

Supporting Information

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Appendix S1: Full initial immigration, repeat immigration, and extinction models

Table S1: Main effects included in the full initial immigration, repeat immigration, and extinction models. Note that each model also included *all* possible interaction terms between the fixed effects indicated below, plus random effects of census and source population. These models were simplified to give the models in *Tables S4–S6*. See *Tables S2–S3* for a complete list of terms included in each model. TIB refers to models based on the Theory of Island Biogeography— that is, excluding any trophic interactions.

	Main effects						
	Distance from mainland	Island diameter	Interval between censuses	Species richness	Presence of predators	Ability to consume basal resources	Presence of animal prey
<hr/>							
(a) Initial and repeat immigration models							
Null							
TIB	X	X	X				
Species-richness	X	X	X	X			
Top-down	X	X	X		X		
Top-down & Species-richness	X	X	X	X	X		
Bottom-up	X	X	X			X	X
Bottom-up & Species-richness	X	X	X	X		X	X
Top-down & Bottom-up	X	X	X		X	X	X
<hr/>							
(b) Extinction models							
Null							
TIB		X	X				
Species-richness		X	X	X			
Top-down		X	X		X		
Top-down & Species-richness		X	X	X	X		
Bottom-up		X	X			X	X
Bottom-up & Species-richness		X	X	X		X	X
Top-down & Bottom-up		X	X		X	X	X

Table S2: Symbols used in mathematical description of the statistical models.

Symbol	Description
C_{ijk+1}	Probability of immigration for species i on island j between census k and census $k + 1$
X_{ijk+1}	Probability of extinction for species i on island j between census k and census $k + 1$
δ_j	Distance of island j from the mainland (meters)
λ_j	Diameter of island j (meters)
τ_{k+1}	Time between census k and census $k + 1$ (days)
Σ_k	Species richness during census k
ρ_{ijk}	Presence of predators of species i on island j during census k : $\rho_{ijk}=1$ if predators of species i were observed on island j during census k , $\rho_{ijk}=0$ otherwise
η_i	Ability of species i to eat plants: $\eta_i=1$ if species i is able to eat basal resources, $\eta_i=0$ otherwise
α_{ijk}	Presence of animal prey for species i on island j during census k : $\alpha_{ijk}=1$ if prey of species i were observed on island j during census k , $\alpha_{ijk}=0$ otherwise
E_{k+1}	Random effect of period between censuses k and $k + 1$
S_i	Random effect of species i
W_{ijq}	Random effect of source population (i.e., the interaction between species i , island j , and event window q)
ϵ_{ijk+1}	Residual error for species i on island j between census k and census $k + 1$

Table S3: Mathematical structure of the full initial immigration models. Mathematical structure of the repeat immigration models was identical except that the random effect of species (S_i) was replaced with a random effect of the interaction between species, island, and colonisation interval (W_{ijq}) as in the full extinction models (Table S4). All symbols are as in Table S2. TIB refers to a model based on the original Theory of Island Biogeography, without any trophic effects.

Model	Mathematical structure
Null	$C_{ijk+1} = E_{k+1} + \epsilon_{ijk+1}$
TIB	$C_{ijk+1} = \delta_j + \lambda_j + \tau_{k+1} + \delta_j \lambda_j + \delta_j \tau_{k+1} + \lambda_j \tau_{k+1} + \delta_j \lambda_j \tau_{k+1} + E_{k+1} + S_i + \epsilon_{ijk+1}$
Species-richness	$C_{ijk+1} = \delta_j + \lambda_j + \tau_{k+1} + \Sigma_k + \delta_j \lambda_j + \delta_j \tau_{k+1} + \delta_j \Sigma_k + \lambda_j \tau_{k+1} + \lambda_j \Sigma_k + \tau_{k+1} \Sigma_k + \delta_j \lambda_j \tau_{k+1} + \delta_j \lambda_j \Sigma_j + \delta_j \tau_{k+1} \Sigma_j + \lambda_j \tau_{k+1} \Sigma_j + \delta_j \lambda_j \tau_{k+1} \Sigma_j + E_{k+1} + S_i + \epsilon_{ijk+1}$
Top-down	$C_{ijk+1} = \delta_j + \lambda_j + \tau_{k+1} + \rho_{ijk} + \delta_j \lambda_j + \delta_j \tau_{k+1} + \delta_j \rho_{ijk} + \lambda_j \tau_{k+1} + \lambda_j \rho_{ijk} + \tau_{k+1} \rho_{ijk} + \delta_j \lambda_j \tau_{k+1} + \delta_j \lambda_j \rho_{ijk} + \delta_j \tau_{k+1} \rho_{ijk} + \lambda_j \tau_{k+1} \rho_{ijk} + \delta_j \lambda_j \tau_{k+1} \rho_{ijk} + E_{k+1} + S_i + \epsilon_{ijk+1}$
Top-down & Species-richness	$C_{ijk+1} = \delta_j + \lambda_j + \tau_{k+1} + \Sigma_k + \rho_{ijk} + \delta_j \lambda_j + \delta_j \tau_{k+1} + \delta_j \Sigma_j + \delta_j \rho_{ijk} + \lambda_j \tau_{k+1} + \lambda_j \Sigma_j + \lambda_j \rho_{ijk} + \tau_{k+1} \Sigma_k + \tau_{k+1} \rho_{ijk} + \Sigma_k \rho_{ijk} + \delta_j \lambda_j \tau_{k+1} + \delta_j \lambda_j \Sigma_k + \delta_j \lambda_j \rho_{ijk} + \delta_j \tau_{k+1} \Sigma_k + \delta_j \tau_{k+1} \rho_{ijk} + \delta_j \Sigma_k \rho_{ijk} + \lambda_j \tau_{k+1} \Sigma_k + \lambda_j \tau_{k+1} \rho_{ijk} + \tau_{k+1} \Sigma_k \rho_{ijk} + \delta_j \lambda_j \tau_{k+1} \Sigma_k + \delta_j \lambda_j \tau_{k+1} \rho_{ijk} + \delta_j \lambda_j \Sigma_k \rho_{ijk} + \delta_j \tau_{k+1} \Sigma_k \rho_{ijk} + \lambda_j \tau_{k+1} \Sigma_k \rho_{ijk} + \delta_j \lambda_j \tau_{k+1} \Sigma_k \rho_{ijk} + E_{k+1} + S_i + \epsilon_{ijk+1}$
Bottom-up	$C_{ijk+1} = \delta_j + \lambda_j + \tau_{k+1} + \eta_i + \alpha_{ijk} + \delta_j \lambda_j + \delta_j \tau_{k+1} + \delta_j \eta_i + \delta_j \alpha_{ijk} + \lambda_j \tau_{k+1} + \lambda_j \eta_i + \lambda_j \alpha_{ijk} + \tau_{k+1} \eta_i + \tau_{k+1} \alpha_{ijk} + \eta_i \alpha_{ijk} + \delta_j \lambda_j \tau_{k+1} + \delta_j \lambda_j \eta_i + \delta_j \lambda_j \alpha_{ijk} + \delta_j \tau_{k+1} \eta_i + \delta_j \tau_{k+1} \alpha_{ijk} + \delta_j \eta_i \alpha_{ijk} + \lambda_j \tau_{k+1} \eta_i + \lambda_j \tau_{k+1} \alpha_{ijk} + \lambda_j \eta_i \alpha_{ijk} + \tau_{k+1} \eta_i \alpha_{ijk} + \delta_j \lambda_j \tau_{k+1} \eta_i + \delta_j \lambda_j \tau_{k+1} \alpha_{ijk} + \delta_j \lambda_j \eta_i \alpha_{ijk} + \delta_j \tau_{k+1} \eta_i \alpha_{ijk} + \lambda_j \tau_{k+1} \eta_i \alpha_{ijk} + E_{k+1} + S_i + \epsilon_{ijk+1}$
Bottom-up & Species-richness	$C_{ijk+1} = \delta_j + \lambda_j + \tau_{k+1} + \Sigma_k + \eta_i + \alpha_{ijk} + \delta_j \lambda_j + \delta_j \tau_{k+1} + \delta_j \Sigma_k + \delta_j \eta_i + \delta_j \alpha_{ijk} + \lambda_j \tau_{k+1} + \lambda_j \Sigma_k + \lambda_j \eta_i + \lambda_j \alpha_{ijk} + \tau_{k+1} \Sigma_k + \tau_{k+1} \eta_i + \tau_{k+1} \alpha_{ijk} + \Sigma_k \eta_i + \Sigma_k \alpha_{ijk} + \eta_i \alpha_{ijk} + \delta_j \lambda_j \tau_{k+1} + \delta_j \lambda_j \Sigma_k + \delta_j \lambda_j \eta_i + \delta_j \lambda_j \alpha_{ijk} + \delta_j \tau_{k+1} \Sigma_k + \delta_j \tau_{k+1} \eta_i + \delta_j \tau_{k+1} \alpha_{ijk} + \lambda_j \tau_{k+1} \Sigma_k + \lambda_j \tau_{k+1} \eta_i + \lambda_j \tau_{k+1} \alpha_{ijk} + \lambda_j \Sigma_k \eta_i + \lambda_j \Sigma_k \alpha_{ijk} + \lambda_j \eta_i \alpha_{ijk} + \tau_{k+1} \Sigma_k \eta_i + \tau_{k+1} \Sigma_k \alpha_{ijk} + \tau_{k+1} \eta_i \alpha_{ijk} + \Sigma_k \eta_i \alpha_{ijk} + \delta_j \lambda_j \tau_{k+1} \Sigma_k + \delta_j \lambda_j \tau_{k+1} \eta_i + \delta_j \lambda_j \tau_{k+1} \alpha_{ijk} + \delta_j \lambda_j \Sigma_k \eta_i + \delta_j \lambda_j \Sigma_k \alpha_{ijk} + \delta_j \lambda_j \eta_i \alpha_{ijk} + \delta_j \tau_{k+1} \Sigma_k \eta_i + \delta_j \tau_{k+1} \Sigma_k \alpha_{ijk} + \delta_j \tau_{k+1} \eta_i \alpha_{ijk} + \delta_j \Sigma_k \eta_i \alpha_{ijk} + \lambda_j \tau_{k+1} \Sigma_k \eta_i + \lambda_j \tau_{k+1} \Sigma_k \alpha_{ijk} + \lambda_j \tau_{k+1} \eta_i \alpha_{ijk} + \lambda_j \Sigma_k \eta_i \alpha_{ijk} + \tau_{k+1} \Sigma_k \eta_i \alpha_{ijk} + \delta_j \lambda_j \tau_{k+1} \Sigma_k \eta_i + \delta_j \lambda_j \tau_{k+1} \Sigma_k \alpha_{ijk} + \delta_j \lambda_j \tau_{k+1} \eta_i \alpha_{ijk} + \delta_j \lambda_j \Sigma_k \eta_i \alpha_{ijk} + \delta_j \lambda_j \Sigma_k \alpha_{ijk} + \lambda_j \tau_{k+1} \Sigma_k \eta_i \alpha_{ijk} + \lambda_j \tau_{k+1} \Sigma_k \alpha_{ijk} + E_{k+1} + S_i + \epsilon_{ijk+1}$
Top-down & Bottom-up	$C_{ijk+1} = \delta_j + \lambda_j + \tau_{k+1} + \rho_{ijk} + \eta_i + \alpha_{ijk} + \delta_j \lambda_j + \delta_j \tau_{k+1} + \delta_j \rho_{ijk} + \delta_j \eta_i + \delta_j \alpha_{ijk} + \lambda_j \tau_{k+1} + \lambda_j \rho_{ijk} + \lambda_j \eta_i + \lambda_j \alpha_{ijk} + \tau_{k+1} \rho_{ijk} + \tau_{k+1} \eta_i + \tau_{k+1} \alpha_{ijk} + \rho_{ijk} \eta_i + \rho_{ijk} \alpha_{ijk} + \eta_i \alpha_{ijk} + \delta_j \lambda_j \tau_{k+1} + \delta_j \lambda_j \rho_{ijk} + \delta_j \lambda_j \eta_i + \delta_j \lambda_j \alpha_{ijk} + \delta_j \tau_{k+1} \rho_{ijk} + \delta_j \tau_{k+1} \eta_i + \delta_j \tau_{k+1} \alpha_{ijk} + \delta_j \rho_{ijk} \eta_i + \delta_j \rho_{ijk} \alpha_{ijk} + \delta_j \tau_{k+1} \rho_{ijk} + \delta_j \tau_{k+1} \eta_i + \delta_j \tau_{k+1} \alpha_{ijk} + \lambda_j \tau_{k+1} \rho_{ijk} + \lambda_j \tau_{k+1} \eta_i + \lambda_j \tau_{k+1} \alpha_{ijk} + \lambda_j \rho_{ijk} \eta_i + \lambda_j \rho_{ijk} \alpha_{ijk} + \lambda_j \eta_i \alpha_{ijk} + \tau_{k+1} \rho_{ijk} \eta_i + \tau_{k+1} \rho_{ijk} \alpha_{ijk} + \tau_{k+1} \eta_i \alpha_{ijk} + \rho_{ijk} \eta_i \alpha_{ijk} + \delta_j \lambda_j \tau_{k+1} \rho_{ijk} + \delta_j \lambda_j \tau_{k+1} \eta_i + \delta_j \lambda_j \tau_{k+1} \alpha_{ijk} + \delta_j \lambda_j \rho_{ijk} \eta_i + \delta_j \lambda_j \rho_{ijk} \alpha_{ijk} + \delta_j \lambda_j \eta_i \alpha_{ijk} + \delta_j \tau_{k+1} \rho_{ijk} \eta_i + \delta_j \tau_{k+1} \rho_{ijk} \alpha_{ijk} + \delta_j \tau_{k+1} \eta_i \alpha_{ijk} + \delta_j \rho_{ijk} \eta_i \alpha_{ijk} + \lambda_j \tau_{k+1} \rho_{ijk} \eta_i + \lambda_j \tau_{k+1} \rho_{ijk} \alpha_{ijk} + \lambda_j \tau_{k+1} \eta_i \alpha_{ijk} + \lambda_j \rho_{ijk} \eta_i \alpha_{ijk} + \tau_{k+1} \rho_{ijk} \eta_i \alpha_{ijk} + \delta_j \lambda_j \tau_{k+1} \rho_{ijk} \eta_i + \delta_j \lambda_j \tau_{k+1} \rho_{ijk} \alpha_{ijk} + \delta_j \lambda_j \tau_{k+1} \eta_i \alpha_{ijk} + \delta_j \lambda_j \rho_{ijk} \eta_i \alpha_{ijk} + \delta_j \tau_{k+1} \rho_{ijk} \eta_i \alpha_{ijk} + \lambda_j \tau_{k+1} \rho_{ijk} \eta_i \alpha_{ijk} + E_{k+1} + S_i + \epsilon_{ijk+1}$

Table S4: Mathematical structure of the full extinction models. All symbols are as in Table S2. TIB refers to a model based on the original Theory of Island Biogeography, without any trophic effects.

Model	Mathematical structure
Null	$X_{ijk+1} = E_{k+1} + W_{ijq} + \epsilon_{ijk+1}$
TIB	$X_{ijk+1} = \lambda_j + \tau_{k+1} + \lambda_j \tau_{k+1} + E_{k+1} + W_{ijq} + \epsilon_{ijk+1}$
Species-richness	$X_{ijk+1} = \lambda_j + \tau_{k+1} + \Sigma_k + \lambda_j \tau_{k+1} + \lambda_j \Sigma_k + \tau_{k+1} \Sigma_k + \lambda_j \tau_{k+1} \Sigma_j + E_{k+1} + W_{ijq} + \epsilon_{ijk+1}$
Top-down	$X_{ijk+1} = \lambda_j + \tau_{k+1} + \rho_{ijk} + \lambda_j \tau_{k+1} + \lambda_j \rho_{ijk} + \tau_{k+1} \rho_{ijk} + \lambda_j \tau_{k+1} \rho_{ijk} + E_{k+1} + W_{ijq} + \epsilon_{ijk+1}$
Top-down & Species-richness	$X_{ijk+1} = \lambda_j + \tau_{k+1} + \Sigma_k + \rho_{ijk} + \lambda_j \tau_{k+1} + \lambda_j \Sigma_j + \lambda_j \rho_{ijk} + \tau_{k+1} \Sigma_k + \tau_{k+1} \rho_{ijk} + \Sigma_k \rho_{ijk} + \lambda_j \tau_{k+1} \Sigma_k + \lambda_j \tau_{k+1} \rho_{ijk} + \lambda_j \Sigma_k \rho_{ijk} + \tau_{k+1} \Sigma_k \rho_{ijk} + \lambda_j \tau_{k+1} \Sigma_k \rho_{ijk} + E_{k+1} + W_{ijq} + \epsilon_{ijk+1}$
Bottom-up	$X_{ijk+1} = \lambda_j + \tau_{k+1} + \eta_i + \alpha_{ijk} + \lambda_j \tau_{k+1} + \lambda_j \eta_i + \lambda_j \alpha_{ijk} + \tau_{k+1} \eta_i + \tau_{k+1} \alpha_{ijk} + \eta_i \alpha_{ijk} + \lambda_j \tau_{k+1} \eta_i + \lambda_j \tau_{k+1} \alpha_{ijk} + \lambda_j \eta_i \alpha_{ijk} + \tau_{k+1} \eta_i \alpha_{ijk} + \lambda_j \tau_{k+1} \eta_i \alpha_{ijk} + E_{k+1} + W_{ijq} + \epsilon_{ijk+1}$
Bottom-up & Species-richness	$X_{ijk+1} = \lambda_j + \tau_{k+1} + \Sigma_k + \eta_i + \alpha_{ijk} + \lambda_j \tau_{k+1} + \lambda_j \Sigma_k + \lambda_j \eta_i + \lambda_j \alpha_{ijk} + \tau_{k+1} \Sigma_k + \tau_{k+1} \eta_i + \tau_{k+1} \alpha_{ijk} + \Sigma_k \eta_i + \Sigma_k \alpha_{ijk} + \eta_i \alpha_{ijk} + \lambda_j \tau_{k+1} \Sigma_k + \lambda_j \tau_{k+1} \eta_i + \lambda_j \tau_{k+1} \alpha_{ijk} + \lambda_j \Sigma_k \eta_i + \lambda_j \Sigma_k \alpha_{ijk} + \lambda_j \eta_i \alpha_{ijk} + \tau_{k+1} \Sigma_k \eta_i + \tau_{k+1} \Sigma_k \alpha_{ijk} + \tau_{k+1} \eta_i \alpha_{ijk} + \Sigma_k \eta_i \alpha_{ijk} + \lambda_j \tau_{k+1} \Sigma_k \eta_i + \lambda_j \tau_{k+1} \Sigma_k \alpha_{ijk} + \lambda_j \tau_{k+1} \eta_i \alpha_{ijk} + \lambda_j \Sigma_k \eta_i \alpha_{ijk} + \tau_{k+1} \Sigma_k \eta_i \alpha_{ijk} + \lambda_j \tau_{k+1} \Sigma_k \eta_i \alpha_{ijk} + E_{k+1} + W_{ijq} + \epsilon_{ijk+1}$
Top-down & Bottom-up	$X_{ijk+1} = \lambda_j + \tau_{k+1} + \rho_{ijk} + \eta_i + \alpha_{ijk} + \lambda_j \tau_{k+1} + \lambda_j \rho_{ijk} + \lambda_j \eta_i + \lambda_j \alpha_{ijk} + \tau_{k+1} \rho_{ijk} + \tau_{k+1} \eta_i + \tau_{k+1} \alpha_{ijk} + \rho_{ijk} \eta_i + \rho_{ijk} \alpha_{ijk} + \eta_i \alpha_{ijk} + \lambda_j \tau_{k+1} \rho_{ijk} + \lambda_j \tau_{k+1} \eta_i + \lambda_j \tau_{k+1} \alpha_{ijk} + \lambda_j \rho_{ijk} \eta_i + \lambda_j \rho_{ijk} \alpha_{ijk} + \lambda_j \eta_i \alpha_{ijk} + \tau_{k+1} \rho_{ijk} \eta_i + \tau_{k+1} \rho_{ijk} \alpha_{ijk} + \tau_{k+1} \eta_i \alpha_{ijk} + \rho_{ijk} \eta_i \alpha_{ijk} + \lambda_j \tau_{k+1} \rho_{ijk} \eta_i + \lambda_j \tau_{k+1} \rho_{ijk} \alpha_{ijk} + \lambda_j \tau_{k+1} \eta_i \alpha_{ijk} + \lambda_j \rho_{ijk} \eta_i \alpha_{ijk} + \tau_{k+1} \rho_{ijk} \eta_i \alpha_{ijk} + \lambda_j \tau_{k+1} \rho_{ijk} \eta_i \alpha_{ijk} + E_{k+1} + W_{ijq} + \epsilon_{ijk+1}$

Appendix S2: Best-fit initial immigration, repeat immigration, and extinction models

Table S5: Mathematical structure of the best-fitting initial immigration models after model simplification. All symbols are as in Table S2. TIB refers to a model based on the original Theory of Island Biogeography, without any trophic effects.

Model	Mathematical structure
TIB	$C_{ijk+1} = \delta_j + \lambda_j + \tau_{k+1} + \delta_j \lambda_j + E_{k+1} + S_i + \epsilon_{ijk+1}$
Species-richness	$C_{ijk+1} = \delta_j + \lambda_j + \tau_{k+1} + \Sigma_{k+1} + \delta_j \lambda_j + \lambda_j \Sigma_{k+1} + E_{k+1} + S_i + \epsilon_{ijk+1}$
Top-down	$C_{ijk+1} = \delta_j + \lambda_j + \tau_{k+1} + \rho_{ijk+1} + \delta_j \lambda_j + \delta_j \rho_{ijk+1} + \tau_{k+1} \rho_{ijk+1} + E_{k+1} + S_i + \epsilon_{ijk+1}$
Top-down & Species-richness	Equivalent to Top-down model
Bottom-up	$C_{ijk+1} = \delta_j + \lambda_j + \tau_{k+1} + \alpha_{ijk+1} + \delta_j \lambda_j + \delta_j \alpha_{ijk+1} + \lambda_j \alpha_{ijk+1} + \delta_j \lambda_j \alpha_{ijk+1} + E_{k+1} + S_i + \epsilon_{ijk+1}$
Bottom-up & Species-richness	$C_{ijk+1} = \delta_j + \lambda_j + \tau_{k+1} + \Sigma_{k+1} + \alpha_{ijk+1} + \delta_j \lambda_j + \lambda_j \Sigma_{k+1} + \lambda_j \alpha_{ijk+1} + E_{k+1} + S_i + \epsilon_{ijk+1}$
Top-down & Bottom-up	$C_{ijk+1} = \delta_j + \lambda_j + \tau_{k+1} + \rho_{ijk+1} + \alpha_{ijk+1} + \delta_j \lambda_j + \lambda_j \rho_{ijk+1} + \lambda_j \alpha_{ijk+1} + \tau_{k+1} \rho_{ijk+1} + E_{k+1} + \epsilon_{ijk+1}$

Table S6: Mathematical structure of the best-fitting repeat immigration models after model simplification. All symbols are as in Table S2. TIB refers to a model based on the original Theory of Island Biogeography, without any trophic effects.

Model	Mathematical structure
TIB	$C_{ijk+1} = \lambda_j + \tau_{k+1} + \lambda_j \tau_{k+1} + E_{k+1} + W_{ijq} + \epsilon_{ijk+1}$
Species-richness	Equivalent to TIB model
Top-down	Equivalent to TIB model
Top-down & Species-richness	Equivalent to TIB model
Bottom-up	$C_{ijk+1} = \lambda_j + \tau_{k+1} + \eta_i + \lambda_j \tau_{k+1} + \lambda_j \eta_i + \tau_{k+1} \eta_i + E_{k+1} + W_{ijq} + \epsilon_{ijk+1}$
Bottom-up & Species-richness	Equivalent to Bottom-up model
Top-down & Bottom-up	Equivalent to Bottom-up model

Table S7: Mathematical structure of the best-fitting extinction models after model simplification. All symbols are as in Table S2. TIB refers to a model based on the original Theory of Island Biogeography, without any trophic effects.

Model	Mathematical structure
TIB	$X_{ijk+1} = \lambda_j + \tau_{k+1} + \lambda_j \tau_{k+1} + E_{k+1} + W_{ijq} + \epsilon_{ijk+1}$
Species-richness	$X_{ijk+1} = \lambda_j + \tau_{k+1} + \Sigma_k + \lambda_j \tau_{k+1} + \lambda_j \Sigma_k + \tau_{k+1} \Sigma_k + \lambda_j \tau_{k+1} \Sigma_k + E_{k+1} + W_{ijq} + \epsilon_{ijk+1}$
Top-down	Equivalent to TIB model
Top-down & Species-richness	Equivalent to Species-richness model
Bottom-up	$X_{ijk+1} = \tau_{k+1} + \eta_i + \alpha_{ijk} + \tau_{k+1} \eta_i + \eta_i \alpha_{ijk} + W_{ijq} + E_{k+1} + \epsilon_{ijk+1}$
Bottom-up & Species-richness	$X_{ijk+1} = \lambda_j + \tau_{k+1} + \Sigma_k + \eta_i + \alpha_{ijk} + \lambda_j \Sigma_k + \tau_{k+1} \Sigma_k + \tau_{k+1} \eta_i + \tau_{k+1} \alpha_{ijk} + \Sigma_k \eta_i + E_{k+1} + W_{ijq} + \epsilon_{ijk+1}$
Top-down & Bottom-up	Equivalent to Bottom-up model

Appendix S3: Summary tables for best-fit models

Table S8: Summary tables of the best-fit Theory of Island Biogeography (TIB), Species-richness (SR), Top-down (TD), Bottom-up (BU), Bottom-up & Species-richness (BU & SR), and Top-down & Bottom-up (TD & BU) models for probability of initial immigration. The best-fit Top-down & Species-richness model was identical to the best-fit species-richness model and is not shown. Standardised effects (β s) and intercepts shown refer to the same scale as the logit-transformed data (e.g., a 1 day increase in time between censuses or a 1m increase in distance from the mainland). Models are as in Table S5. The intercept of the null model was -3.84 ($p < 0.001$). Standardised effects of 0 were not included in the best-fit versions of each model. An empty cell indicates that the term was not part of the full model and hence could not appear in the best-fit version.

Fixed effect	TIB		SR		TD		Bottom-up		BU & SR		TD & BU	
	β	<i>p</i> -value	β	<i>p</i> -value	β	<i>p</i> -value	β	<i>p</i> -value	β	<i>p</i> -value	β	<i>p</i> -value
Intercept	-3.77	<0.001	-3.78	<0.001	-3.98	<0.001	-3.87	<0.001	-3.84	<0.001	-4.02	<0.001
Distance	-55.7	<0.001	-56.5	<0.001	-57.1	<0.001	-61.7	<0.001	-55.3	<0.001	-56.3	<0.001
Diameter	0.977	0.015	0.938	0.016	-0.122	0.865	-0.041	0.938	0.425	0.353	-0.711	0.34
Timesince	11.1	<0.001	10.7	<0.001	17.8	<0.001	11.1	<0.001	10.7	<0.001	18.1	<0.001
Species			1.19	0.07					1.1	0.103		
Predators					0.251	0.081					0.239	0.104
Animal Prey							0.22	0.112	0.125	0.368	0.119	0.387
Distance:Diameter	327	<0.001	304	<0.001	322.7	<0.001	205	0.045	314	<0.001	333	<0.001
Distance:Animals							12.7	0.568	0	NA	0	NA
Diameter:Species			7.31	0.026					6.59	0.048		
Diameter:Predators					1.29	0.08					1.29	0.077
Diameter:Animals							2.27	0.002	1.13	0.027	1.32	0.009
Time:Predators					-9.01	0.108					-9.32	0.099
Distance:Diameter:Animals							285	0.05	0	NA	0	NA

∞

Table S9: Summary tables of the best-fit Theory of Island Biogeography (TIB) and Bottom-up models for probability of repeat immigration. The best-fit Top-down, Species-richness, and Top-down & Species-richness models were identical to the best-fit TIB model, while the best-fit Bottom-up & Species-richness and Top-down & Bottom-up models were identical to the best-fit Bottom-up model and are not shown. Standardised effects (β s) and intercepts shown refer to the same scale as the logit-transformed data (e.g., a 1 day increase in time between censuses or a 1m increase in distance from the mainland). The best-fitting Species-richness, Top-down, and Top-down & Species-richness models were identical to the best-fitting TIB model, and the best-fit Bottom-up & Species-richness and Top-down & Bottom-up models were identical to the Bottom-up model. Models are as in Table S6. The intercept of the null model was -2.77 ($p < 0.001$). Standardised effects of 0 were not included in the best-fit versions of each model. An empty cell indicates that the term was not part of the full model and hence could not appear in the best-fit version.

Fixed effect	TIB		Bottom-up	
	β	p -value	β	p -value
Intercept	-2.91	<0.001	-2.82	<0.001
Diameter	-0.671	0.486	0.504	0.637
Time	-46.8	0.137	-76.8	0.027
Basal resources			-0.164	0.431
Diameter:Time	-464	0.052	-431	0.073
Diameter:Basal			-2.52	0.025
Time:Basal			51.5	0.024

Table S10: Summary tables of the best-fit Theory of Island Biogeography (TIB), Species-richness, Top-down, Bottom-up, and Bottom-up & Species-richness (BU & SR) models for extinction probability. The best-fit Top-down model was identical to the best-fit TIB model, the best-fit Top-down & Species-richness model was identical to the best-fit Species-richness model, and the best-fit Top-down & Bottom-up model was identical to the best-fit Bottom-up model. None are shown here. Standardised effects (β s) and intercepts shown refer to the same scale as the logit-transformed data (e.g., a 1 day increase in time between censuses or a 1m increase in distance from the mainland). The best-fitting Top-down model was identical to the best-fitting TIB model, the best-fitting Top-down & Species-richness model was identical to the best-fitting Species-richness model, and the best-fitting Top-down & Bottom-up model was identical to the best-fitting Bottom-up model. Models are as in Table S7. The intercept of the null model was -0.587 ($p < 0.001$). Standardised effects of 0 were not included in the best-fit versions of each model. An empty cell indicates that the term was not part of the full model and hence could not appear in the best-fit version.

Fixed effect	TIB		Species-richness		Bottom-up		BU & SR	
	β	p -value	β	p -value	β	p -value	β	p -value
Intercept	-0.462	<0.001	-0.59	<0.001	-0.174	0.863	1.22	0.007
Diameter	0.437	0.419	-0.836	0.276	0	NA	0.009	0.987
Time	60.0	<0.001	23.9	0.252	91.9	<0.001	117	<0.001
Species-richness			4.00	0.001			4.75	<0.001
Basal resources					-0.470	0.646	-1.87	<0.001
Animals					0.201	0.844	-1.19	0.003
Diameter:Time	140	0.008	-209	0.210	0	NA	0	NA
Diameter:Species			-2.55	0.652			-9.02	0.031
Time:Species			546	0.017			166	0.016
Time:Basal					-57.7	<0.001	-69.4	<0.001
Time:Animals							-20.4	0.146
Species:Basal							-3.70	0.036
Basal:Animals					-1.64	0.135	0	NA
Diameter:Time:Species			2.74x10 ³	0.037			0	NA

Appendix S4: Details of models not described in the main text

Initial immigration

The best-fitting TIB model for initial immigration included main effects for diameter, distance from the mainland, interval between censuses, and interactions between diameter and both distance and interval between censuses (Table S5). This model significantly improved upon the AIC of the null model ($\chi^2=52.0$, $df=4$, $p<0.001$; *Table 2A, main text*). As we expected, species were less likely to immigrate to more isolated islands ($\beta_{Distance}=-55.7$), although this effect was reversed on large islands ($\beta_{Distance:Diameter}=327$). More intuitively, probability of immigration also increased when the interval between censuses was long ($\beta_{Time}=11.1$; Fig. S1).

The best-fitting species-richness model also improved on the fit of the null model ($\chi^2=60.9$, $df=6$, $p<0.001$). As in the TIB model, a species' probability of immigration increased with increasing island diameter and interval between censuses, and decreased with increasing distance from the mainland. All effect sizes were very similar to those in the TIB model (Table S8). Contrary to our expectations, species' probability of immigration also increased with increasing species richness ($\beta_{Species}=7.31$).

The best-fitting top-down model also significantly improved upon the fit of the null model ($\chi^2=60.7$, $df=7$, $p<0.001$). As with the species-richness model, in the top-down model a species' probability of immigration decreased with increasing distance from the mainland, except on large islands (Table S8). Species with predators present were more likely to immigrate, especially on large islands ($\beta_{Predators}=0.251$, $\beta_{Diameter:Predators}=1.29$). However, for these species likelihood of immigration increased less with increasing interval between censuses than for other species ($\beta_{Time}=17.8$, $\beta_{Time:Predators}=-9.01$).

The bottom-up model, which also significantly improved upon the null model ($\chi^2=63.7$,

df=8, $p < 0.001$), also included similar terms for distance from the mainland, interval between censuses, and the interaction between distance and island diameter (Table S8). Contrary to our expectations, the bottom-up model did not include any terms for the ability to consume basal resources. However, species with animal prey present were more likely to immigrate than those without animal prey present ($\beta_{Animals}=0.22$). This effect was stronger on larger islands, islands farther from the mainland, and especially on large, isolated islands ($\beta_{Distance:Animal}=12.7$, $\beta_{Diameter:Animal}=2.27$, $\beta_{Distance:Diameter:Animal}=285$).

The best-fit top-down & species-richness model was identical to the best-fit species-richness model. The best-fit bottom-up & species-richness model, however, included terms for species richness and the presence of animal prey similar to those in the species-richness and bottom-up models in addition to similar terms to those in the TIB model (Table S8). Despite combining features of the species-richness and bottom-up models, the bottom-up & species-richness model did not significantly improve upon the fit of either ($\chi^2=5.92$, df=2, $p=0.052$ and $\chi^2=0$, df=0, $p > 0.999$). Each of the species-richness, bottom-up, and bottom-up & species-richness models all fit data generated by any of the other models extremely well (Fig. S3).

Repeat immigration models

The best-fitting TIB model did not significantly improve upon the null model ($\chi^2=6.09$, df=3, $p=0.107$). The TIB model included terms for island diameter, interval between censuses, and their interaction, but no terms relating to distance from the mainland (Table S6). In this model, a species' probability of re-immigration decreased with increasing island diameter ($\beta_{Diameter}=-0.671$), an effect which was strengthened when the interval between censuses was large ($\beta_{Diameter:Time}=-464$; Fig. S1). The species-richness and top-down models both reduced to the best-fitting TIB model, indicating that the number

of species or presence of predators on an island explained little variation in the data. Unsurprisingly, the combined model including species-richness and top-down effects also reduced to the best-fitting TIB model.

Extinction models

The best-fitting TIB model for extinction was the full model ($\chi^2=59.8$, $df=3$, $p<0.001$; Table S7), and this model had a lower AIC than the null model (Table 2C, main text). Contrary to our expectations, the data indicated that extinction probability increased on larger islands ($\beta_{Diameter}=0.437$). More intuitively, extinction probability also increased with increasing intervals between censuses ($\beta_{Time}=60.0$). The larger the island, the larger this effect ($\beta_{Diameter:Time}=140$; Fig. S1).

Similarly, the best-fitting species-richness model was the full model, which had a lower AIC than both the null and TIB models (Table 2C, main text). Unlike the TIB model, the species-richness model predicted that extinction probability would decrease on larger islands ($\beta_{Diameter}=-0.836$), and that this effect would be stronger with large census intervals ($\beta_{Diameter:Time}=-209$). As expected, probability of extinction increased with species richness ($\beta_{Species}=4.00$), although this effect was weaker on larger islands ($\beta_{Diameter:Species}=-2.55$). Because of a strong three-way interaction between diameter, species richness, and time between censuses, any of the above relationships could be reversed when both species richness and the interval between censuses were sufficiently large (or when both were small) ($\beta_{Diameter:Time:Species}=2740$). Nevertheless, overall the species-richness model generated very similar predictions to those of the TIB model (Fig. S5). The best-fitting top-down model was identical to the TIB model while the best-fitting top-down & species-richness model was identical to the species-richness model.

The bottom-up & species-richness model provided significant statistical improvement

over both the species-richness and bottom-up models ($\chi^2=44.8$, $df=3$, $p<0.001$ and $\chi^2=19.5$, $df=5$, $p=0.002$, respectively). In this model, as in the bottom-up model, extinction probabilities were lower for species with animal prey available or able to consume basal resources ($\beta_{Animals}=-1.19$, $\beta_{Basal}=-1.87$). Further, the increase in probability of extinction with increasing interval between censuses was weaker for these species. Unlike the bottom-up model, the bottom-up & species-richness model also included positive effects of species-richness and the interaction between species-richness and census interval on probability of extinction ($\beta_{Species}=4.75$ and $\beta_{Time:Species}=166$). Despite these additional terms, the bottom-up & species-richness model captured similar variation in the data to the bottom-up model (average pairwise AUC = 0.618, Fig. S6). In addition, the parameters of the combined and bottom-up models were qualitatively similar (Table S10), suggesting that the statistical gains of the combined model may be due to over-fitting.

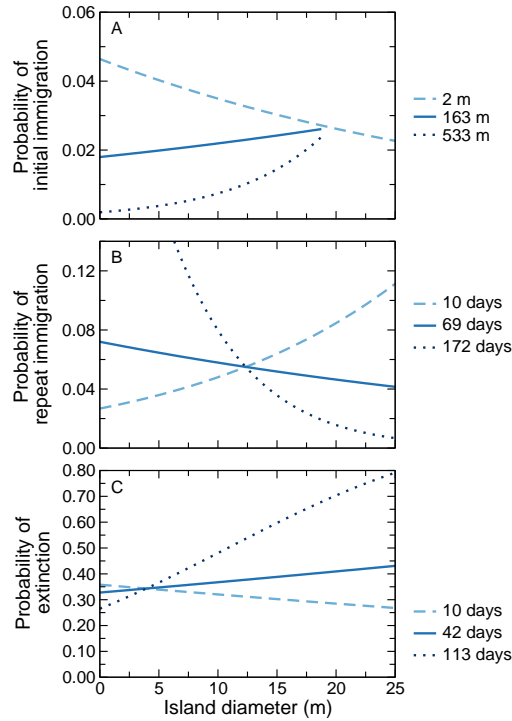


Figure S1: Predicted per-species probabilities of initial immigration, repeat immigration, and extinction as a function of island diameter in models based on the classic Theory of Island Biogeography. **(A)** Predicted initial immigration probability was affected by island diameter, distance from the mainland, and interval between censuses. For islands that were relatively far from the mainland, a species' immigration probability increased with island size. The opposite trend occurred for islands close to the mainland. Predictions are shown for an island close to the mainland (2m, light, dashed line), a moderate distance from the mainland (163 m, solid line), and far from the mainland (533 m, dark, dotted line). All predictions used the mean observed interval between censuses of 37 days and were based on a sample size of 18,420 opportunities for initial immigration. Predicted probability of initial immigration increased linearly with an increasing interval between censuses (not shown). **(B)** Predicted repeat immigration probability varied with island diameter and interval between censuses. For short to moderate intervals between censuses, repeat immigration probability increased with island diameter. When the interval between censuses was short, immigration probability decreased with increasing island diameter. **(C)** Predicted extinction probability increased with increasing island diameter, and this increase was steeper when the interval between censuses was long. In panels **(B)** and **(C)**, predicted per-species probabilities of immigration and extinction are shown for the minimum observed interval between censuses of 10 days (dashed line), a moderate interval of 28 days (solid line), and a large interval between censuses (76 days). Predictions were based on N=1,674 and N=1,943 opportunities for repeat immigration and extinction, respectively.

Appendix S5: Hypothesis comparison figures

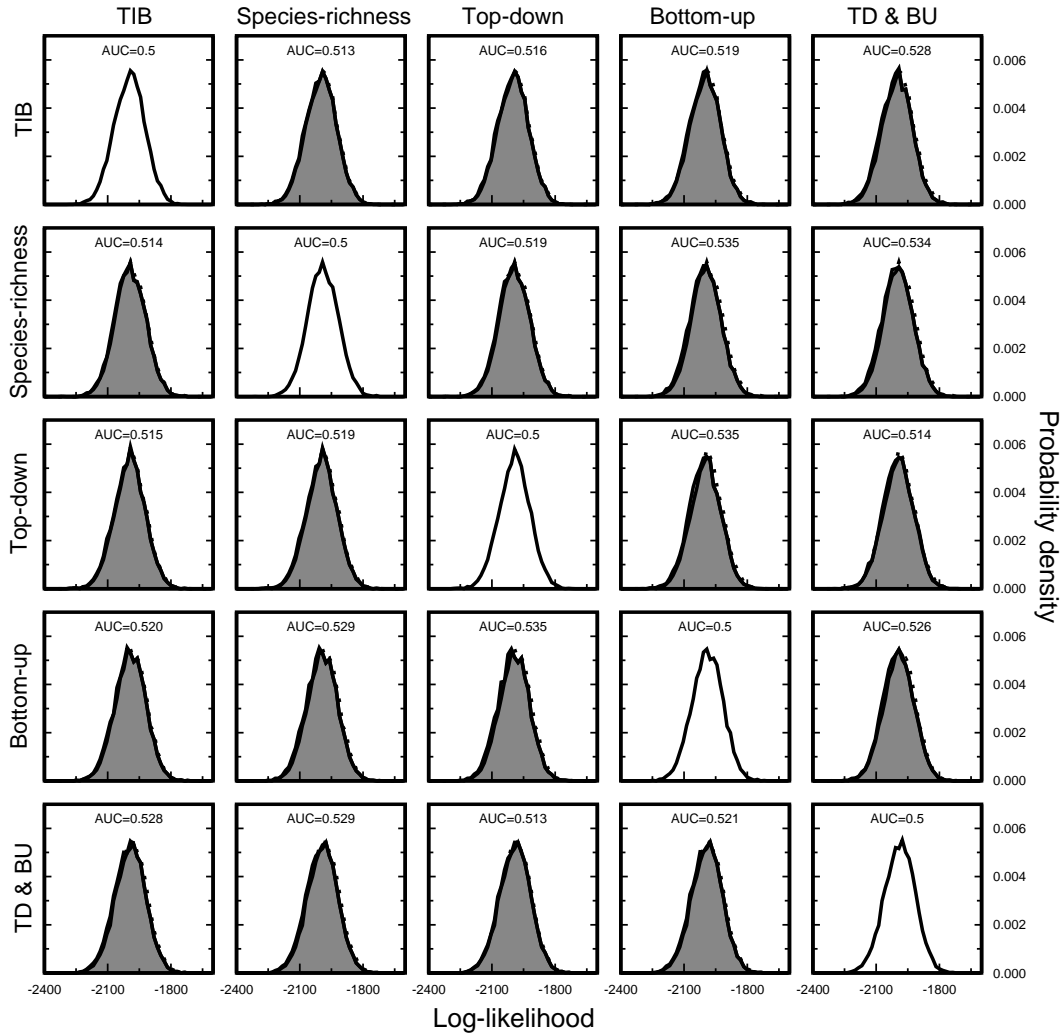


Figure S2: Hypothesis comparison for Theory of Island Biogeography (TIB), species-richness, top-down, bottom-up, and top-down & bottom-up (TD & BU) initial immigration models. Row names indicate the model from which test data was generated; column names indicate the model used to fit the test data. Each plot shows the histogram of log-likelihoods of obtaining test data from one model using another, based on 10,000 randomly-generated test datasets. Dotted curves indicate the success of a given model at predicting itself, as do plots on the diagonal. The grey shaded regions indicate overlap between the two models, where a given dataset was equally likely to have come from either model. All pairs of models have AUC's close to 0.5, indicating that the likelihood of observing a given dataset was approximately equal assuming either model were true.

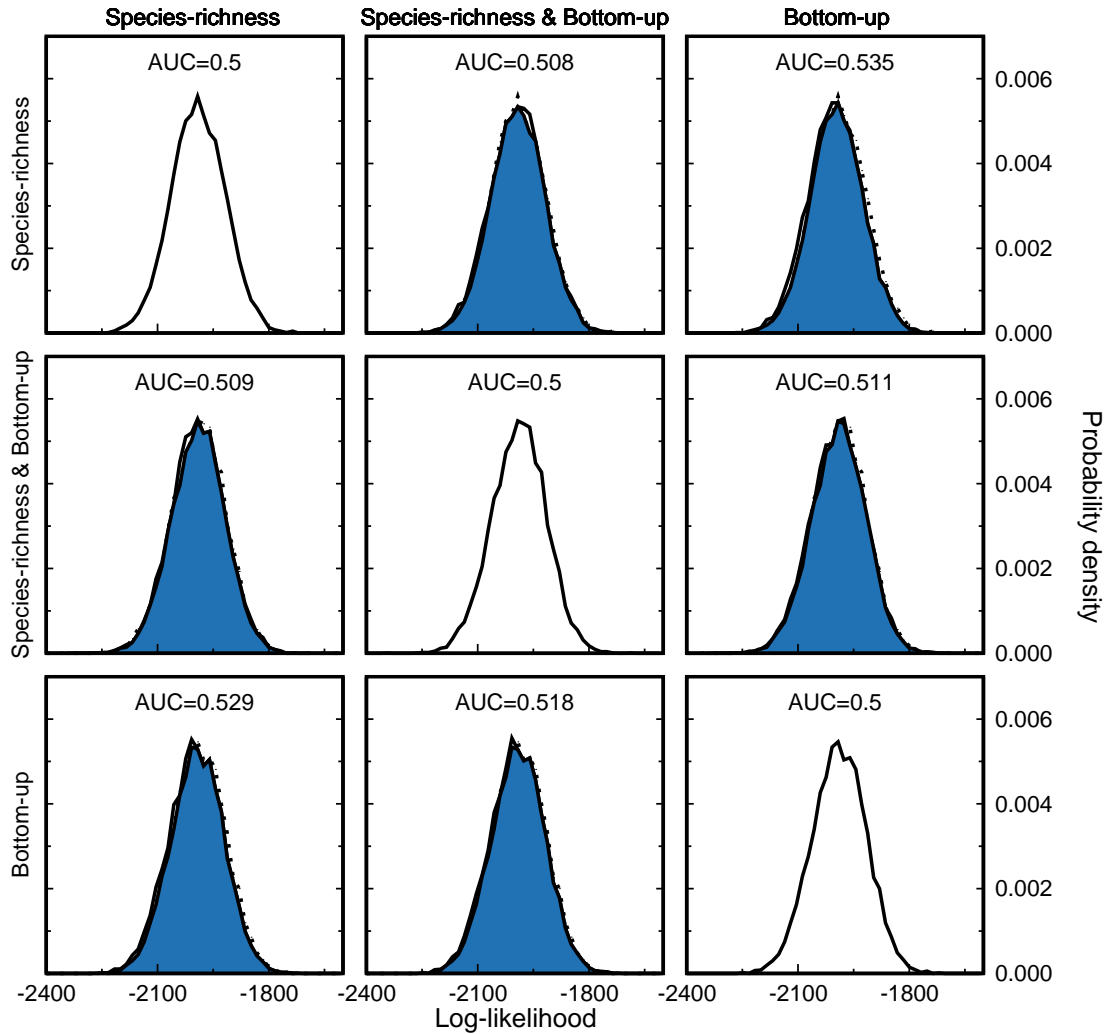


Figure S3: Hypothesis comparison for species-richness, species-richness & bottom-up, and bottom-up initial immigration models. Row names indicate the model from which test data was generated; column names indicate the model used to fit the test data. Each plot shows the histogram of log-likelihoods of obtaining test data from one model using another, based on 10,000 randomly-generated test datasets. Dotted curves indicate the success of a given model at predicting itself, as do plots on the diagonal. The grey shaded regions indicate overlap between the two models, where a given dataset was equally likely to have come from either model. Data generated by each model was fit well by either of the other models. This indicates that all three models capture very similar variation in the data.

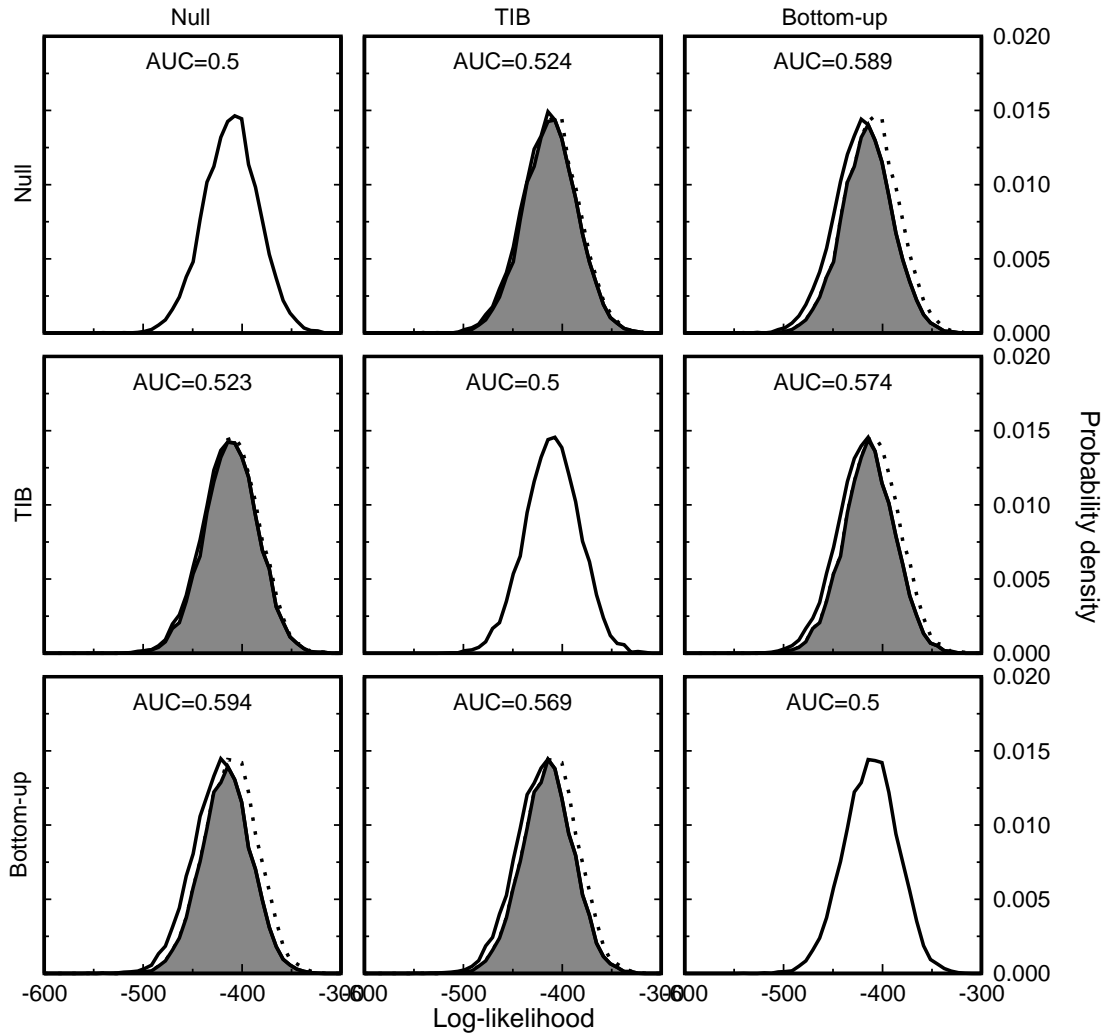


Figure S4: Hypothesis comparison for null, Theory of Island Biogeography (TIB), and bottom-up repeat immigration models. Note that the best-fitting species-richness and top-down models were identical to the best-fitting TIB model while the best-fitting top-down & bottom-up model was identical to the best-fitting bottom-up model. Row names indicate the model from which test data was generated; column names indicate the model used to fit the test data. Each plot shows the histogram of log-likelihoods of obtaining test data from one model using another, based on 10,000 randomly-generated test datasets. Dotted curves indicate the success of a given model at predicting itself, as do plots on the diagonal. The grey shaded regions indicate overlap between the two models, where a given dataset was equally likely to have come from either model. All pairs of models have AUC's close to 0.5, indicating that the likelihood of observing a given dataset was approximately equal assuming either model were true.

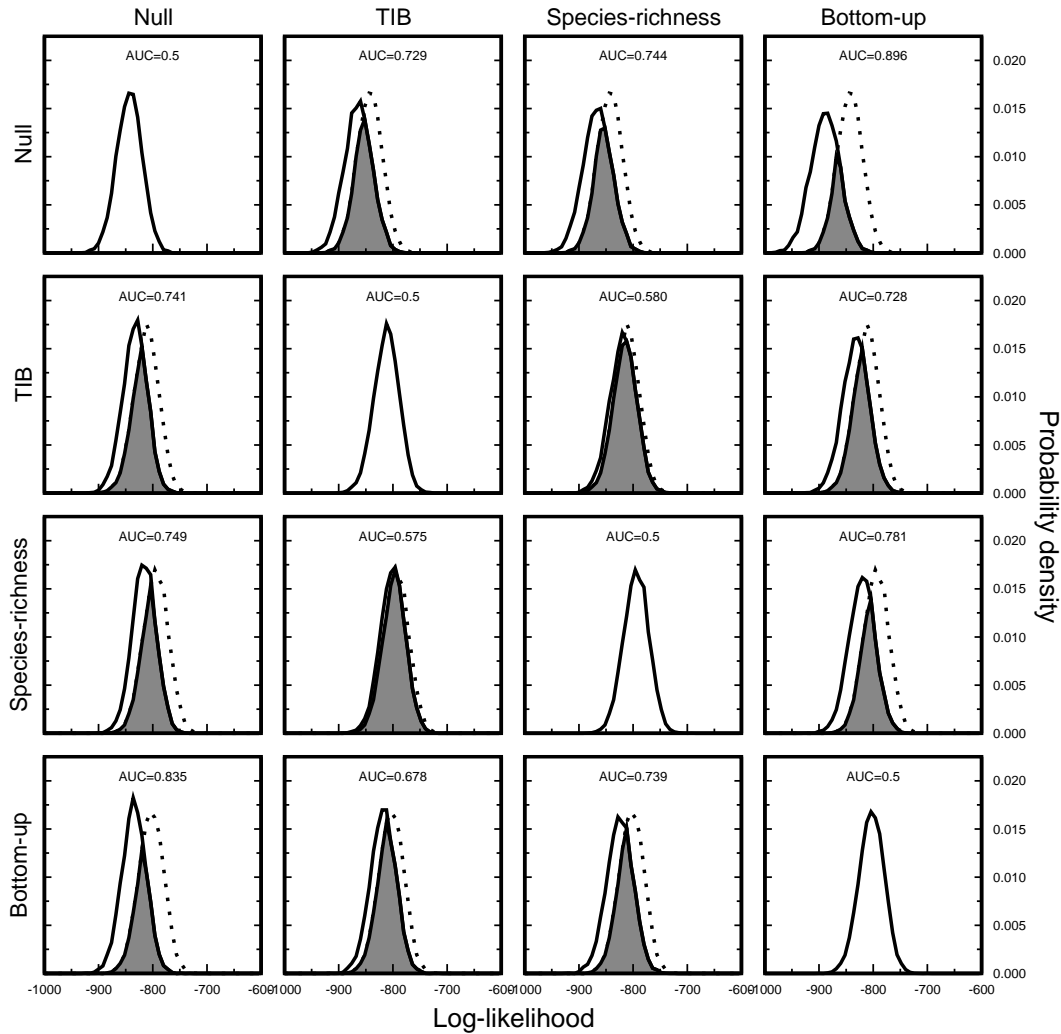


Figure S5: Hypothesis comparison for null, Theory of Island Biogeography (TIB), species-richness and bottom-up extinction models. The top-down model was identical to the TIB model while the top-down & bottom-up was identical to the bottom-up model. Row names indicate the model from which test data were generated; column names indicate the model used to fit the test data. Each plot shows the histogram of log-likelihoods of obtaining test data from one model using another, based on 10,000 randomly-generated test datasets. Dotted curves indicate the success of a given model at predicting itself, as do plots on the diagonal. The grey shaded regions indicate overlap between the two models, where a given dataset was equally likely to have come from either model.

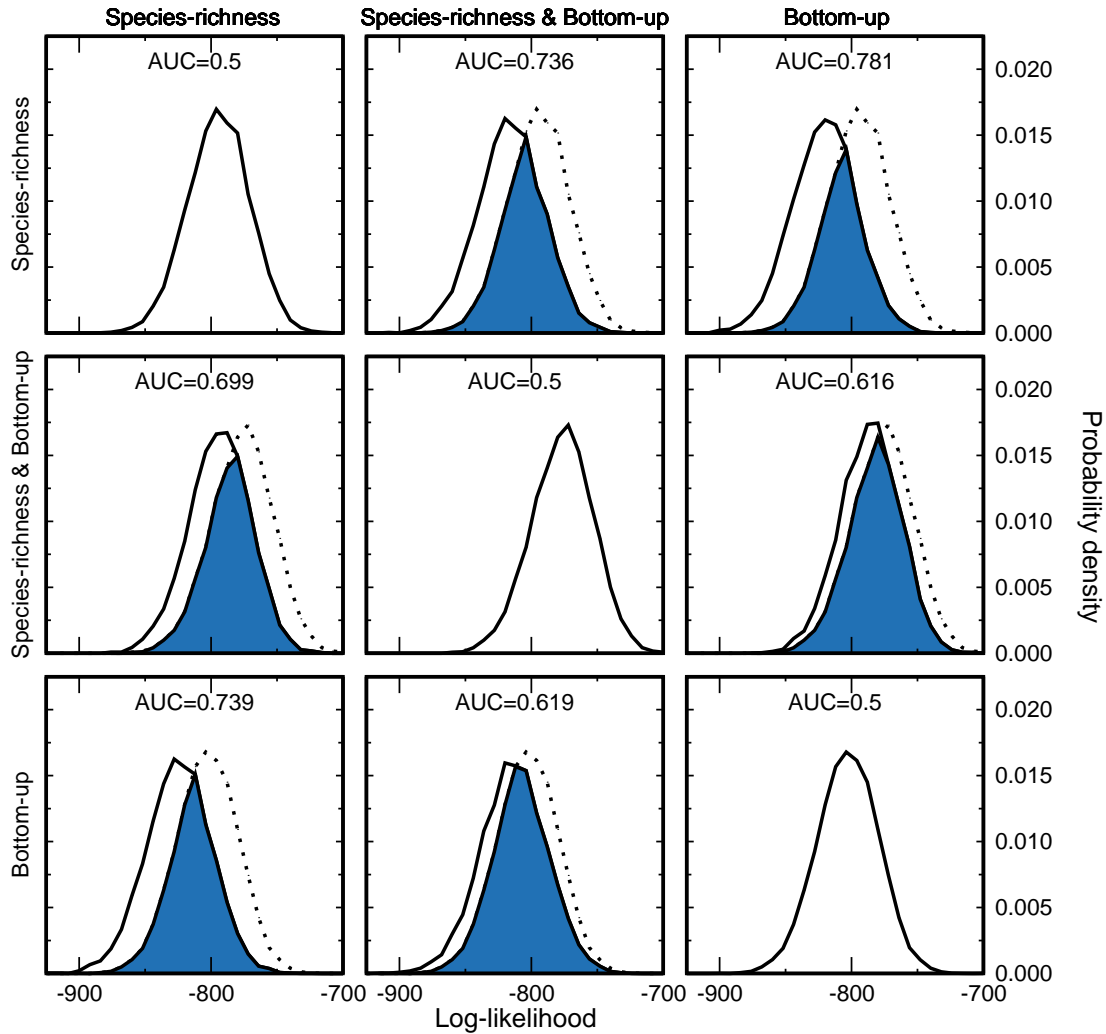


Figure S6: Hypothesis comparison for species-richness, species-richness & bottom-up, and bottom-up extinction models. Row names indicate the model from which test data was generated; column names indicate the model used to fit the test data. Each plot shows the histogram of log-likelihoods of obtaining test data from one model using another, based on 10,000 randomly-generated test datasets. Dotted curves indicate the success of a given model at predicting itself, as do plots on the diagonal. The grey shaded regions indicate overlap between the two models, where a given dataset was equally likely to have come from either model. Data generated by the species-richness model was poorly fit by the bottom-up and combined models, and vice versa. In contrast, pairings of the bottom-up and combined models had AUC's close to 0.5. This indicates that adding species-richness effects to the bottom-up model did not capture any variation not already explained by bottom-up effects.

Appendix S6: Cumulative species richness plots for islands not shown in the main text

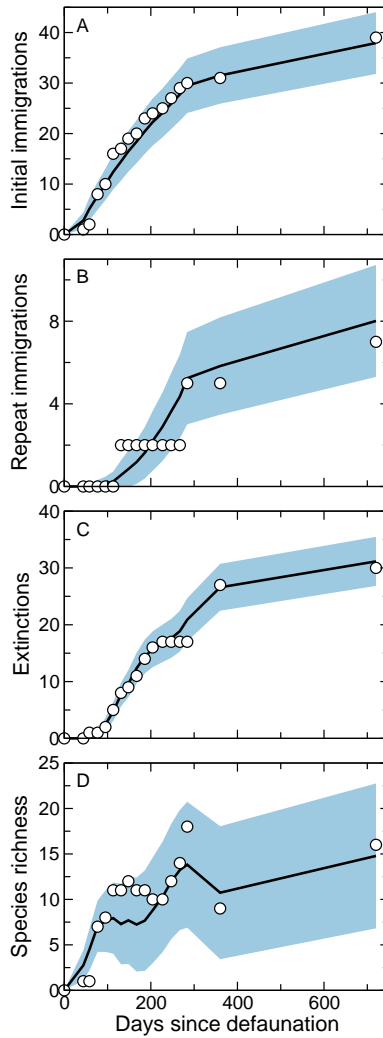


Figure S7: Initial immigrations, repeat immigrations, extinctions, and species richness over time for island E1, (11m in diameter, 533m from the mainland). (A)-(D) We show the cumulative values for the observed experiment (white circles) along with the equivalent values as predicted by the the best-fitting models for initial immigration, repeat immigration, and extinction (i.e., top-down & bottom-up, bottom-up, and bottom-up models, respectively). We obtained the model predictions for total species richness at each census by adding predicted immigrants and subtracting predicted extinctions. In all panels, the solid line indicates the mean prediction while the shaded area corresponds to one standard deviation.

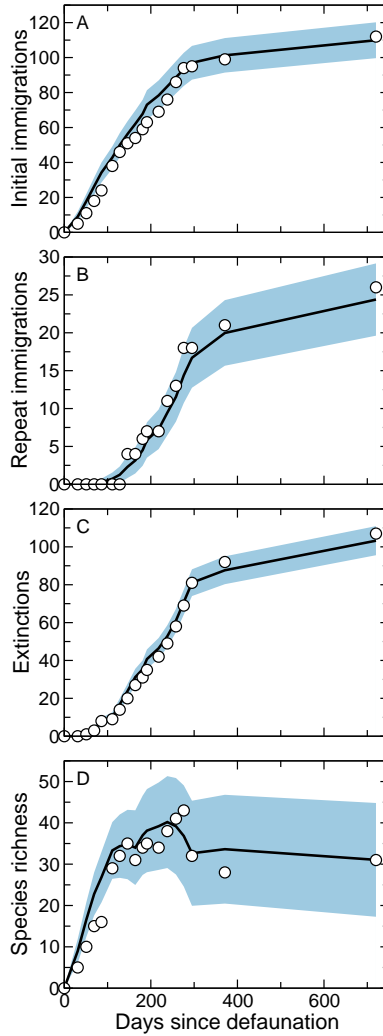


Figure S8: Initial immigrations, repeat immigrations, extinctions, and species richness over time for island E2 (12m in diameter, 2m from the mainland). **(A)-(D)** We show the cumulative values for the observed experiment (white circles) along with the equivalent values as predicted by the the best-fitting models for initial immigration, repeat immigration, and extinction (i.e., top-down & bottom-up, bottom-up, and bottom-up models, respectively). We obtained the model predictions for total species richness at each census by adding predicted immigrants and subtracting predicted extinctions. In all panels, the solid line indicates the mean prediction while the shaded area corresponds to one standard deviation.

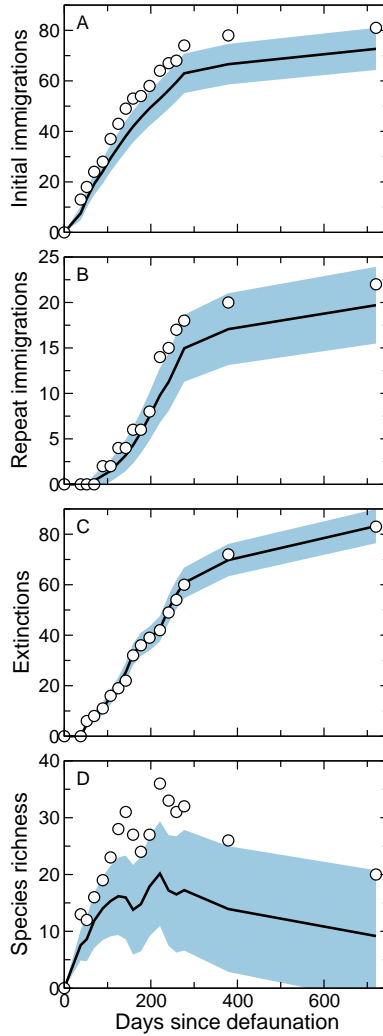


Figure S9: Initial immigrations, repeat immigrations, extinctions, and species richness over time for island E3 (12m in diameter, 172m from the mainland). **(A)-(D)** We show the cumulative values for the observed experiment (white circles) along with the equivalent values as predicted by the the best-fitting models for initial immigration, repeat immigration, and extinction (i.e., top-down & bottom-up, bottom-up, and bottom-up models, respectively). We obtained the model predictions for total species richness at each census by adding predicted immigrants and subtracting predicted extinctions. In all panels, the solid line indicates the mean prediction while the shaded area corresponds to one standard deviation.

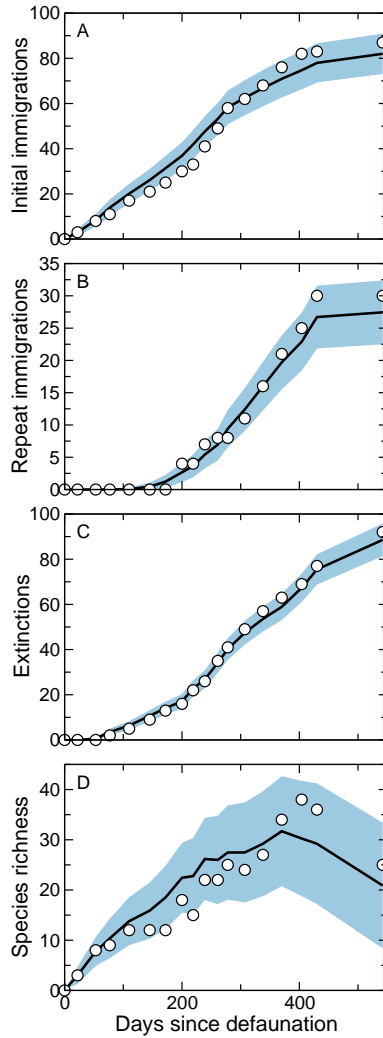


Figure S10: Initial immigrations, repeat immigrations, extinctions, and species richness over time for island E7 (25m in diameter, 15m from the mainland). **(A)-(D)** We show the cumulative values for the observed experiment (white circles) along with the equivalent values as predicted by the the best-fitting models for initial immigration, repeat immigration, and extinction (i.e., top-down & bottom-up, bottom-up, and bottom-up models, respectively). We obtained the model predictions for total species richness at each census by adding predicted immigrants and subtracting predicted extinctions. In all panels, the solid line indicates the mean prediction while the shaded area corresponds to one standard deviation.

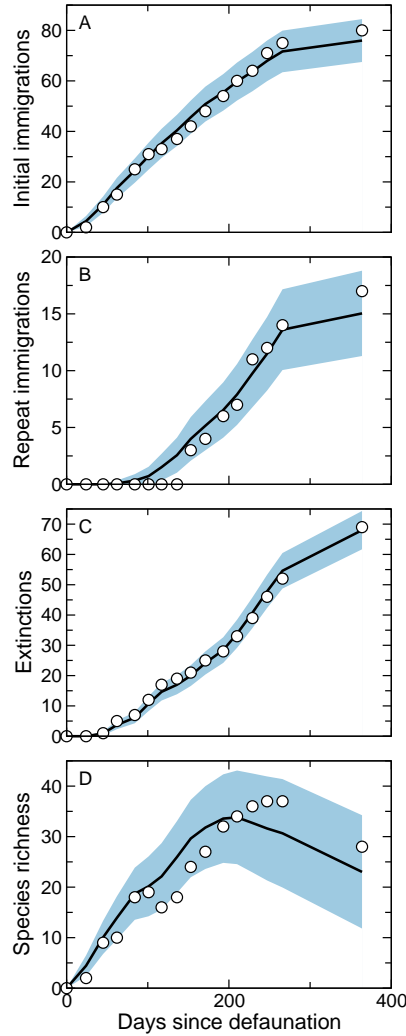


Figure S11: Initial immigrations, repeat immigrations, extinctions, and species richness over time for island E9 (18m in diameter, 379m from the mainland). **(A)-(D)** We show the cumulative values for the observed experiment (white circles) along with the equivalent values as predicted by the the best-fitting models for initial immigration, repeat immigration, and extinction (i.e., top-down & bottom-up, bottom-up, and bottom-up models, respectively). We obtained the model predictions for total species richness at each census by adding predicted immigrants and subtracting predicted extinctions. In all panels, the solid line indicates the mean prediction while the shaded area corresponds to one standard deviation.

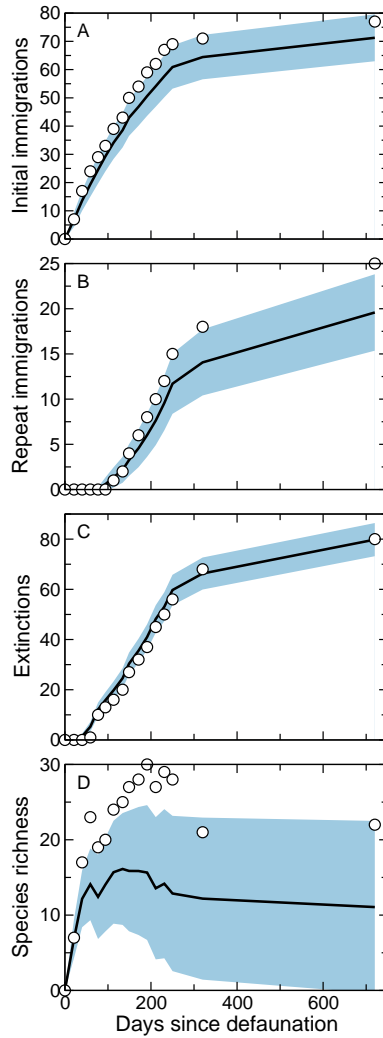


Figure S12: Initial immigrations, repeat immigrations, extinctions, and species richness over time for island ST2 (11m in diameter, 154m from the mainland). **(A)-(D)** We show the cumulative values for the observed experiment (white circles) along with the equivalent values as predicted by the the best-fitting models for initial immigration, repeat immigration, and extinction (i.e., top-down & bottom-up, bottom-up, and bottom-up models, respectively). We obtained the model predictions for total species richness at each census by adding predicted immigrants and subtracting predicted extinctions. In all panels, the solid line indicates the mean prediction while the shaded area corresponds to one standard deviation.