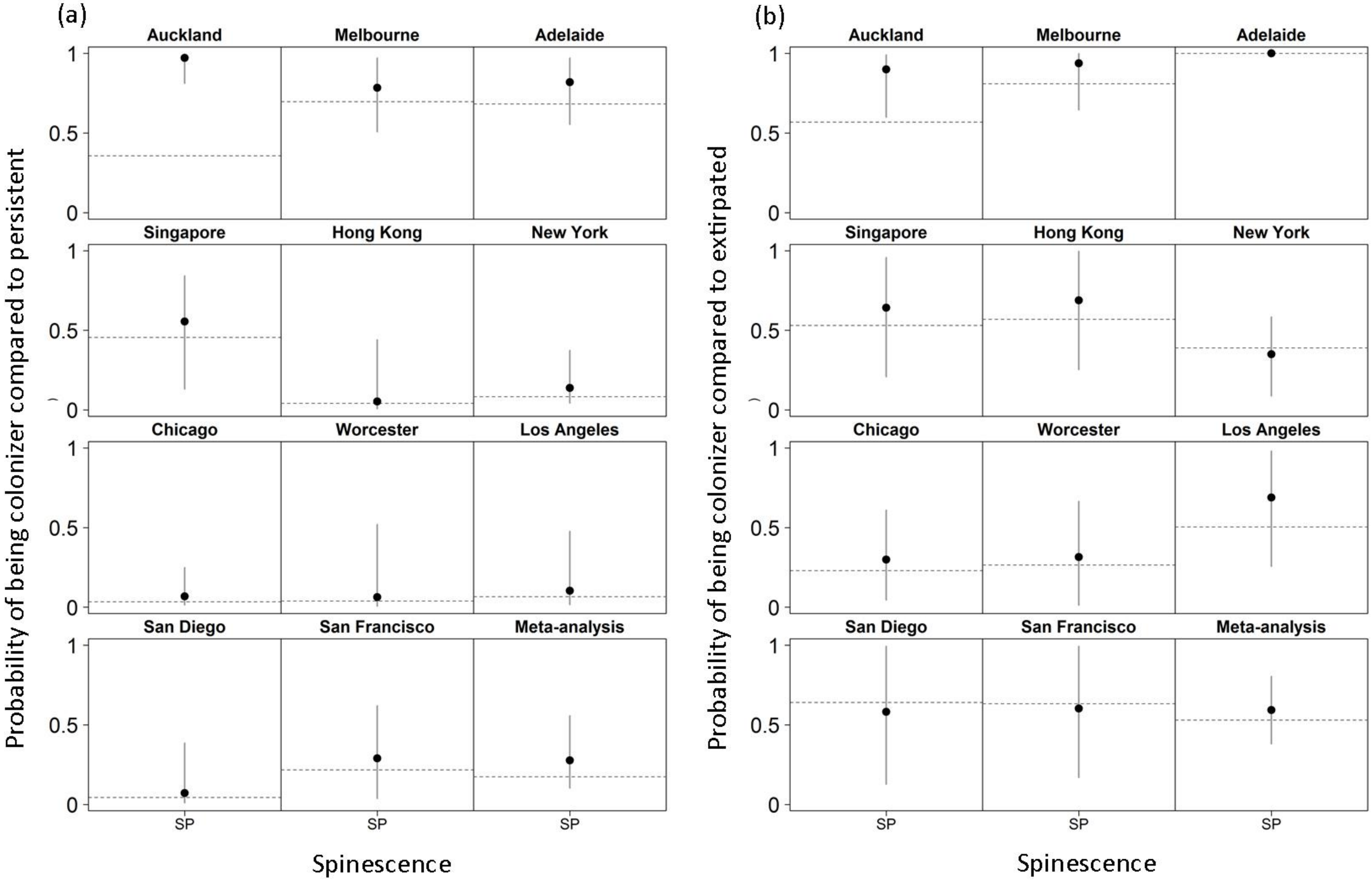

(a)
Auckland
Melbourne
Adelaide
Singapore
Hong Kong
New York
Chicago
Worcester
Los Angeles
San Diego
San Francisco
Meta-analysis
Probability of being colonizer compared to persistent
SP
Spinescence
(b)
Auckland
Melbourne
Adelaide
Singapore
Hong Kong
New York
Chicago
Worcester
Los Angeles
San Diego
San Francisco
Meta-analysis
Probability of being colonizer compared to extirpated
SP
Spinescence

Figure A4.

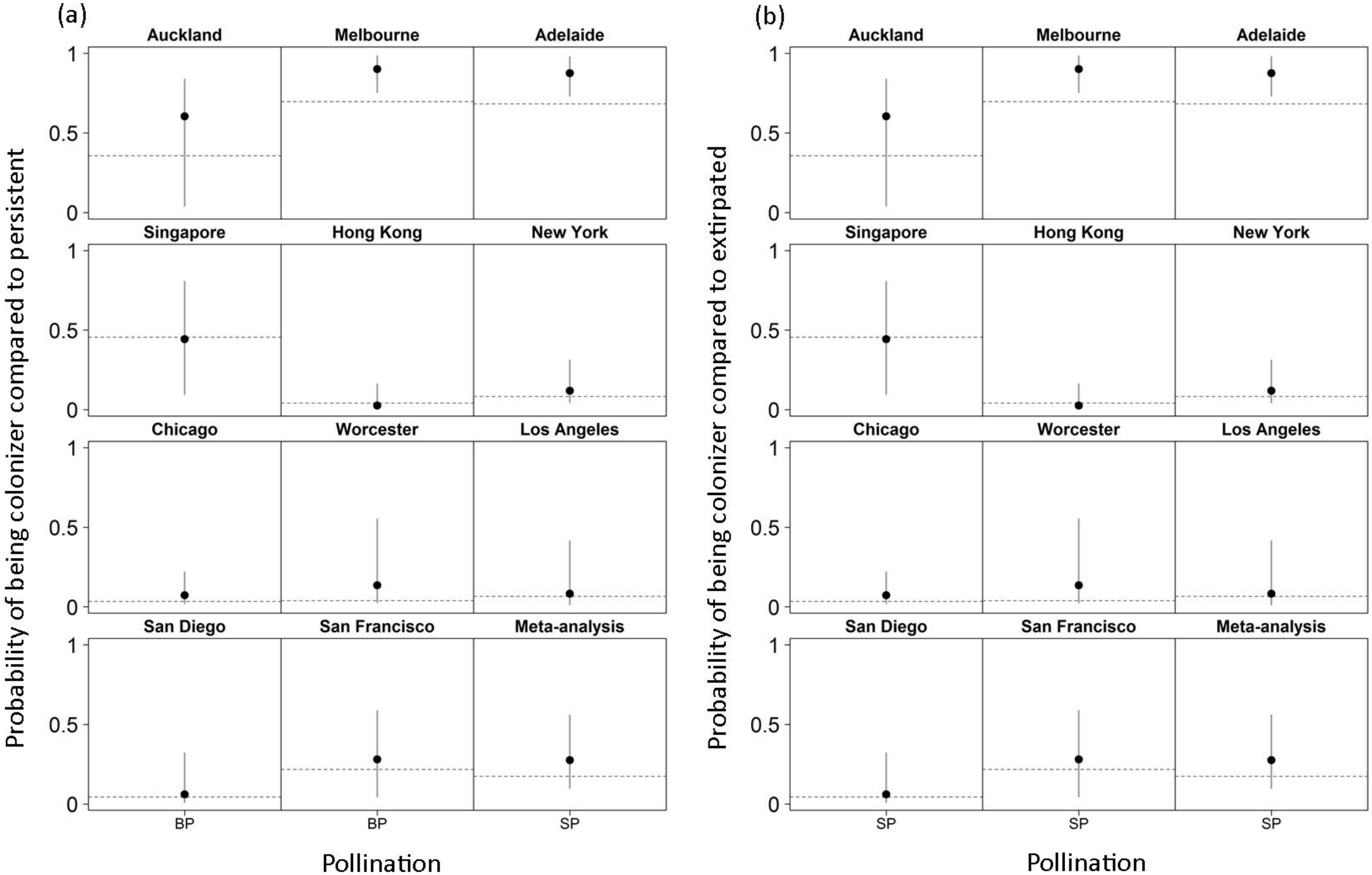

(a)
(b)
Auckland
Melbourne
Adelaide
Singapore
Hong Kong
New York
Chicago
Worcester
Los Angeles
San Diego
San Francisco
Meta-analysis
Probability of being colonizer compared to persistent
Probability of being colonizer compared to extirpated
0
0.5
1
BP
SP
Pollination

Figure A5.

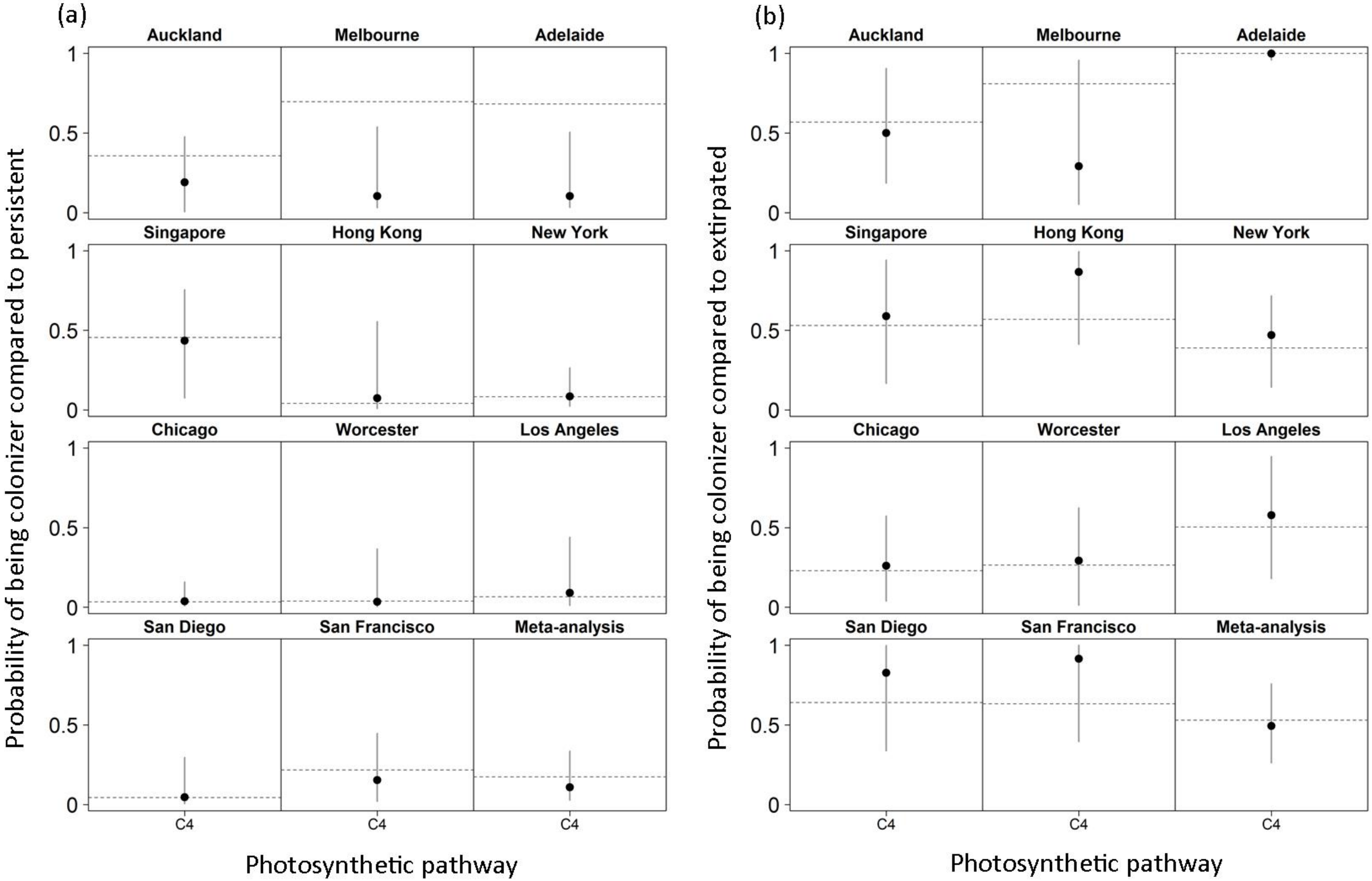

(a)
Auckland
Melbourne
Adelaide
Singapore
Hong Kong
New York
Chicago
Worcester
Los Angeles
San Diego
San Francisco
Meta-analysis
Probability of being colonizer compared to persistent
1
0.5
0
C4
Photosynthetic pathway
(b)
Auckland
Melbourne
Adelaide
Singapore
Hong Kong
New York
Chicago
Worcester
Los Angeles
San Diego
San Francisco
Meta-analysis
Probability of being colonizer compared to extirpated
1
0.5
0
C4
Photosynthetic pathway

Figure A6.

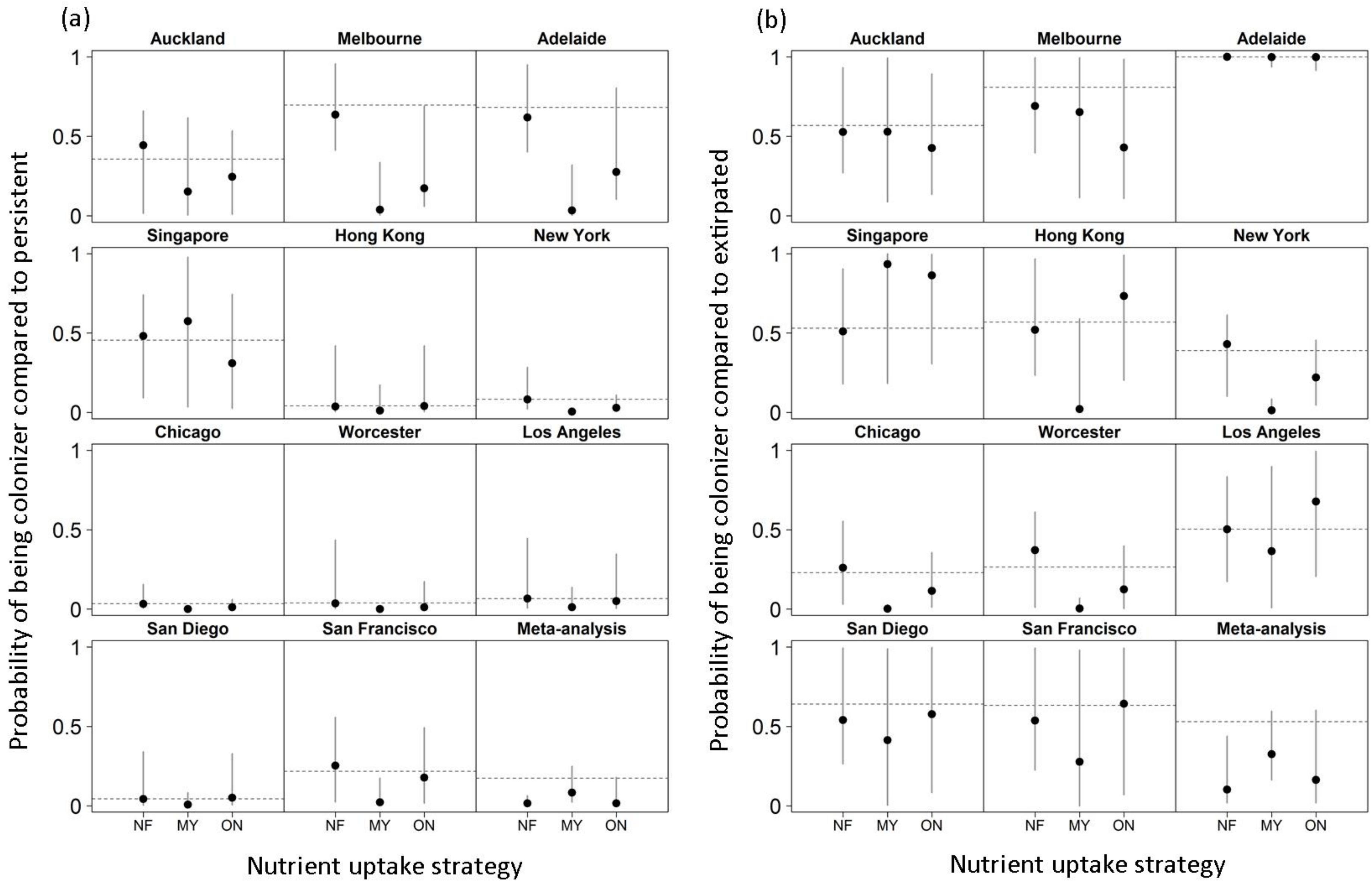

(a)
Auckland
Melbourne
Adelaide
Singapore
Hong Kong
New York
Chicago
Worcester
Los Angeles
San Diego
San Francisco
Meta-analysis
Probability of being colonizer compared to persistent
1
0.5
0
NF
MY
ON
Nutrient uptake strategy
(b)
Auckland
Melbourne
Adelaide
Singapore
Hong Kong
New York
Chicago
Worcester
Los Angeles
San Diego
San Francisco
Meta-analysis
Probability of being colonizer compared to extirpated
Nutrient uptake strategy

Figure A7.

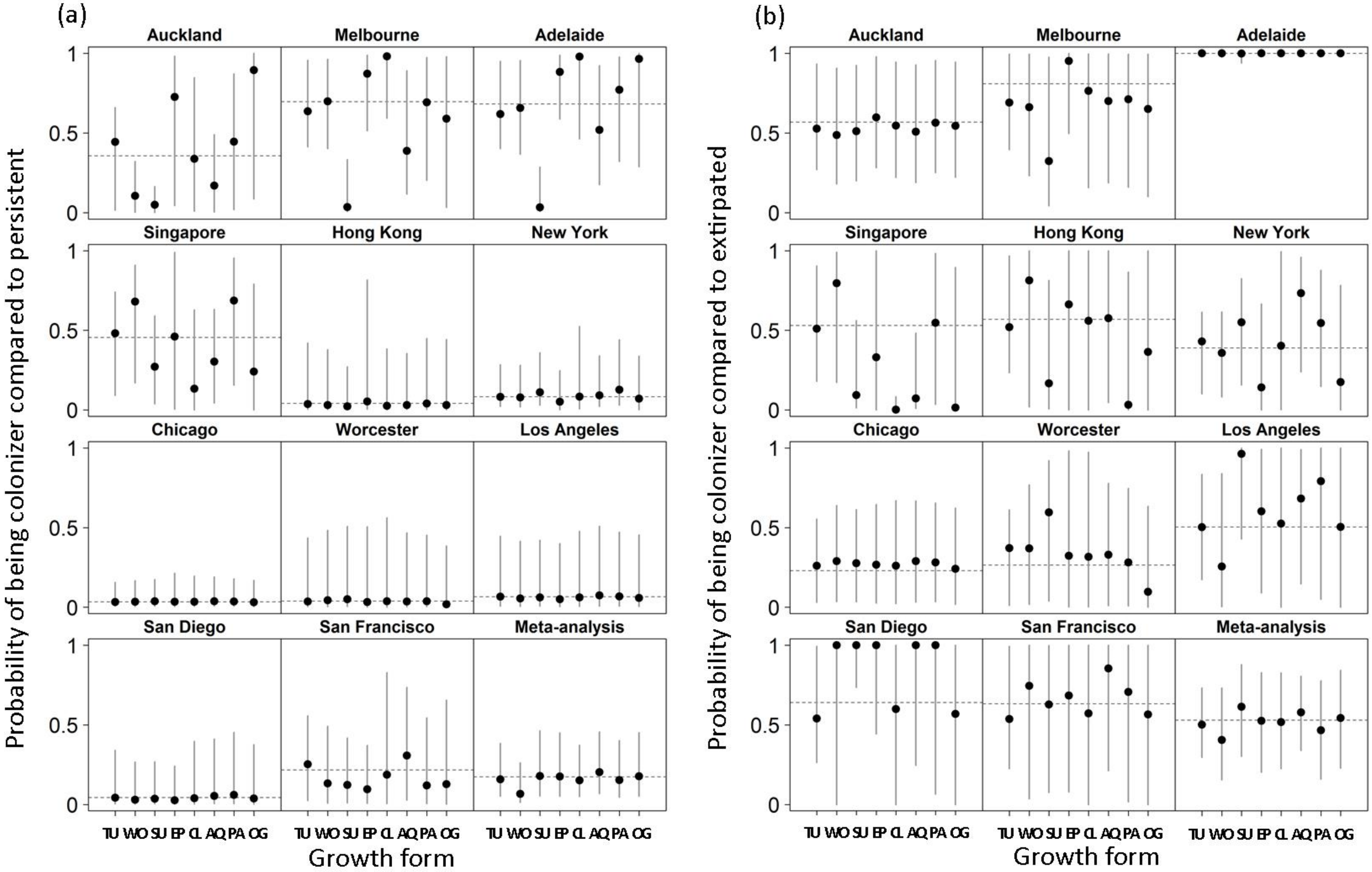
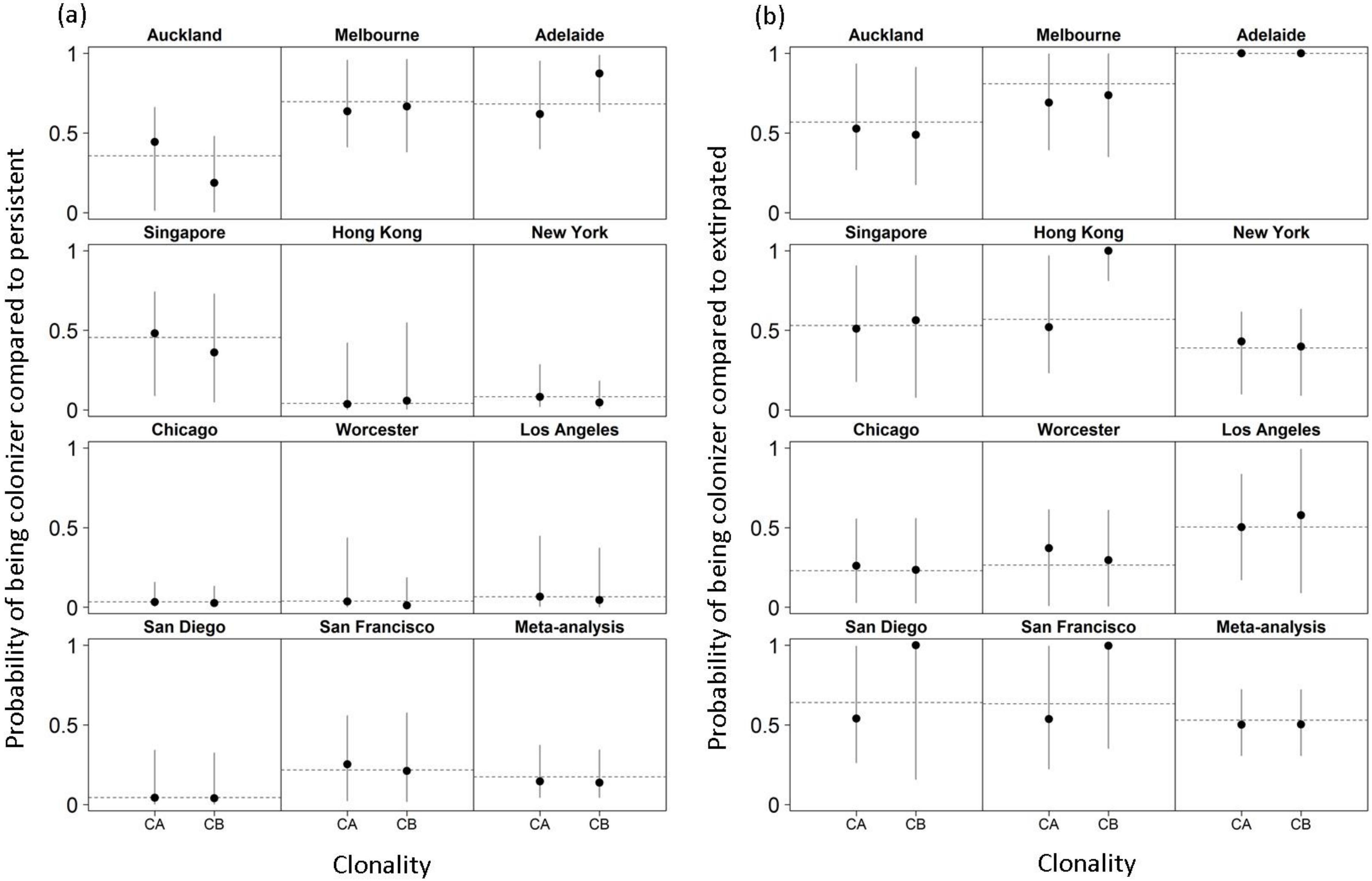
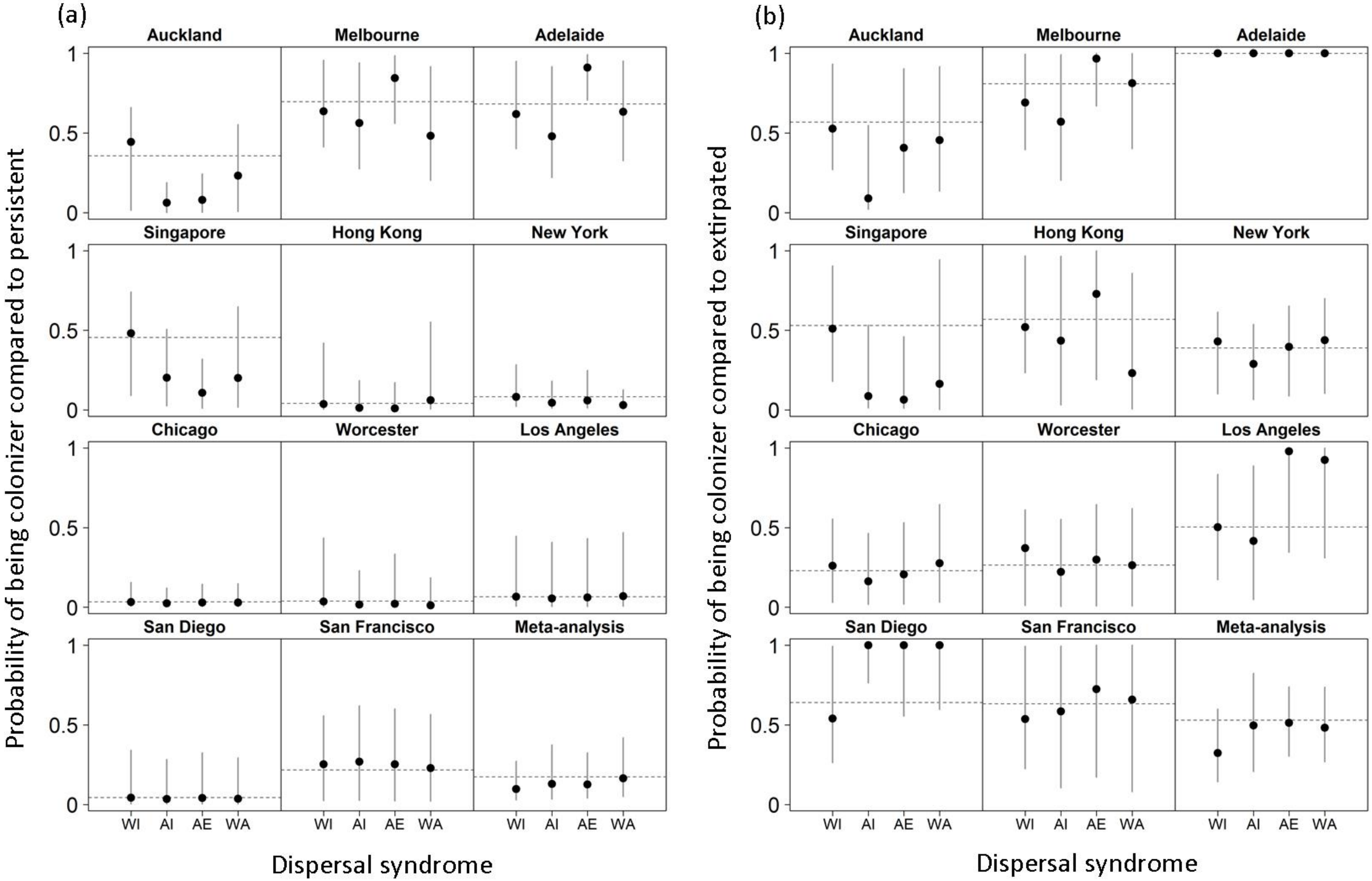

(a)
Auckland
Melbourne
Adelaide
Singapore
Hong Kong
New York
Chicago
Worcester
Los Angeles
San Diego
San Francisco
Meta-analysis
Probability of being colonizer compared to persistent
TU WO SU EP CL AQ PA OG
Growth form
(b)
Probability of being colonizer compared to extirpated

Figure A8.



(a)
Auckland
Melbourne
Adelaide
Singapore
Hong Kong
New York
Chicago
Worcester
Los Angeles
San Diego
San Francisco
Meta-analysis
Probability of being colonizer compared to persistent
CA
CB
Clonality
(b)
Probability of being colonizer compared to extirpated

Figure A9.



(a)
Auckland
Melbourne
Adelaide
Singapore
Hong Kong
New York
Chicago
Worcester
Los Angeles
San Diego
San Francisco
Meta-analysis
Probability of being colonizer compared to persistent
WI AI AE WA
Dispersal syndrome
(b)
Auckland
Melbourne
Adelaide
Singapore
Hong Kong
New York
Chicago
Worcester
Los Angeles
San Diego
San Francisco
Meta-analysis
Probability of being colonizer compared to extirpated
WI AI AE WA
Dispersal syndrome

Figure A10

Figure A11. Floral similarity among cities included in the study, based on paired comparisons using the Jaccard's index; larger points represent larger similarities between two cities for their pre-urbanization (a) or introduced flora (b). Codes for cities as follows: LA= Los Angeles, SD= San Diego, SF= San Francisco, WO= Worcester, CH= Chicago, NY= New York, HK= Hong Kong, SI= Singapore, AD= Adelaide, ME= Melbourne, AU= Auckland.

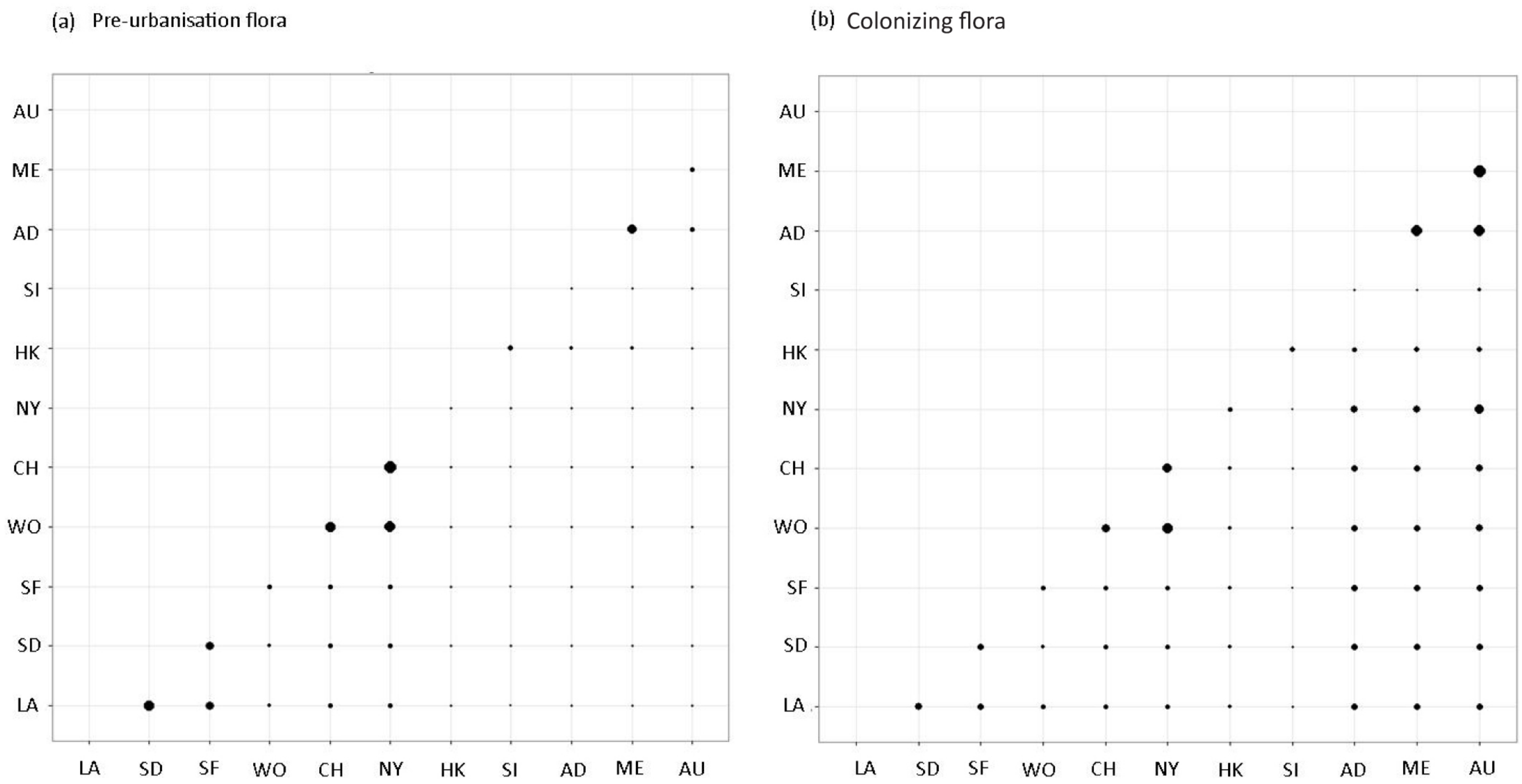

(a) Pre-urbanisation flora
(b) Colonizing flora
AU
ME
AD
SI
HK
NY
CH
WO
SF
SD
LA
LA
SD
SF
WO
CH
NY
HK
SI
AD
ME
AU

Figure A11

Figures A12-a13. Estimated effect of traits on the prevalence of colonizers over persistent (Fig. A12) and extirpated (Fig. A13) urban plants, within four biogeographic regions. Black dots represent mean effects and grey lines represent 95% credible intervals. Credible intervals over 10 or under -10 not represented.

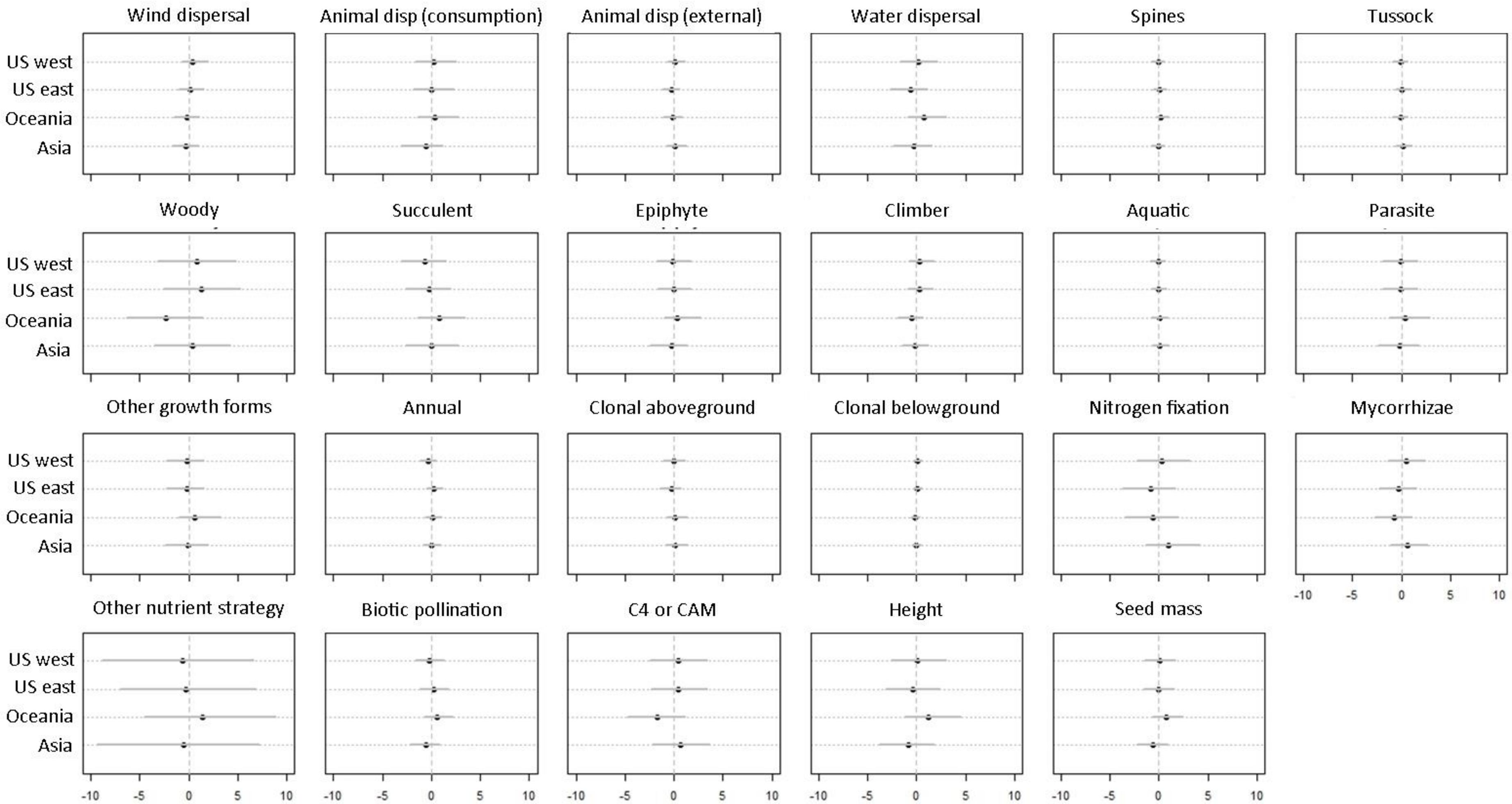

Wind dispersal
Animal disp (consumption)
Animal disp (external)
Water dispersal
Spines
Tussock
Woody
Succulent
Epiphyte
Climber
Aquatic
Parasite
Other growth forms
Annual
Clonal aboveground
Clonal belowground
Nitrogen fixation
Mycorrhizae
Other nutrient strategy
Biotic pollination
C4 or CAM
Height
Seed mass
US west
US east
Oceania
Asia
-10
-5
0
5
10

Figure A12

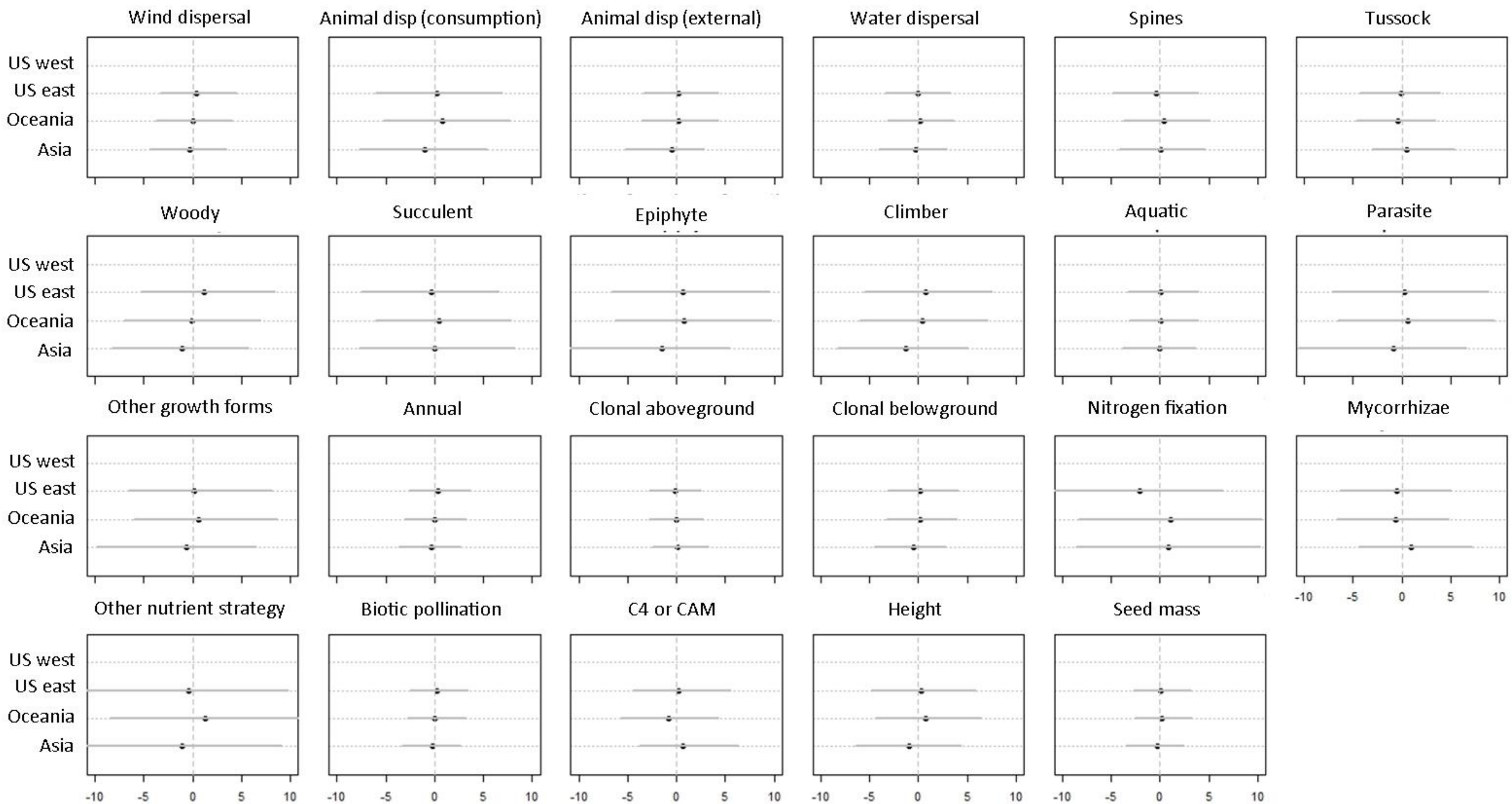

Wind dispersal
Animal disp (consumption)
Animal disp (external)
Water dispersal
Spines
Tussock
Woody
Succulent
Epiphyte
Climber
Aquatic
Parasite
Other growth forms
Annual
Clonal aboveground
Clonal belowground
Nitrogen fixation
Mycorrhizae
Other nutrient strategy
Biotic pollination
C4 or CAM
Height
Seed mass
US west
US east
Oceania
Asia
-10
-5
0
5
10

Figure A13

Appendix 2: Sampling bias –temporal and spatial grain of plant surveys

Olden and Poff (2003) state that our inference on the biotic change occurring in plant communities will depend on both the spatial and temporal scale of the data we use to analyse those changes. To check if these elements could have affected our results, we analysed their effect in the annual rates of extirpation and colonization found in the 11 cities under consideration. Specific values of the aforementioned rates can be found in Table A1.

Regarding the temporal scale, we checked how time elapsed between initial and final surveys in each city (refer to Table S1 for details) correlated with their annual rates of extirpation and colonization. To do so, we run a simple linear model where the annual rate was a function of survey length.

Regarding the spatial scale, we checked how urban surface (as reported in Demographia (April 2016) Demographia World Urban Areas (12th ed.); URL: http://demographia.com/db-worldua.pdf) affects the same rates. We have used urban surface as a surrogate of the area surveyed in each city. Unfortunately there is no accurate information as to how exactly the urban boundaries were delimited for the surveys. However, the current surrogate allows us to investigate the possible effect of the spatial extent of the surveys, as pointed out by Olden and Poff (2003).

None of the reported effects are significant (Fig A14, the 95% credible intervals cross zero). Therefore, we conclude that, in the present work, survey length and urban area have non consistent effect on the annual rates of extirpation and colonization and they do not affect the inference we drew on biotic change across urban areas.

Figure A14. Effects of survey length and urban area on the annual extirpation and colonization rate reported for the 11 cities. Black dots represent mean effects and grey lines represent 95% credible intervals.

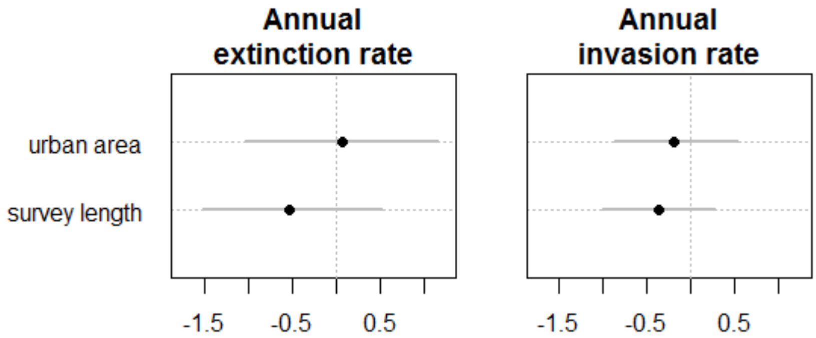

Annual
extinction rate
Annual
invasion rate
urban area
survey length
-1.5
-0.5
0.5
-1.5
-0.5
0.5

Figure A14

Appendix 3: Code used for modelling.

1. City-level logistic regressions

'DATA' includes the classification of species recorded in each city as colonizer or persitent/extirpated and trait characterization for each species

Load dataset and call for the packages

```
DATA <- read.csv("~/dataset.csv")
library(R2jags)
```

Choose city

```
city.list <- levels(DATA $city)
acity <- city.list[1] # Adelaide – Repeat for the rest of the cities
```

Create data set for city

```
int <- DATA [DATA $city==acity, ]
int.miss <- int # make an additional city data frame with missing values
int.miss$ne <- rep(NA, length(int.miss$ne))
int <- rbind(int, int.miss)  # duplicates the rows with the same info, except for the response (which contains NAs)
rest <- DATA [DATA $city!=acity, ] # takes all records except those for the city under consideration
rest <- rest[duplicated(rest$sci)==F, ] # remove species duplicates
ny <- rbind(int, rest)
rm(rest)
```

Set response variable

```
ne <- int$ne # 0=persistent or extirpated, 1=colonizer, NA=for prediction
```

Set predictors and other variables

```
height <- log(ny$height)
height <- (height - mean(height, na.rm=T)) / (2*sd(height, na.rm=T))
seed.mass <- log(ny$seed.mass)
seed.mass <- (seed.mass - mean(seed.mass, na.rm=T)) / (2*sd(seed.mass, na.rm=T))
growth.form <- as.numeric(ny$growth.form)
annual <- as.numeric(ny$annual)
clonal <- as.numeric(ny$clonal)
dispersal <- as.numeric(ny$dispersal)
nutrient <- as.numeric(ny$nutrient)
pollination <- as.numeric(ny$pollination)
photo.path <- as.numeric(ny$photo.path)
spines <- as.numeric(ny$spines)
N <- dim(ny)[1]
```

```
fam <- as.numeric(ny$family)
N.fam <- max(fam)
CN <- length(ne)
Cfam <- as.numeric(int$family)
CN.fam <- max(Cfam)
ncat.growth.form <- length(table(growth.form))
ncat.annual <- length(table(annual))
ncat.clonal <- length(table(clonal))
ncat.dispersal <- length(table(dispersal))
ncat.nutrient <- length(table(nutrient))
ncat.pollination <- length(table(pollination))
ncat.photo.path <- length(table(photo.path))
ncat.spines <- length(table(spines))
```

Run model

```
cat('   model {
# model to impute missing values (uncertainty at family level is propagated when imputing missing values)
  for(i in 1:N) {
    # continuous variables
      height[i] ~ dnorm(m.height[fam[i]], t.height[fam[i]])
      seed.mass[i] ~ dnorm(m.seed.mass[fam[i]], t.seed.mass[fam[i]])
    # categorical variables
      growth.form[i] ~ dcat(p.growth.form[fam[i], 1:ncat.growth.form])
      annual[i]      ~ dcat(p.annual[fam[i], 1:ncat.annual])
      clonal[i]      ~ dcat(p.clonal[fam[i], 1:ncat.clonal])
      dispersal[i]   ~ dcat(p.dispersal[fam[i], 1:ncat.dispersal])
      nutrient[i]    ~ dcat(p.nutrient[fam[i], 1:ncat.nutrient])
      pollination[i] ~ dcat(p.pollination[fam[i], 1:ncat.pollination])
      photo.path[i]  ~ dcat(p.photo.path[fam[i], 1:ncat.photo.path])
      spines[i]      ~ dcat(p.spines[fam[i], 1:ncat.spines])
    }
  # family level
    for(j in 1:N.fam) {
      m.height[j] ~ dnorm(fmm.height, pow(fms.height, -2))
      t.height[j] ~ dgamma(pow(fsm.height, -2), pow(fst.height, -2))
      m.seed.mass[j] ~ dnorm(fmm.seed.mass, pow(fms.seed.mass, -2))
      t.seed.mass[j] ~ dgamma(pow(fsm.seed.mass, -2), pow(fst.seed.mass, -2))
      p.growth.form[j, 1:ncat.growth.form] ~ ddirch(alpha1[1:ncat.growth.form])
      p.annual[j, 1:ncat.annual] ~ ddirch(alpha2[1:ncat.annual])
      p.clonal[j, 1:ncat.clonal] ~ ddirch(alpha3[1:ncat.clonal])
      p.dispersal[j, 1:ncat.dispersal]  ~ ddirch(alpha4[1:ncat.dispersal])
      p.nutrient[j, 1:ncat.nutrient]  ~ ddirch(alpha5[1:ncat.nutrient])
      p.pollination[j, 1:ncat.pollination] ~ ddirch(alpha6[1:ncat.pollination])
      p.photo.path[j, 1:ncat.photo.path] ~ ddirch(alpha7[1:ncat.photo.path])
      p.spines[j, 1:ncat.spines] ~ ddirch(alpha8[1:ncat.spines])
      }
  # priors; missing values for height
    fmm.height ~ dnorm(0, 0.0001)
    fms.height ~ dunif(0, 10)
```

```
   fsm.height ~ dunif(0, 10)
   fst.height ~ dunif(0, 10)
  # proirs; missing values for seed mass
   fmm.seed.mass ~ dnorm(0, 0.0001)
   fms.seed.mass ~ dunif(0, 10)
   fsm.seed.mass ~ dunif(0, 10)
   fst.seed.mass ~ dunif(0, 10)

 # model response
  for(i in 1:CN) {
   ne[i] ~ dbern(p[i])
   logit(p[i]) <- min(max(b0 + b1[dispersal[i]] + b2[growth.form[i]] + b3*annual[i]
         + b4[clonal[i]] + b5[nutrient[i]] + b6*pollination[i] + b7*photo.path[i]
         + b8*height[i] + b9*seed.mass[i] + b10*spines[i] + ran.fam[Cfam[i]], -999), 999)
   }
  # family random effect
   for(j in 1:CN.fam) {
    ran.fam[j] ~ dnorm(0,pow(s.fam, -2))
    }
  # priors; explanatory variables
   b0 ~ dt(0, 10, 1)
   b1[1] <- 0
   for(i in 2:ncat.dispersal) {b1[i] ~ dnorm(0, pow(sigma.b1, -2))}
   b2[1] <- 0
   for(i in 2:ncat.growth.form) {b2[i] ~ dnorm(0, pow(sigma.b2, -2))}
   b3 ~ dt(0, 2.5, 1)
   b4[1] <- 0
   for(i in 2:ncat.clonal) {b4[i] ~ dnorm(0, pow(sigma.b4, -2))}
   b5[1] <- 0
   for(i in 2:ncat.nutrient) {b5[i] ~ dnorm(0, pow(sigma.b5, -2))}
   b6 ~ dt(0, 2.5, 1)
   b7 ~ dt(0, 2.5, 1)
   b8 ~ dt(0, 2.5, 1)
   b9 ~ dt(0, 2.5, 1)
   b10 ~ dt(0, 2.5, 1)
   sigma.b1 ~ dt(0, 0.0016, 1)T(0,)
   sigma.b2 ~ dt(0, 0.0016, 1)T(0,)
   sigma.b4 ~ dt(0, 0.0016, 1)T(0,)
   sigma.b5 ~ dt(0, 0.0016, 1)T(0,)
  # priors; random effect for family
   s.fam ~ dt(0, 0.0016, 1)T(0,)
  } '
   , file=(modelfile <- tempfile()))

 # Bundle data
 jags.data <- list(ncat.dispersal=ncat.dispersal, ncat.growth.form=ncat.growth.form,
         ncat.annual=ncat.annual, ncat.clonal=ncat.clonal,
         ncat.nutrient=ncat.nutrient, ncat.pollination=ncat.pollination,
         ncat.photo.path=ncat.photo.path, ncat.spines=ncat.spines, N=N, ne=ne,
         N.fam=N.fam, fam=fam, CN=CN, Cfam=Cfam, CN.fam=CN.fam, height=height,
```

```
        seed.mass=seed.mass, growth.form=growth.form, annual=annual, clonal=clonal,
        dispersal=dispersal, nutrient=nutrient, pollination=pollination,
        photo.path=photo.path, spines=spines,
        alpha1=rep(1,ncat.growth.form), alpha2=rep(1,ncat.annual),
        alpha3=rep(1,ncat.clonal), alpha4=rep(1,ncat.dispersal),
        alpha5=rep(1,ncat.nutrient), alpha6=rep(1,ncat.pollination),
        alpha7=rep(1,ncat.photo.path), alpha8=rep(1,ncat.spines))

# Inits function
n.ch=1
b1<-rep(NA,times=ncat.dispersal)
for(i in 2:ncat.dispersal) {b1[i]=rnorm(n.ch)}
b2<-rep(NA,times=ncat.growth.form)
for(i in 2:ncat.growth.form) {b2[i]=rnorm(n.ch)}
b4<-rep(NA,times=ncat.clonal)
for(i in 2:ncat.clonal) {b4[i]=rnorm(n.ch)}
b5<-rep(NA,times=ncat.nutrient)
for(i in 2:ncat.nutrient) {b5[i]=rnorm(n.ch)}
inits <- function() list(fmm.height=rnorm(n.ch), fms.height=runif(n.ch),
          fsm.height=runif(n.ch), fst.height=runif(n.ch), fmm.seed.mass=rnorm(n.ch),
          fms.seed.mass=runif(n.ch), fsm.seed.mass=runif(n.ch),
          fst.seed.mass=runif(n.ch), b0=rnorm(n.ch), b1=b1, b2=b2, b3=rnorm(n.ch),
          b4=b4,b5=b5,b6=rnorm(n.ch),b7=rnorm(n.ch),b10=rnorm(n.ch),
          sigma.b1=runif(n.ch), sigma.b2=runif(n.ch), sigma.b4=runif(n.ch),
          sigma.b5=runif(n.ch), b8=rnorm(n.ch), b9=rnorm(n.ch), s.fam=runif(n.ch))

# Parameters to estimate
parameters <- c("b0", "b1", "b2", "b3", "b4", "b5", "b6", "b7", "b8", "b9", "b10", "s.fam", "ran.fam",
"sigma.b1", "sigma.b2", "sigma.b4", "sigma.b5", "ne")

n.chains=3
n.iter=50000
n.burnin=20000

# Start Gibbs sampling
OUT<- jags(data = jags.data, inits = inits, parameters.to.save = parameters, model.file = modelfile,
n.chains=n.chains, n.iter=n.iter, n.burnin=n.burnin)
```

2. Meta-analysis

'MEAN' includes the average estimated effect for each trait (rows) and city (columns) - represented by β_k in the Methods section

'SD' includes the standard deviations estimated for the effect of each trait (rows) and city (columns) - represented by $\sigma_{\beta k}$ in the Methods section.

1.1. Without spatial correction

Set some variables

```
Ncity <- ncol(MEAN)
Nvar <- nrow(MEAN)
```

Run model

```
cat('   model {
    for(j in 1:Ncity) {      # for each data set
      for(i in 1:Nvar) {
        m[i,j] ~ dnorm(gm[i], tau[i,j])          # observed estimate drawn from a distribution of estimates
        tau[i,j] <- 1 / (gv[i] + s[i,j]*s[i,j])       # variances are additive
      }
    }
  for(i in 1:Nvar) {
    gm[i] ~ dnorm(0,0.0001)      # mean effect size of all possible data sets
    gv[i] <- sd[i]*sd[i]                 # between dataset variance in effect size
    sd[i] ~ dunif(0,100)
  }
}'
    , file=(modelfile <- tempfile()))

# Bundle data
jags.data <- list(Ncity=Ncity, Nvar=Nvar, m=MEAN, s=SD)

# Inits function
inits <- function() list(gm=rnorm(Nvar), sd=runif(Nvar))

# Parameters to estimate
parameters <- c("gm","gv")

n.chains=3
n.iter=50000
n.burnin=20000
n.thin=10

# Start Gibbs sampling
META <- jags(data = jags.data, inits = inits, parameters.to.save = parameters, model.file = modelfile,
n.chains=n.chains, n.iter=n.iter, n.burnin=n.burnin, n.thin=n.thin)
```

1.2. Including a random effect to correct for spatial autocorrelation

Set some variables

```
Ncity <- ncol(MEAN)
Nvar <- nrow(MEAN)
```

```
region <- as.factor(c("Oceania", "Oceania", "USeast", "Asia", "USwest", "Oceania", "USeast", "USwest",
"USwest", "Asia", "USeast"))
Nregions <- max(as.numeric(region))
```

Run model

```
cat('   model {
    for(i in 1:Nvar) {
      for(j in 1:Ncity) {
        m[i,j] ~ dnorm(city.m[i,j], tau[i,j])         # observed estimate drawn from a distribution of estimates, where city.m
is the real city-level mean
        city.m[i,j] <- gm[i] + beta[i,region[j]]    # gm is the mean effect across cities, and beta the regional level effect
        tau[i,j] <- 1 / (gv[i] + s[i,j]*s[i,j])           # variances are additive
      }
    }
    for(i in 1:Nvar) {
      gm[i] ~ dnorm(0,0.001)
      for (j in 1:Nregions){
        beta[i,j] ~ dnorm(0, pow(s.beta[i], -2))
        }
      s.beta[i] ~ dt(0,0.0016,1)T(0,)        # variance in effect size among regions
      gv[i] <- sd[i] * sd[i]                         # between cities variance in effect size (within regions)
       sd[i] ~ dt(0,0.0016,1)T(0,)
    }
  }'
    , file=(modelfile <- tempfile()))

## Bundle data
jags.data <- list(Ncity=Ncity, Nvar=Nvar, m=IP.MEAN, s=IP.SD, region=as.numeric(region), Nregions=Nregions)

## Inits function
inits <- function() list(gm=rnorm(Nvar), s.beta=runif(Nvar), sd=runif(Nvar))

## Parameters to estimate
parameters <- c("city.m", "gm", "beta", "gv", "s.beta", "sd")

n.chains=3
n.iter=100000
n.burnin=50000
n.thin=10

## Start Gibbs sampling
META <- jags(data = jags.data, inits = inits, parameters.to.save = parameters, model.file = modelfile,
n.chains=n.chains, n.iter=n.iter, n.burnin=n.burnin, n.thin=n.thin)
```