Maintenance of biodiversity on islands

Chisholm, Ryan A., et al. "Maintenance of biodiversity on islands." *Proc. R. Soc. B*. Vol. 283. No. 1829. The Royal Society, 2016.

Lab Journal club

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Reasons for choosing this article

- This paper tackles a relevant theory problem (predicting biodiversity with niche and dispersal models)
- This paper presents parsimonious mechanistic model (4 parameters)
- The model might be applicable to scenarios that people in the lab care about (perhaps):
  - e.g. how to interpret gut microbial diversity observed in different mammals

Background

- Small-area effect:
  - Below a threshold island area, island species richness apparently varies independently of area
- Previous explanations: i) extinction rates are high in small islands; ii) small islands contain small subsets of habitats available on large islands
- Criticism on previous explanations:
  - immigration: Larger small islands still receive more immigration than smaller small islands
  - inconsistence with data
  - qualitative

Prototypical example of small-island effect: vascular plants in the Kapingamarangi Atoll in Micronesia

This paper's approach provides excellent fit to prototypical data

- Introduce niche diversity K -- number of equal-sized, non-overlapping niche spaces -- into existing neutral models
- Treat migration (island), demographic stochasticity (island and mainland) and speciation (mainland) within each niche.
- 4 parameters:
- J: number of individuals
- m: immigration
- K: niche
- Theta: speciation

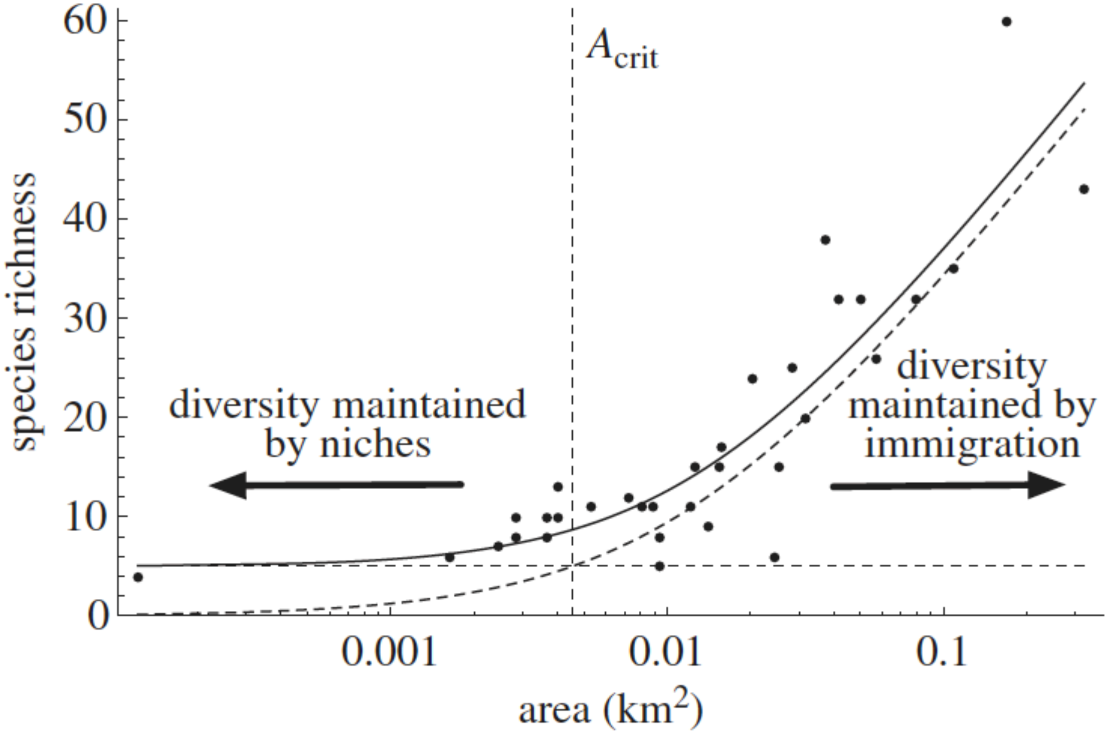

Figure 1. SAR for vascular plants on islands in the Kapingamarangi Atoll [10] (points) along with the fitted SAR from the model (solid curve; $n = 33$, $\theta = 15.2$, $m = 6.9 \times 10^{-5}$, $K = 5$, $R^2 = 0.93$). The horizontal dashed line and dashed curve show the diversity predicted by, respectively, the niche and neutral components of the model in isolation. The transition between the two regimes occurs at area $A_{crit} = 0.0045\ km^2$ (grey dashed vertical line; equation (2.8)).

Diphasic pattern was generated in other data sets

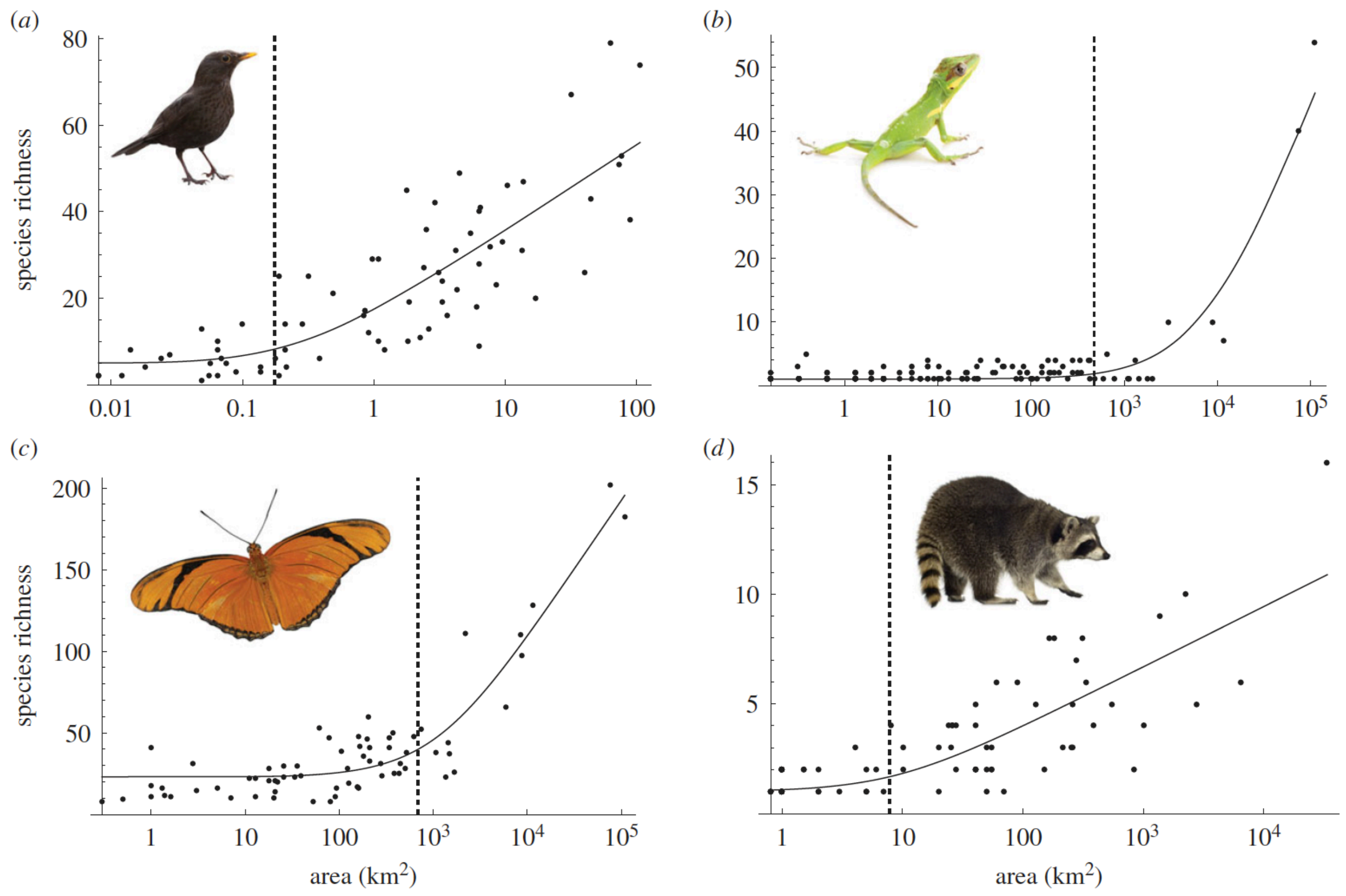

Figure 2. SARs for four datasets (points), with best-fit models (solid curves): (*a*) birds, British Isles ($n = 73$, $\theta = 8.6$, $m = 0.012$, $K = 5$, $R^2 = 0.87$); (*b*) anoline lizards, West Indies ($n = 136$, $\theta = 16.6$, $m = 1.1 \times 10^{-9}$, $K = 1$, $R^2 = 0.93$); (*c*) butterflies, West Indies ($n = 68$, $\theta = 37.2$, $m = 2.3 \times 10^{-9}$, $K = 23$, $R^2 = 0.92$); and (*d*) mammals, Islands of British Columbia ($n = 75$, $\theta = 1.2$, $m = 1.8 \times 10^{-5}$, $K = 1$, $R^2 = 0.84$). As in figure 1, a transition from a niche-structured regime to a colonization–extinction regime occurs in each panel as area increases past a critical area A_{crit} (dashed vertical lines; equation (2.8)). Inset images (obtained with permission from www.shutterstock.com) show common blackbird (*Turdus merula*), Knight anole (*Anolis equestris*), Julia heliconian (*Dryas iulia*) and common raccoon (*Procyon lotor*). (Online version in colour.)

Critical area is smaller when immigration is stronger

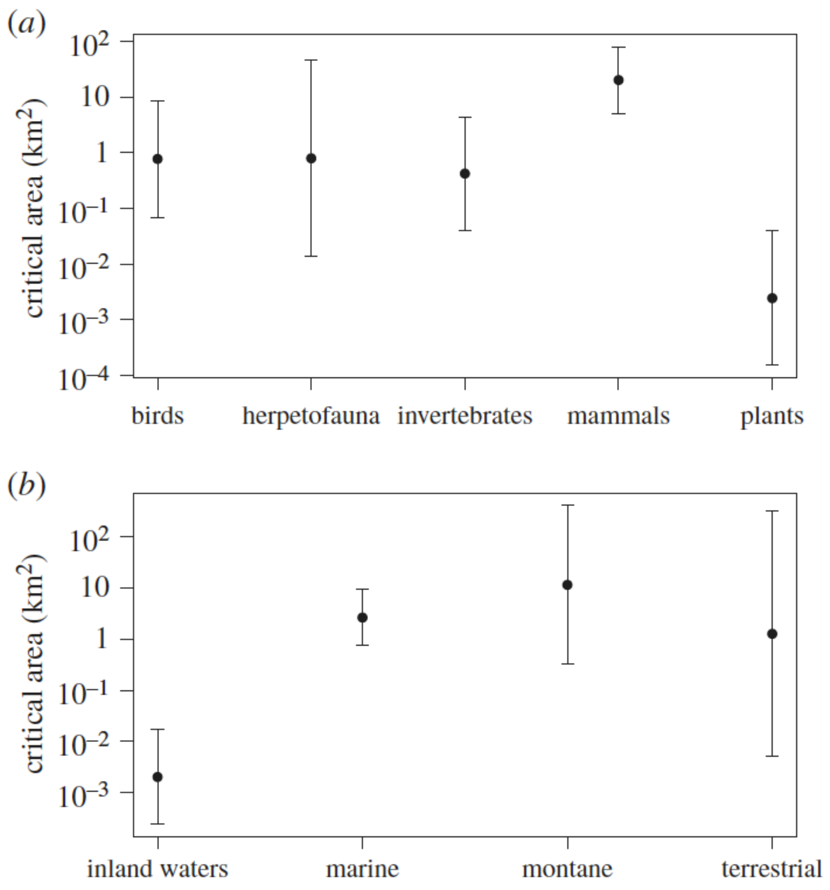

Figure 3. Critical area by (*a*) taxonomic group and (*b*) archipelago type. Points show means on a log scale; whiskers show estimated 95% CIs using a normal approximation on a log scale.

	estimated effect on log A_{crit} (km^2) [95% CI]		*p*-value
intercept (birds, inland waters)	−6.59	[−9.56, −3.62]	2.9×10^{-5}
taxonomic group			1.4×10^{-9}
herpetofauna	1.73	[−2.10, 5.55]	0.37
invertebrates	0.65	[−2.15, 3.45]	0.65
mammals	4.17	[1.58, 6.76]	0.0019
plants	−4.11	[−7.03, −1.19]	0.0062
archipelago type			8.3×10^{-7}
marine	6.49	[4.28, 8.70]	8.2×10^{-8}
montane	7.88	[4.28, 11.48]	3.5×10^{-5}
terrestrial	4.72	[1.11, 8.32]	0.011