

Supplementary Table S1: Best models determining the relationship between host density and four distance measurements from the host species' range center in fish, macroinvertebrates and birds taxa. The coefficients (Trend), standard errors (SE), test statistics (t ratio), p-values, degrees of freedom (df), and 95% Bayesian credible intervals (Low BCI, High BCI) for each predictor variable are shown. Distance measurements include: CMCH (Distance to centroid of minimum convex hull), CP (Distance to polygon range centroid), EMCH (Distance to edge of minimum convex hull range), and EP (Distance to edge of polygon range). Host species density peaks near range centers and decreases toward range edges for fish and benthic macroinvertebrates, regardless of whether distance to the range centroid or nearest edge was used as the distance metric the polygon level. Birds did not show a clear center-to-periphery density gradient, likely because robust detection of such patterns depends on standardized sampling, sufficient sample sizes, and taxa with more limited dispersal than birds.

Taxa	Measurement	t ratio	p-value	Trend	SE	df	Low BCI	High BCI
Invertebrates	CMCH	1.787	0.07391	0.081	0.046	200083	-0.008	0.171
Fish	CMCH	-4.863	0.00000	-0.266	0.055	200083	-0.373	-0.159
Bird	CMCH	-2.354	0.01859	-0.639	0.271	200083	-1.170	-0.107
Invertebrates	CP	-3.148	0.00165	-0.102	0.032	200083	-0.165	-0.038
Fish	CP	-4.220	0.00002	-0.159	0.038	200083	-0.233	-0.085
Bird	CP	1.150	0.25012	0.161	0.140	200083	-0.113	0.434
Invertebrates	EMCH	-1.036	0.30043	-0.088	0.085	200083	-0.254	0.078
Fish	EMCH	4.402	0.00001	0.421	0.096	200083	0.233	0.608
Bird	EMCH	2.264	0.02360	1.269	0.561	200083	0.170	2.368
Invertebrates	EP	3.017	0.00255	0.305	0.101	200083	0.107	0.503
Fish	EP	7.593	0.00000	0.990	0.130	200083	0.734	1.245
Bird	EP	-2.544	0.01096	-1.614	0.635	200083	-2.858	-0.371

Supplementary Table S2: Comparison of the five best-performing models to determine the relationship between disease prevalence, disease transmission mode and distance from the species' range center using four distance calculations and host taxa. The table includes the model structure, Akaike Information Criterion (AIC) values, ΔAIC , and model weights. Models were ranked based on AIC, with lower values indicating better model fit. The best-supported model (lowest AIC) was used for the final interpretation, as shown in Figure 3, Extended Data Fig. 2, and Supplementary Table S4.

	Variables	AICc	ΔAIC	weight
<u>Distance to edge of polygon range (EP)</u>				
Mod 1	EP, Host_taxa, Latitude, EP:Host_taxa	26738.9	0.0	1.00
Mod 2	EP, Host_taxa, EP:Host_taxa	26982.2	243.4	0
Mod 3	EP, Latitude	27207.7	468.9	0
Mod 4	EP, Host_taxa, Latitude	27218.6	479.8	0
Mod 5	Latitude	27244.0	505.1	0
<u>Distance to edge of minimum convex hull range (EMCH)</u>				
Mod 1	EMCH, Host_taxa, Latitude, EMCH:Host_taxa	26533.6	0.0	1.00
Mod 2	EMCH, Host_taxa, EMCH:Host_taxa	26591.8	58.2	0
Mod 3	EMCH, Latitude	26938.4	404.8	0
Mod 4	EMCH, Host_taxa, Latitude	26949.2	415.6	0
Mod 5	EMCH	27057.8	524.2	0
<u>Distance to polygon range centroid (CP)</u>				
Mod 1	CP, Host_taxa, Latitude, CP:Host_taxa	26714.1	0.0	1.00
Mod 2	CP, Host_taxa, CP:Host_taxa	26736.8	22.7	0
Mod 3	CP, Latitude	27158.8	444.7	0
Mod 4	CP, Host_taxa, Latitude	27169.6	455.5	0
Mod 5	Latitude	27244.0	529.9	0
<u>Distance to centroid of minimum convex hull (CMCH)</u>				
Mod 1	CMCH, Host_taxa, Latitude, CMCH:Host_taxa	26647.1	0.0	1.00
Mod 2	CMCH, Host_taxa, CMCH:Host_taxa	26673.0	26.0	0
Mod 3	CMCH, Latitude	26984.4	337.4	0
Mod 4	CMCH, Host_taxa, Latitude	26995.4	348.3	0
Mod 5	CMCH	27140.4	493.3	0

Supplementary Table S3: Comparison of the five best-performing models to determine the relationship between disease prevalence, pathogen taxa and distance from the species' range center using four distance calculations and pathogen type. The table includes the model structure, Akaike Information Criterion (AIC) values, Δ AIC, and model weights. Models were ranked based on AIC, with lower values indicating better model fit. The best-supported model (lowest AIC) was used for the final interpretation, as shown in Figure 4, Extended Data Fig. 3, and Supplementary Table S5.

Rank	Variables	AICc	Δ AIC	weight
<u>Distance to edge of polygon range (EP)</u>				
Mod 1	agent_vect, EP, Latitude, agent_vect:EP	26510.1	0.0	1.0
Mod 2	agent_vect, EP, agent_vect:EP	26762.2	252.1	0.0
Mod 3	agent_vect, EP, Latitude	27142.0	632.0	0.0
Mod 4	EP, Latitude	27145.0	634.9	0.0
Mod 5	agent_vect, Latitude	27178.0	668.0	0.0
<u>Distance to edge of minimum convex hull range (EMCH)</u>				
Mod 1	agent_vect, EMCH, Latitude, agent_vect:EMCH	26413.4	0.0	1.0
Mod 2	agent_vect, EMCH, agent_vect:EMCH	26501.4	88.1	0.0
Mod 3	agent_vect, EMCH, Latitude	26871.7	458.4	0.0
Mod 4	EMCH, Latitude	26875.5	462.1	0.0
Mod 5	agent_vect, EMCH	26991.4	578.0	0.0
<u>Distance to polygon range centroid (CP)</u>				
Mod 1	agent_vect, CP, Latitude, agent_vect:CP	26546.4	0.0	1.0
Mod 2	agent_vect, CP, agent_vect:CP	26624.6	78.2	0.0
Mod 3	agent_vect, CP, Latitude	27092.4	546.0	0.0
Mod 4	CP, Latitude	27095.9	549.5	0.0
Mod 5	agent_vect, Latitude	27178.0	631.6	0.0
<u>Distance to centroid of minimum convex hull (CMCH)</u>				
Mod 1	agent_vect, CMCH, Latitude, agent_vect:CMCH	26468.5	0.0	1.0
Mod 2	agent_vect, CMCH, agent_vect:CMCH	26534.5	66.0	0.0
Mod 3	agent_vect, CMCH, Latitude	26917.9	449.4	0.0
Mod 4	CMCH, Latitude	26921.8	453.3	0.0
Mod 5	agent_vect, CMCH	27074.2	605.7	0.0

Supplementary Table S4: Best models assessing the relationship between disease prevalence, disease transmission mode and four distances from the species' range center. The coefficients, standard errors (Std. Error), test statistics (Z values), and p-values for each predictor variable are shown here. Results indicate that the prevalence of density-dependent pathogens in amphibians, insects, fish, and mammals significantly decreases as distance from the range core increases. In contrast, the prevalence of frequency-dependent pathogens, such as vector-borne diseases in birds and mammals, remains consistent or increases across ranges depending on the measurement used. In our cross-validation, our models achieved a mean correlation of $r=0.52$ (SE= 0.011) and explained on average $R^2=0.25$ (SE=0.013) across all distance metrics (Supplementary Table S4).

Variable	Estimate	Std. Error	Z value	P-value
<u>Distance to edge of polygon range (EP)</u>				
(Intercept)	-4.200	2.608	-1.610	0.107
EP	1.734	0.438	3.963	<0.0001
Host_taxaAmphibia/Reptilia	0.559	2.842	0.197	0.844
Host_taxaInsecta	-4.158	4.252	-0.978	0.328
Host_taxaMammalia Vector Borne No	-0.547	2.697	-0.203	0.839
Host_taxaAves Vector Borne No	16.716	4.300	3.887	0.000
Host_taxaMammalia Vector Borne Yes	1.517	2.739	0.554	0.580
Host_taxaAves Vector Borne Yes	0.693	2.880	0.241	0.810
Latitude	0.071	0.005	15.344	<0.0001
EP:Host_taxaAmphibia/Reptilia	0.446	0.624	0.715	0.475
EP:Host_taxaInsecta	11.493	0.934	12.307	<0.0001
EP:Host_taxaMammalia Vector Borne No	13.688	1.595	8.580	<0.0001
EP:Host_taxaAves Vector Borne No	-206.402	36.031	-5.729	<0.0001
EP:Host_taxaMammalia Vector Borne Yes	-10.097	1.080	-9.347	<0.0001
EP:Host_taxaAves Vector Borne Yes	-4.423	0.701	-6.311	<0.0001
<u>Distance to edge of minimum convex hull range (EMCH)</u>				
(Intercept)	-3.626	2.201	-1.647	0.100
EMCH	4.571	0.293	15.607	<0.0001
Host_taxaAmphibia/Reptilia	1.088	2.438	0.446	0.655
Host_taxaInsecta	-1.964	3.711	-0.529	0.597
Host_taxaMammalia Vector Borne No	-1.565	2.284	-0.685	0.493
Host_taxaAves Vector Borne No	-1.522	3.582	-0.425	0.671
Host_taxaMammalia Vector Borne Yes	2.312	2.328	0.993	0.321
Host_taxaAves Vector Borne Yes	1.082	2.480	0.436	0.663
Latitude	0.035	0.005	7.700	<0.0001
EMCH:Host_taxaAmphibia/Reptilia	-2.897	0.441	-6.573	<0.0001
EMCH:Host_taxaInsecta	-2.100	0.796	-2.640	0.008
EMCH:Host_taxaMammalia Vector Borne No	7.900	0.733	10.771	<0.0001
EMCH:Host_taxaAves Vector Borne No	6.624	10.758	0.616	0.538
EMCH:Host_taxaMammalia Vector Borne Yes	-7.006	0.633	-11.061	<0.0001

EMCH:Host_taxaAves Vector Borne Yes	-4.032	0.491	-8.205	<0.0001
<i>Distance to polygon range centroid (CP)</i>				
(Intercept)	-0.912	2.278	-0.400	0.689
CP	-2.859	0.187	-15.327	<0.0001
Host_taxaAmphibia/Reptilia	-0.608	2.509	-0.242	0.808
Host_taxaInsecta	-3.547	3.797	-0.934	0.350
Host_taxaMammalia Vector Borne No	1.479	2.359	0.627	0.531
Host_taxaAves Vector Borne No	-13.809	4.711	-2.931	0.003
Host_taxaMammalia Vector Borne Yes	-1.168	2.400	-0.487	0.626
Host_taxaAves Vector Borne Yes	-1.260	2.548	-0.495	0.621
Latitude	0.025	0.005	4.957	<0.0001
CP:Host_taxaAmphibia/Reptilia	2.183	0.211	10.365	<0.0001
CP:Host_taxaInsecta	2.594	0.404	6.420	<0.0001
CP:Host_taxaMammalia Vector Borne No	-1.991	0.378	-5.269	<0.0001
CP:Host_taxaAves Vector Borne No	45.827	13.182	3.476	0.001
CP:Host_taxaMammalia Vector Borne Yes	4.044	0.377	10.717	<0.0001
CP:Host_taxaAves Vector Borne Yes	2.895	0.196	14.778	<0.0001
<i>Distance to centroid of minimum convex hull (CMCH)</i>				
(Intercept)	-0.670	2.175	-0.308	0.758
CMCH	-4.446	0.225	-19.792	<0.0001
Host_taxaAmphibia/Reptilia	-1.047	2.403	-0.436	0.663
Host_taxaInsecta	-3.440	3.672	-0.937	0.349
Host_taxaMammalia Vector Borne No	0.365	2.249	0.162	0.871
Host_taxaAves Vector Borne No	1.752	3.456	0.507	0.612
Host_taxaMammalia Vector Borne Yes	-0.950	2.292	-0.415	0.678
Host_taxaAves Vector Borne Yes	-1.393	2.448	-0.569	0.569
Latitude	0.025	0.005	5.255	<0.0001
CMCH:Host_taxaAmphibia/Reptilia	3.814	0.264	14.456	<0.0001
CMCH:Host_taxaInsecta	3.252	0.474	6.855	<0.0001
CMCH:Host_taxaMammalia Vector Borne No	0.114	0.417	0.273	0.785
CMCH:Host_taxaAves Vector Borne No	-0.079	2.887	-0.027	0.978
CMCH:Host_taxaMammalia Vector Borne Yes	4.842	0.436	11.103	<0.0001
CMCH:Host_taxaAves Vector Borne Yes	4.177	0.279	14.953	<0.0001

Supplementary Table S5: Best models assessing the relationship between disease prevalence, pathogen taxa and four distances from the species' range center. The coefficients, standard errors (Std. Error), test statistics (Z values), and p-values for each predictor variable are shown here. Results indicate that the prevalence of density-dependent pathogens in amphibians, insects, fish, and mammals significantly decreases as distance from the range core increases. In contrast, the prevalence of frequency-dependent pathogens, such as vector-borne diseases in birds and mammals, remains consistent or increases across ranges depending on the measurement used. In our cross-validation, our models achieved a mean correlation of $r=0.52$ ($SE=0.01$) and explained on average $R^2=0.24$ ($SE=0.02$) across all distance metrics (Supplementary Table S4).

Variable	Estimate	Std. Error	Z value	P-value
<i>Distance to edge of polygon range (EP)</i>				
(Intercept)	-2.277	0.913	-2.496	0.013
agent_vectBacteria	-3.672	0.904	-4.062	<0.0001
agent_vectFungi	-2.861	1.511	-1.893	0.058
agent_vectHelminths	-1.231	0.843	-1.460	0.144
agent_vectProtozoans	-6.600	1.144	-5.769	<0.0001
agent_vectViruses	-1.234	0.866	-1.425	0.154
agent_vectBacteria Vector-Borne	-3.228	1.313	-2.459	0.014
agent_vectProtozoans Vector-Borne	-0.843	1.101	-0.765	0.444
agent_vectViruses Vector-Borne	-4.310	1.289	-3.343	0.001
EP	-10.882	5.998	-1.814	0.070
Latitude	0.072	0.005	15.537	<0.0001
agent_vectBacteria:EP	16.956	6.684	2.537	0.011
agent_vectFungi:EP	17.103	6.014	2.844	0.004
agent_vectHelminths:EP	14.495	6.104	2.374	0.018
agent_vectProtozoans:EP	60.234	6.665	9.038	<0.0001
agent_vectViruses:EP	11.739	6.011	1.953	0.051
agent_vectBacteria Vector-Borne:EP	-0.262	6.103	-0.043	0.966
agent_vectProtozoans Vector-Borne:EP	8.196	6.022	1.361	0.174
agent_vectViruses Vector-Borne:EP	42.133	8.464	4.978	<0.0001
<i>Distance to edge of minimum convex hull range (EMCH)</i>				
(Intercept)	-5.291	1.316	-4.020	<0.0001
agent_vectBacteria	1.652	1.413	1.169	0.243
agent_vectFungi	1.128	1.731	0.652	0.514
agent_vectHelminths	0.753	1.246	0.604	0.546
agent_vectProtozoans	-2.068	1.467	-1.410	0.159

agent_vectViruses	2.289	1.296	1.766	0.077
agent_vectBacteria Vector-Borne	1.660	1.658	1.001	0.317
agent_vectProtozoans Vector-Borne	2.886	1.462	1.975	0.048
agent_vectViruses Vector-Borne	0.728	1.601	0.455	0.649
EMCH	11.887	4.414	2.693	0.007
Latitude	0.043	0.005	9.372	<0.0001
agent_vectBacteria:EMCH	-15.640	4.918	-3.180	0.001
agent_vectFungi:EMCH	-9.150	4.425	-2.068	0.039
agent_vectHelminths:EMCH	-2.493	4.438	-0.562	0.574
agent_vectProtozoans:EMCH	3.085	4.502	0.685	0.493
agent_vectViruses:EMCH	-8.418	4.422	-1.904	0.057
agent_vectBacteria Vector-Borne:EMCH	-15.466	4.456	-3.471	0.001
agent_vectProtozoans Vector-Borne:EMCH	-11.360	4.431	-2.564	0.010
agent_vectViruses Vector-Borne:EMCH	-5.171	4.801	-1.077	0.281
<u>Distance to polygon range centroid (CP)</u>				
(Intercept)	0.652	1.177	0.554	0.580
agent_vectBacteria	-4.751	1.192	-3.986	<0.0001
agent_vectFungi	-3.886	1.649	-2.356	0.018
agent_vectHelminths	-1.142	1.111	-1.029	0.304
agent_vectProtozoans	-0.156	1.325	-0.117	0.907
agent_vectViruses	-2.402	1.157	-2.076	0.038
agent_vectBacteria Vector-Borne	-4.479	1.468	-3.051	0.002
agent_vectProtozoans Vector-Borne	-3.178	1.309	-2.427	0.015
agent_vectViruses Vector-Borne	-4.721	1.403	-3.366	0.001
CP	-5.887	1.872	-3.145	0.002
Latitude	0.045	0.005	8.848	<0.0001
agent_vectBacteria:CP	5.304	1.900	2.793	0.005
agent_vectFungi:CP	5.007	1.875	2.671	0.008
agent_vectHelminths:CP	2.221	1.882	1.180	0.238
agent_vectProtozoans:CP	-5.135	1.986	-2.586	0.010
agent_vectViruses:CP	4.548	1.878	2.422	0.015
agent_vectBacteria Vector-Borne:CP	6.573	1.899	3.461	0.001
agent_vectProtozoans Vector-Borne:CP	5.949	1.873	3.176	0.001
agent_vectViruses Vector-Borne:CP	11.006	2.288	4.811	<0.0001
<u>Distance to centroid of minimum convex hull (CMCH)</u>				
(Intercept)	0.010	1.011	0.010	0.992

agent_vectBacteria	-4.212	1.063	-3.963	<0.0001
agent_vectFungi	-3.013	1.536	-1.961	0.050
agent_vectHelminths	-0.900	0.961	-0.937	0.349
agent_vectProtozoans	0.086	1.184	0.073	0.942
agent_vectViruses	-0.823	0.999	-0.824	0.410
agent_vectBacteria Vector-Borne	-4.195	1.331	-3.152	0.002
agent_vectProtozoans Vector-Borne	-2.057	1.169	-1.760	0.078
agent_vectViruses Vector-Borne	-1.391	1.231	-1.130	0.259
CMCH	-5.525	2.016	-2.741	0.006
Latitude	0.039	0.005	8.151	<0.0001
agent_vectBacteria:CMCH	6.129	2.127	2.882	0.004
agent_vectFungi:CMCH	4.508	2.020	2.231	0.026
agent_vectHelminths:CMCH	2.659	2.023	1.315	0.189
agent_vectProtozoans:CMCH	-8.031	2.176	-3.690	<0.0001
agent_vectViruses:CMCH	2.602	2.023	1.286	0.198
agent_vectBacteria Vector-Borne:CMCH	6.708	2.051	3.271	0.001
agent_vectProtozoans Vector-Borne:CMCH	5.248	2.022	2.595	0.009
agent_vectViruses Vector-Borne:CMCH	-1.472	2.282	-0.645	0.519

Supplementary Table S6: Comparison of the five best-performing models to determine the relationship between disease prevalence in density-dependent pathogens, host thermal biology (i.e., endotherms and ectotherms) and distance from the species' range center using four distance calculations. The table includes the model structure, Akaike Information Criterion (AIC) values, ΔAIC , and model weights. Models were ranked based on AIC, with lower values indicating better model fit. The best-supported model (lowest AIC) was used for the final interpretation, as shown in Figure 5, Extended Data Fig. 4, and Supplementary Table S7.

	Variables	AICc	ΔAIC	weight
<u>Distance to edge of polygon range (EP)</u>				
Mod 1	EP, Latitude, EP:Thermal.biology	18474.0	0.0	1.0
Mod 2	EP, Host_taxa, EP:Thermal.biology	18480.8	6.8	0.0
Mod 3	EP, Latitude	18539.0	65.0	0.0
Mod 4	EP, Host_taxa, Latitude	18546.1	72.1	0.0
Mod 5	Latitude	18672.4	198.4	0.0
<u>Distance to edge of minimum convex hull range (EMCH)</u>				
Mod 1	EMCH, Latitude, EMCH:Thermal.biology	18132.4	0.0	0.9
Mod 2	EMCH, Host_taxa, Latitude, EMCH:Thermal.biology	18136.9	4.5	0.1
Mod 3	EMCH, Latitude	18346.9	214.5	0.0
Mod 4	EMCH, Host_taxa, Latitude	18354.0	221.6	0.0
Mod 5	EMCH, Distance_total_edge:Thermal.biology	18430.3	297.8	0.0
<u>Distance to polygon range centroid (CP)</u>				
Mod 1	CP, Latitude, CP:Thermal.biology	18352.6	0.0	0.9
Mod 2	CP, Host_taxa, Latitude, CP:Thermal.biology	18357.9	5.3	0.1
Mod 3	CP, Latitude	18501.9	149.4	0.0
Mod 4	CP, Host_taxa, Latitude	18509.1	156.6	0.0
Mod 5	Latitude	18672.4	319.9	0.0
<u>Distance to centroid of minimum convex hull (CMCH)</u>				
Mod 1	CMCH, Latitude, CMCH:Thermal.biology	18373.7	0.0	0.9
Mod 2	CMCH, Host_taxa, Latitude, CMCH:Thermal.biology	18379.3	5.6	0.1
Mod 3	CMCH, Latitude	18434.4	60.6	0.0
Mod 4	CMCH, Host_taxa, Latitude	18441.5	67.7	0.0
Mod 5	Latitude	18672.4	298.7	0.0

Supplementary Table S7: Best models assessing the relationship between disease prevalence, host thermal biology (i.e., endotherms and ectotherms) and four distances from the species' range center. The coefficients, standard errors (Std. Error), test statistics (Z values), and p-values for each predictor variable are shown here. Results indicate that the prevalence of density-dependent pathogens in amphibians, insects, fish, and mammals significantly decreases as distance from the range core increases. In contrast, the prevalence of frequency-dependent pathogens, such as vector-borne diseases in birds and mammals, remains consistent or increases across ranges depending on the measurement used. In our cross-validation, our models achieved a mean correlation of $r=0.61$ (SE= 0.011) and explained on average $R^2=0.34$ (SE=0.015) across all distance metrics (Supplementary Table S4).

Variable	Estimate	Std. Error	Z value	P-value
<u>Distance to edge of polygon range (EP)</u>				
(Intercept)	-6.575	0.765	-8.593	<0.0001
EP	2.958	0.301	9.815	<0.0001
Latitude	0.127	0.006	20.737	<0.0001
EP:Thermal.biologyEndothermic	12.958	1.635	7.925	<0.0001
<u>Distance to edge of minimum convex hull range (EMCH)</u>				
(Intercept)	-6.838	0.743	-9.208	<0.0001
EMCH	2.606	0.214	12.160	<0.0001
Latitude	0.105	0.006	16.579	<0.0001
EMCH:Thermal.biologyEndothermic	9.641	0.714	13.495	<0.0001
<u>Distance to polygon range centroid (CP)</u>				
(Intercept)	-3.674	0.764	-4.808	<0.0001
CP	-0.818	0.090	-9.069	<0.0001
Latitude	0.114	0.006	17.830	<0.0001
CP:Thermal.biologyEndothermic	-4.043	0.348	-11.610	<0.0001
<u>Distance to centroid of minimum convex hull (CMCH)</u>				
(Intercept)	-3.781	0.725	-5.215	<0.0001
CMCH	-1.426	0.120	-11.871	<0.0001
Latitude	0.111	0.006	17.471	<0.0001
CMCH:Thermal.biologyEndothermic	-2.925	0.382	-7.659	<0.0001