

Behavioral Ecology and Sociobiology

Electronic Supplemental Material: Online Resource 1

**Moving beyond the plane: measuring 3D home ranges of juvenile salamanders with Passive
Integrated Transponder (PIT) tags**

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Table S1 Comparison of calculated Clark-Evans aggregation index (R) using different edge correction factors across our surveyed sites, habitat groups, and seasons. Naïve does not include a correction factor, Donnelly is an edge correction used for rectangular search windows, and CDF is a cumulative distribution function method. $R = 1$ indicates random spatial distribution, $R < 1$ indicates clumped spatial distribution, and $R > 1$ indicates a uniform spatial distribution

Site	Habitat	Clark-Evans correction metric		
		Naïve	Donnelly	CDF
<i>Fall</i>				
1	Grassland	1.023	0.905	0.827
1	Forest	1.121	1.027	1.130
2	Forest	1.255	1.100	0.550
<i>Winter</i>				
1	Grassland	1.790	1.408	-
1	Forest	1.058	0.915	0.306
2	Forest	1.121	0.919	0.495
<i>Spring</i>				
1	Grassland	0.937	0.778	0.046
1	Forest	1.042	0.916	0.145
2	Forest	1.164	0.969	0.045

Table S2 Effects of number of relocations and distance moved (m) between relocations on estimates of 2D and 3D home range size. Core and Extent refer to 50% and 95% kernel density estimates (KDE), respectively. Estimate refers to predicted effects and 95% CI is the upper and lower 95% Confidence interval. $P < 0.05$ are bolded

Response	Relocations			Distance moved		
	Estimate	95% CI	P	Estimate	95% CI	P
2D Core	-0.14	(-0.23, -0.05)	0.002	0.03	(0.01, 0.04)	< 0.001
2D Extent	-0.02	(-0.08, 0.04)	0.460	0.03	(0.02, 0.04)	< 0.001
3D Core	-0.15	(-0.26, -0.04)	0.008	0.04	(0.02, 0.07)	< 0.001
3D Extent	0.01	(-0.08, 0.10)	0.853	0.04	(0.02, 0.06)	< 0.001

Table S3 Results from the Clark and Evans test of spatial aggregation (R) for our enclosures by season, site, and habitat. Seasons were delineated as Fall (12 October 2013 – 18 November 2014), Winter (01 January 2014 – 21 February 2014), and Spring (01 March 2014 – 03 April 2014). $R = 1$ indicates random spatial distribution, $R < 1$ indicates clumped spatial distribution, and $R > 1$ indicates a uniform spatial distribution. Pattern is the pattern of spatial aggregation corresponding to the p-value. When two-sided hypothesis tests were nonsignificant, individuals are randomly distributed

Site	Habitat	R	Pattern	P
<i>Fall</i>				
1	Grassland	0.93	random	0.318
1	Forest	1.01	random	0.736
2	Forest	1.10	random	0.276
<i>Winter</i>				
1	Grassland	1.99	uniform	0.011
1	Forest	1.01	random	0.910
2	Forest	0.52	clustered	0.002
<i>Spring</i>				
1	Grassland	1.14	random	0.700
1	Forest	0.96	random	0.776
2	Forest	0.93	random	0.546

Fig. S1 Schematic of enclosure array (not to scale). At Site 1, the pond was 75 m from the nearest grassland enclosure and 100 m from the nearest forest enclosure. At Site 2, the pond was 125 m from the nearest forest enclosure.

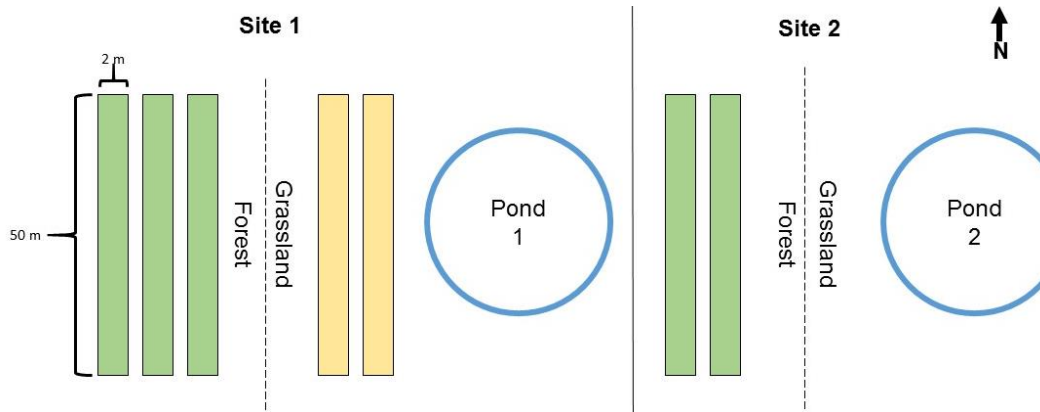


Fig. S2 The effect of the number of relocations on 2D (a and c) and 3D KDEs (b and d). Each line represents the mean KDE size for one individual. Means are based on 500 bootstrap iterations for each individual and number of relocations

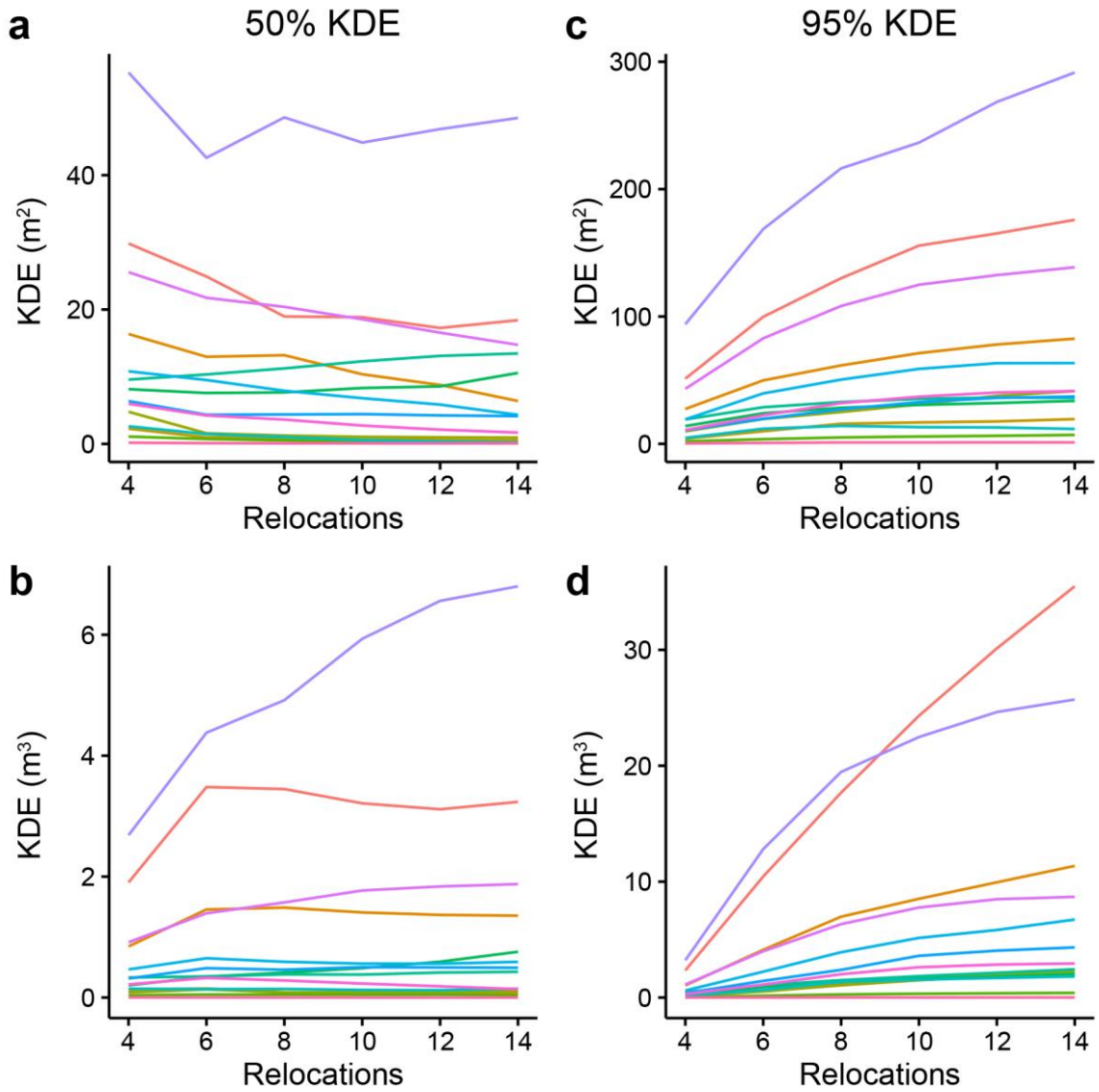


Fig. 3S Effect of habitat type on 3D KDE a) core area and b) extent. Open symbols are individual observations. Filled symbols represent predicted mean values and error bars represent 95% confidence intervals. Figures for 2D core area and extent are presented in the main text

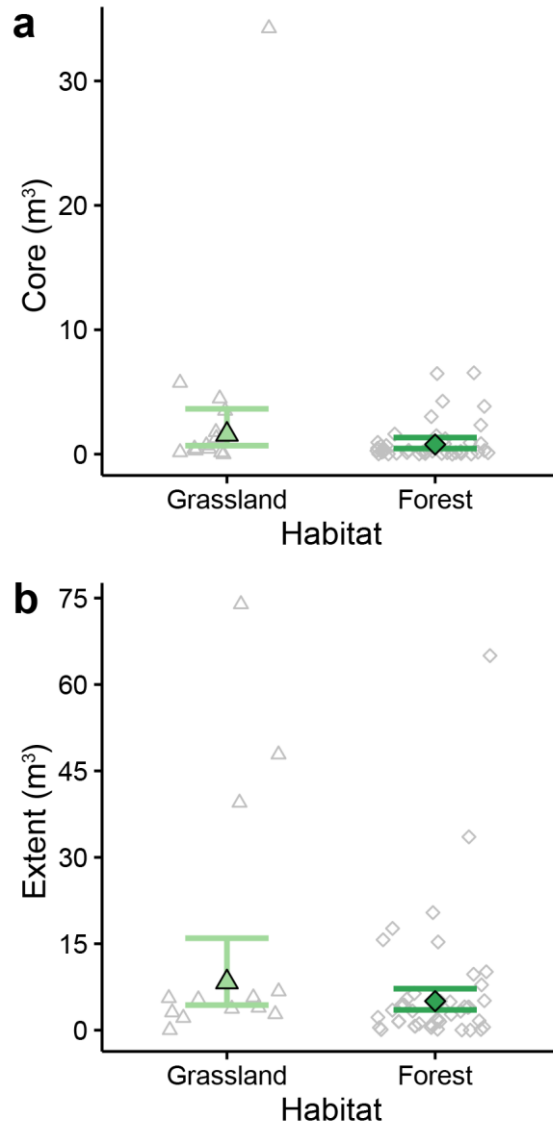


Fig. S4 Effect of habitat type (a, d, g), species (b, e, h), and the interaction between habitat type and species (c, f, i) on the KDE overlap index. Filled symbols represent predicted mean values and error bars represent 95% confidence intervals.

