

# Ladybirds in the UK: can biological traits explain distribution patterns?

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## Data used

**Species:** The 26 ladybirds resident in the UK

**Distribution data:** 30 year period (1980-end 2009), c.90,000 verified records  
Summarised as range size and aggregation (after Wilson *et al*, 2004)

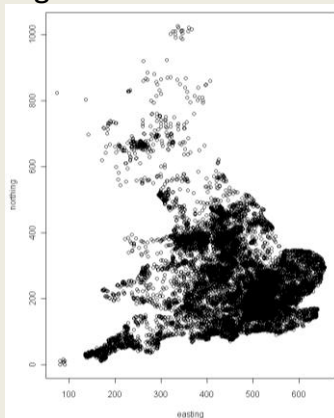
**Traits:** From the literature – 794 sources included in final analysis

- Categories – many investigated, only those with good data for all species used
- Intrinsic (largely genetic)
- Interactions with environment (split into habitat & diet)
- Activity (thermal regulation & voltinism)

Intrinsic	Env (diet)	Env (habitat)	Activity	Range size & Aggregation
Minimum size	# species predated by larvae	# EUNIS level 1 habitats	Usual voltinism	Range size
Maximum size	# species predated by adults	# EUNIS level 2 habitats	Maximum voltinism recorded	Aggregation (10 km scale)
Median size	# species predated, total			Aggregation (20 km scale)
Number of polymorphisms (UK)	# families predated by larvae			Aggregation (50 km scale)
	# families predated by adults			Aggregation (100 km scale)
	# families predated, total			

## Range size

**Range Size:**  
Sum of squares with at least 1 record during the recording period



## Aggregation

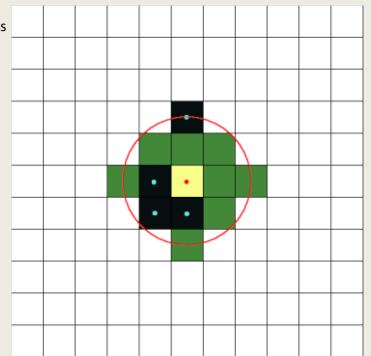
**Aggregation = NR/NRmax = decimal between 0 and 1**

**NR** = Mean number of occupied squares in circular radii of 10, 20, 50 and 100 km around each record (10km square)

**NRmax** = Maximum number of records possible for that circle of squares (usually 4, 12, 80 or 317, respectively)

NRmax varies as only terrestrial squares used for analysis

- Aggregation at the 10 km scale
- Aggregation at the 20 km scale
- Aggregation at the 50 km scale
- Aggregation (20km)  
NRmax = 12  
NR = 4  
 $4/12 = 0.333$



## Saturated models

### Linear regression models

- **Dependent variables** - range size or aggregation
- **Explanatory variables** - all traits

**Problem** – Many similar traits, causing multicollinearity

**Solution** - Hierarchical partitioning.

Traits tested to leave one from each category in final saturated models, eg:

**Range size** ~ Diet + Habitat + Size + Voltinism + Polymorphism

Diet = # families predated by the species

Habitat = # EUNIS level 2 habitat categories

Size = Median length

Voltinism = Usual number of generations in the UK

## Final models

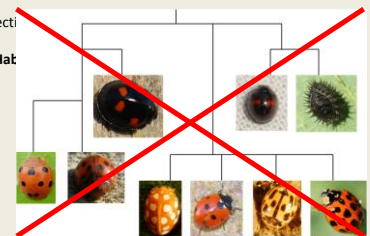
1000 replicates of stepwise selection

**Aggregation (100km) ~ Diet + Habitat**

**BUT:**

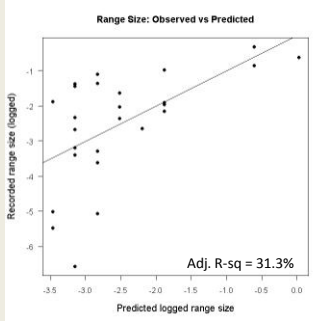
Phylogenetic influence?

- Therefore the phylogenetic models were dropped.



## Final models

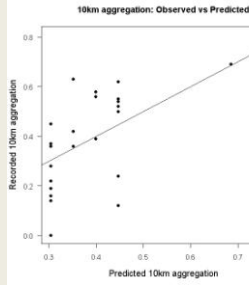
Range size ~ Diet



Dietary range is a critical niche dimension, and has been found to correlate with range size in many other insects

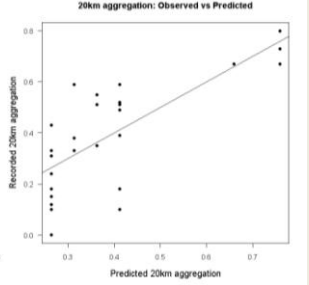
## Final models

Aggregation (10 km) ~ Habitat



Adj. R-sq = 50.45%

Aggregation (20 km) ~ Habitat



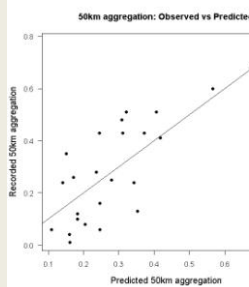
Adj. R-sq = 53.1%



More habitats occupied allows a more homogeneous distribution

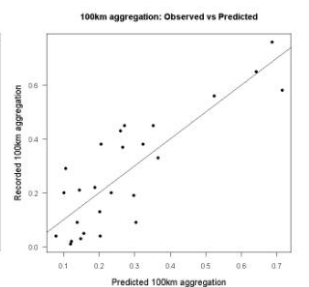
## Final models

Aggregation (50 km) ~ Diet + Habitat - Size



Adj. R-sq = 63.7%

Aggregation (100 km) ~ Diet + Habitat - Size



Adj. R-sq = 67.03%

Larger species = larger appetites = larger habitat patches



Habitat-limited species:  
 • Aggregated at small scale  
 • Patchy at large scale



## Acknowledgements

Ladybird recorders – for the data!



The Harlequin Ladybird Survey



JNCC  
 Joint Nature Conservation Committee

BRC  
 Biological Records Centre

CEH  
 Centre for Ecology & Hydrology  
 NATURAL ENVIRONMENT RESEARCH COUNCIL

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