

The MEGA Murray-Darling Microbat Project

Results of a citizen science project
2017–2019

November 2019





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For further details contact

Natural Resources SA Murray-Darling Basin
Department for Environment and Water
Upper Level, Cnr Mann & Walker Sts, Mt Barker,, South Australia, 5251.
Phone: (08) 8391 7500
Website: <http://www.naturalresources.sa.gov.au/samurraydarlingbasin>

Microbat image on front cover courtesy : Dennis Matthews

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1 Summary

The South Australian portion of the Murray-Darling Basin is home to 18 species of insectivorous bat or 'microbat', which have persisted when many other species of native mammal have declined or disappeared entirely. However, due to their nocturnal habits, relatively little is known about their populations and their habitat associations. An opportunity was created to encourage citizen scientists to participate in a project to generate new records of occurrence of microbat species and collect information relevant to microbat conservation and management, while contributing to improved understanding and appreciation of native mammals more generally in society. Data collection through citizen science leading to conservation action was the ultimate goal.

The MEGA Murray-Darling Microbat Project citizen science project aimed to:

- Contribute to improved understanding and appreciation of microbats more generally in society, by engaging the community in data collection and conservation initiatives on their own land
- Collect new records of occurrence and habitat associations on microbat species across the SA Murray-Darling Basin region, to help inform state conservation reassessments and guide decisions effecting conservation of these species across the region
- Promote the program to other regions within the Murray-Darling Basin and beyond to increase knowledge of bat distributions, while creating opportunity for community to engage with native fauna and science.

The MEGA Murray-Darling Microbat Project was a partnership between the South Australian Museum, Natural Resources South Australian Murray-Darling Basin (Department for Environment and Water), the University of South Australia, and Mid Murray Landcare SA. Funding was received from the Australian Government Inspiring Australia – Science Engagement Program through their Citizen Science Grants.

Members of the public were initially engaged in the project through 'Bat Nights', local networks and the media. Anabat Swift 'bat detectors' were loaned out to people who conducted overnight acoustic surveys at locations of their choice, and provided habitat data and site photos via a BioCollect (Atlas of Living Australia) portal. Community participation was facilitated through seven local Landcare and three Natural Resources SA Murray-Darling Basin offices.

Between October 2017 and May 2019, over 300 people participated in the project in various ways. Anabat surveys were conducted by 158 people resulting in 3,000 new microbat records for the region. This compares with just 2591 records from the Atlas of Living Australia compiled for the same region since 1890.

The overall biological outcome from the MEGA microbat citizen science project is evidence of a species-rich assemblage of microbats that still exists through the Murray-Darling Basin in South Australia. Most microbat species were present throughout the range of broad habitat types in the region, and any one recording site had four species present on average. The habitats that appeared to provide more resources for bats were tall forests and woodlands, which had six species on average; and the Murray River corridor, which had five species on average at any one site. These habitats offer roost sites in the large old trees and a variety of insects for food, and should be a priority for protection and effective management. Modified landscapes such as urban gardens, cropping paddocks and grazing land also supported a relatively high number of bat species: an average of 4 bat species.

Management of vegetation remnants should take into consideration that native mammals still exist in these areas, and their roosting and food resources need to be maintained consistently for them to persist. Hollow protection and fire management is particularly relevant, but a range of other considerations are relevant to microbat conservation. When species results were communicated to participants, a message (as a brochure) was given that was designed to empower and inform the person to undertake conservation-related efforts on their own land.

These results are available to inform state conservation status reassessments of individual microbat species, especially with regard to current population extents in the lower Murray-Darling Basin. Some of the observations for individual microbat species were particularly informative in the context of their management and conservation. For example, the large-footed Myotis, *Myotis macropus*, which is listed as Threatened under South Australian environmental legislation, was found to use a greater area along the Murray River than previously thought, suggesting the presence of roosts not yet discovered. Other species, like the large forest bat, *Vespadelus darlingtoni*, were also found to have restricted distributions.

There are obvious spatial gaps in sampling to the north-west and south-east of the Murray River corridor, which are relatively unpopulated. These areas should be targets for any future microbat surveys in the region. The single occurrence of Finlayson's cave bat, *Vespadelus finlaysoni* south of Burra also warrants future acoustic recording and trapping effort in this area.

This citizen science model incorporated several aspects: engagement with a wide cross-section of the community; easy-to-use, reliable technology; a publicly accessible database; a rapid species identification technique; and timely reporting to the community, land and threatened species manager and policy makers. It has achieved impressive social and scientific impacts, resulting in an increase in awareness of microbats and their habitat needs in this region, and has already lead to on-ground action to aid in bat conservation.

Effort has been made to encourage natural resources management regions further upstream in the Murray-Darling Basin to undertake a similar citizen science approach to acoustics-based surveys for microbats, and now enquiries are being received from them regarding support. In addition, the bat detectors purchased for the project are beginning to find application in smaller efforts for microbat survey and management in other parts of South Australia, such as on Bush Heritage properties and local government projects in the Adelaide area.

2 Background and Objectives

While many small insectivorous mammals in South Australia (SA) have declined or disappeared entirely, an important native mammal group remaining in these ecosystems is bats. The South Australian portion of the Murray-Darling Basin, which extends 640 km from the Victorian border to the Murray mouth at Goolwa, is home to 18 species of insectivorous echolocating bat (hereafter 'microbat'). Of these, four species are listed under SA environmental legislation as Endangered, and one species is listed as Vulnerable under national environmental legislation.

While microbats have not been in a conspicuous decline from feral predators like many other small Australian mammals, they are sensitive to changes in their environment. This is particularly obvious in closed forest habitats in tropical areas where the removal of forest can result in the decline of species that forage within forest interiors (Jones et al. 2003). In this case, preserving forest structure and extent is the best approach for ensuring the persistence of these species. In ecosystems that have been subject to many years of anthropogenic influence, the causes of decline of bat species may be more subtle, and these can be managed more effectively if data exists on current distribution patterns, habitat availability and population levels. Periodic reassessment of conservation status by Department for Environment and Water (DEW) is currently limited by an almost complete lack of current data. There has been scant resources put into microbat survey and management in South Australia, outside of Naracoorte in the South East. However, at a general level, the biodiversity objectives of DEW and Natural Resources South Australian Murray-Darling Basin (Natural Resources SAMDB) aim to increase the resilience of native ecosystems, and ensure native species and ecological communities are not at a greater risk of extinction. This project was a timely solution to data generation of relevance to both bat conservation and land management in one of Australia's most important multi-land use regions.

The continued popularity of bat information nights held previously across the South Australian Murray-Darling Basin region, and nationally with the Bat Night events run by the Australasian Bat Society, demonstrates great interest amongst a large proportion of the community, particularly children. Many people are interested in finding out how they can be involved in protecting or managing our native species and their habitats. A previous small-scale project to engage citizens to assist in the surveying of microbats was begun by Natural Resources South Australian Murray-Darling Basin (SAMDB) in mid-2015, itself building upon a previous smaller community microbat monitoring projects run by Mid Murray Landcare SA and others. This had some success, with large numbers of people attending bat information nights and landholders borrowing 'bat detectors' to make recordings on their property, returning data for entry via an Atlas of Living Australia (ALA) portal. To build on this success, funding was sought from the Australian Government through their Citizen Science Grants, part of the Inspiring Australia – Science Engagement Program, to increase the scale of the project and generate sufficient data that would be useful on a wider-scale for landholders, Landcare groups, and land and threatened species management policy makers. The resulting MEGA Murray-Darling Microbat Project (hereafter the MEGA Microbat Project) was a partnership between the South Australian Museum, Natural Resources SAMDB, the University of South Australia, and Mid Murray Landcare SA.

There were three primary aims to the MEGA Microbat Project:

- Contribute to improved understanding and appreciation of microbats more generally in society by engaging the community in data collection and conservation initiatives on their own land
- Collect new records of occurrence and habitat associations on microbat species across the SA Murray-Darling Basin region to help inform state conservation reassessments and guide decisions effecting conservation of these species across the region
- Promote the program to other regions within Murray-Darling Basin and beyond to increase knowledge of bat distributions, while creating opportunity for community to engage with native fauna and science .

To achieve the project aims, a diverse project management team consisting of staff from the South Australian Museum, Natural Resources SAMDB, University of South Australia and Mid Murray Landcare SA, engaged with Landcare associations, landholders, and other interested community members across the SA Murray-Darling Basin region, to run a broad-scale citizen science survey for microbat species, and evaluate its social impact.

3 Methods

3.1 Data collection

The core activity in the project was an acoustics-based survey for insectivorous microbat species. Microbats can be detected and identified, without the need for capturing them, by recording and examining their echolocation calls. Each species of microbat produces an echolocation call type that is distinct in some way from calls of other species in the same region, though some species have quite similar calls and cannot be separated reliably with current methods. Electronic recorders with a microphone capable of transforming ultrasound (>20 kHz), 'bat detectors', are used to record these signals onto flash memory cards.

A total of 30 Titley Scientific Anabat Swift bat detectors were used in this project. These record high quality 'full spectrum' sound files in WAV format. They can be set to function during night hours only, and trigger recordings only when ultrasonic signals are received by the microphone. This model of bat detector is one of the best devices available currently for making quality ultrasonic recordings, and it allows the data collected in the project to be forwards-compatible with future efforts.

Each of the 30 bat detectors was labelled with a unique, memorable name (a female name beginning with the letter M; in addition to the factory-provided serial number of six digits) to help track units and data across participants. The units were dispersed via seven local Landcare network offices and three Natural Resource Offices. Community participants were initially engaged in the project at Bat Nights held across the region through Landcare organisations (an initiative of the Australasian Bat Society, Inc), as well as through local networks and various media outlets.

When bat detectors were borrowed, participants received instruction on how to use the device, and collect and submit habitat data. Units were deployed by participants for at least one night at a location of their choice. Additional sites could be surveyed if at least 50 metres away. Units were also placed on houseboats and commercial paddleboats as they travelled the lower Murray River.

A comprehensive social evaluation survey was included as part of the project to measure the attitude of people towards microbats and their general knowledge of microbats. This was developed by Dr. Philip Roetman and Dr. Annette Scanlon from the University of South Australia and completed by participants at the beginning of a Bat Night or before borrowing a bat detector. Participants were surveyed again towards the end of the project when they were also asked if they had changed their land management practices or planned to in the future.

3.2 Collecting covariate data on site characteristics

A specially-created BioCollect data portal on the Atlas of Living Australia (ALA), which could be accessed via either a smartphone app or the website, allowed participants to input site information to the database directly in the field. Project officers could also input site data to the website from paper datasheets submitted by participants who chose not to use the app (**Appendix 1**). A site photo was required to be uploaded to the portal, taken in the same direction that the microphone was pointing, which allowed independent verification of site characteristics, if necessary.

To determine characteristics of the habitat at each site that might explain the diversity and composition of microbats, three categorical variables were recorded by participants at the time of the acoustic survey:

Flight space: represented the type of open area in front of the microphone that might be used for foraging by bats, and gives an indication of the spatial structure of the habitat. Categories included:

- DL—over water body (lake, wide river, dam);
- G—house garden;
- IS—windrow / shelter belt or isolated stand of trees;
- OP—open pasture or parkland with no or sparsely scattered trees;
- R—riparian vegetation around watercourse or lake;
- SC—shrubland, vines or orchard (no overstorey above 2 m);
- WL—woodland and forest (overstorey above 2 m).

Open water source: most microbats in South Australia drink from free water sources, so descriptor categories were included for the nearest water source:

- D—dam;
- L—lake;
- MR—Murray River main channel;
- NWS—no significant water sources within 50 m;
- OSF—other river/stream with flowing water;
- OSP—other river/stream with intermittent pools;
- WT—large open water tank accessible to bats;
- W—wetland.

Vegetation type: major vegetation community types were also included:

- CD—coastal dunes in Coorong region;
- DM—dense mallee, broombush and heath shrubland – south of the Murray River;
- ES—estuarine habitat – Lower Lakes and Coorong;
- GZ—grazing land with scattered gum trees – flanks of eastern hills;
- I—irrigated horticulture and dairy farming along the the Murray River;
- MN—mallee north of the Murray River;
- MS—mallee south of the Murray River;
- NG—native grassland, chenopod shrublands;
- OW—open woodlands with open understorey – low rainfall;
- RMC—Murray River corridor floodplains and wetlands;
- SEW—artificially constructed and managed wetlands and sewerage ponds;
- TFD—tall forests and woodlands with dense shrub understorey;
- TFO—tall forests and woodlands with open shrub understorey;
- U—urban areas;
- WCG—wheat/cropping/grazing land interspersed with mallee – south and west of Murray River.

3.3 Call identification and verification methods

Microbat species were identified in the recordings by comparing the signal structure of recorded echolocation calls, as viewed in a spectrogram, with reference calls collected from South Australia (including one field trip to Chowilla in February 2018) and Victoria (as provided by Dr L. Lumsden, Arthur Rylah Institute, Victoria). Manual inspection

of every sound file is not expedient for datasets that are many gigabytes in size, so a semi-automated analysis method was provided to non-specialists with some previous experience in bat call analysis (The non-specialists were Aimee Linke, Jacqui Wilson, Martin Philcox) to process the recordings efficiently.

This multi-step analysis procedure was adapted from a method developed to process large full spectrum echolocation recording datasets from uncharacterised assemblages of insectivorous bats from Indochina through to New Guinea and northern Australia (Armstrong and Aplin 2014a; Armstrong et al. 2016), which has been the basis of many commercial biodiversity surveys (K.N. Armstrong unpublished reports), as well as several large-scale surveys for conservation organisations (Armstrong and Aplin 2011, 2014b; Armstrong et al. 2015a,b). The MEGA Microbat Project utilised freeware in the process rather than commercial software to make the process available at no cost.

Data was first downloaded from SD memory cards and tracked by recording unit. The detectors organise the WAV recordings into nightly subfolders to assist analysis. These WAV files were loaded into Titley Scientific Anabat Insight freeware (various versions were used during the project as the software was improved by the developers). Once a directory of subfolders from a single unit was loaded, an automated process was used to recognise putative bat pulses and tabulate several measurement parameters from each of these signals. The output from Insight was a large CSV file that tracked WAV filename against numerous measurements for each putative bat pulse.

The file of measurements was run through a process that helped determine if any of the signals could be attributed to one or more species of bat. This was done using a novel 'shiny' app written in the [R] statistical computing language ('SZapp'; screenshot in **Figure 1**). The app allowed the analyst to step through three main tasks:

1. Undertake a Discriminant Function Analysis (DFA) on training data from reference calls from South Australia and Victoria. This analysis maximised separation of clusters of points representing calls from each species, and placed an elliptical confidence region around each cluster (one standard deviation in size);
2. From the measurements of each putative bat pulse from Insight, calculate values for the first two Discriminant Functions that could separate the echolocation call types derived from the analysis of training data, and plot these resulting coordinates over confidence regions for the defined call types; and
3. Check a spectrogram of multiple examples of each call type for each recording night against a reference spectrogram by providing an efficient way to select and open original WAV files containing pulses of interest in Audacity version 2.3.0.

This process enabled verification of the presence of calls from each species that was shown to be present using the DFA, since non-target signals often fall out within species confidence regions. One night of data could be analysed in approximately 10–15 minutes compared to one hour needed when using manual techniques, which was a significant saving of time.

The Snipping Tool in Microsoft Windows was used to save screenshot examples of each species recorded at a site. Verification of some of the more challenging species to distinguish was provided by a person experienced with South Australian bat calls (This was Dennis Matthews).

The resulting species list from each survey night was matched to field site data and uploaded to BioCollect. Screenshot spectrogram examples were also with the identifications and site data to allow a level of verification of the identifications at a later date if needed. This data is available for public viewing and download. The compiled information is consistent with the recommendations for presenting the results of acoustic surveys for bats (ABS 2006).

Species lists were returned to individual participants through Landcare officers, along with an information brochure on how private lands could be modified to promote sustained or increased usage by bats. A newsletter summarising overall results was also distributed periodically at events.

The bulk raw recordings are backed up both on SD cards, external hard drives and a local server at the Mt Barker Natural Resources Office.

A manual that steps through the analysis process in more detail has been produced to allow other regions around the Murray-Darling Basin to use the same expedient process on their own bat assemblage.

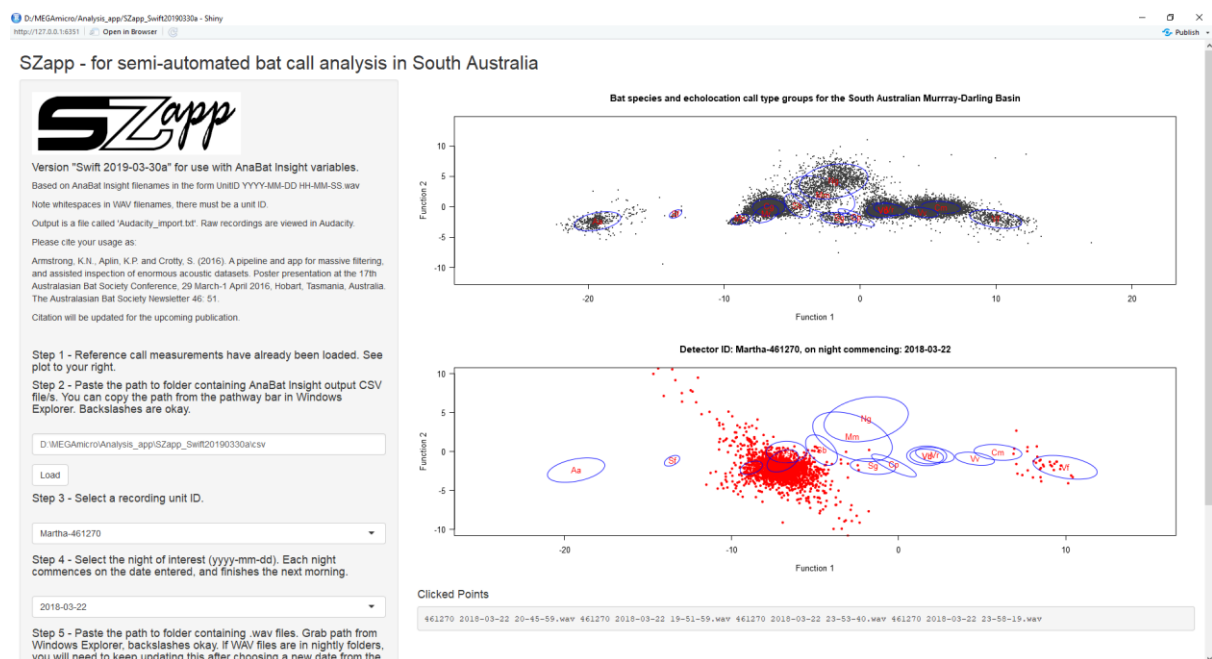


Figure 1. A screenshot of the [R] language 'shiny' app called 'SZapp', showing some of the steps on the left side, a Discriminant Function Analysis plot of reference call data at the top, and a second plot below showing a single night's data. Analysts would select red dots representing individual signals inside the blue confidence ellipses for species. The list of associated WAV files is listed below under 'Clicked Points', and these are then opened in the software Audacity to verify that at least one representative point inside an ellipse is attributable to the species.

3.4 Analysis of species occurrence data

The full dataset consisting of species records and associated site information collected over the two seasons of the project (2018–2019) was downloaded from BioCollect on 2019-06-24.

This comprised 3,042 entries (796 deployment sites, 290 recording nights), which was reduced to 3,000 records (754 deployment sites, 284 recording nights) following the removal of uninformative entries with no microbat species data. Other records of microbat species distributed across South Australia were downloaded from the Atlas of Living Australia on 29-06-2019. There were 2,693 records of bat species within the SAMDB NRM region, representing preserved specimens in museums and direct observations without an associated specimen, with records extending between 1890 and 2018.

Plotting geographic distribution of recording sites and species occurrences was undertaken in Quantum GIS version 3.4.9-Madeira software. Summaries and statistical analyses of the BioCollect and ALA datasets were performed in a script in the [R] language (all code is reproduced in **Appendix 2**).

Analyses were undertaken to summarise microbat species richness in the region. To help understand which types of habitat supported microbats, the habitat was categorised in three different ways—according to vegetation type, the presence of water, and whether the microphone faced open areas, water or vegetation. Microbat species richness was compared amongst the category levels. The composition of the microbat species assemblage was also compared amongst recording sites and habitat categories using multivariate ordination (Non-metric Multi-Dimensional Scaling; NMDS).

4 Results

4.1 Participation by citizen scientists

Over 300 people attended bat information nights across the region to learn about their local microbat species.

Two hundred and fifteen pre-involvement social surveys were completed and 54 post-involvement surveys, including 35 that were able to be matched. Of these, 31% respondents had a higher opinion of microbats after the project and 66% were unchanged. The 'bat acceptance capacity', their willingness to live with microbats, did not change but was quite high to start with among respondents. The most common reason that people gave for their involvement in the project was because native wildlife and conservation were important to them.

Thirty eight respondents (70%) of the post-survey respondents (n=54) indicated that they were likely to do things differently on their property to support wildlife since participating in the project. Results indicate that some activities are more likely to be enacted than others:

- Promote tree hollows, bark crevices, or bird/bat boxes (85% of respondents)
- Protect scattered native trees (including dead trees) (80% of respondents)
- Protect a block of native remnant vegetation (including nearby to your property) (78% of respondents)
- Use land management practices for healthy trees (76% of respondents)
- Plant re-vegetation areas (67% of respondents)
- Reduce pesticide/herbicide use (65% of respondents)
- Manage watercourses and/or dams (56% of respondents)
- 21 respondents (39%) of the post-survey respondents (n=54) indicated that, since participating in the project, they have already changed how they look after or manage their property.

Eighteen respondents (33%) described how they have changed how they look after or manage their property (since participating in the project):

- Planting (7 respondents – 13%)
- Protecting existing trees (including dead trees) (7 respondents – 13%)
- Installing nest boxes (6 respondents – 11%)
- Cease or reduce pesticide/herbicide use (2 respondents – 4%)
- Addition of water source (2 respondents – 4%)

The following feedback was commonly received by participants:

- "Fantastic initiative that allowed families to undertake exciting survey work in their own backyards, great for involving children and spreading the fascination for nature conservation. Brilliant community involvement initiative and look forward to more."
- "Very enjoyable and very encouraging to see our revegetation efforts resulting in such a diversity of bat species"
- "The follow-up letter with information about the specific types of bats identified on our property was very interesting."

Community participants who undertook acoustic surveys showed a demographic diversity of ages and gender. They included urban and rural individuals, and families interested in learning about microbats in their backyard; volunteer groups such as Paiwalla Wetland Trust and North Calperum Volunteers who will add the microbat survey results to a suite of other ecological monitoring they undertake; and horticultural properties with an interest in microbats as a biological control for insect pests.

A National Science Week event was held in Murray Bridge in August 2019 to thank all the participants, promote the results of the project, and release the public report. This was attended by approximately 80 participants and members of the public. Six SAMDB Citizen Science Awards for Outstanding Achievement were awarded to volunteer groups and individuals who had shown above average levels of participation in the project by undertaking multiple surveys and/or assisting with species identification.

A total of 158 citizen scientist individuals are listed as contributing to the BioCollect database as part of the project. The number of records collected in the two survey seasons was significantly greater than all other efforts represented on the Atlas of Living Australia since 1890 (3,000 at 754 unique sites versus 2,693 records) (**Figure 2**).

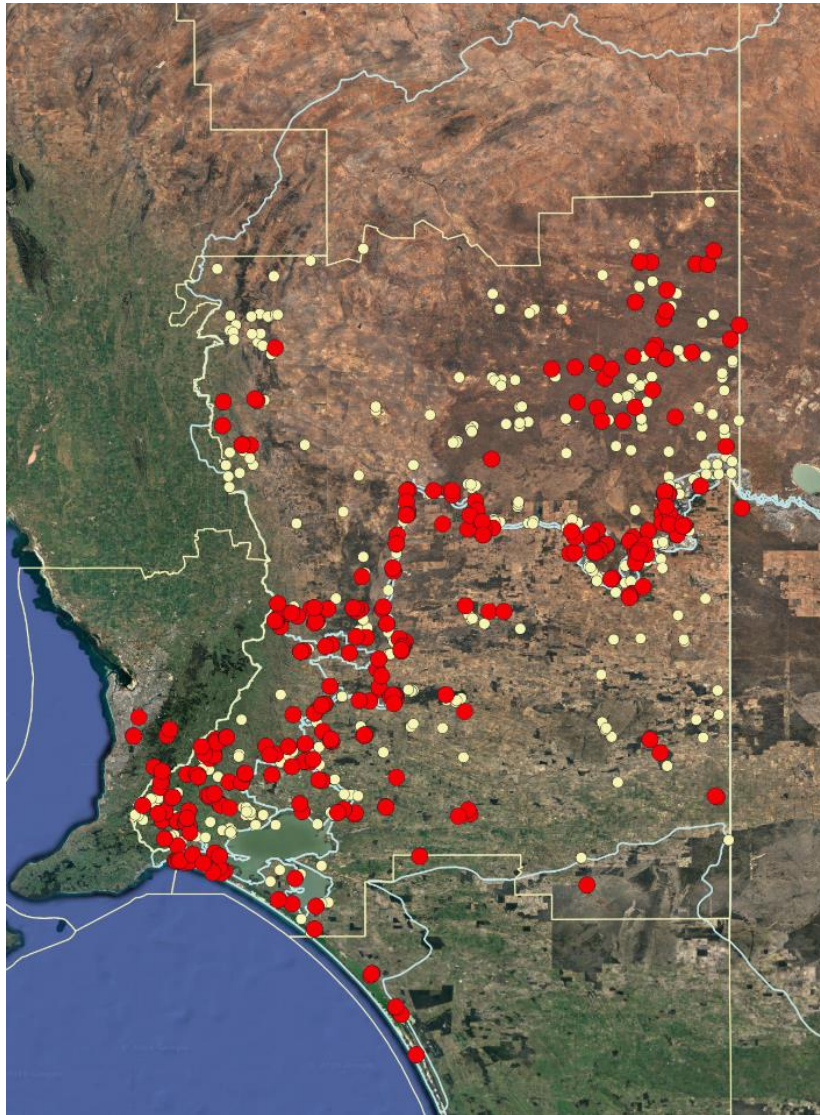


Figure 2. All microbat species occurrence records. Yellow dots are records in ALA up to June 2019 (data from this project was not yet part of official ALA records); red dots overlain are records from the MEGA Microbat Project; yellow outline represents NRM regional boundaries; blue outline is the Murray-Darling Basin boundary, and the Murray-Darling River system in the centre of the region.

4.2 Species occurrence records

The survey produced records of 12 species, plus another three call types that each probably represent more than one species (long-eared bats *Nyctophilus corbeni* and *N. geoffroyi*; evening bats *Vespadelus baverstocki*, *V. darlingtoni* and *V. regulus*; free-tailed bats *Ozimops petersi* and *O. planiceps*) (**Table 1**). Species were lumped into call types if the elliptical confidence regions (68%, or one standard deviation) from the Discriminant Function Analysis overlapped significantly, and there were no characters evident in the spectrograms of the original recordings that allowed unambiguous separation of the candidate species. The distribution of records for each species is summarised in **Figure 3**.

Only three species of echolocating microbat known from the region were not detected unambiguously on the survey—the yellow-bellied sheath-tailed bat *Saccolaimus flaviventris*, little broad-nosed bat *Scotorepens greyii*, and southern bent-winged bat *Miniopterus orianae bassanii*, which were all rare occurrences in the past.

Species records of note are:

- Four locations along the main channel of the Murray River for the large-footed Myotis, *Myotis macropus*.
- A single occurrence of *Vespadelus finalysoni* near Burra
- A single location for *Scotorepens balstoni* was identified north of the Murray River with high confidence

The large-footed Myotis *Myotis macropus*, which is listed as Threatened under South Australian environmental legislation, was only observed foraging over the main channel of the Murray River. These records were collected from a houseboat travelling up and down the river. Low confidence identifications were made elsewhere (Adelaide Hills, Goolwa), where confusion with other calls types such as a species of long-eared bat *Nyctophilus* spp. could not be ruled out. This has extended the known range of *M. macropus* in the lower Murray River and provides the basis for suggesting the presence of roosts not yet discovered.

Some species may be distributed more widely than they appear in the mapped results (**Figure 3**). Due to their calls being effectively indistinguishable from other species, their presence has likely been underestimated. These include: long-eared bats *Nyctophilus corbeni* and *N. geoffroyi*, evening bats *Vespadelus baverstocki*, *V. darlingtoni* and *V. regulus*; free-tailed bats *Ozimops petersi*, *O. ridei* and *O. planiceps*. It can also be difficult to distinguish calls of the inland broad-nosed bat *Scotorepens balstoni* from the higher frequency examples of Gould's wattled bat *Chalinolobus gouldii*.

Most microbat species showed a strong preference for watercourses, particularly the Murray River and its riparian habitats. Some such as *M. macropus* seemed not to occur outside the river corridor. These species are most vulnerable to changes in their habitat, but all species appear to have a strong dependence on the river corridor and/or other significant water bodies.

Some species appear to be relatively restricted in their distribution. In addition to *M. macropus*, a conspicuous example is the large forest bat *Vespadelus darlingtoni*. It was observed at only three locations: Keyneton/Sedan, Mannum and Nangkita.

Table 1. Total records for each species from the two database sources.

	ALA ^a	MEGA ^b
EMBALLONURIDAE Sheath-tailed bats		
<i>Saccolaimus flaviventris</i> Yellow-bellied Sheath-tailed Bat	5	0
VESPERTILIONIDAE Evening bats		
<i>Chalinolobus gouldii</i> Gould's Wattled Bat	625	626
<i>Chalinolobus morio</i> Chocolate Wattled Bat	242	198
<i>Chalinolobus picatus</i> Little Pied Bat	26	12
<i>Myotis macropus</i> Large-footed Myotis (=Fishing Bat)	26	4
<i>Nyctophilus corbeni</i> Corben's Long-eared Bat	56	0
<i>Nyctophilus geoffroyi</i> Lesser Long-eared Bat	434	302
<i>Scotorepens balstoni</i> Inland Broad-nosed Bat	38	1
<i>Scotorepens greyii</i> Little Broad-nosed Bat	1	0
<i>Vespadelus</i> spp. evening bats	78	473
<i>Vespadelus darlingtoni</i> Large Forest Bat	53	^c
<i>Vespadelus regulus</i> Southern Forest Bat	88	^c
<i>Vespadelus baverstocki</i> Inland Forest Bat	192	^c
<i>Vespadelus finlaysoni</i> Finlayson's Cave Bat	1	1
<i>Vespadelus vulturnus</i> Little Forest Bat	105	316
MINIOPTERIDAE Bent-winged bats		
<i>Miniopterus orianae bassanii</i> Southern Bent-winged Bat ^d	1	0
MOLOSSIDAE Free-tailed bats		
<i>Austronomus australis</i> White-striped Free-tailed Bat	114	485
<i>Ozimops petersi</i> Inland Free-tailed Bat	64	2
<i>Ozimops planiceps</i> Southern Free-tailed Bat	417	521
<i>Ozimops ridei</i> Ride's Free-tailed Bat	30	59
Total records	2,591^a	3,000
Total Species Richness	19	up to 15

^a ALA—Atlas of Living Australia records 1890–2018; 105 records attributed to genus only were removed. Also removed were records for *Pteropus poliocephalus*, and questionable records for *Macroderma gigas*, *Nyctophilus bifax*.

^b MEGA—MEGA microbat project BioCollect records;

^c Lumped as *Vespadelus* spp.

^d *Miniopterus orianae bassanii* is present on the ALA database as *M. schreibersii*.

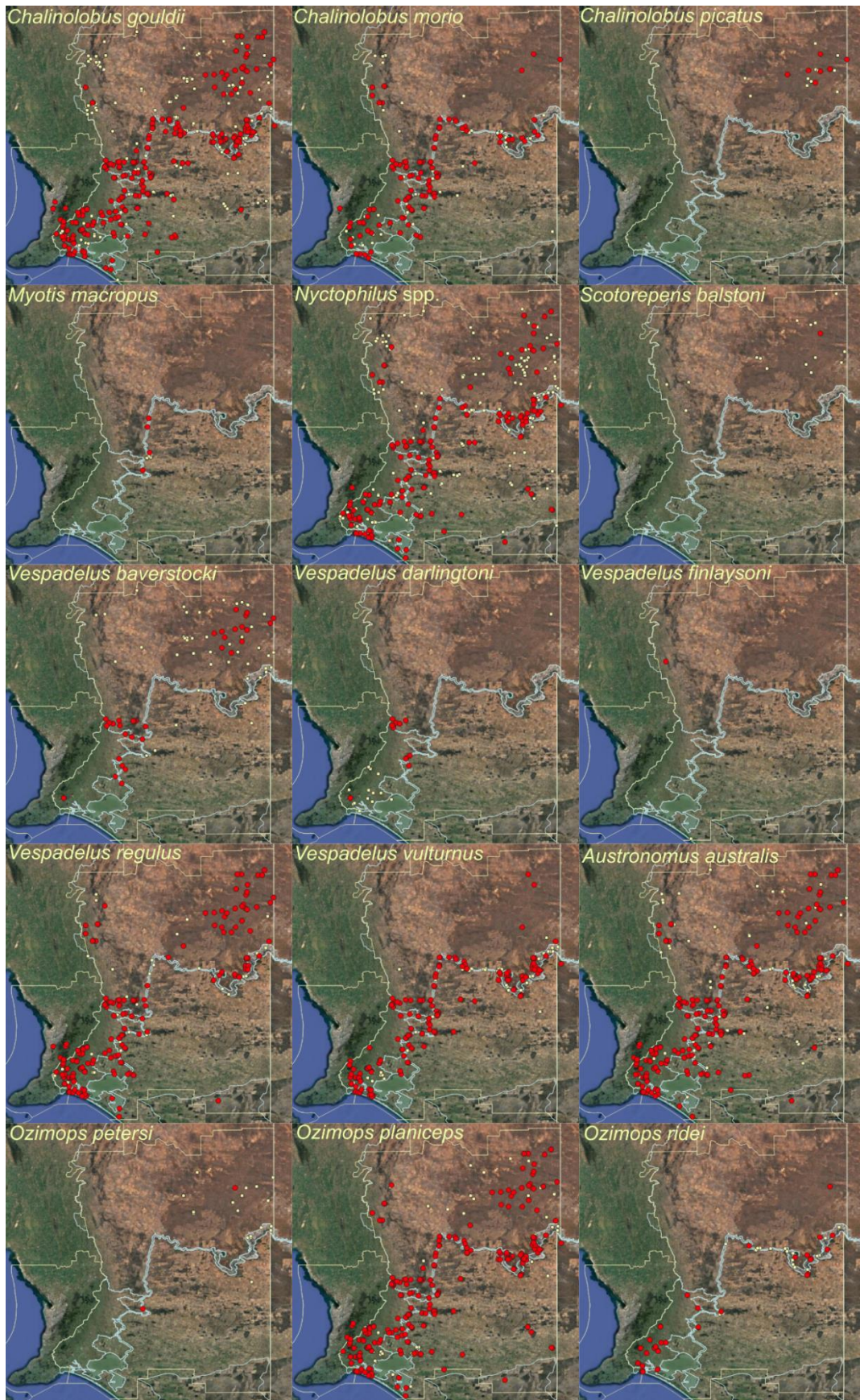


Figure 3. Summary of occurrence records for all bats detected on the MEGA Microbat Project. Yellow dots – historical ALA records, red dots – records from MEGA Microbat Project.

4.3 Species composition

A Non-Metric Multidimensional Scaling (NMDS) analysis was performed to group recording sites based on the similarity of their bat species. The model failed to converge after 20 iterations, and there was no obvious pattern in species composition according to any habitat category (**Figure 4**). This suggested that microbat assemblages across the lower (South Australian) Murray-Darling Basin have a similar composition of species, with no grouping of species according to habitat characteristics such as openness or vegetation type.

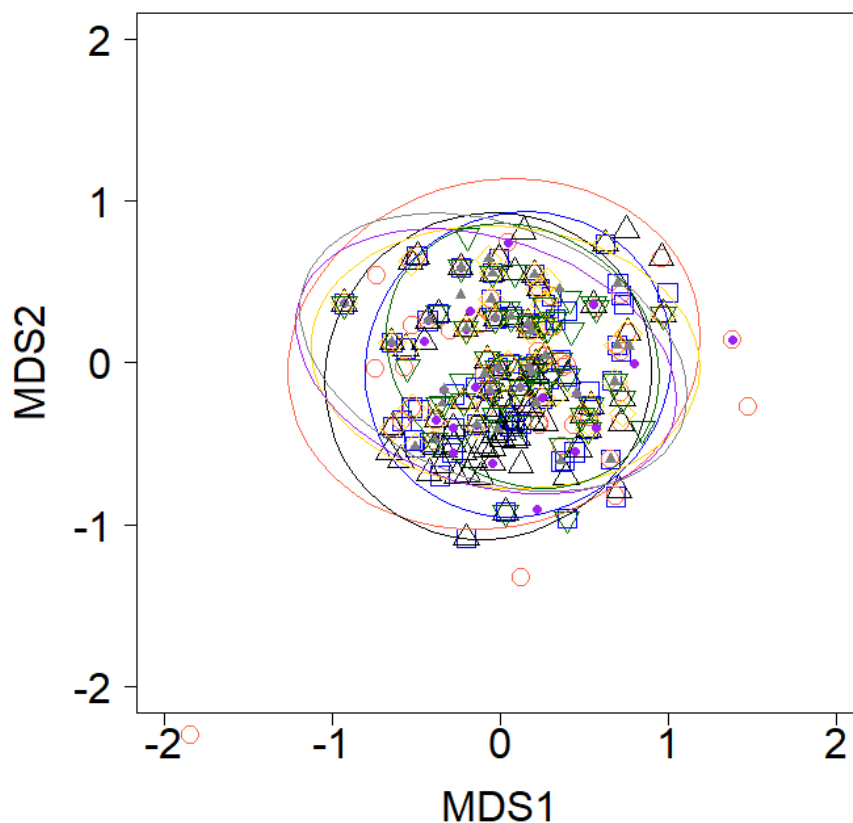


Figure 4. Non-Metric Multidimensional Scaling (NMDS) multivariate analysis was performed to group recording sites based on the similarity of their bat species. In this example, colours represent the different flight spaces.

4.4 Patterns of species richness in different habitat categories

4.4.1 Flight space

The flight space descriptor represents the type of open area in front of the microphone that might be used for foraging by microbats, and gives an indication of the spatial structure of the habitat. The species richness amongst the flight space categories was similar, with most habitats having four species on average (**Figure 5**). The open spaces above dams and lakes (DL), and riparian zones (R) tended to support more species, around five on average, but up to a maximum of eight species. Thus, not only was species composition generally similar across habitats, but the average number of species that could be detected was also similar.

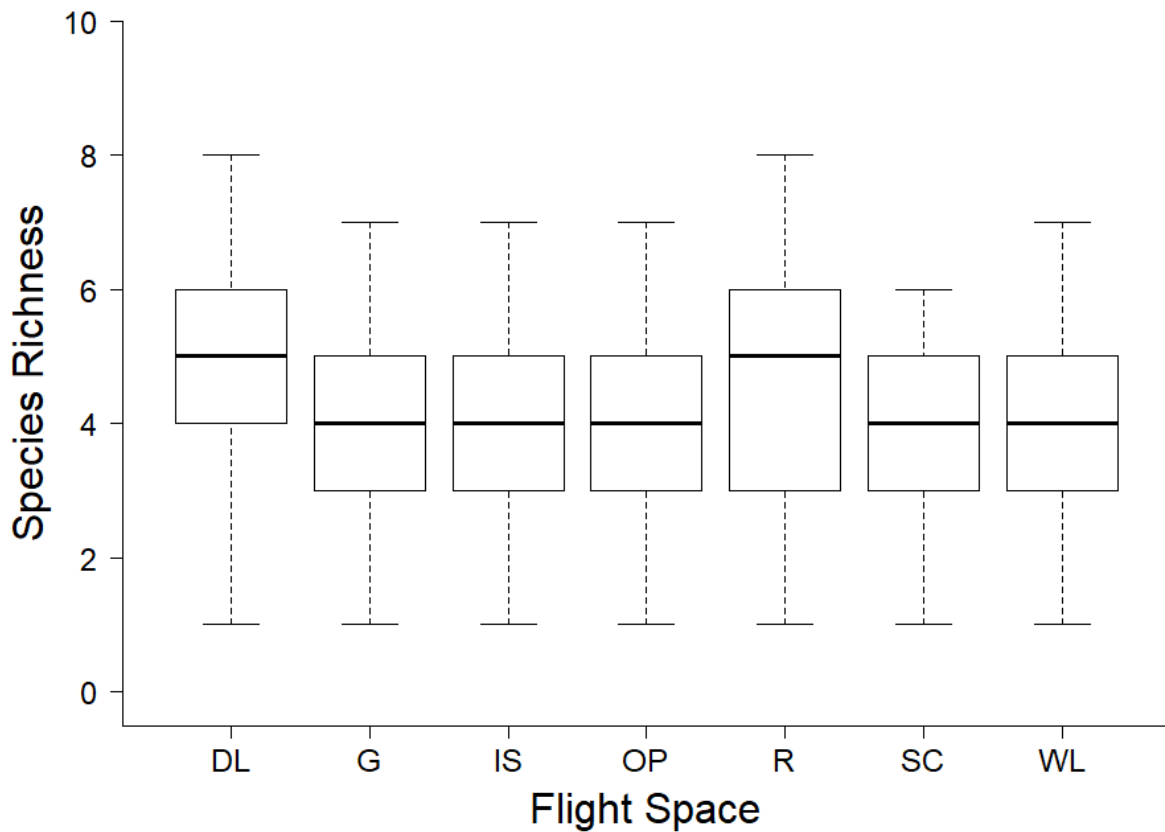


Figure 5. Patterns of species richness amongst the flight space categories (number of surveys for each type in square braces; DL—over water body (lake, wide river, dam) [405]; G—house garden [595]; IS—windrow / shelter belt or isolated stand of trees [206]; OP—open pasture or parkland with no or sparsely scattered trees [266]; R—riparian vegetation around watercourse or lake [599]; SC—shrubland, vines or orchard (no overstorey above 2 m) [194]; WL—woodland and forest (overstorey above 2 m) [777]). [Boxplot components: central bar—median; boxes—inter-quartile range, with second quartile group below median, third quartile group above median; bars—minimum and maximum values; circles—outliers]

4.4.2 Open water sources

Given that most bats in South Australia drink from free-water sources, descriptor categories were included for the nearest water source. The type of open water source closest to the recording site appeared to have a slight influence on bat species richness. The highest tallies (mean five species) were in the main channel of the Murray River (MR), over streams with intermittent pools (OSP), and wetlands (W). Large open water tanks had the lowest diversity of bats (**Figure 6**). The productivity of insect prey is also probably greater in habitats associated with large bodies of water.

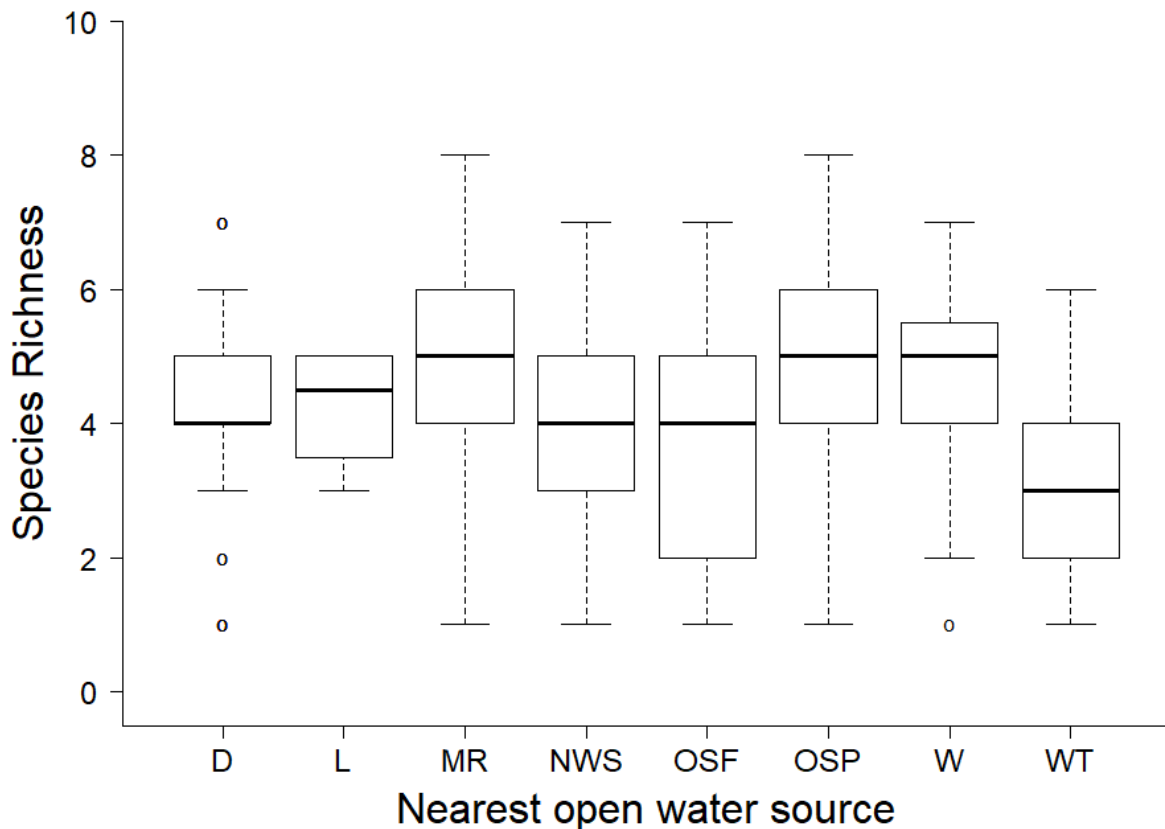


Figure 6. Patterns of species richness amongst the open water source categories (number of surveys for each type in square brackets; D—dam [253]; L—lake [34]; MR—Murray River main channel [530]; NWS—no significant water sources within 50 m [1,584]; OSF—other river/stream with flowing water [126]; OSP—other river/stream with intermittent pools [280]; WT—large open water tank accessible to bats [47]; W—wetland [188]).

4.4.3 Vegetation type

Descriptor categories for major vegetation community types were included to determine if these were a controlling factor for microbat species richness. Most vegetation types appeared to be relatively similar for microbat species richness (**Figure 7**). However, it was clear that tall forests and woodlands with a dense shrub understorey had the highest diversity of bats, with most of these sites having six species, and some having up to seven species. This shows clearly that forests and woodlands are important for bats. The Murray River corridor, which contains both riparian vegetation and flight spaces over water, also had relatively high numbers of bat species. This is probably related to the productivity of this vegetation type in terms of providing insect food, and different types of flight space available to accommodate a range of bat foraging strategies.

Of interest is the relatively high species richness in native grassland and chenopod shrublands vegetation communities, as well as grazing land with scattered gum trees on the eastern flanks of hills. While such vegetation types do not provide as many flight spaces as forests, woodlands and riparian zones, it does suggest that they are productive and provide foraging opportunity for microbats.

It is notable also that highly modified landscapes supported a mean of four species of bat—at least for foraging. This included people’s backyards (U—urban areas), as well as wheat/cropping/grazing land interspersed with mallee south and west of the Murray River. Microbats are clearly able to use a range of habitats in the SAMDB region, and

almost the same level of bat diversity is present in highly modified landscapes as the more intact forested landscapes.

Those vegetation types with the lowest species richness values (DM—dense mallee, broombush and heath shrubland south of River Murray; SEW—artificially constructed and managed wetlands and sewerage ponds) had relatively low sampling effort.

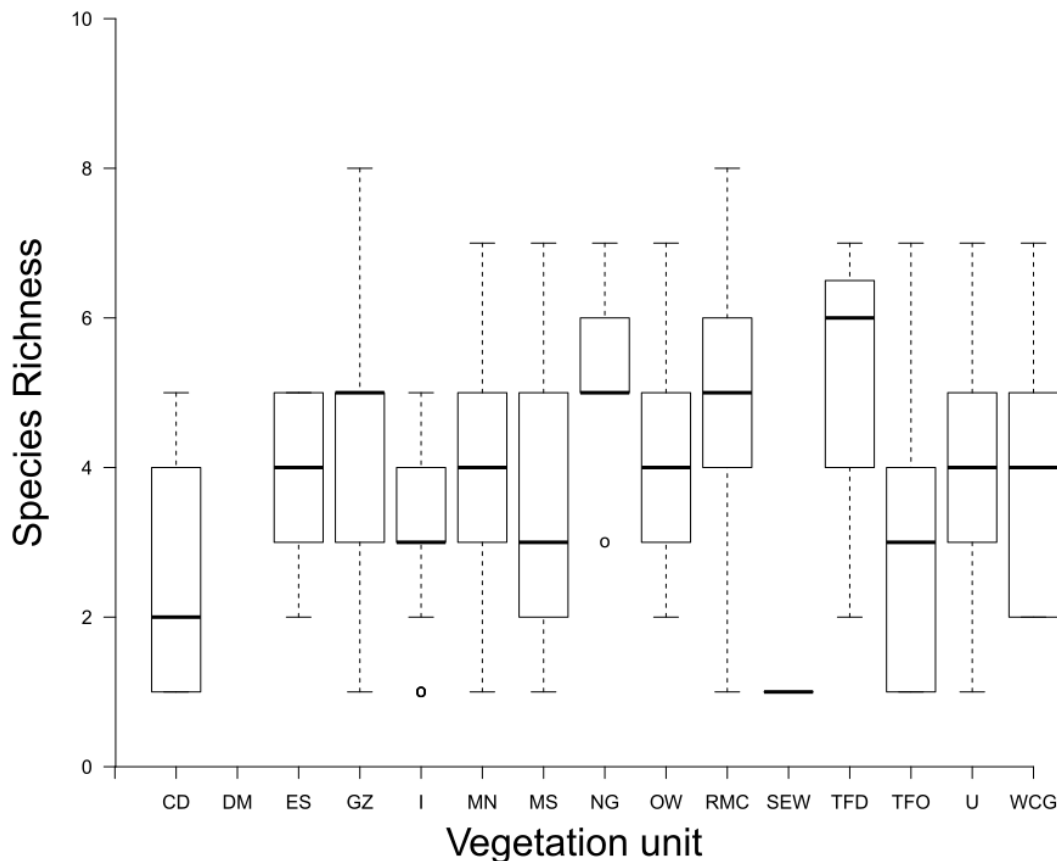


Figure 7. Patterns of species richness amongst the vegetation community categories (number of surveys for each type in square brackets; CD—coastal dunes in Coorong region [28]; DM—dense mallee, broombush and heath shrubland – south of the Murray River [1]; ES—estuarine habitat – Lower Lakes and Coorong [41]; GZ—grazing land with scattered gum trees - flanks of eastern hills [381]; I—irrigated horticulture and dairy farming along the Murray River [97]; MN—mallee north of the Murray River [424]; MS—mallee south of the Murray River [174]; NG—native grassland, chenopod shrublands [37]; OW—open woodlands with open understorey – low rainfall [176]; RMC—the Murray River corridor floodplains and wetlands [672]; SEW—artificially constructed and managed Wetlands and sewerage ponds [1]; TFD—tall forests and woodlands with dense shrub understorey [16]; TFO—tall forests and woodlands with open shrub understorey [116]; U—urban areas [322]; WCG—wheat/cropping/grazing land interspersed with mallee – south and west of Murray River [96]; habitat not recorded—460).

4.4.4 Habitat faced by the microphone

It is interesting to consider if the microphone placement affected the likelihood of detecting bats. Microphones placed in thick vegetation probably have a slightly reduced detection volume compared with those facing open spaces because of acoustic reflections away from the microphone. There was no detectable difference in the mean

number of species detected by microphones facing into vegetated areas compared with those facing wide open spaces (**Figure 8**), indicating that detectability in the different habitats was probably equivalent. However, it was clear that more bats species were present in habitats that had large open water sources and presumably larger insect productivity.

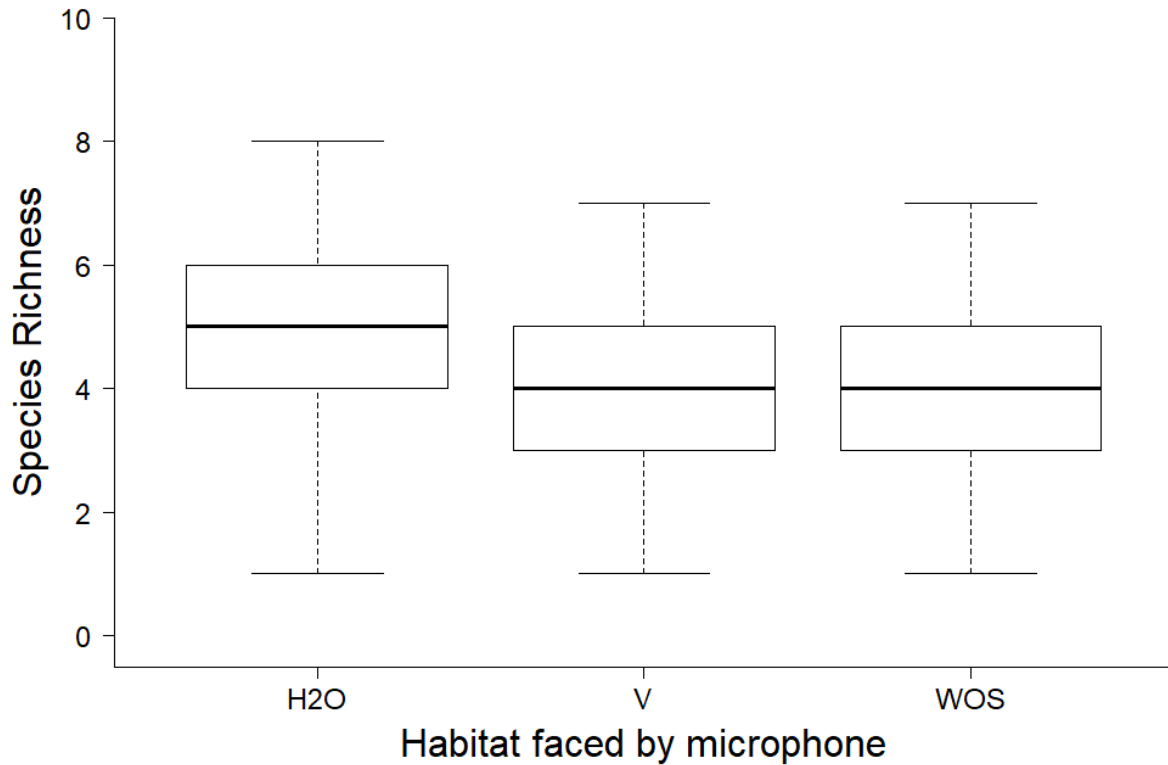


Figure 8. Patterns of species richness amongst the categories for microphone placement (number of surveys for each type in square brackets; H2O—pointing directly over water [698]; V—pointing into vegetation or gaps between vegetation nearby [1,497]; WOS—pointing into wide open space [847]).

4.4.5 Indicator species

The indicator species index (Dufrene and Legendre 1997) is calculated using presence/absence data and is similar to relative abundance, but highlights the association of each species with particular habitats. Species found in many habitat types tend to have low scores, and those with higher scores may have a specialist requirement for that particular habitat. In the present study, the measure allows comment on which species may be negatively or positively affected by modifying the original native vegetation, or that may show a particular preference for one type of habitat. In this case, we used flight space categories to represent the broad structural habitats that bat species used.

The indices show a pattern that suggests most bat species did not have a strong preference for or against certain habitats, modified or otherwise (**Figure 9**). However, it was clear that the chocolate wattled bat *Chalinolobus morio*, large-footed Myotis *Myotis macropus*, and the little forest bat *Vespadelus vulturnus* had an obvious preference for foraging over large water sources and riparian habitats compared with drier habitats. Other species of *Vespadelus* and the little pied bat *Chalinolobus picatus* had a clear preference for woodland habitats.

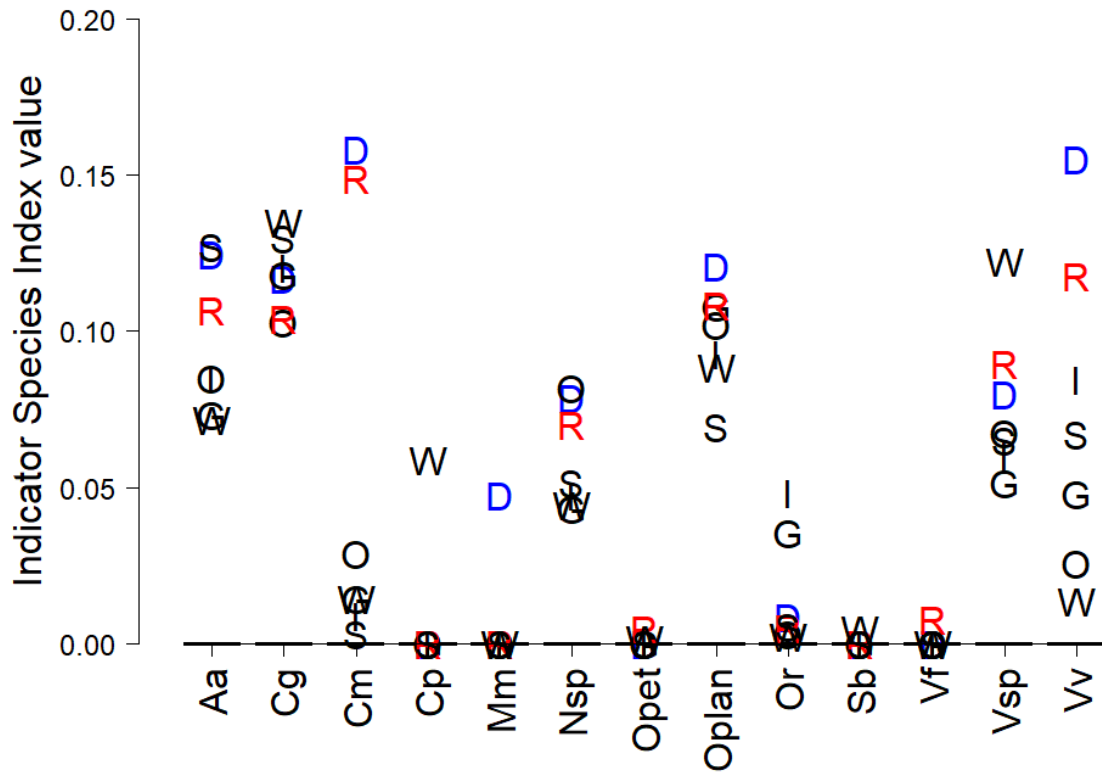


Figure 9. Indicator species indices for each species, in each flight space (see symbology below). Coloured symbols are those of most interest, particularly the relatively high values suggesting a positive association of *Chalinolobus morio* and *Vespadelus vulturnus* over large water bodies and in riparian zones. Modified flight space symbols on the plot are: D—over water body (lake, wide river, dam); G—house garden; I—windrow / shelter belt or isolated stand of trees; O—open pasture or parkland with no or sparsely scattered trees; R—riparian vegetation around watercourse or lake; S—shrubland, vines or orchard (no overstorey above 2 m); W—woodland and forest (overstorey above 2 m). Species are: Aa—*Austronomus australis* white-striped free-tailed bat; Cg—*Chalinolobus gouldii* Gould's wattled bat; Cm—*Chalinolobus morio* chocolate wattled bat; Cp—*Chalinolobus picatus* little pied bat; Mm—*Myotis macropus* large-footed Myotis; Nsp—*Nyctophilus corbeni* / *Nyctophilus geoffroyi*; Opet—*Ozimops petersi* inland free-tailed bat; Oplan—*Ozimops planiceps* southern free-tailed bat; Or—*Ozimops ridei* Ride's free-tailed bat; Sb—*Scotorepens balstoni* inland broad-nosed bat; Vf—*Vespadelus finlaysoni* Finlayson's cave bat; Vsp—*Vespadelus baverstocki* / *Vespadelus darlingtoni* / *Vespadelus regulus*; Vv—*Vespadelus vulturnus* little forest bat.

5 Conclusions and Management Suggestions

The overall biological outcome from the MEGA Microbat Project is evidence of a species-rich assemblage of microbats that still exists through the Murray-Darling Basin in South Australia (**Figure 2**).

Most microbat species were present throughout the range of broad habitat types in the region, and any one recording site had four species present on average. This finding was communicated to the community via stickers and a fridge magnet with the theme: "Bats are everywhere (except Antarctica)" (**Figure 10**).



Figure 10. A fridge magnet given to participants.

The habitats that appeared to provide more resources for bats were tall forests and woodlands, which had six species on average, and the Murray River corridor that had five species on average at any one site. These habitats offer roost sites in the large old trees and a variety of insects for food, and should be a priority for protection and effective management.

Modified landscapes such as urban gardens, cropping paddocks and grazing land supported an average of four bat species, which was often a source of surprise for participants. We were able to reinforce a message that there is a largely intact assemblage of microbats still present in areas where human habitation has encroached on native habitats.

When results were communicated to participants, along with detailed information on each of the species, a message (as a brochure) was given that was designed to empower and inform the person to undertake conservation-related effort on their own land. It was communicated that everyone can help microbats to persist and flourish by protecting their habitat (maintaining large trees, promoting understorey growth for native insect prey, and water sources) and keeping cats inside, especially at night.

Some of the observations for individual microbat species were particularly informative in the context of their management and conservation. The survey extended the known range of the large-footed Myotis, *M. macropus* in the lower Murray River, which is listed as Threatened under South Australian environmental legislation, and provided the basis for suggesting the presence of roosts not yet discovered. The survey also improved

understanding of the distribution of some other species, including the large forest bat *Vespadelus darlingtoni* that appears to have a restricted distribution, and confirmed the persistence of other listed species such as the little pied bat *Chalinolobus picatus* which appears to be closely affiliated with the presence of woodland in the arid rangelands areas. These results are available to inform state conservation status reassessments of microbat species, especially with regard to current population extents in the lower Murray-Darling Basin.

Management of vegetation remnants should take into consideration that microbats still exist in these areas, and their roosting and food resources need to be maintained consistently for them to persist. Fire management is particularly relevant, since high fire frequency and intensity can remove the largest and oldest trees that are more likely to provide roosting opportunity in hollows and under exfoliating bark. Management of vegetation remnants can also consider practices that maintain the diversity and cover of the understorey plant community, which provides abundant insect prey resources for bats. Fencing remnant vegetation and wetland areas against intrusion by stock will also maintain the plant understorey and the quality of freshwater resources.

There are obvious spatial gaps in sampling to the north-west and south-east of the Murray River corridor, which is unsurprising since these areas are relatively unpopulated. These areas should be targets for future sampling. The South Australian Museum has close ties with the University of Adelaide, and it is anticipated that the MEGA Microbat Project will be the foundation for several student projects that could examine ecological and bioacoustics processing questions stemming from this project in the near future. Natural Resources SAMDB plans to run another extensive citizen science microbat survey in a couple of years' time to look for any trends and engage more of the community.

This citizen science model incorporated several aspects: engagement with a wide cross-section of the community; easy-to-use, reliable technology; a publicly accessible database; a rapid species identification technique; and timely reporting to the community, land and threatened species managers and policy makers. It has achieved impressive social and scientific impacts. It has resulted in an increase in awareness of microbats and their habitat needs in this region and has already led to on-ground action to aid in their conservation.

This project has demonstrated that the community in this region is generally interested in microbats and many are more than willing to be part of conservation efforts by changing their land management practices to improve available habitat. The fact that being involved in this project has prompted people to act (enact positive behaviours that promote microbat conservation) is a powerful outcome. It is very likely that a similar result would be realised in other regions of the Murray-Darling Basin.

Effort has been made to encourage natural resources management regions further upstream in the Murray-Darling Basin to undertake a similar citizen science approach to acoustics-based surveys for microbats, and now enquiries are being received from them regarding support. All techniques and templates used in this project, including the BioCollect database and technical manual, are freely-available for others to use. The Mallee Catchment Management Authority in Victoria will be using this citizen science model to undertake microbat surveys in their region over the summer of 2019–2020. In addition, the bat detectors purchased for the project are beginning to find application in smaller efforts for bat survey and management in other parts of South Australia, such as on Bush Heritage properties and local government projects in the Adelaide area. An opportunity may also exist in Fiji.

6 Acknowledgements

This project would not have been possible without...

- Our Very Important Participants (VIPs)
- Project Team – Dr. Kyle Armstrong & Professor Steve Donnellan (South Australian Museum), Dr. Sylvia Clarke (Natural Resources SA Murray-Darling Basin, Dept. Environment & Water), Aimee Linke (Mid Murray Landcare SA), Dr. Philip Roetman & Dr. Annette Scanlon (University of South Australia), & Jacqui Wilson (Goolwa to Wellington LAP).
- Landcare Officers – Berri Barmera Landcare, Coorong Tatiara LAP, Eastern Hills & Murray Plains Catchment Group, Murray Mallee LAP, Renmark Paringa LAP, Riverland West Landcare.
- Special Others – Terry Reardon, Dennis Matthews, Chris Grant, Matthew Humphrey and Martin Philcox.
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8 Appendix 1 - Datasheet

Property and Site Information



This form is to be completed for all bat monitoring.
Please fill in a separate sheet for each site and night of recording.

The MEGA Microbat Project is a collaborative initiative of the South Australian Museum, South Australian Murray-Darling Basin Natural Resources Management Board, Mid Murray Landcare South Australia, and the University of South Australia to engage with Landcare associations, landholders, land managers, and other interested community members within the Murray-Darling Basin region to collect information on microbats!

Microbats are a MEGA-important part of our environment, but little is known about them in the Murray-Darling region

Any technical issues with using the equipment please call your local officer or Mid Murray Landcare SA Aimee Linke 0427 590 344 or Natural Resources SA Murray-Darling Basin Sylvia Clarke 0428 743 487

Name:		Site Name:	
Date:		Unit Name:	
Contact Number:		GPS location/street address:	
Bat Flight Space (choose one) <input type="checkbox"/> Open pasture or parkland with no or sparsely scattered trees <input type="checkbox"/> Windrow/Shelter Belt or isolated stand of trees <input type="checkbox"/> House Garden		<input type="checkbox"/> Shrubland, vines or orchard (no overstorey above 2m) <input type="checkbox"/> Woodland & forest (overstorey above 2m) <input type="checkbox"/> Riparian vegetation around water course or lake <input type="checkbox"/> Over water body (lake, wide river, dam)	
Water sources (currently holding water) within 50m of Anabat location <input type="checkbox"/> No significant water sources within 50m <input type="checkbox"/> Murray River main channel <input type="checkbox"/> Other River/Stream with flowing water		<input type="checkbox"/> Other River/Stream with intermittent pools <input type="checkbox"/> Wetland <input type="checkbox"/> Dam <input type="checkbox"/> Lake <input type="checkbox"/> Large open water tank accessible to bats	
Microphone direction <input type="checkbox"/> Into wide open space <input type="checkbox"/> Pointing directly over water <input type="checkbox"/> Pointing into vegetation or gaps between Vegetation nearby		Photo taken of microphone direction (stand behind the detector and take a photo of the view the detector would have) <input type="checkbox"/> Yes <input type="checkbox"/> No Please send photo to LAP/Landcare officer	

9 Appendix 2 - R code

```
#MEGAmicro bat community ecological data analysis in R

#-----#
#
# 1. Data frame preparation
#-----#

# Type in the path where all data files have been placed, and where all output will appear
setwd("D:/MEGAmicro/Bat_ecol_analysis/MEGAmicro_Biocollect_20190624")

# read in the main data matrix and check
y <-read.delim("MEGAmicro.csv", header=TRUE, sep=",")

#select and modify columns for analysis in new dataframe
colnames(y)

x <-y[,c("Activity.ID",
        "Unit.name",
        "Species.name",
        "Date.set..night.of.",
        "Latitude",
        "Longitude",
        "Bat.Flight.Space...Anabat.Placement..choose.one.",
        "Water.sources..currently.holding.water.",
        "Vegetation.type..habitat...of.Site..choose.one.",
        "Microphone.facing..")]

colnames(x)[colnames(x)=="Activity.ID"] <- "site"
colnames(x)[colnames(x)=="Unit.name"] <- "unit"
colnames(x)[colnames(x)=="Species.name"] <- "sp"
colnames(x)[colnames(x)=="Date.set..night.of."] <- "nightof"
colnames(x)[colnames(x)=="Latitude"] <- "lat"
colnames(x)[colnames(x)=="Longitude"] <- "lon"
colnames(x)[colnames(x)=="Bat.Flight.Space...Anabat.Placement..choose.one."] <- "FS"
colnames(x)[colnames(x)=="Water.sources..currently.holding.water."] <- "water"
colnames(x)[colnames(x)=="Vegetation.type..habitat...of.Site..choose.one."] <- "veg"
colnames(x)[colnames(x)=="Microphone.facing.."] <- "mic"

x$site <-as.character(x$site)
x$unit <-as.factor(x$unit)
x$sp <-as.factor(x$sp)
x$nightof <-as.Date(x$nightof)
x$lat <-as.numeric(x$lat)
x$lon <-as.numeric(x$lon)
x$FS <-as.factor(x$FS)
x$water <-as.factor(x$water)
x$veg <-as.factor(x$veg)
x$mic <-as.factor(x$mic)

# #add a counter for doing stats - not needed
# x$count <-as.numeric(rep("1", nrow(x)))

#check
str(x)
head(x)

#make factor strings smaller
unique(x$unit) #'Tricia' is an AnaBat Express

unique(x$FS)
x$FS <-gsub("R - Riparian vegetation around watercourse or lake", "R", x$FS)
x$FS <-gsub("G - House garden", "G", x$FS)
x$FS <-gsub("WL - Woodland and forest \\(overstorey above 2 m\\)", "WL", x$FS)
x$FS <-gsub("WL - Woodland and forest \\(overstorey above 2 m\\)", "WL", x$FS)
x$FS <-gsub("OP - Open pasture or parkland with no or sparsely scattered trees", "OP", x$FS)
x$FS <-gsub("DL - Over water body \\(lake, wide river, dam\\)", "DL", x$FS)
x$FS <-gsub("SC - Shrubland, vines or orchard \\(no overstorey above 2 m\\)", "SC", x$FS)
x$FS <-gsub("IS - Windrow/ Shelter Belt or isolated stand of trees", "IS", x$FS)
unique(x$FS)
```

```

unique(x$water)
x$water <-gsub("W - Wetland", "W", x$water)
x$water <-gsub("NWS - No significant water sources within 50 m", "NWS", x$water)
x$water <-gsub("WT - Large open water tank accessible to bats", "WT", x$water)
x$water <-gsub("MR - Murray River main channel", "MR", x$water)
x$water <-gsub("D - Dam", "D", x$water)
x$water <-gsub("OSP - Other River/Stream with intermittent pools", "OSP", x$water)
x$water <-gsub("OSF - Other River/Stream with flowing water", "OSF", x$water)
x$water <-gsub("L - Lake", "L", x$water)
unique(x$water)

unique(x$veg)
x$veg <-gsub("RMC - River Murray corridor - floodplains & wetlands", "RMC", x$veg)
x$veg <-gsub("U - Urban areas", "U", x$veg)
x$veg <-gsub("MS - Mallee - south of River Murray", "MS", x$veg)
x$veg <-gsub("OW - Open woodlands with open understorey - Low rainfall", "OW", x$veg)
x$veg <-gsub("WCG - Wheat/cropping/grazing land interspersed with mallee - south & west of
River Murray", "WCG", x$veg)
x$veg <-gsub("SEW - Artificially constructed and managed Wetlands and Sewerage Ponds", "SEW",
x$veg)
x$veg <-gsub("TFO - Tall Forests and Woodlands with open shrub understorey", "TFO", x$veg)
x$veg <-gsub("NG - Native grassland, chenopod shrublands", "NG", x$veg)
x$veg <-gsub("TFD - Tall Forests and Woodlands with dense shrub understorey", "TFD", x$veg)
x$veg <-gsub("ES - Estuarine habitat - Lower Lakes & Coorong", "ES", x$veg)
x$veg <-gsub("CD - Coastal dunes in Coorong region", "CD", x$veg)
x$veg <-gsub("GZ - Grazing land with scattered gum trees - flanks of eastern hills", "GZ",
x$veg)
x$veg <-gsub("MN - Mallee - north of River Murray", "MN", x$veg)
x$veg <-gsub("DM - Dense Mallee, Broombush & Heath shrubland - south of River Murray", "DM",
x$veg)
x$veg <-gsub("I - Irrigated horticulture and dairy farming along the River Murray", "I",
x$veg)
x$veg <-gsub("OW - Open woodlands with open understorey - Low rainfall", "OW", x$veg)
unique(x$veg)

unique(x$mic)
x$mic <-gsub("V - Pointing into vegetation or gaps between vegetation nearby", "V", x$mic)
x$mic <-gsub("WOS - Into wide open space", "WOS", x$mic)
x$mic <-gsub("H2O - pointing directly over water", "H2O", x$mic)
unique(x$mic)

#check
str(x)
head(x)

x$FS <-as.factor(x$FS)
x$water <-as.factor(x$water)
x$veg <-as.factor(x$veg)
x$mic <-as.factor(x$mic)

#Note that the Vespadelus are combined in the next lines
unique(x$sp)
x$sp <-gsub("Australopus australis \\(White-Striped Freetail-Bat\\)", "Aa", x$sp)
x$sp <-gsub("Chalinolobus gouldii \\(Gould's Wattled Bat\\)", "Cg", x$sp)
x$sp <-gsub("Chalinolobus morio \\(Chocolate Wattled Bat\\)", "Cm", x$sp)
x$sp <-gsub("Chalinolobus picatus \\(Little Pied Bat\\)", "Cp", x$sp)
x$sp <-gsub("Mormopterus \\(Ozimops\\) petersi \\(Inland Free-Tailed Bat\\)", "Opet", x$sp)
x$sp <-gsub("Mormopterus \\(Ozimops\\) planiceps \\(South-Eastern Free-Tailed Bat\\)",
"Oplan", x$sp)
x$sp <-gsub("Mormopterus \\(Ozimops\\) ridei \\(Ride's Free-Tailed Bat\\)", "Or", x$sp)
x$sp <-gsub("Myotis macropus \\(Southern Myotis\\)", "Mm", x$sp)
x$sp <-gsub("Nyctophilus geoffroyi geoffroyi", "Ng", x$sp)
x$sp <-gsub("Nyctophilus geoffroyi \\(Lesser Long-Eared Bat\\)", "Ng", x$sp)
x$sp <-gsub("Saccolaimus flaviventris \\(Yellow-Bellied Sheath-tail-Bat\\)", "Sf", x$sp)
x$sp <-gsub("Scotorepens balstoni \\(Inland Broad-Nosed Bat\\)", "Sb", x$sp)
x$sp <-gsub("Vespadelus baverstocki \\(Inland Forest Bat\\)", "Vsp", x$sp)
x$sp <-gsub("Vespadelus darlingtoni \\(Large Forest Bat\\)", "Vsp", x$sp)
x$sp <-gsub("Vespadelus finalysoni", "Vf", x$sp)
x$sp <-gsub("Vespadelus regulus \\(Southern Forest Bat\\)", "Vsp", x$sp)
x$sp <-gsub("Vespadelus vulturinus \\(Little Forest Bat\\)", "Vv", x$sp)
# x$sp <-gsub("Vespadelus baverstocki \\(Inland Forest Bat\\)", "Vb", x$sp)
# x$sp <-gsub("Vespadelus darlingtoni \\(Large Forest Bat\\)", "Vd", x$sp)
# x$sp <-gsub("Vespadelus finalysoni", "Vf", x$sp)
# x$sp <-gsub("Vespadelus regulus \\(Southern Forest Bat\\)", "Vr", x$sp)
str(x)
dim(x)

```

```

write.csv(x, "for_summary_table.csv", row.names=FALSE)

selected <-c("Aa","Cg","Cm","Cp","Mm","Ng","Opet","Oplan","Or","Sb","Sf","Vsp","Vf","Vv")
z <-x[x$sp %in% selected,]
dim(z); unique(z$sp)
head(z)
str(z)
# _____ #
#
# 2. Community analysis: ordinations
# _____ #

library(ape) #Version 4.3; Paradis E., Claude J. and Strimmer K. 2004. APE: analyses of
phylogenetics and evolution in R language. Bioinformatics 20: 289-290.
library(vegan) #Version 2.3-5; Oksanen, J., Blanchet, F.G., Kindt, R., Legendre, P., Minchin,
P.R., O'Hara, R.B., Simpson, G.L., Solymos, P., Henry, M., Stevens, H. and Wagner, H. 2016.
vegan: Community Ecology Package. R package version 2.3-5. https://CRAN.R-
project.org/package=vegan
library(car) #Version 2.1-2; Fox, J. and Weisberg, S. 2011. An {R} Companion to Applied
Regression, Second Edition. Sage, Thousand Oaks, California.

#data preparation
z$site <-paste(z$lat, z$lon, sep="_") #no longer required

library(reshape2)
z2 <-dcast(z, site+unit+nightof+lat+lon+FS+water+veg+mic ~ sp)
#sort by unit
z2 <-z2[order(z2$unit, z2$nightof),]
duplicated(z2$site); length(unique(z2$site)); dim(z2)

row.names(z2) <- z2$site
head(z2); str(z2)

#check for any sites with richness of 0 - zero rows must be removed from the dataset before
NMDS
z2$total_richness <-rowSums(z2[,10:21])
z2[z2$total_richness==0,] #show rows with no bats
z3 <-z2[!z2$total_richness==0, ] #remove rows with sum of 0
dim(z2); dim(z3)

#Must remove all factors and leave data vectors
z3 <-z3[,c(10:22)]
str(z3)

#MDS 1
z3.bray.mds <-metaMDS(z3, dist = "bray")

# MDS1 plot by veg
unique(x$FS)

mds.fig <-ordiplot(z3.bray.mds, type = "none", las=1, xlab="MDS1", ylab="MDS2", cex.lab=2,
cex.axis=2, ylim=c(-1.5,1.5), main="", cex.main=2)
z4 <-cbind(z2, mds.fig$sites)
head(z4)

par(xpd = T, mar=c(5, 5, 2, 1)+0.1, mgp=c(3.5, 1, 0))
plot(z4$NMDS1, z4$NMDS2, las=1, xlab="MDS1", ylab="MDS2", cex.lab=2, cex.axis=2, xlim=c(-2,2),
ylim=c(-2,2), main="", cex.main=2, col="white")
points(z4$NMDS1[z4$FS=="R"], z4$NMDS2[z4$FS=="R"], pch = 0, col = "blue", cex=2)
points(z4$NMDS1[z4$FS=="G"], z4$NMDS2[z4$FS=="G"], pch = 1, col = "tomato", cex=2)
points(z4$NMDS1[z4$FS=="WL"], z4$NMDS2[z4$FS=="WL"], pch = 2, col = "black", cex=2)
points(z4$NMDS1[z4$FS=="OP"], z4$NMDS2[z4$FS=="OP"], pch = 5, col = "gold", cex=2)
points(z4$NMDS1[z4$FS=="DL"], z4$NMDS2[z4$FS=="DL"], pch = 6, col = "darkgreen", cex=2)
points(z4$NMDS1[z4$FS=="SC"], z4$NMDS2[z4$FS=="SC"], pch = 16, col = "purple", cex=1)
points(z4$NMDS1[z4$FS=="IS"], z4$NMDS2[z4$FS=="IS"], pch = 17, col = "grey50", cex=1)

ell.1 <-dataEllipse(z4$NMDS1[z4$FS=="R"], z4$NMDS2[z4$FS=="R"], levels=0.95, draw=FALSE);
points(ell.1, type = "l", col = "blue")
ell.2 <-dataEllipse(z4$NMDS1[z4$FS=="G"], z4$NMDS2[z4$FS=="G"], levels=0.95, draw=FALSE);
points(ell.2, type = "l", col = "tomato")
ell.3 <-dataEllipse(z4$NMDS1[z4$FS=="WL"], z4$NMDS2[z4$FS=="WL"], levels=0.95, draw=FALSE);
points(ell.3, type = "l", col = "black")
ell.4 <-dataEllipse(z4$NMDS1[z4$FS=="OP"], z4$NMDS2[z4$FS=="OP"], levels=0.95, draw=FALSE);
points(ell.4, type = "l", col = "gold")
ell.5 <-dataEllipse(z4$NMDS1[z4$FS=="DL"], z4$NMDS2[z4$FS=="DL"], levels=0.95, draw=FALSE);
points(ell.5, type = "l", col = "darkgreen")

```

```

ell.6 <-dataEllipse(z4$NMDS1[z4$FS=="SC"], z4$NMDS2[z4$FS=="SC"], levels=0.95, draw=FALSE);
points(ell.6, type = "l", col = "purple")
ell.7 <-dataEllipse(z4$NMDS1[z4$FS=="IS"], z4$NMDS2[z4$FS=="IS"], levels=0.95, draw=FALSE);
points(ell.7, type = "l", col = "grey50")

#another habitat variable
par(xpd = T, mar=c(5, 5, 2, 1)+0.1, mgp=c(3.5, 1, 0))
plot(z4$NMDS1, z4$NMDS2, las=1, xlab="MDS1", ylab="MDS2", cex.lab=2, cex.axis=2, xlim=c(-2,2),
ylim=c(-2,2), main="", cex.main=2, col="white")
points(z4$NMDS1[z4$water=="D"], z4$NMDS2[z4$water=="D"], pch = 0, col = "blue", cex=2)
points(z4$NMDS1[z4$water=="L"], z4$NMDS2[z4$water=="L"], pch = 1, col = "tomato", cex=2)
points(z4$NMDS1[z4$water=="MR"], z4$NMDS2[z4$water=="MR"], pch = 2, col = "black", cex=2)
points(z4$NMDS1[z4$water=="NWS"], z4$NMDS2[z4$water=="NWS"], pch = 5, col = "gold", cex=2)
points(z4$NMDS1[z4$water=="OSF"], z4$NMDS2[z4$water=="OSF"], pch = 6, col = "red", cex=2)
points(z4$NMDS1[z4$water=="OSP"], z4$NMDS2[z4$water=="OSP"], pch = 16, col = "purple", cex=1)
points(z4$NMDS1[z4$water=="WT"], z4$NMDS2[z4$water=="WT"], pch = 17, col = "grey50", cex=1)
points(z4$NMDS1[z4$water=="W"], z4$NMDS2[z4$water=="W"], pch = 17, col = "pink", cex=1)

ell.1 <-dataEllipse(z4$NMDS1[z4$water=="D"], z4$NMDS2[z4$water=="D"], levels=0.95,
draw=FALSE); points(ell.1, type = "l", col = "blue")
ell.2 <-dataEllipse(z4$NMDS1[z4$water=="L"], z4$NMDS2[z4$water=="L"], levels=0.95,
draw=FALSE); points(ell.2, type = "l", col = "tomato")
ell.3 <-dataEllipse(z4$NMDS1[z4$water=="MR"], z4$NMDS2[z4$water=="MR"], levels=0.95,
draw=FALSE); points(ell.3, type = "l", col = "black")
ell.4 <-dataEllipse(z4$NMDS1[z4$water=="NWS"], z4$NMDS2[z4$water=="NWS"], levels=0.95,
draw=FALSE); points(ell.4, type = "l", col = "gold")
ell.5 <-dataEllipse(z4$NMDS1[z4$water=="OSF"], z4$NMDS2[z4$water=="OSF"], levels=0.95,
draw=FALSE); points(ell.5, type = "l", col = "red")
ell.6 <-dataEllipse(z4$NMDS1[z4$water=="OSP"], z4$NMDS2[z4$water=="OSP"], levels=0.95,
draw=FALSE); points(ell.6, type = "l", col = "purple")
ell.7 <-dataEllipse(z4$NMDS1[z4$water=="WT"], z4$NMDS2[z4$water=="WT"], levels=0.95,
draw=FALSE); points(ell.7, type = "l", col = "grey50")
ell.8 <-dataEllipse(z4$NMDS1[z4$water=="W"], z4$NMDS2[z4$water=="W"], levels=0.95,
draw=FALSE); points(ell.8, type = "l", col = "pink")

#check
#write.csv(z2, "species_MEGAmicro_Biocollect_20190714_z2.csv", row.names = FALSE)

#-----#
#
# 3. Distributions
#-----#

#All mapping done in QGIS
#write.csv(z, "species_MEGAmicro_Biocollect_20190714.csv", row.names = FALSE)

#-----#
#
# 4. Summaries of Species Richness
#-----#
library(dplyr) #Hadley Wickham, Romain François, Lionel Henry and Kirill Müller (2019). dplyr:
A Grammar of Data Manipulation. R package version 0.8.1. https://CRAN.R-
project.org/package=dplyr
library(tidyr)

#Starting dataframe
head(z2)
str(z2)

#remove everything except factors and total richness

#FS
z5 <-z2[,c(6,23)]
str(z5)

FS <-z5 %>%
  group_by(FS) %>%
  summarise_all(funs(mean, median, min, max, sd)) %>%
  gather(key, value, -FS) %>%
  separate(key, into = c("variable", "stats")) %>%
  spread(stats, value)
#write.csv(FS, "summary_FS.csv")
#plot
par(mar=c(5, 5, 1, 1)+0.1, mgp=c(3, 1, 0))
plot(z2$FS, z2$total_richness, type="n", pch="o", yaxs="i", cex=1, las=1, xlab="Flight Space",
ylab="Species Richness", cex.lab=2, cex.axis=1.5, ylim=c(-0.5,10), frame=FALSE )
box(bty="l")

```



```

#water
z5 <-z2[,c(7,23)]
str(z5)

water <-z5 %>%
  group_by(water) %>%
  summarise_all(funs(mean, median, min, max, sd)) %>%
  gather(key, value, -water) %>%
  separate(key, into = c("variable", "stats")) %>%
  spread(stats, value)
#write.csv(water, "summary_water.csv")

par(mar=c(5, 5, 1, 1)+0.1, mgp=c(3, 1, 0))
plot(z5$water, z5$total_richness, type="n", pch="o", yaxs="i", cex=1, las=1, xlab="Nearest
open water source", ylab="Species Richness", cex.lab=2, cex.axis=1.5, ylim=c(-0.5,10),
frame=FALSE )
box(bty="l")

#veg
z5 <-z2[,c(8,23)]
str(z5); dim(z5)
#remove rows with no value for veg habitat
#note there are no NAs
z5 <-z5[Reduce(`&`, lapply(z5, function(x) !(is.na(x)|x==""))),]
dim(z5)
tail(z5, 136)
veg <-z5 %>%
  group_by(veg) %>%
  summarise_all(funs(mean, median, min, max, sd)) %>%
  gather(key, value, -veg) %>%
  separate(key, into = c("variable", "stats")) %>%
  spread(stats, value)
#write.csv(veg, "summary_veg.csv")

par(mar=c(5, 5, 1, 1)+0.1, mgp=c(3, 1, 0))
plot(z2$veg, z2$total_richness, type="n", pch="o", yaxs="i", cex=1, las=1, xlab="Vegetation
unit", ylab="Species Richness", cex.lab=2, cex.axis=1, ylim=c(0,10), frame=FALSE )
box(bty="l")

#mic
z5 <-z2[,c(9,23)]
str(z5)

mic <-z5 %>%
  group_by(mic) %>%
  summarise_all(funs(mean, median, min, max, sd)) %>%
  gather(key, value, -mic) %>%
  separate(key, into = c("variable", "stats")) %>%
  spread(stats, value)
#write.csv(mic, "summary_mic.csv")

par(mar=c(5, 5, 1, 1)+0.1, mgp=c(3, 1, 0))
plot(z5$mic, z5$total_richness, type="n", pch="o", yaxs="i", cex=1, las=1, xlab="Habitat faced
by microphone", ylab="Species Richness", cex.lab=2, cex.axis=1.5, ylim=c(-0.5,10), frame=FALSE
)
box(bty="l")

#-----#
#
# 5. Community analysis 5: Indicator Species analysis
#-----#

library(labdsv)
#Dufrene M, Legendre P. 1997. Species assemblages and indicator species: the need for a
flexible asymmetrical approach. Ecol Monogr. 67:345-366.

#Starting dataframe
head(z2)
str(z2)

#Remove sites with no bats
z2$total_richness; z2$total_richness!=0
z2[z2$total_richness==0,]
dim(z2); z2 <-z2[z2$total_richness!=0,]; dim(z2) #remove no rows with sum of 0
z2[z2$total_richness==0,]

```

```

#Remove species in no sites
str(z2)
absences <-colSums(z2[,10:22]); absences #gives a sum per species

#Indicator Species
z2 <-z2[, -c(23)]; str(z2) #removed total_richness
FS <-z2$FS
veg <-z2$veg

#make a custom ordering vector
sp <-c("Aa","Cg","Cm","Cp","Mm","Ng","Opet","Oplan","Or","Sb","Sf","Vsp","Vf","Vv"); sp
df <-data.frame(sp)

#Distance
z2 <-z2[, -c(1:9)]; str(z2)
iv <-indval(z2, FS, numitr=10)
a <-data.frame(iv$indval)
a$sp <-as.factor(rownames(a))
a$zero <-rep(0, nrow(a))
str(a); a
#write.csv(a, "indspp.csv", row.names=FALSE)
#Plot
plot(a$sp, a$zero, type="n", yaxs="i", axes=FALSE, main="", las=1, xlab="xxx", ylim=c(0,
0.2), ylab= "yyy")
lines(a$sp, a$DL, type="o", lty=1, pch=1, col="blue", cex=1)
lines(a$sp, a$G, type="o", lty=1, pch=1, col="red", cex=1)
lines(a$sp, a$IS, type="o", lty=1, pch=1, col="darkgreen", cex=1)
lines(a$sp, a$OP, type="o", lty=1, pch=1, col="orange", cex=1)
lines(a$sp, a$R, type="o", lty=1, pch=1, col="grey75", cex=1)
lines(a$sp, a$SC, type="o", lty=1, pch=1, col="yellow", cex=1)
lines(a$sp, a$WL, type="o", lty=1, pch=1, col="purple", cex=1)
axis(1, at=c(1:13), las=2,
labels=c("Aa","Cg","Cm","Cp","Mm","Ng","Opet","Oplan","Or","Sb","Vf","Vsp","Vv"))
axis(2)

#FS
#FS: DL G IS OP R SC WL

#"R - Riparian vegetation around watercourse or lake"
#"G - House garden"
#"WL - Woodland and forest \\(overstorey above 2 m\\)"
#"WL - Woodland and forest \\(overstorey above 2 m\\)"
#"OP - Open pasture or parkland with no or sparsely scattered trees"
#"DL - Over water body \\(lake, wide river, dam\\)"
#"SC - Shrubland, vines or orchard \\(no overstorey above 2 m\\)"
#"IS - Windrow/ Shelter Belt or isolated stand of trees"

plot(a$sp, a$zero, type="p", yaxs="i", axes=FALSE, main="", las=1, xlab="xxx", ylim=c(0,
0.2), ylab= "yyy")
lines(a$sp, a$DL, type="p", lty=1, pch="D", col="blue", cex=1)
lines(a$sp, a$G, type="p", lty=1, pch="G", col="red", cex=1)
lines(a$sp, a$IS, type="p", lty=1, pch="I", col="darkgreen", cex=1)
lines(a$sp, a$OP, type="p", lty=1, pch="O", col="orange", cex=1)
lines(a$sp, a$R, type="p", lty=1, pch="R", col="grey75", cex=1)
lines(a$sp, a$SC, type="p", lty=1, pch="S", col="yellow", cex=1)
lines(a$sp, a$WL, type="p", lty=1, pch="W", col="purple", cex=1)
axis(1, at=c(1:13), las=2,
labels=c("Aa","Cg","Cm","Cp","Mm","Ng","Opet","Oplan","Or","Sb","Vf","Vsp","Vv"))
axis(2)

plot(a$sp, a$zero, type="p", yaxs="i", axes=FALSE, main="", las=1, xlab="xxx", ylim=c(0,
0.2), ylab= "yyy")
lines(a$sp, a$DL, type="p", lty=1, pch=16, col="blue", cex=5)
lines(a$sp, a$G, type="p", lty=1, pch=17, col="red", cex=3)
lines(a$sp, a$R, type="p", lty=1, pch=18, col="darkgreen", cex=3)
lines(a$sp, a$OP, type="p", lty=1, pch=0, col="orange", cex=3)
lines(a$sp, a$IS, type="p", lty=1, pch=1, col="grey75", cex=3)
lines(a$sp, a$SC, type="p", lty=1, pch=2, col="yellow", cex=3)
lines(a$sp, a$WL, type="p", lty=1, pch=3, col="purple", cex=3)
axis(1, at=c(1:13), las=2,
labels=c("Aa","Cg","Cm","Cp","Mm","Ng","Opet","Oplan","Or","Sb","Vf","Vsp","Vv"))
axis(2)

par(mar=c(6, 7, 1, 1)+0.1, mgp=c(4, 1, 0))

```

```

plot(a$sp, a$zero, type="p", yaxs="i", axes=FALSE, main="", las=1, xlab="", ylim=c(0, 0.2),
ylab= "Indicator Species Index value", cex.lab=2, cex.axis=1.5)
lines(a$sp, a$DL, type="p", lty=1, pch="D", col="blue", cex=2)
lines(a$sp, a$G, type="p", lty=1, pch="G", col="black", cex=2)
lines(a$sp, a$IS, type="p", lty=1, pch="I", col="black", cex=2)
lines(a$sp, a$OP, type="p", lty=1, pch="O", col="black", cex=2)
lines(a$sp, a$R, type="p", lty=1, pch="R", col="red", cex=2)
lines(a$sp, a$SC, type="p", lty=1, pch="S", col="black", cex=2)
lines(a$sp, a$WL, type="p", lty=1, pch="W", col="black", cex=2)
axis(1, at=c(1:13), las=2, cex.axis=2,
labels=c("Aa", "Cg", "Cm", "Cp", "Mm", "Nsp", "Opet", "Oplan", "Or", "Sb", "Vf", "Vsp", "Vv"))
axis(2, cex.axis=1.5, las=1)

#end

```