Mygalomorphae Spider Hot Spots

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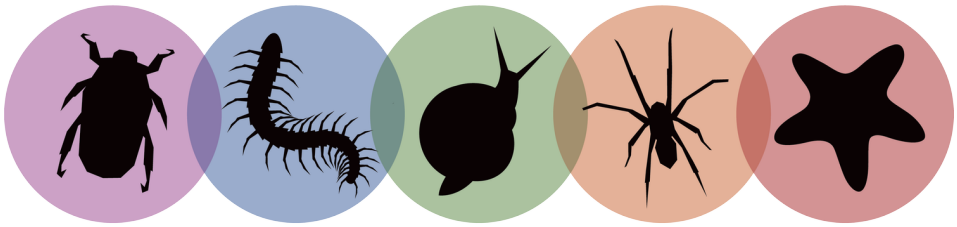
Executive Summary



INVERTEBRATES AUSTRALIA

Aim

The goal of this project is to design a fully reproducible, end-to-end workflow to identify biodiversity hotspots for Australian Invertebrates. Here, the workflow was applied to *Mygalomorphae* spiders, a group known to consist of trapdoor spiders, funnel webs and tarantlas).

Method

We used occurrence data from the Atlas of Living Australia for this analysis. We created two datasets for analyses:

1. 'Citizen science + preserved specimen' dataset (number of species = 219, number of observations = 6051)
2. 'Preserved specimen only' (number of species = 213, number of observations = 4663)

We computed alpha-hulls, a form of spatial polygon to represent each species distribution for endemism analyses.

Species richness (SR), weighted endemism (WE) and corrected weighted endemsim (CEW) were used as metrics to define hotspots. [Briefly describe each of these]

Moran's I test was used to test whether spatial patterns were statistically significant.

Results

- Overall signals for 'hotspots' were weak for *Mygalomorphae* spiders.
- No 'hotspots' were identified using the 'citizen science + preserved specimen' dataset
- In the 'preserved specimen only' dataset, there was some evidence of 'hotspots' using WE and CWE

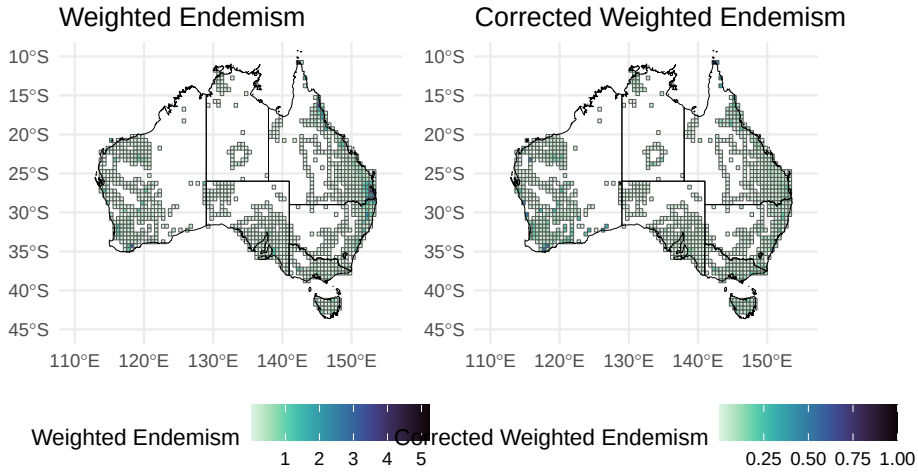


Figure 1: Maps showing (left) weighted endemism and (right) corrected weighted endemism of Mygalmorphae spiders. These maps were created using the 'preserved specimen data only'

Conclusions

Preserved specimen data provided better detection rates of endemism hotspots in *Mygalomorphae* spiders

Notable endemism hotspots identified for *Mygalomorphae* spiders in this analyses include:

- Tropical far north Queensland
- South East coast of New South Wales
- Rural Victoria
- Adelaide and Kangaroo Island
- South West coast of Perth
- Southern coast of Perth

There is still value for citizen science data for endemism analyses particularly for taxonomic groups that can be identified to species level using photographs.

Acknowledgements

This project was conducted on the unceded lands of the Bedegal and Gadigal people of the Eora Nation (Sydney), the Kaurna people (South Australia), the Whadjuk people of the Nyoongar nation (Perth), the Wurundjeri Woi-wurrung and Bunurong people of the Kulin nation (Melbourne). We recognise the original scientists of the native lands and their connection to the ecosystem.

We thank Dr. Jessica Marsh, Dr. Bruno Buzatto, Dr. Aaron Greenville and Professor Shawn Laffan for their expertise and advice on this project.

1 Introduction

Invertebrates are an often overlooked but vital component of healthy ecosystems. They perform a variety of critical ecological functions and ecosystem services, including pollination, soil modification, organic matter decomposition, nutrient cycling, pest control, and food provisioning to other animals and humans (Lavelle et al. 2006; Macadam and Stockan 2015; Griffiths et al. 2021; Porto et al. 2021). They are ubiquitous across land and seascapes, constituting the vast majority of Earth's biodiversity. Over 1.25 million invertebrate species have been documented, representing around 95% of animal species (Eisenhauer and Hines 2021). However, many invertebrate species and populations around the globe are under threat, as are the services they provide and the ecosystems they support (Hallmann et al. 2017; Ulrich et al. 2020; Wagner et al. 2021; Eisenhauer et al. 2023).

Australia has a high proportion of endemic fauna and is home to around 320,000 invertebrate species, of which around 35% have been described (Murphy and Leeuwen 2021). These include invertebrates of cultural significance to Indigenous Australians, such as freshwater crayfish (marron), beetle larvae (witchetty grubs), and Bogong moths, used for food, medicine, and ceremonies for thousands of years (Faast and Weinstein 2020; Stephenson et al. 2020; Murphy and Leeuwen 2021). Invertebrates also play vital roles in Australian agriculture, land management, and environmental monitoring (Andersen and Majer 2004; Holloway, Furlong, and Bowden 2008). Despite their ecological, cultural, social, and economic importance, invertebrates are often neglected in conservation and management plans, and a lack of taxonomic and ecological knowledge hinders their protection (Braby 2018, 2019; Sands 2018). Invertebrates constitute 95% of Australia's faunal diversity but only 15% of species assessed under the Environment Protection and Biodiversity Conservation Act (EPBC Act), and only around 480 species of Australian invertebrates are listed as threatened (invertebratesaustralia.org).

Invertebrates face a multitude of anthropogenic and environmental threats, including habitat loss, climate change (and associated events such as fires, floods, and droughts), pollution, pesticides, and introduced species (Wagner et al. 2021; Marsh et al. 2022; Reddin et al. 2022). There is growing evidence that such pressures, which have seen widespread invertebrate declines around the globe, are impacting Australian species (Braby, Yeates, and Taylor 2021). While there is an urgent need for further research on invertebrate biodiversity and conservation in relation to these threats, conservation measures can help to mitigate their effects, protect and restore biodiversity, and prevent extinctions.

Biological conservation is hampered by limited resources, and identifying priority areas to focus conservation efforts can help to maximise their effectiveness (Myers et al. 2000). Species

richness and endemism are key indices of biodiversity that reflect biological complexity and uniqueness, and can be used to identify 'biodiversity hotspots' to prioritise for conservation (Myers 1988; Caldecott et al. 1996; Reid 1998). **Species richness refers to the number of species in an area**. Numerous definitions of **endemism exist but generally a taxon is considered endemic to a particular area if it occurs only in that area (Anderson 1994)**. Quantifying endemism and identifying areas of high endemism is important in conservation because narrowly endemic taxa have small ranges by definition and are therefore more vulnerable to threats such as habitat loss and climate change (Harvey et al. 2011). The 10 known invertebrate extinctions in Australia were all narrow-range endemics (Braby 2019). There is a need to identify hotspots of invertebrate biodiversity to enhance their conservation, particularly within Australia (Taylor et al. 2018). Designation of protected areas and other landscape management practices can be informed by spatial quantification of endemism. Identifying hotspots helps to focus limited resources and improve the efficiency of biodiversity conservation efforts.

Identifying hotspots for all invertebrates is not logistically feasible at present, so as a proof of concept we focussed on spiders in the infraorder *Mygalomorphae*, using spatial analyses to identify hotspots of species richness and endemism across Australia. Mygalomorph spiders have poor dispersal capabilties and sedentary habits, making them well-suited to endemism analyses (Ferretti, González, and Pérez–Miles 2014). Australian mygalomorphs are diverse and many may face a greater level of threat than what is formally recognised (Castalanelli et al. 2014; Rix et al. 2017). Our methods can be used as a framework and extended to other taxonomic groups. Identifying hotspots of endemism in the Australian invertebrate fauna will help guide research and conservation efforts and improve outcomes, not only for invertebrates, but for the ecological communities they support.

(to move to methods) Quantification of endemism depends on the spatial scale being considered (Townsend Peterson and Watson 1998), and numerous calculation methods exist (). Endemism can be quantified on a continuous scale across a spatial grid with reference to the constituent grid cells, based on how many cells taxa occupy.

2 Methods

2.1 Data retrieval

> **Note**
>
> We downloaded data for this report on the 2024-03-13 and the raw download contained 9395 records

> **Source code**
>
> The data retrieval workflow can be found here

We used data from Atlas of Living Australia (ALA) for this study. We downloaded occurrence records using the `galah` R package using the following criterion:

1. Found in Australian mainland and Tasmania.
2. Identified to a taxon rank of species.
3. Basis of record of either:
    i) Preserved specimen
    ii) Material sample
    iii) Machine observation
    iv) Human observation
4. Coordinate uncertainty of less than 1000 meters or has a value of NA (citizen science records or human observations are typically entered as NA)

We also used ALA's data quality assertions to further refine our download. We excluded occurrence records using the following criterion:

1. Coordinates are equal to 0
2. Coordinates are presumed swapped e.g. when latitude is entered as longitude
3. Latitude and longitude values are presumed negated
4. Coordinates our out of range
5. Taxon excluded by the ALA
6. Taxon considered as a questionable species

See Section 2.2.5 to learn more about which assertions we used for this project.

2.2 Data overview

> **Note**
>
> The full data overview report can be found here

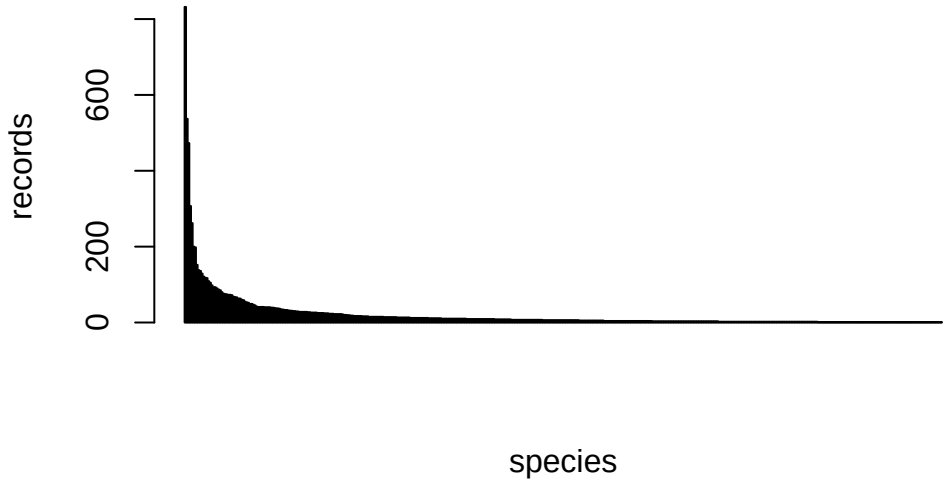
> **Source code**
>
> The data overview workflow can be found here

After the initial data retrieval the data were summarised to provide an overview of the number of records, species, and families represented, as well as the broad distribution of these across Australian states. The basis of records and data quality assertions were also investigated. This provided a broad overview of data quality and facilitated review by taxonomic experts.

2.2.1 Species

There are **457 species** in total in the original download.

The below barplot shows the distribution of the number of records across species.



The below table shows the number of records of each species.

Show 10 entries Search:

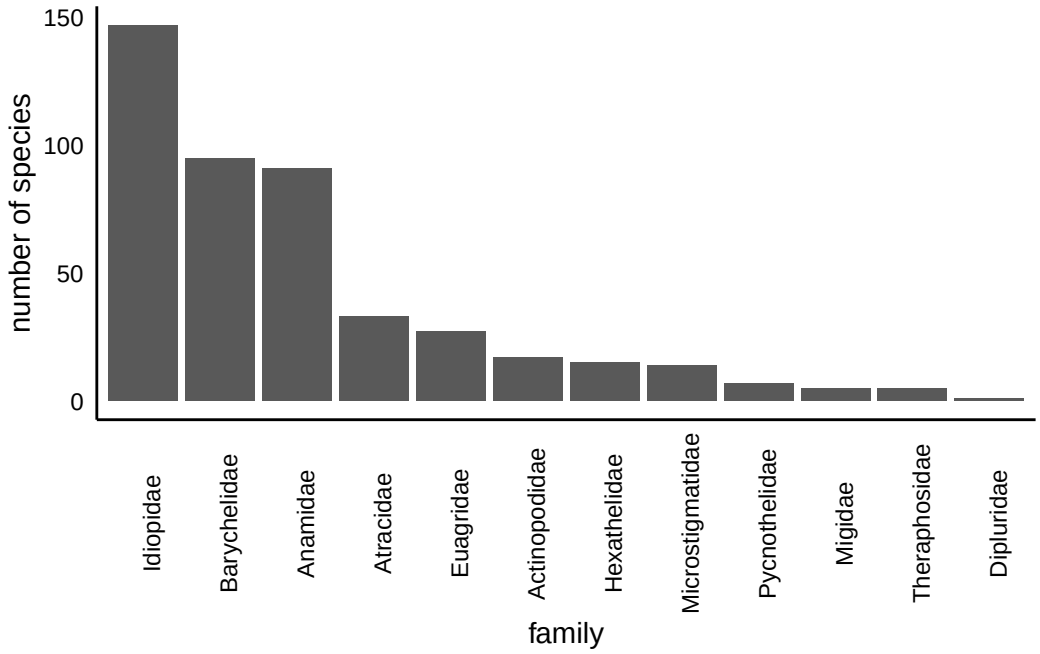
	species	n	percent
1	Missulena occatoria	832	8.86
2	Missulena bradleyi	537	5.72
3	Aname mellosa	473	5.03
4	Seqocrypta jakara	307	3.27
5	Atrax robustus	262	2.79
6	Blakistonia aurea	200	2.13
7	Hadronyche infensa	198	2.11
8	Idiosoma subtriste	152	1.62
9	Hadronyche modesta	138	1.47
10	Aname pallida	136	1.45

Showing 1 to 10 of 457 entries

Previous 1 2 3 4 5 … 46 Next

2.2.2 Family

Barplot showing the number of species in each family:



2.2.3 Taxonomic overview by state

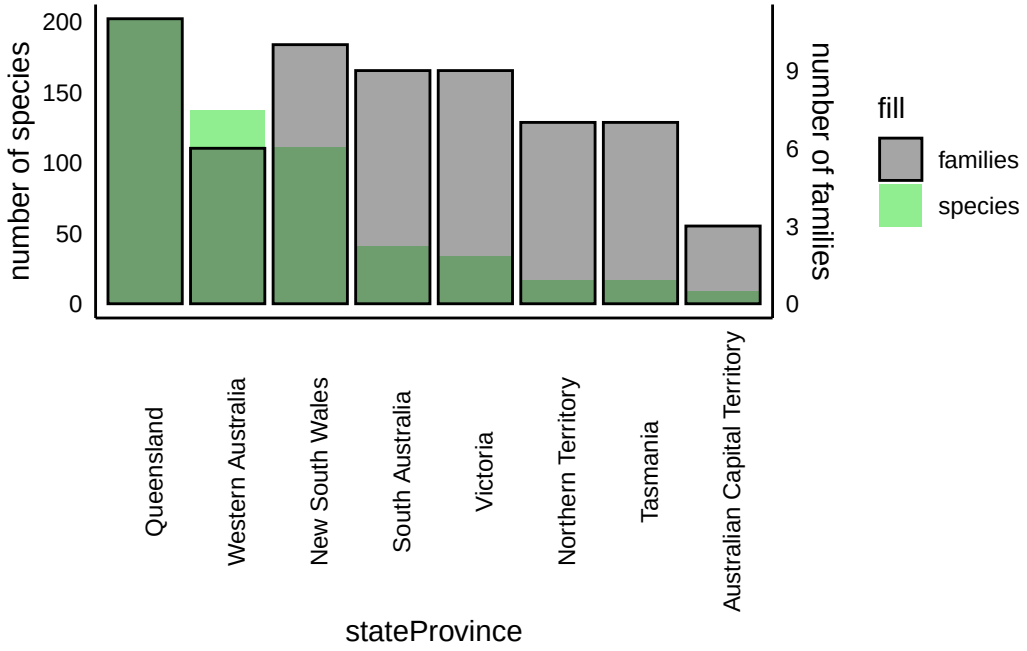


Figure 2.1: Barplot showing the number of species and families by state

	species	n
Australian Capital Territory	Missulena occatoria	69
	Atrax yorkmainorum	22
	Paraembolides brindabella	11
New South Wales	Atrax robustus	258
	Missulena bradleyi	164
	Missulena occatoria	97
Northern Territory	Missulena pruinosa	33
	Selenocosmia stirlingi	31
	Aname humptydoo	11
Queensland	Missulena occatoria	330
	Missulena bradleyi	292
	Seqocrypta jakara	266
South Australia	Blakistonia aurea	199
	Missulena occatoria	156
	Idiosoma subtriste	151
Tasmania	Hadronyche venenata	72
	Teranodes montana	63
	Chenistonia trevallynia	47
Victoria	Missulena occatoria	155
	Hadronyche modesta	137
	Hadronyche meridiana	85
Western Australia	Aname mellosa	473
	Bungulla bertmaini	121
	Aname lorica	117

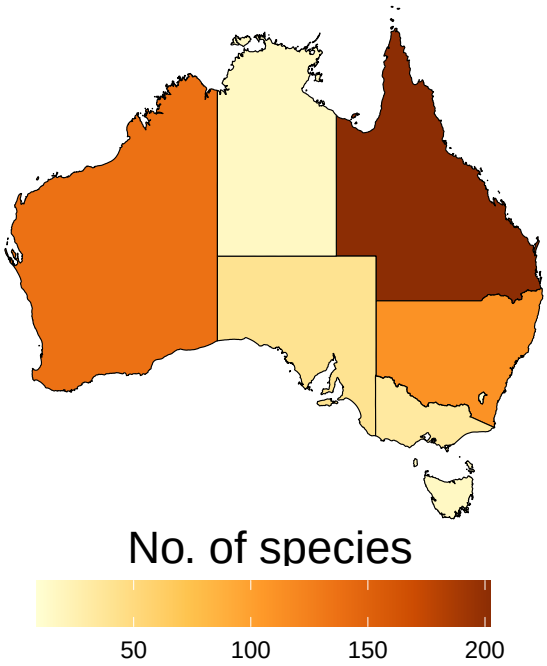


Figure 2.2: Map showing the number of species by state

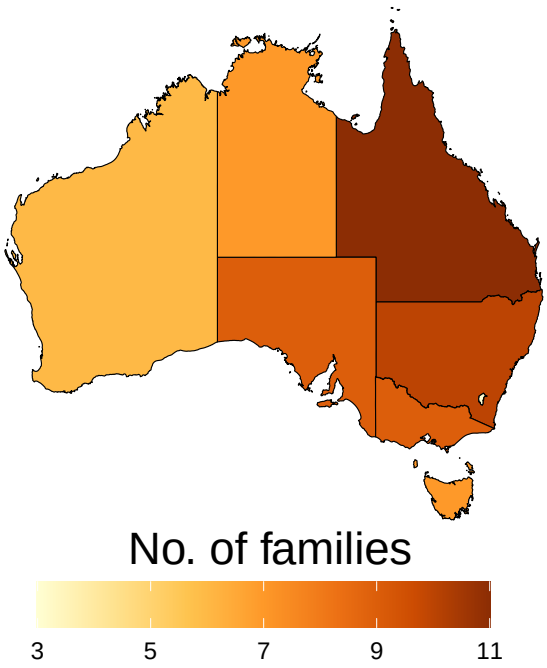


Figure 2.3: Map showing the number of families by state

basisOfRecord	n	percent
PRESERVED_SPECIMEN	7828	83.32
HUMAN_OBSERVATION	1514	16.11
MATERIAL_SAMPLE	52	0.55
MACHINE_OBSERVATION	1	0.01

2.2.4 Basis of record

Total counts of basis of record types.

`PRESERVED_SPECIMEN`: An occurrence record describing a preserved specimen.
`HUMAN_OBSERVATION`: An occurrence record describing an observation made by one or more people.
`MATERIAL_SAMPLE`: An occurrence record based on samples taken from other specimens or the environment.
`MACHINE_OBSERVATION`: An occurrence record describing an observation made by a machine.

2.2.5 Assertions

Various tests are run on occurrence data in the Atlas of Living Australia, resulting in assertions about the content and quality of the data. These assertions help users gauge whether data is fit for their purposes and allow for easy data filtering. Assertions are logical variables (`TRUE/FALSE`) and take the value TRUE when they apply to the associated occurrence record. Descriptions of Assertions can be found at here

Here, we have focused on spatial and taxonomic assertions because accurate identification of taxa and their spatial distributions is imperative to the calculation of endemism metrics and subsequent mapping.

2.2.5.1 Spatial assertions

We investigated a range of spatial assertions and deemed the following safe to bypass when refining the data download:

- `COORDINATE_UNCERTAINTY_METERS_INVALID`
  We performed visual checks and flagged records did not seem to be out of species' range. They were mostly cases where `coordinateUncertaintyinMeters` was NA. We know iNaturalist records input NA for `coordinateUncertaintyinMeters`, therefore in refining the data download we will include records where `coordinateUncertaintyinMeters` is NA or less than 1000 m. We will remove flagged values for a sensitivity analysis later on.

- `COORDINATE_ROUNDED`
  The original coordinates were rounded to six decimals (~ 1 m precision) to simplify processing. The level of precision lost will not affect the endemism analysis.

The following will be used to refine the data download as they indicate coordinates outside of the given country (records flagged as TRUE will be excluded):

- `COORDINATE_OUT_OF_RANGE`
- `PRESUMED_NEGATED_LONGITUDE`
- `PRESUMED_NEGATED_LATITUDE`
- `PRESUMED_SWAPPED_COORDINATE`
- `ZERO_COORDINATE`

2.2.5.2 Taxonomic assertions

The following assertions were used to identify taxonomic discrepancies in the data and allow for review by taxonomic experts:

`TAXON_MATCH_FUZZY` - is flagged when the supplied scientific name (`raw_scientificName`) does not exactly match the taxonomic backbone of the Atlas.

2.3 Data cleaning

> **Note**
>
> The full data cleaning report can be found here

> **Source code**
>
> The data overview workflow can be found here

The following criterion were used to identify and remove records for the endemism analyses:

- Taxonomic errors, invalid species names or synonyms
- Species introduced to Australia
- Marine taxa
- Records with geographic errors
- Any subspecies level identifications were reclassified to species level
- Duplicates

ALA_names	AFD_synonyms
Eucyrtops eremaeus	Eucyrtops eremaea
Kwonkan turriger	NA
Proshermacha wilga	NA
Selenocosmia crassipes	NA

2.3.1 Taxonomic Errors

2.3.1.1 Invalid names

The (AFD) is an online catalogue of taxonomic and biological information on all animal species known to occur within Australia and its territories.

The Australian Faunal Directory (AFD) was used to cross validate the records from ALA to ensure all records had valid species names.

A list of valid species names was downloaded from the AFD and was compared to the species names in our dataset, subsetting any records that did not have a matching valid name.

The AFD lists any applicable synonyms for each species within their database. The 4 unmatched species might be synonyms of valid species.

The potential synonym matches are as follows:

These will be verified by experts to determine how to best handle them. For now,taxa in our dataset that are not matched in the AFD will be excluded.

> **!** Important
>
> As such, we decide to exclude these 4 taxa from our dataset (15 observations, 0.002% of raw dataset).

> **i** Note
>
> After removing the taxonomic errors, we have 9380 observations after the exclusion, 453 species.

2.3.2 Introduced Species

Any species which are not native to Australia were removed from our dataset. To identify all introduced species in the dataset, we used species lists from the World Spider Catalogue (WSC) and the Global Register of Invasive and Introduced Species (GRIIS).

The (WSC) is a comprehensive online database of spiders from around the world, with detailed taxonomic information, distribution maps, references and images.

> **Important**
>
> Introduced species in the WSC matched with 0 records in our data.

(GRIIS) is a project by the IUCN SSC Invasive Species Specialist Group to compile annotated and verified country-wise inventories of introduced and invasive species.

> **Important**
>
> There are no arachnids in the Australian GRIIS list

> **Note**
>
> For the purpose of this project, we conclude there are no introduced spiders in our dataset.

2.3.3 Marine Species

The World Register of Marine Species (WoRMS) was used to identify and remove marine species from the data. WoRMS provides a authoritative and comprehensive list of names of marine organisms, including currently valid and alternative names.

Using the `worrms` R package, we supplied our list of 453 species to the `wm_records_taxamatch()` function to check whether any our taxa are classified as marine.

> **Note**
>
> In the case of this project, we found 0 taxa that matched with marine species in the WoRMS database.

2.3.4 Geographic Errors

Biodiversity data, especially citizen science data can have various geographic imperfections. For example, occurrence records may include data from institutions such as botanic gardens or zoos which may not be reflective of a specie's natural range. There may be data entry errors where the default location of a taxa is assumed to be the center of particular region. For these reasons, we used the R package `CoordinateCleaner` to investigate potential errors in our dataset.

Test	Number of Observations
.val	0
.equ	0
.zer	0
.cap	48
.cen	0
.sea	418
.urb	1292
.otl	119
.gbf	0
.inst	26
.dpl	2970
.summary	4125

We used the `clean_coordinates()` function and tested whether any of our coordinates were the following:

- General coordinate validity
- Country and province centroids
- Capital coordinates
- Coordinates of biodiversity institutions
- Spatial outliers
- Temporal outliers
- Assigned to the location of the GBIF headquarters
- Located in Urban areas
- Located in the sea
- Duplicated values
- Plain zeros

Table of the number of observations flagged by CoordinateCleaner's testing suite:

CoordinateCleaner, identified a large number of duplicates which we have a separate workflow in Section 2.3.5 so we decided to ignore the duplicates flagged by CoordinateCleaner.

After some consideration:

- 48 records excluded due to being near a capital vicinity (0.51%)
- 26 records excluded due to being in the vicinity of biodiversity institutions (0.28%).
- 418 records excluded due to being in sea (4.45%).

> **Note**
>
> After removing these geographic errors, we have 8888 observations after the exclusion, 437 species.

2.3.5 Duplicate Records

Duplicate records can affect statistical analyses by pseudoreplication (increasing sample size but not adding information). We noticed that some records that had the *same* coordinate values for a large number of *different* species. These records were typically from museum record providers, we suspect this was due to the sampling method e.g. pitfall traps. For this reason, we decided to remove records if they fulfiled the following critiera:

- the record was duplicated at the species level
- had same exact coordinates
- had same time and date of collection

> **Important**
>
> Using this method, we excluded 2513 from the dataset (26.75%).

> **Note**
>
> After deduplication, we have 6375 observations after the exclusion, 404 species.

2.3.6 Minimum number of observations

The final step in our data cleaning workflow is to exclude any species that have fewer than three observations as this is a key requirement for the generation of alpha hulls.

> **Important**
>
> We identified 185 species with fewer than three observations. This resulted in an exclusion of 324 observations (3.45%).

> **Note**
>
> After removing data-deficient taxa, we have 6051 observations after the exclusion, 219 species.

2.3.7 Citizen science data

While citizen science is an increasingly important source of data that informs research, it's accuracy and quality impact statistical inference. This is likely due to improper species identification.

As such, we decided to conduct the endemism analysis using the cleaned data that includes citizen science data (e.g. basis of record = `"HUMAN_OBSERVATION"`), as well as a dataset with we exclude citizen science data (e.g. basis of record = `"PRESERVED_SPECIMEN"`)

> **!** Important
>
> There were 1388 records that were flagged with basis of record = `"HUMAN_OBSERVATION"`. This resulted in an exclusion of 14.77% of the original data) in the "preserved specimen only" dataset.

> **i** Note
>
> After removing data-deficient taxa, we have 4663 observations after the exclusion, 213 species.

2.4 Generation of α hulls

> Source code
>
> The alpha-hull workflow can be found here

Spatial data for invertebrates are typically sparse, often resulting in exclusion of entire species when using advanced spatial modelling methods such as species distribution models.

One way to retain as many species as possible in a spatial analysis is to represent species range with alpha-hulls, a form of spatial polygon. An alpha-hull can be computed using a minimum of three data points, which allows the inclusion of data-deficient invertebrates in our endemism analysis

Using the cleaned data, we applied the `EOO.computing()` function from R package `ConR` to quantify alpha-hulls for all species that had at least 3 records (n =). We used an alpha value of 2 and a buffer size of 0.000001 (which approximates to ~100m). The alpha-hull workflow is laid out in this document.

Alpha-hulls were converted into `SpatialPolgyon` objects using the `sp` R package and exported for endemism analysis

2.5 Biodiversity metrics

> Source code
>
> The biodiversity metrics workflow can be found here

In order to quantify patterns of species richness and endemism, we need to convert our point based (i.e. coordinates for each occurrence of a species) into a community matrix, whereby each row in the matrix corresponds to a different site, while each column represents a different species. The entries in the matrix indicate whether a species is present at a particular site (often with a 1 for presence and 0 for absence) or how abundant the species is at that site. See here for further information.

We converted our alpha-hulls into a community matrix using the `poly2comm()` function in the `phyloregion` R package. The resolution or grid size is set at 0.5 decimal degrees. The `poly2comm()` also computes abundance (the number of individuals in each cell) and species rich (number of species in each cell).

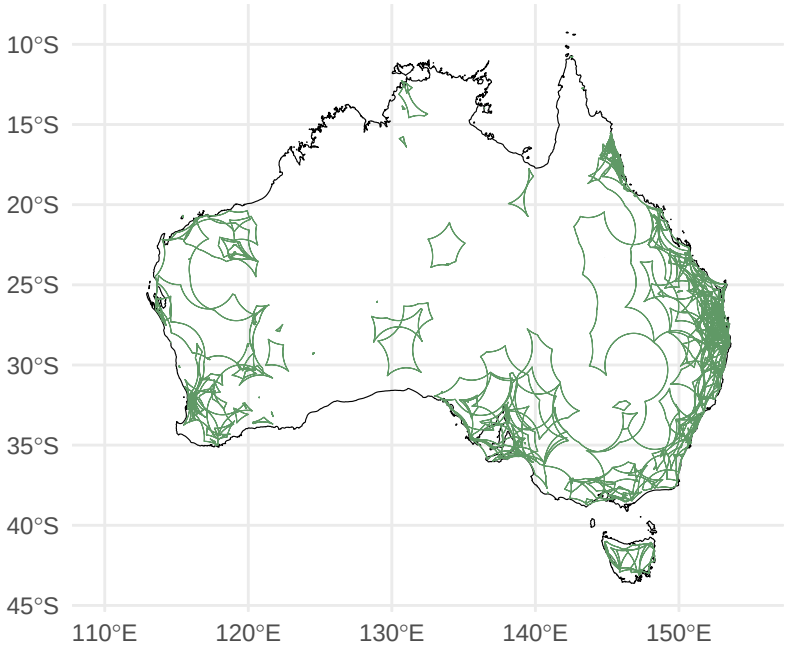


Figure 2.4: Community matrix of Mygalomorphae spiders from our cleaned dataset

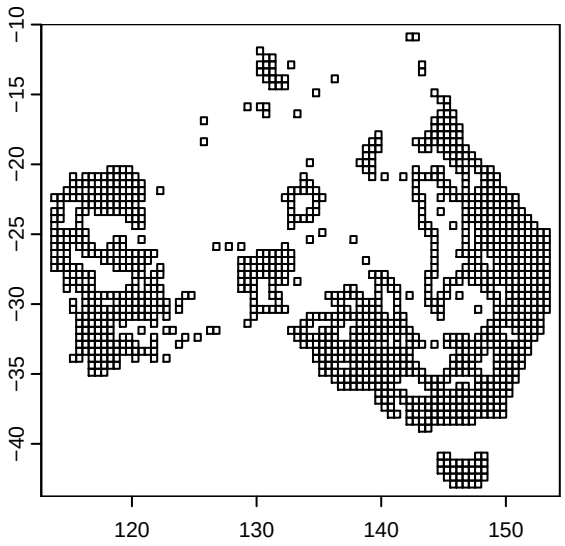


Figure 2.5: Community matrix of Mygalomorphae spiders from our cleaned dataset

2.5.1 Quantifying endemism

Endemism is a measure of rarity relative to other species (refs). There are multiple metrics to assess which areas are of importance for Mygal spiders, each have their own caveats. In order to get a fuller picture of the distribution of species and importantly, rare species that are limited in their range, we need to use a combination of endemism metrics.

2.5.1.1 Weighted endemism

Weighted endemism is species richness inversely weighted by species ranges(Crisp et al. 2001),(Laffan and Crisp 2003),(Barnabas H. Daru et al. 2020). It gives higher weight to species with smaller ranges, emphasizing areas with many range-restricted species. WE highlights areas with a high concentration of rare species, which can be crucial for conservation efforts, however regions with high species richness can have inflated WE values simply because they have more species, not necessarily more endemics (https://www.jstor.org/stable/3554498).

We calculated WE using the `weighted_endemism()` from `phyloregion` package.

2.5.1.2 Corrected weighted endemism

Corrected weighted endemism accounts for species richness in each cell. This correction accounts for the fact that areas with more species are likely to have more endemics by chance

alone (Crisp and Laffan). It provides a balanced measure, considering rarity and richness and range sizes.

We calculated CWE by dividing the WE in each grid cell by species richness.

2.5.2 Statistical inference

We calculated the Moran's I test statistic, to determine whether spatial patterns of species richness, abundance and endemism for Mygalomorphs are distributed in a way that is not expected by random chance. Moran's I is a statistical measure used to assess spatial autocorrelation, which is the degree to which a set of spatial features e.g occurrences or polygons are clustered, dispersed, or randomly distributed across a geographic area (ref).

Moran's I ranges from -1 to 1:

- 1: Perfect positive spatial autocorrelation (values are highly clustered).
- 0: No spatial autocorrelation (random distribution).
- -1: Perfect negative spatial autocorrelation (values are perfectly dispersed).

2.6 Data and code availability

All data and code to reproduce the R portion of our analyses can be found at our Github repository.

3 Results

3.1 All data from ALA

3.1.1 Species richness

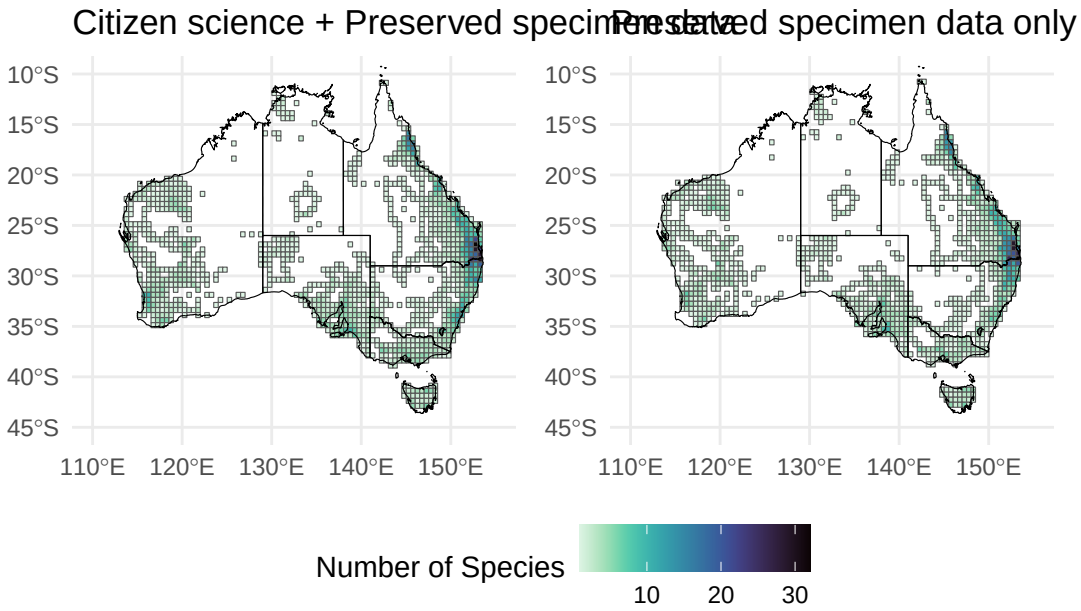


Figure 3.1: Figure 1: Map showing species richness estimated of Mygalmorphae spiders. Left: All data from the cleaned dataset is used i.e contains citizen science data (basis of record == `HUMAN_OBSERVATION`) Right: Only expert data is used (basis of record == `PRESERVED_SPECIMEN` only)

> **Note**
>
> There was **no evidence** for spatial clustering in **species richness** in either the combined dataset or in the preserved specimen only dataset (Table 1).

Table 1. Summary statistics for species richness in both datasets

Dataset	Z statistic	P value	N species	N observations
Citizen Science + Preserved Specimen	-0.00087	0.35	219	6051
Preserved Specimen only	-0.00092	0.27	213	4663

Dataset	Z statistic	P value	N species	N observations
Citizen Science + Preserved Specimen	-0.00087	0.560	219	6051
Preserved Specimen only	-0.00092	0.015	213	4663

3.1.2 Weighted endemism

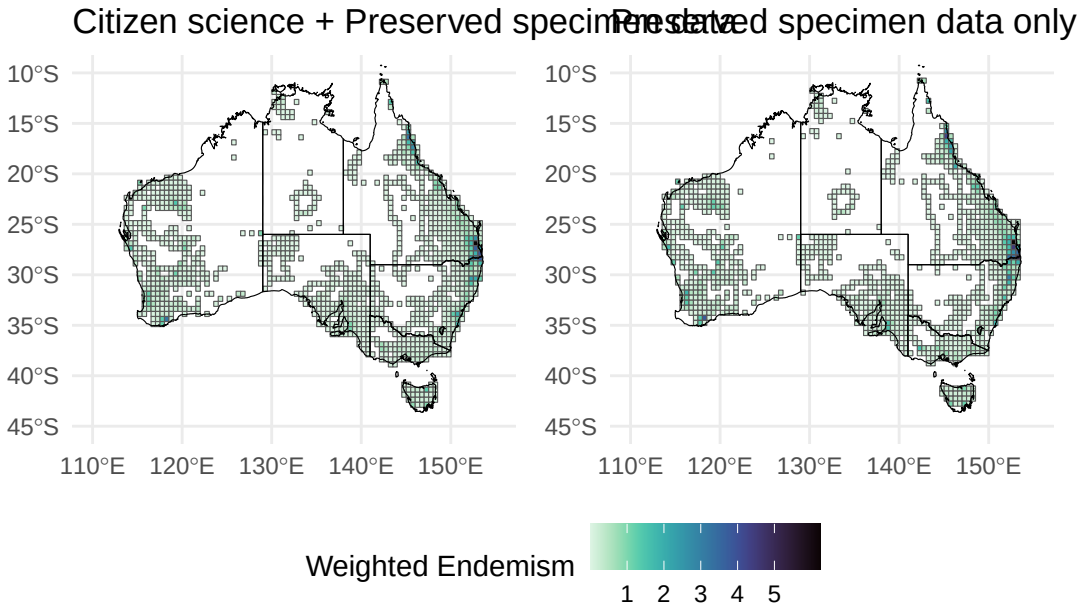


Figure 3.2: Figure 2: Map showing weighted endemism estimated of Mygalmorphae spiders. Left: All data from the cleaned dataset is used i.e contains citizen science data (basis of record == `HUMAN_OBSERVATION`) Right: Only expert data is used (basis of record == `PRESERVED_SPECIMEN` only)

> **Note**
>
> There was **some evidence** for spatial clustering in **weighted endemism** in the preserved specimen only dataset (Table 2).

Table 2. Test statistic and p value for weighted endemsim

Dataset	Z statistic	P value	N species	N observations
Citizen Science + Preserved Specimen	-0.00087	1.00	219	6051
Preserved Specimen only	-0.00092	0.02	213	4663

3.1.3 Corrected weighted endemism

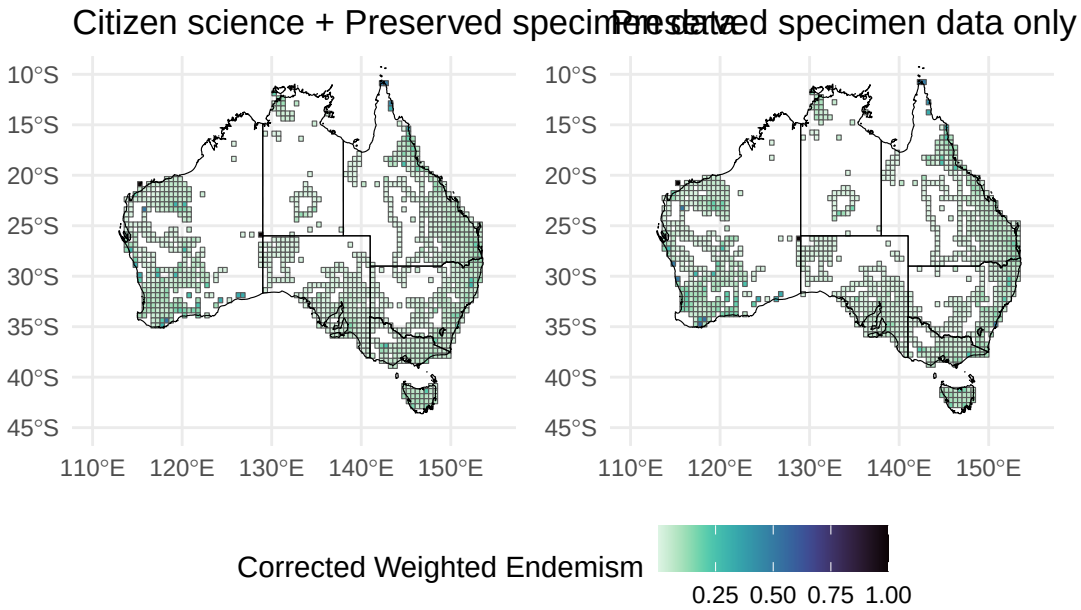


Figure 3.3: Figure 2: Map showing corrected weighted endemism estimated of Mygalmorphae spiders. Left: All data from the cleaned dataset is used i.e contains citizen science data (basis of record == `HUMAN_OBSERVATION`) Right: Only expert data is used (basis of record == `PRESERVED_SPECIMEN` only)

> **Note**
>
> There was **some evidence** for spatial clustering in **corrected weighted endemism** in the preserved specimen only dataset (Table 3).

Table 3. Test statistic and p value for corrected weighted endemsim

4 Discussion

5 Summary

In summary, this book has no content whatsoever.

```
1 + 1
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```
[1] 2
```

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