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)

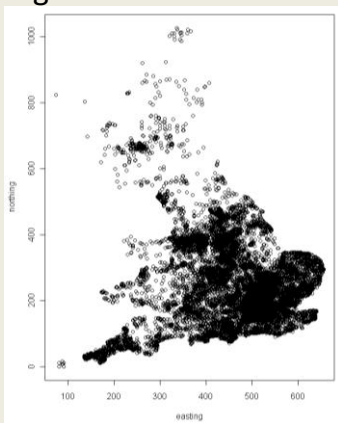
Traits: From the literature – 794 sources included in final analysis

- 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

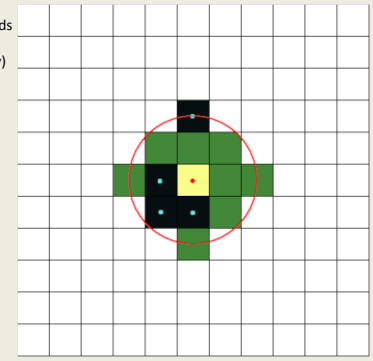


Aggregation

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 multicolinearity

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

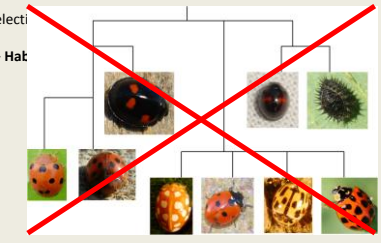
Final models

1000 replicates of stepwise selecti

Aggregation (100km) ~ Diet + Hab

BUT:

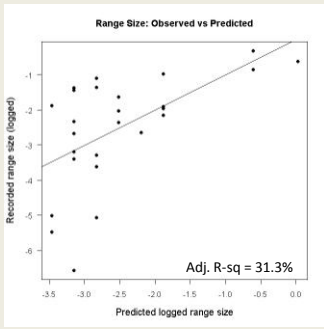
Phylogenic influence?



- Therefore the phylogenetic models were dropped.

Final models

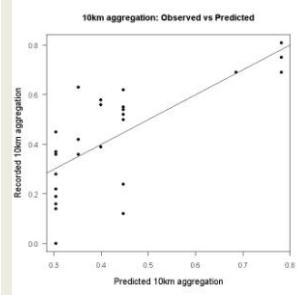
Range size ~ Diet



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

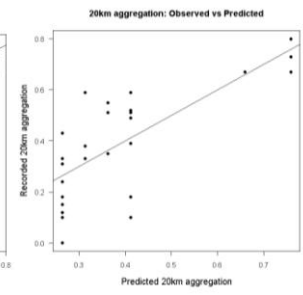
Final models

Aggregation (10 km) ~ Habitat



Adj. R-sq = 50.45%

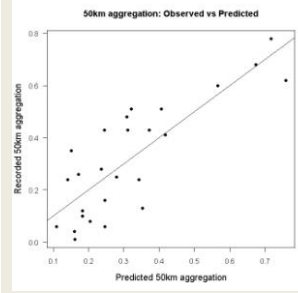
Aggregation (20 km) ~ Habitat



Adj. R-sq = 53.1%

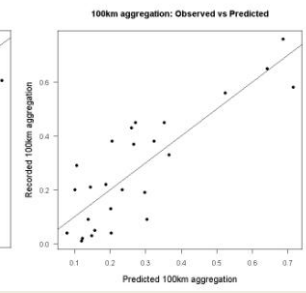
Final models

Aggregation (50 km) ~ Diet + Habitat - Size

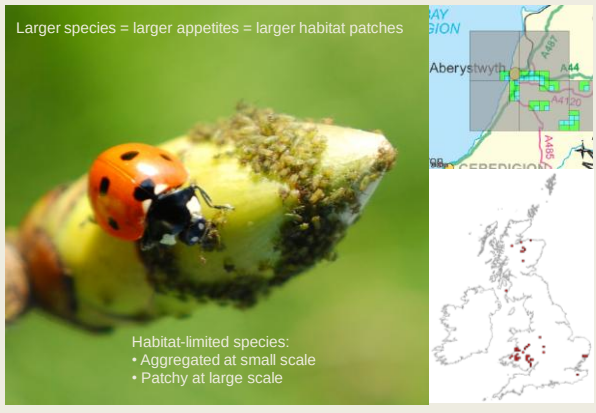


Adj. R-sq = 63.7%

Aggregation (100 km) ~ Diet + Habitat - Size



Adj. R-sq = 67.03%



Acknowledgements

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UK Ladybird Survey

JNCC Joint Nature Conservation Committee

ROTHAMSTED RESEARCH

BRC Biological Records Centre

CEH Centre for Ecology & Hydrology NATURAL ENVIRONMENT RESEARCH COUNCIL

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