ORIGINAL PAPER

Check for
updates

Undergraduate entomology field excursions are a valuable source of biodiversity data: a case for spider (Araneae) bycatches in ecological studies

Charles Richard Haddad[1] ⬡

Abstract

As part of an undergraduate Entomology module, field excursions were undertaken to a mixed livestock farm in central South Africa, during March–April 2015, 2016 and 2018–2020. The aim was for groups to determine and compare terrestrial arthropod biodiversity in three strata of three contrasting biotopes, with particular emphasis on insects. To determine the contributions such excursions make to documenting biodiversity of a non-target taxon, the spider (Arachnida: Araneae) data generated by students was compared with the local species richness (LSR) for the area. The LSR for the farm Bankfontein included a total of 242 species, representing 40 families. Over the 5 years, student groups sampled a total of 158 spider species, representing 65.3% of the LSR. The number of species sampled per year ranged between 57 and 94 for undergraduate students (1–3 groups), and was 119 species for the final year of the study carried out by the author and two post-graduate students (2 groups), which could be attributed to collector experience and modification of the sorting process for beat sampling, particularly. This study emphasizes the importance of utilizing students as a valuable resource to generate biodiversity data, particularly where financial and human resources may be limited.

Keywords Beating · Grassland · Insects · Litter sifting · Local species richness · Nama Karoo · Pitfalls · Student's field work data

Introduction

The Global Biodiversity Crisis is an important challenge facing humankind, which is largely driven by the degradation and loss of natural habitat (Mokany et al. 2020). Although the Convention on Biological Diversity was signed in 1992 to try to reduce biodiversity

✉ Charles Richard Haddad
  haddadcr@ufs.ac.za

1 Department of Zoology & Entomology, University of the Free State, P.O. Box 339,
  Bloemfontein 9300, South Africa

loss, the shortage of financial and human resources to comprehensively document, describe and conserve global biodiversity (Barbier et al. 2018) has exacerbated species declines. As a result, some species are assumed to have gone extinct before they have been described (e.g. Costello 2015; Lees and Pimm 2015).

Contributing to this problem is the lack of human resources and time to intensively and effectively sample habitats and describe new taxa from the material collected, resulting in considerable gaps in our knowledge of the taxonomy, distribution, biology and ecology of organisms (e.g. Victor et al. 2015). This situation is particularly evident in countries that do not have adequate financial resources or human capacity to extensively sample and document their fauna and flora (Hochkirch et al. 2021). This problem is exacerbated in certain megadiverse countries such as South Africa, which often have high levels of endemism (e.g. Cowling and Hilton-Taylor 1994; Tolley et al. 2019; Foord et al. 2020) and feature global biodiversity hotspots (Myers et al. 2000; Mittermeier et al. 2011).

One potential solution to this problem is to optimise the available human resources through atlas projects, to more effectively generate biodiversity data and acquisition of specimens for natural history collections, improving the documentation of species occurrences (Robertson et al. 2010; Dippenaar-Schoeman et al. 2015). Data generation for various organismal groups benefits greatly from the involvement of volunteers (Lovell et al. 2010; Lewandowski and Specht 2015), citizen scientists (Theobald et al. 2015; Chandler et al. 2016) or students (e.g. Cardoso et al. 2017; Kiljunen et al. 2020; Soukainen et al. 2020; Supriatna et al. 2020) to assist with field sampling. Further, the extraction of non-target groups as bycatch in surveys can also provide data that is comparable to dedicated surveys of those particular non-target groups (e.g. Oberprieler et al. 2019).

Insects are the largest component of terrestrial biodiversity and play various significant ecological roles in ecosystems (Yang and Gratton 2014). Training undergraduate students in Entomology requires a broad scope and approach to provide adequate knowledge in the core disciplines, e.g. ecology, systematics, physiology and pest management. Considering the importance of the Global Biodiversity Crisis, an understanding of the planet's biodiversity and the importance of conserving species richness is critical in the education process (Dikmenli 2010; Lamarre et al. 2018). This creates an understanding of natural systems and the organisms occupying them. Skills development in biodiversity and ecology, specifically, can be enhanced by exposing students to various sampling techniques and methodological approaches through field excursions and practicals (e.g. Yli-Panula et al. 2018).

Training in insect biodiversity and ecology equips students to understand the importance of (1) identifying an ecological scenario or problem, (2) planning a protocol to sample adequately and effectively to determine ecological patterns, (3) executing sampling, sorting and identification of material, (4) analysing data using appropriate statistical tests, and (5) preparing a written report to a hypothetical client that provides evidence and solutions to a particular problem or scenario. Further, they gain an understanding of the guilds or functional feeding groups of insects (Kaiser et al. 2009; Buschke and Seaman 2011), and how these organisms utilise the available food resources in the biotopes sampled.

In the current study, the contribution of an annual undergraduate Entomology student field excursion to generating biodiversity data on a relatively well-studied non-target arthropod group, spiders (Arachnida: Araneae), was documented over the course of 5 years. A standardised sampling protocol was used to sample terrestrial arthropods, with spiders as a bycatch taxon, to determine the proportion of the local species richness for the site sampled by each student year-group, and also by each group of students. This way, the success of student groups in contributing biodiversity data could be assessed and compared with more experienced arachnologists, who conducted the sampling in the final year of the

study. The data generated through this study contributed towards an ongoing atlas project in South Africa, the South African National Survey of Arachnida (Dippenaar-Schoeman et al. 2015), by surveying in a historically undersampled degree-square of the Free State Province (Foord et al. 2011; Haddad et al. 2013).

By exposing students to such a field trip, they can develop a variety of skills related to ecological surveys and data processing. Further, they can develop an appreciation for the contribution that their sampling may make to generating baseline biodiversity data for an area, even for non-target taxa, as well as the value that specimens collected can make to national atlas programmes and future taxonomic research.

Materials and methods

General background

This study was based on data generated as part of an annual field excursion forming part of the 3rd year Entomology curriculum at the University of the Free State in Bloemfontein, South Africa. The excursion was an assessment component contributing to the ENTO3714 module, titled "Advanced Insect Ecology". The core purposes of the excursion are to expose students to an environment not encountered during their regular practical assignments in the Grassland Biome; to sample arthropods using a standardised protocol and to apply sampling methods (beating, litter sifting and pitfalls) not used during their regular practical sessions (sweep-netting); and to learn various statistical techniques to analyse the datasets generated to evaluate differences in abundance, species richness and composition of functional feeding groups (guilds) in different biotopes.

The current study focused on biotopes in the transition zone between the Grassland and Nama Karoo biomes in the western Free State Province. The Grassland Biome dominates the central plateau of South Africa, and is recognized by a field layer dominated by grasses and forbs, with woody vegetation largely restricted to hillsides and drainage lines (Mucina and Rutherford 2006). The Nama Karoo Biome covers a large area in the semi-arid and arid western half of South Africa, with vegetation dominated by low-growing Asteraceae, Fabaceae and Poaceae, and trees generally rare due to the predominantly shallow soils (Mucina and Rutherford 2006). Previous field excursions exposed students to other biomes, e.g. Fynbos in the Western Cape and Afromontane Forests in the Eastern Cape. The number of groups was determined by the number of students registered for the ENTO3714 module each year, and varied from one to three groups comprising two or three students each.

Study area and period

Field excursions were undertaken at the farm Bankfontein in the Luckhof district in the western Free State Province, South Africa (Fig. 1a), during the March–April recess or over a national long weekend at the end of April, in 2015, 2016 and 2018–2020. During 2017, only two students registered for the ENTO3714 module, so the excursion during that year was combined with the annual Zoology excursion (ZLGY3714 module) to the Gariep Dam in the south-western Free State. The farm is predominantly utilised for sheep farming, although some cattle are also managed on the property.
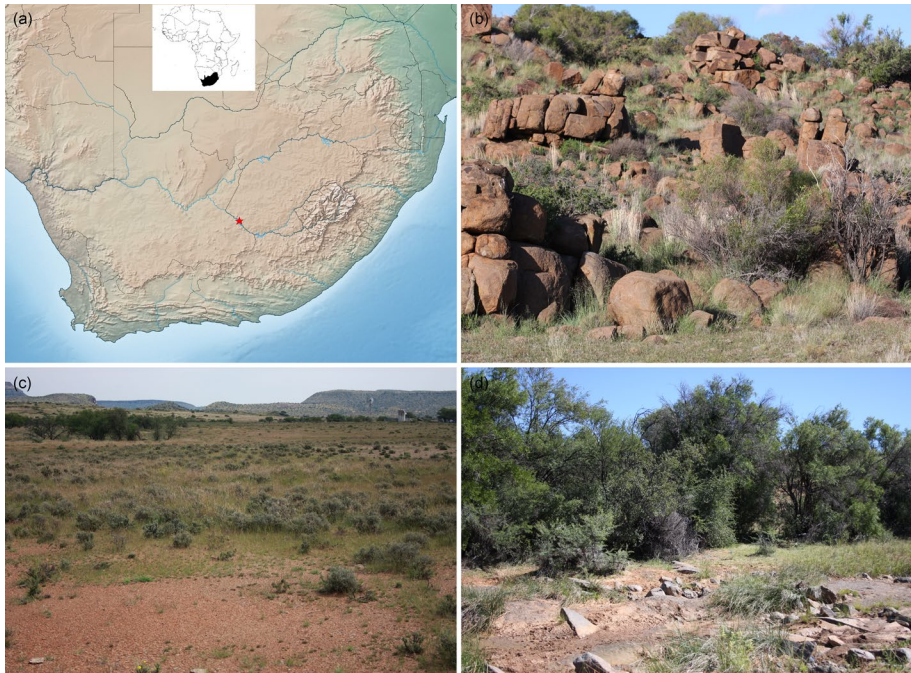
Fig. 1 **a** Map of South Africa, red star indicating the location of Bankfontein farm in the western Free State Province; **b–d** Habitats sampled for spiders and other arthropods: **b** Hillside grassland; **c** Nama Karoo veld; **d** Riparian woodland. Map **a** created on www.simplemappr.net

The first biotope sampled was the west-facing slopes of hillsides (referred to as hillside grassland; 30°04.526′ S, 24°53.039′ E), which are classified as Besemkaree Koppies Shrubland (vegetation unit Gh 4 of Mucina et al. 2006a) that include scattered dolerite formations (Fig. 1b). Woody vegetation was dominated by *Searsia burchellii*, *S. ciliata* and *S. erosa*, with scattered *Diospyros lycioides*, *Ehretia rigida*, *Grewia occidentalis*, *S. lancea* and *Ziziphus mucronata*. Common grasses include *Aristida*, *Eragrostis* and *Tragus* spp., *Heteropogon contortus* and *Themeda triandra*, with *Osteospermum leptolobum* the most common karooid bushes. The substrate could be classified as sandy shale.

The second biotope, referred to as Nama Karoo veld (30°04.974′ S, 24°54.297′ E), was dominant in the lower lying parts of the farm, and was classified as Northern Upper Karoo (vegetation unit NKu 3 of Mucina et al. 2006b). The vegetation at the site sampled was dominated by the karooid bushes *Asparagus capensis*, *Eriocephalus ericoides*, *E. spinescens*, *Lycium cinereum*, *Nenax microphylla* and *O. leptolobum*, and the grasses *Aristida congesta*, *Enneapogon* sp. and *Eragrostis* sp., on a shale substrate, with isolated *Senegalia mellifera* and *Vachellia karroo* trees (Fig. 1c).

The third biotope (riparian woodland; 30°04.421′ S, 24°53.013′ E) was surrounded by dolerite formations and formed part of the Upper Karoo Hardeveld (vegetation unit NKu 2 of Mucina et al. 2006b), but specifically parts restricted to the drainage lines that led to the Vanderkloof Dam on the Orange River (Fig. 1d). *Searsia lancea*, *V. karroo* and *Z. mucronata* were the dominant trees present, but were interspersed with *Diospyros austro-africana* and *Lotononis divaricata* shrubs. Grass richness was low in this biotope, but *Cynodon*

dactylon and *Eragrostis* spp. were very abundant, as were Restionaceae, *Asparagus* spp. and other herbs.

Sampling methodology and intensity

Each student group was required to implement a standardised sampling protocol in each of the three biotopes. Considering the paucity and low growth of grasses in the Nama Karoo veld, no sweep-net sampling was undertaken. This contrasts with their regular practical assignments, which rely exclusively on sweep-net sampling. Three methods were employed in each biotope by each group to sample arthropods:

(1) 10 pitfall traps (6 cm diameter 250 ml bottles) were set out 5 m apart in a line transect. Ethylene glycol (50 ml) was added to each pitfall trap as a preservative, with traps kept open for 4 days (96 h) before being removed. Where multiple student groups sampled in a single year, trapping transects were separated by at least 10 m to minimise interference. Arthropods were sorted from the collected material in white plastic trays and preserved in 70% ethanol in separate vials for each sample;

(2) 10 leaf litter samples were taken by filling 5 l plastic freezer bags with litter from beneath woody plants. The collected material was sifted over a large white sheet using a round steel sieve with a diameter of 45 cm, height of 10 cm and mesh spacing of 8 mm. Specimens sampled by litter sifting were collected with forceps or clean glass vials and put into separate vials containing 70% ethanol for each sample. For this method, either the author or one senior post-graduate student assisted each student group with collecting specimens from the sheet; and

(3) 10 beating samples were taken by striking the branches of woody foliage 50 times over a standard sweep-net with a diameter of 40 cm. Each of the 50 beat units comprised striking a single branch at the same point three times before moving onto the next unit. Once 50 units had been completed, the sampled material was transferred to a 5 l plastic freezer bag until sorting in the laboratory. Beat samples were euthanized using toilet paper doused in ethyl acetate, which was added to each bag on return to the field laboratory. This was to ensure that flying insects could not escape during sorting. The material was then emptied into large white plastic trays, and the arthropods removed using forceps and transferred to vials containing 70% ethanol.

The number of samples per habitat and method was determined by the number of student groups on each trip: 30 (2015), 20 (2016), 10 (2018), 30 (2019) and 20 (2020). In all of the years, students were responsible for all sampling and processing of material, except for 2020, when the University of the Free State closed in the week prior to the proposed excursion due to the COVID-19 pandemic. The author and two post-graduate Arachnology students (one Ph.D and one M.Sc level) consequently undertook the sampling before national government imposed a national lockdown on 27 March 2020, and executed collecting for the two student groups that would have undertaken the excursion.

In 2020, we were only interested in extracting spiders from the samples for the purpose of completing this study. We therefore deviated from the methodology above slightly by emptying beat samples into white sorting trays without euthanasia, so that live spiders could be easily recognised and collected while walking on the plant material or walls of the tray. Insects were ignored and not sampled, as students would not have had an opportunity to process the material during lockdown. Consequently, students in the 2020 cohort

prepared their excursion reports based on a hypothetical visit to Bankfontein, utilizing the datasets of one of the 2019 groups.

Spider sorting and identification

Normal sorting and identification procedures for arthropods were implemented for each of the 10 method-samples taken by each group. Insects were identified to family level using the keys of Triplehorn and Johnson (2005) and further separated into morphospecies, while arachnids and other non-insect arthropods (woodlice, millipedes and centipedes etc.) were identified by the author. Students were instructed to keep all arachnids and other non-insect arthropods in a vial labelled for each sample taken, so that material could be allocated to the correct sample once identified.

Initial sorting and morphospecies identification of arachnid samples was done in the field laboratory to ensure inclusion of fine resolution data in the student reports, with final identifications performed at the University of the Free State by the author. For the purposes of this study, both adult and immature spiders were identified and tallied. Immature morphospecies were separated on the basis of colouration or morphological attributes until adults were sampled from the same biotope, which were linked to a particular morphospecies and identified. In some species-rich genera (Gnaphosidae: *Zelotes* and Thomisidae: *Thomisus*), there were inadequate characters to separate potential immature morphospecies, and these were then pooled and treated as a single morphospecies; adults of these genera were identified and tallied separately (Appendix 1). Adult material was identified to species level using taxonomic literature available from the World Spider Catalog (2021) for all families. In some cases, spiders could not be identified to species level, due to the lack of modern revisions or redescriptions, and otherwise because new species had been discovered. Voucher specimens of adult arachnids have been deposited in the National Collection of Arachnida at the ARC—Plant Health and Protection in Pretoria, South Africa.

The local species richness (LSR) for spiders was determined by incorporating all spider data sampled from Bankfontein by students during the excursions, as well as additional collecting by the author, post-graduate students and other arachnologists on the farm during the period 2014–2021. Prior to this period, no sampling had been undertaken there. The LSR therefore includes all spider species records, irrespective of sampling method. Other sampling methods used by more experienced collectors included ad hoc hand collecting from rocks and logs, sweep-netting, searching in grass tussocks, night collecting, and a single canopy fogging sample. In addition, extra samples were taken at other non-student sites by beating, litter sifting and pitfalls.

Statistical analysis

To assess the effectiveness of the sampling protocol in determining species richness, the number of species per sample was used to calculate the mean ± SD species richness for each year for each method-biotope combination. Values were calculated and graphs prepared in GraphPad InStat version 3.00.

Using PAST version 2.07 (Hammer et al. 2001), sample rarefaction curves were prepared for each method-biotope combination. In preparing these curves, datasets were prepared based on annual accumulation of samples, i.e. 2015 alone (3 groups), 2015 + 2016 (5 groups), 2015 + 2016 + 2018 (6 groups), 2015 + 2016 + 2018 + 2019 (9 groups), and 2015 + 2016 + 2018−2020 (11 groups). This was done to assess whether the rarefaction

curves would approach an asymptote. In PAST, sample rarefaction implements the "Mao tau" analytical procedure, with standard errors indicated as 95% confidence intervals on the resulting graphs. The confidence intervals were only indicated for the full dataset, i.e. 11 groups.

To assess the contribution of each year-group in sampling spider species richness, the total number of species sampled per year (all groups pooled) was determined and divided by the LSR. Sample completeness for each year-group was calculated as the ratio of the observed species richness (S_{obs}) and the Chao1-estimated species richness (S_{Chao1}), with the latter calculated as:

$$S_{Chao1} = S_{obs} + \left(f_1^2/2f_2\right)$$

where f_1 is the number of singleton species (represented by one individual only) and f_2 is the number of doubleton species (represented by two individuals only).

Coverage-based rarefaction and extrapolation was used to assess community richness and sampling effort (Chao and Jost 2012). Sample coverage (C_n) was defined as the proportion of the total number of individuals in a community that belong to the species represented in the sample. By subtracting the sample coverage from 1, the proportion of the community belonging to as yet unsampled species can be calculated, which Chao and Jost (2012) referred to as "coverage deficit". This metric can be interpreted as the likelihood that a new, previously unsampled species will be collected if the sample were to be increased by one individual (Chao and Jost 2012). Coverage for each year-group was calculated using the following equation:

$$Cn = 1 - \frac{f_1}{n}\left[\frac{(n-1)f_1}{\left((n-1)f_1\right) + 2f_2}\right]$$

where n represents the number of individuals in the sample, and f_1 the number of singleton species and f_2 the number of doubleton species. Chao and Lee (1992) proposed that coverage values should be at least 0.5 for a sample to be considered representative of the assemblage.

Based on the cumulative species sampled by student groups over the course of the study, the similarity in faunal composition sampled using each method was compared between biotopes using Sørensen's Quotient of Similarity, $SQ = 2j/a + b$, where j is the number of species shared between the two compared biotopes, and a and b represent the species richness sampled in each biotope (Magurran 2004). A value closer to 1 indicates a high degree of similarity, and closer to 0 indicates greater uniqueness of the fauna of each biotope.

Results

Overall abundance and richness patterns

The LSR for the farm Bankfontein included a total of 242 species, representing 40 families (Table 1; Appendix 1). The most species-rich families were Gnaphosidae (36 spp.), Salticidae (35 spp.), Thomisidae (21 spp.) and Theridiidae (18 spp.). Over the 5 years, students sampled a total of 158 spider species, representing 65.3% of the LSR. The total abundance and number of species sampled by each group in the three biotopes using

Table 1 Family diversity of spiders sampled from the farm Bankfontein in central South Africa, indicating the number of species in each family contributing to the local species richness (LSR) and the number of species sampled each year by students (% of LSR in parenthesis)

Family	LSR	2015	2016	2018	2019	2020	Total
Agelenidae	2	1 (50)	1 (50)	0 (0)	1 (50)	0 (0)	2 (100)
Amaurobiidae	4	2 (50)	2 (50)	1 (25)	2 (50)	1 (25)	2 (50)
Ammoxenidae	2	0 (0)	0 (0)	0 (0)	0 (0)	1 (50)	1 (50)
Araneidae	11	1 (9.1)	2 (18.2)	2 (18.2)	2 (18.2)	5 (45.5)	5 (45.4)
Caponiidae	1	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
Cheiracanthiidae	2	1 (50)	1 (50)	1 (50)	1 (50)	2 (100)	2 (100)
Clubionidae	1	1 (100)	1 (100)	1 (100)	0 (0)	1 (100)	1 (100)
Corinnidae	4	0 (0)	1 (25)	0 (0)	1 (25)	2 (50)	2 (50)
Cyatholipidae	2	0 (0)	1 (50)	0 (0)	0 (0)	1 (50)	2 (100)
Cyrtaucheniidae	2	1 (50)	0 (0)	0 (0)	1 (50)	0 (0)	2 (100)
Dictynidae	2	1 (50)	1 (50)	1 (50)	2 (100)	2 (100)	2 (100)
Eresidae	2	0 (0)	0 (0)	0 (0)	1 (50)	0 (0)	1 (50)
Gnaphosidae	36	9 (25)	6 (16.7)	5 (13.9)	17 (47.2)	17 (47.2)	23 (63.9)
Hersiliidae	2	1 (50)	1 (50)	1 (50)	1 (50)	0 (0)	2 (100)
Idiopidae	2	1 (50)	1 (50)	0 (0)	1 (50)	1 (50)	1 (50)
Linyphiidae	14	2 (14.3)	1 (7.1)	2 (14.3)	4 (28.6)	7 (50)	7 (50)
Liocranidae	1	0 (0)	0 (0)	0 (0)	0 (0)	1 (100)	1 (100)
Lycosidae	13	3 (23.1)	4 (30.8)	3 (23.1)	6 (46.2)	6 (46.2)	9 (69.2)
Migidae	1	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
Mimetidae	1	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
Oonopidae	6	2 (33.3)	1 (16.7)	1 (16.7)	1 (16.7)	2 (33.3)	4 (66.7)
Orsolobidae	2	1 (50)	1 (50)	1 (50)	1 (50)	1 (50)	2 (100)
Oxyopidae	8	2 (25)	2 (25)	4 (50)	3 (37.5)	4 (50)	5 (62.5)
Palpimanidae	2	1 (50)	2 (100)	2 (100)	1 (50)	2 (100)	2 (100)
Philodromidae	10	3 (30)	3 (30)	4 (40)	5 (50)	6 (60)	7 (70)
Pholcidae	1	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
Pisauridae	2	1 (50)	1 (50)	0 (0)	1 (50)	1 (50)	1 (50)
Salticidae	35	10 (28.6)	11 (31.4)	10 (28.6)	12 (34.3)	17 (48.6)	22 (62.9)
Selenopidae	3	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
Sparassidae	3	1 (33.3)	0 (0)	0 (0)	0 (0)	1 (33.3)	2 (66.7)
Stasimopidae	1	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
Symphytognathidae	1	0 (0)	0 (0)	0 (0)	1 (100)	0 (0)	1 (100)
Tetragnathidae	1	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
Theraphosidae	1	0 (0)	0 (0)	0 (0)	0 (0)	1 (100)	1 (100)
Theridiidae	18	5 (27.8)	3 (16.7)	6 (33.3)	10 (55.6)	12 (66.7)	15 (83.3)
Theridiosomatidae	1	0 (0)	0 (0)	0 (0)	1 (100)	1 (100)	1 (100)
Thomisidae	21	8 (38.1)	6 (28.6)	10 (47.6)	10 (47.6)	12 (57.1)	13 (61.9)
Trachelidae	9	4 (44.4)	2 (22.2)	2 (22.2)	2 (22.2)	5 (55.6)	8 (88.9)
Uloboridae	2	1 (50)	0 (0)	0 (0)	0 (0)	1 (50)	1 (50)
Zodariidae	10	4 (40)	2 (20)	3 (30)	6 (60)	6 (60)	8 (80)
Total species	242	67	57	60	94	119	158
% of LSR	100	27.7	23.6	24.8	38.8	49.2	65.3
Coverage	–	0.979	0.966	0.948	0.977	0.987	0.994
Sample completion	–	0.743	0.760	0.677	0.813	0.740	0.831

Table 1 (continued)

Student species richness includes all morphospecies (i.e. adults and juveniles)

three methods was considerably variable: 2015, three groups ($n = 282$, $S = 37$; $n = 353$, $S = 47$; $n = 210$, $S = 48$), 2016, two groups ($n = 338$, $S = 46$; $n = 193$, $S = 34$), 2018, one group ($n = 382$, $S = 60$), 2019, three groups ($n = 308$, $S = 47$; $n = 483$, $S = 66$; $n = 358$, $S = 64$) and 2020, two groups ($n = 1351$, $S = 95$; $n = 1237$, $S = 99$). When the number of species per year were pooled, however, species richness ranged between 57 and 94 for undergraduate student groups (2015–2019). Sampling in the final year of the study (2020), carried out by the author and two post-graduate students, yielded 119 species, representing almost half of the LSR (Table 1).

Sample coverage was high in all 5 years (> 0.940), with overall coverage for the cumulative fauna sampled over all 5 years 0.994. Sample completion values were more indicative of the number of groups involved in sampling, being lowest in 2018 when a single group participated in sampling (0.667), and > 0.740 when two or more groups participated (Table 1).

Over the course of the study, total spider abundance and species richness were relatively similar between the three habitats (Table 2). Species richness was slightly higher in the hillside grassland than the other two biotopes, while abundance was highest in the Nama Karoo veld and similar in the riparian woodland and hillside grassland. Sample coverage was above 0.75 for all three biotopes, and was highest in the hillside grassland, with 0.89 (Table 2).

Of the 40 families collected from Bankfontein, seven were only sampled by experienced collectors and not by student groups (Caponiidae, Migidae, Mimetidae, Pholcidae, Selenopidae, Stasimopidae and Tetragnathidae). These families are generally rare and often collected in particular microhabitats, explaining their absence from student samples. Depending on the family and habitat stratum, students collected variable proportions of the local species richness. For the most part, aside from the above exceptions, most families represented by only one or two species were successfully collected by students (Appendix 1). In total, 24 new species (~ 10% local species richness) can be confirmed from Bankfontein from recently revised genera or those currently being researched, although more than that number of species could not be identified with current literature, and may also be undescribed.

Table 2 Summary of overall spider abundance and species richness patterns sampled over 5 years on the farm Bankfontein in central South Africa, arranged by method and biotope

	Biotopes			Sampling methods			Total
	HG	NK	RW	BT	LL	PT	
S_{obs}	113	103	97	92	98	84	158
S_{Chao1}	126.921	135.000	113.133	148.250	166.643	110.281	192.133
Abundance	1740	1993	1762	2570	2144	781	5495
Coverage	0.987	0.988	0.988	0.988	0.986	0.963	0.994
Sample completion	0.890	0.763	0.857	0.621	0.588	0.762	0.822

BT vegetation beats, *HG* hillside grassland, *LL* leaf litter sifting, *NK* Nama Karoo veld, *PT* pitfall traps, *RW* riparian woodland

Success of sampling methods

The methodology employed by students was successful in sampling almost two-thirds of the LSR over a period of 5 years. The three sampling methods were similarly successful in generating species richness data, with litter sifting yielding the highest richness overall (98 spp.), followed by beating (92 spp.) and pitfall trapping (84 spp.). However, abundance was considerably more skewed: of the 5495 individuals collected, 2570 were collected by beating, 2144 by litter sifting, while pitfall trapping was far less successful (n = 781).

Of the three methods used, pitfall traps sampled the lowest number of species in all biotopes (Fig. 2a–c), while leaf litter sifting (Fig. 2d–f) and foliage beating (Fig. 2g–i) sampled more than twice as many species in all of the biotopes. The Nama Karoo veld produced the largest number of species for sifting and beating, while the hillside grassland had the highest species richness for pitfalls. On an annual accumulation basis, the slopes of the pitfalls had a generally consistent trajectory, suggesting that many additional species could still be sampled by this method. In contrast, the curves for beats and litter sifting increased sharply initially, but had declining slopes with an increasing
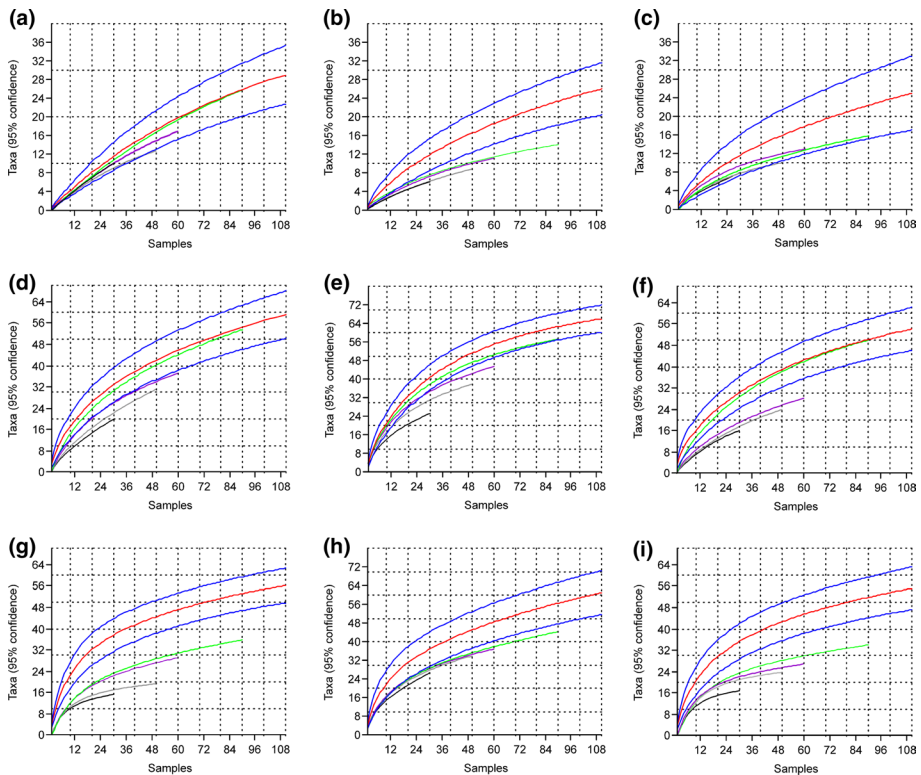

Fig. 2 Cumulating sample rarefaction curves of spider assemblages sampled using pitfall trapping (**a–c**), leaf litter sifting (**d–f**) and foliage beating (**g–i**) in hillside grassland (**a**, **d**, **g**), Nama Karoo veld (**b**, **e**, **h**) and riparian woodland (**c**, **f**, **i**) on the farm Bankfontein in central South Africa. Curve colours: black (2015; 30 samples), grey (2015–6; 50 samples), purple (2015–6, 2018; 60 samples), green (2015–6, 2018–9; 90 samples) and red (2015–6, 2018–2020; 110 samples). Blue lines indicate 95% confidence intervals for the full set of 110 samples

number of samples, suggesting that the majority of the species in the local species richness in these microhabitats had been sampled. Greater saturation was particularly evident for the beating sampling. However, none of the biotope-method curves approached an asymptote, indicating that more species could be sampled, as supported by the estimated species richness of each biotope (Table 2).

The numerically dominant families differed considerably between sampling methods (Table 3). Over the course of the study, Theridiidae, Oxyopidae, Philodromidae, Araneidae and Thomisidae each represented between 10–20% of the fauna sampled by beating. Almost half of the individuals sampled by litter sifting belonged to Gnaphosidae (48.74%), with Linyphiidae (27.71%) also very abundant. Pitfall traps were also strongly dominated by Gnaphosidae (40.72%) and Linyphiidae (28.17%), and to a lesser extent, Lycosidae (8.07%).

For eight of the nine site-method combinations, the 2020 samples yielded the largest number of species per sample, with the exception of the riparian woodland pitfall traps, which were highest in 2018 (Fig. 3). The pitfall traps and leaf litter sifting samples showed the least variability between years (Fig. 3a–f), but for beating the 2020 samples were considerably more profitable in generating species than the preceding years (Fig. 3g–i).

The distinctness of the pitfall samples was supported by the Sorensen's Quotient values generated for the three methods, which were markedly lower for pitfalls than the other two methods, indicating a relatively unique fauna in each biotope. Values were highest for beating, indicating considerable overlap between the arboreal spider faunas of the three biotopes (Table 4).

Table 3 Overall percentage spider family abundance sampled in three biotopes over 5 years on the farm Bankfontein in central South Africa using vegetation beating (BT), leaf litter sifting (LL) and pitfall traps (PT)

| Family	BT	LL	PT	Family	BT	LL	PT
Agelenidae	0.04	0.05	0.26	Oonopidae	0.04	1.21	0.38
Amaurobiidae	0.00	2.33	1.79	Orsolobidae	0.00	0.37	0.38
Ammoxenidae	0.00	0.00	0.13	Oxyopidae	17.04	0.33	0.38
Araneidae	12.65	0.84	1.28	Palpimanidae	0.00	0.65	0.38
Cheiracanthiidae	2.30	0.93	1.02	Philodromidae	14.24	4.15	1.15
Clubionidae	1.17	0.09	0.13	Pisauridae	1.79	0.14	0.26
Corinnidae	0.04	0.19	0.38	Salticidae	9.57	3.45	2.82
Cyatholipidae	0.04	0.05	0.00	Sparassidae	0.08	0.00	0.00
Cyrtaucheniidae	0.00	0.00	0.38	Symphytognathidae	0.04	0.00	0.00
Dictynidae	4.36	0.00	0.13	Theraphosidae	0.00	0.00	0.38
Eresidae	0.00	0.05	0.00	Theridiidae	19.46	2.52	3.07
Gnaphosidae	0.31	48.74	40.72	Theridiosomatidae	1.87	0.05	0.00
Hersiliidae	0.08	0.09	0.00	Thomisidae	11.83	2.10	1.54
Idiopidae	0.00	0.00	0.77	Trachelidae	2.14	0.89	0.77
Linyphiidae	0.70	27.71	28.17	Uloboridae	0.08	0.05	0.00
Liocranidae	0.00	0.00	0.51	Zodariidae	0.00	1.77	4.74
Lycosidae	0.16	1.26	8.07	Total	~100.00	~100.00	~100.00
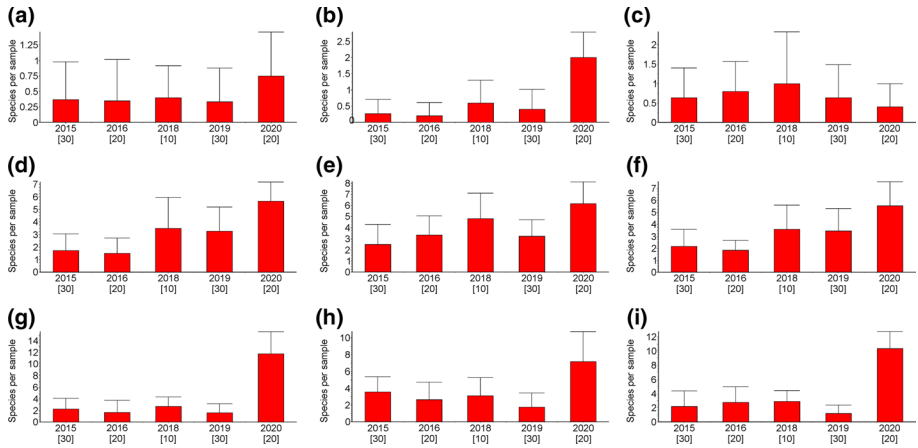
Fig. 3 Mean ± SD of spider species richness per sample collected using pitfall trapping (**a–c**), leaf litter sifting (**d–f**) and foliage beating (**g–i**) in hillside grassland (**a**, **d**, **g**), Nama Karoo veld (**b**, **e**, **h**) and riparian woodland (**c**, **f**, **i**) on the farm Bankfontein in central South Africa. Numbers in square parenthesis indicate the number of samples per year for each method, determined by the number of student groups

Table 4 Sorensen's quotient of similarity comparing species composition between habitats for three methods used to sample spiders at Bankfontein farm, South Africa

	Pitfalls		Litter		Beats	
	NK	HG	NK	HG	NK	HG
HG	0.433	–	0.542	–	0.655	–
RW	0.384	0.324	0.536	0.602	0.655	0.603

HG hillside grassland, *NK* Nama Karoo veld, *RW* riparian woodland

Discussion

Field excursions play a critical role in the development of students in the biological science fields of Zoology, Entomology and Botany, exposing them to the environment and the biodiversity components that they might spend their careers working on. By creating an understanding for the ecological roles of the fauna and flora in ecosystems, students are able to foster an appreciation for the interactions between organisms and the influence of anthropogenic impacts on biodiversity.

In the current study, the contribution of an undergraduate Entomology excursion in generating biodiversity data on a non-target arthropod group, spiders, was investigated. The annual spider species richness sampled by student groups was found to vary between 23.6 and 38.8% of the local species richness (i.e. all species sampled historically at the site). However, the highest value, generated in 2020 (49.2%) could be attributed to sampling having been undertaken by the author, a professional arachnologist with more than 20 years' experience, and two senior postgraduate students, because of the impacts of the COVID-19 pandemic prohibiting undergraduate excursions. The collecting effort in 2020 was therefore a simulation of two "student" groups, but the results clearly benefited by the considerably greater field experience of the three collectors. Furthermore, sorting spiders from the beat samples while specimens were still alive also had a strong positive effect on

their detectability and successful capture, compared to extracting dead spiders from euthanized samples, as was done by student groups.

While it could be suggested that the proportion of the local species richness sampled each year by students was not remarkably high, over the course of the 5 years' sampling the pooled data represented almost two-thirds of the local species richness (65.3%). Individually, sample completion values for each year ranged between 67.7 and 81.3%, indicating that the standardised protocol (i.e. 10 samples taken with each of three methods in three biotopes by each student group) was very effective in sampling the species that could potentially be sampled by these three methods.

When the Chao1 estimated species richness of Bankfontein based on the student sampling is considered (192 spp.; Table 2), there would still be 50 species forming part of the local species richness pool (242 spp.; Appendix 1) not collected by the three methods. Similarly, the disparity between the proportion of local species richness sampled and the sample completion values of student groups could be attributed to the sampling of rare and ecologically specialised species by more experienced arachnologists, particularly in microhabitats not sampled as part of the protocol (e.g. grass tussocks, on or beneath rocks and logs, etc.), and hand collecting at night, which would have sampled nocturnally active species.

Although the three methods sampled quite similar spider species richness, the abundance of spiders sampled by pitfall traps was approximately three times lower than by litter sifting or beating. Creating a more comparable sampling protocol by increasing the numbers of individuals sampled by pitfalls to a level similar to the other methods could follow either of three approaches: (1) the number of pitfalls per biotope could be tripled, (2) considerably larger pitfall traps could be employed, to sample a larger number of rare species (see Work et al. 2002), or (3) drift fences could be added to the trapping setup, which in the case of spiders, dramatically increases pitfall catches (Boetzl et al. 2018).

Two of these proposed changes present their own problems. Although increasing the pitfall trap size to 15 cm might approximately triple the spider catch (Work et al. 2002), making it more comparable, digging such large holes would certainly be more time-consuming, which in the context of a time-restricted field excursion may not be practical. Using a ground augur to rapidly dig holes that fit the 6 cm bottles is a lot more feasible, and even tripling the sampling effort may take less time than digging large holes. In either case, increasing the sampling effort to generate comparable numbers of individuals would considerably boost the species richness of pitfall samples, probably to levels far higher than the other two methods, as suggested by the sample rarefaction curves and Sørensen's Quotient values. A drawback of fences is that they show a strong bias to sampling highly active spider species, which skews abundance data and assemblage composition (Brennan et al. 2005). It would therefore seem that tripling the sampling effort for pitfalls of the same size used in this study would be the simplest approach to generate abundance data comparable to beating and litter sifting in future surveys.

It is informative that despite pitfalls sampling far fewer individuals than the other two methods, and approximately only half the number of species than the other methods in each biotope, that overall pitfall species richness was quite similar to them (Table 2). This suggests that the litter and foliage assemblages each show considerable overlap between biotopes, while pitfalls generate far more distinctive assemblages and more unique species per biotope, which is supported by the Sørensen's similarity values, species richness estimators, and slopes of the sample rarefaction curves.

Patterns in the faunistic composition of the assemblages sampled are quite consistent with other studies in semi-arid South Africa. Gnaphosidae are frequently the most abundant

and/or species richness family of ground-dwelling (e.g. Lotz et al. 1991; Haddad and Dippenaar-Schoeman 2002, 2005; Haddad et al. 2015; Haddad and Butler 2018) and litter-dwelling spiders (Butler and Haddad 2011; Haddad et al. 2019) in grasslands and Nama Karoo biotopes in central South Africa, and were strongly dominant in both respects here (Appendix 1; Table 3). In contrast, vegetation sampled by beating did not have a strongly dominant family, but rather several moderately dominant families (10–20% of abundance), which is generally similar to patterns seen in two grassland studies (Fourie et al. 2013; Neethling & Haddad 2013), where Araneidae, Philodromidae, Salticidae, Theridiidae and Thomisidae were the most abundant and species-rich groups.

In conclusion, this study demonstrated the value of utilizing student groups for sampling arthropods using a standardised protocol to generate biodiversity data, supporting recent studies on spiders (e.g. Cardoso et al. 2017; Kiljunen et al. 2020; Soukainen et al. 2020). The data generated can be utilised to elucidate patterns in biodiversity between different biotopes and sampling years, and also facilitates comparison of the efficacy of different sampling methods by students. It is worthwhile pointing out to students that despite the hard work and effort required to successfully complete sampling and processing of the collected material, that the data generated has broader application value to the biological and conservation community. Further, such training may foster an interest in future participation in citizen science, expanding their impact in the generation of biodiversity data (Theobald et al. 2015; Chandler et al. 2016).

These results also highlight the need to use opportunities such as student excursions, BioBlitz field trips or international volunteer programmes to address the biodiversity deficit in developing countries across the globe, but particularly in under-resourced Africa. This approach need not be restricted to arthropods such as spiders (although any order could potentially benefit greatly from such data and specimen generation), but also to any group of animals and plants that students may potentially be exposed to during their undergraduate or graduate training. The basic principle of developing a suitable standardised sampling protocol for use on a particular organismal group would set the foundation for successful generation and use of biodiversity data for conservation and management purposes.

Appendix 1

Local species richness of spiders sampled from Bankfontein farm, South Africa. Numbers recorded for each species refer to specimens sampled exclusively as part of student sampling during 2015, 2016 and 2018–2020. Numbers in family rows indicate number of species sampled by students, followed by % of species sampled by a particular method by total species per family sampled by students overall, followed by % of species sampled by students of the local species richness for that family. Symbols: ?—uncertain identification; †—new species; imm—immatures only; indet—undetermined due to lack of taxonomic resources

Family/species	Pitfalls	Litter	Beats
Agelenidae	1/50.0/50.0	1/50.0/50.0	1/50.0/50.0
Agelena sp. indet	2		1
Benoitia sp. indet		1	
Amaurobiidae	1/50.0/25.0	2/100.0/50.0	0

Family/species	Pitfalls	Litter	Beats
Obatala sp. indet	14	15	
Pseudauximus sp. indet			
New genus 1[†]		35	
New genus 2[†]			
Ammoxenidae	2/100.0/50.0	0	0
Ammoxenus pentheri Simon, 1896	1		
Ammoxenus sp. 2[†]			
Araneidae	2/40.0/18.2	3/60.0/27.3	5/100.0/45.5
Argiope australis (Walckenaer, 1805)			
Cyclosa insulana (Costa, 1834)		5	65
Cyphalonotus sp. indet			3
Hypsosinga sp. indet	6	6	1
Isoxya stuhlmanni (Bösenberg & Lenz, 1885)			
Nemoscolus elongatus Lawrence, 1947			
Nemoscolus tubicola (Simon, 1887)			
Neoscona blondeli (Simon, 1885)			
Neoscona subfusca (C.L. Koch, 1837)	4	7	251
Neoscona triangula (Keyserling, 1864)			
Pararaneus spectator (Karsch, 1886)			5
Caponiidae	0	0	0
Caponia hastifera Purcell, 1904			
Cheiracanthiidae	1/50.0/50.0	1/50.0/50.0	2/100.0/100.0
Cheiracanthium furculatum Karsch, 1879	8	20	56
Cheiramiona upperbyensis Lotz, 2015			3
Clubionidae	1/100.0/100.0	1/100.0/100.0	1/100.0/100.0
Clubiona sp. 1[†]	1	2	30
Corinnidae	2/100.0/50.0	1/50.0/25.0	1/50.0/25.0
Castianeira sp. 1[†]			
Castianeira sp. 2[†]			
Copa flavoplumosa Simon, 1885	2	4	1
Copuetta lacustris (Strand, 1916)	1		
Cyatholipidae	0	1/50.0/50.0	1/50.0/50.0
Cyatholipus hirsutissimus Simon, 1894		1	
Cyatholipus sp. 2[†]			1
Cyrtaucheniidae	2/100.0/100.0	0	0
Ancylotrypa sp. indet	2		
Homostola sp. indet	1		
Dictynidae	1/50.0/50.0	0	2/100.0/100.0
Dictyna sp. 1 indet	1		96
Dictyna sp. 2 indet			16
Eresidae	0	1/50.0/50.0	0
Dresserus sp. indet		1	
Seothyra schreineri Purcell, 1903			
Gnaphosidae	15/65.2/41.7	20/87.0/55.6	7/30.4/19.4
Aphantaulax sp. indet			1
Asemesthes albovittatus Purcell, 1908	18	6	1

Family/species	Pitfalls	Litter	Beats
Asemesthes lineatus Purcell, 1908	2	9	
Asemesthes oconnori Tucker, 1923	3	4	
Asemesthes purcelli Tucker, 1923			
Asemesthes reflexus Tucker, 1923			
Austrodomus scaber (Purcell, 1904)	2	5	
Camillina cordifera (Tullgren, 1910)	86	310	
Camillina maun Platnick & Murphy, 1987	2	94	
Drassodes sp. indet	13	16	1
Eilica lotzi FitzPatrick, 2002	5	2	
Eleleis sp.[†]		1	
Leptodrassex sp.[†]			
Megamyrmaekion sp.			
Micaria beaufortia (Tucker, 1923)	26	11	2
Micaria felix Booysen & Haddad, 2021			
Nomisia sp. indet		6	
Pterotricha sp. indet	1		
Setaphis subtilis (Simon, 1879)			
Smionia lineatipes (Purcell, 1908)			
Theuma ababensis Tucker, 1923			
Theuma fusca Purcell, 1907	6	3	
Trachyzelotes sp. indet		1	
Trichothyse sp. indet			1
Upognampa sp. indet		5	
Xerophaeus aridus Purcell, 1907	3	3	1
Xerophaeus spoliator Purcell, 1907			
Zelotes albanicus (Hewitt, 1915)			
Zelotes capensis FitzPatrick, 2007			
Zelotes florisbad FitzPatrick, 2007			
Zelotes frenchi Tucker, 1923	12	171	
Zelotes fuligineus (Purcell, 1907)	1	3	
Zelotes lavus Tucker, 1923			
Zelotes sclateri Tucker, 1923		48	
Zelotes scrutatus (O.P.-Cambridge, 1872)		10	
Zelotes sp. imm	138	337	1
Hersiliidae	0	1/50.0/50.0	1/50.0/50.0
Hersilia sp.[†]			2
Tyrotama australis (Simon, 1893)		2	
Idiopidae	1/50.0/50.0	0	0
Idiops monticola (Hewitt, 1916)	6		
Segregara sp. indet			
Linyphiidae	5/71.4/35.7	3/42.9/21.4	7/100.0/50.0
Agyneta habra (Locket, 1968)	39	214	5
Agyneta prosectoides (Locket & Russell-Smith, 1980)			3
Agyneta sp. 3 indet			
Ceratinopsis dippenaari Jocqué, 1984			
Ceratinopsis idanrensis Locket & Russell-Smith, 1980?			

Family/species	Pitfalls	Litter	Beats
Metaleptyphantes familiaris Jocque, 1984			1
Microlinyphia sterilis (Pavesi, 1883)			
Nereine sp. indet	1		1
Ostearius melanopygius (O.P.-Cambridge, 1879)	9	26	1
Pelecopsis janus Jocqué, 1984	169	354	5
Pelecopsis sp. 2 indet			
Proelauna humicola (Miller, 1970)			
Prinerigone sp. indet	2		2
Tybaertiella sp. indet.?			
Liocranidae	1/100.0/100.0	0	0
Rhaeboctesis sp. indet	4		
Lycosidae	9/100.0/69.2	5/55.6/38.5	2/22.2/15.4
Allocosa sp. indet			
Amblyothele sp. indet	1		
Evippomma squamulatum (Simon, 1898)	3		
Hogna transvaalica (Simon, 1898)	1	1	
Pardosa clavipalpis Purcell, 1903?			
Pardosa crassipalpis Purcell, 1904	13		3
Pardosa manubriata Simon, 1898			
Proevippa albiventris (Simon, 1898)	12	23	1
Proevippa fascicularis (Purcell, 1903)			
Trabea purcelli Roewer, 1951	1	1	
Tricassa sp. indet	1	1	
Trochosa sp. indet	30	1	
Zenonina mystacina Simon, 1898	1		
Migidae	0	0	0
Moggridgea sp. indet			
Mimetidae	0	0	0
Mimetus sp.[†]			
Oonopidae	1/25.0/16.7	4/100.0/66.7	1/25.0/16.7
Australoonops sp.[†]			
Dysderina sp. indet		1	
Opopaea sp.[†]		11	
Orchestina sp.[†]		5	1
Oonopidae sp. 1 indet	3	9	
Oonopidae sp. 2 indet			
Orsolobidae	1/50.0/50.0	2/100.0/100.0	0
Afrilobus sp.[†]	3	6	
Azanialobus sp.[†]		2	
Oxyopidae	2/40.0/25.0	1/20.0/12.5	5/100.0/62.5
Oxyopes bothai Lessert, 1915	2	7	220
Oxyopes russoi Caporiacco, 1940			20
Oxyopes sp. 3 indet			1
Oxyopes sp. 4 indet	1		182
Peucetia transvaalica Simon, 1896			15
Oxyopes jacksoni Lessert, 1915			

Family/species	Pitfalls	Litter	Beats
Oxyopes vogelsangeri Lessert, 1946?			
Peucetia viridis (Blackwall, 1858)			
Palpimanidae	2/100.0/100.0	2/100.0/100.0	0
Diaphorocellus biplagiatus Simon, 1893	2	4	
Palpimanus sp. indet	1	10	
Philodromidae	5/71.4/50.0	6/85.7/60.0	5/71.4/50.0
Hirriusa arenacea (Lawrence, 1927)	2		
Hirriusa bidentata (Lawrence, 1927)			
Philodromus bigibbus (O. P.-Cambridge, 1876)	1	3	14
Philodromus brachycephalus Lawrence, 1952	1	69	
Philodromus browningi Lawrence, 1952		1	29
Philodromus sp. 4 indet	4	13	288
Philodromus sp. 5 indet		1	20
Thanatus lamottei Jézéquel, 1964?	1	2	15
Thanatus vulgaris Simon, 1870			
Tibellus minor Lessert, 1919			
Pholcidae	0	0	0
Smeringopus lotzi Huber, 2012			
Pisauridae	1/100.0/50.0	1/100.0/50.0	1/100.0/50.0
Rothus vittatus Simon, 1898	2	3	46
Cispius kimbius Blandin, 1978			
Salticidae	9/40.1/25.7	13/59.1/37.1	17/77.2/48.9
Baryphas ahenus Simon, 1902		1	17
Cyrba nigrimana Simon, 1900		1	
Evarcha denticulata Wesołowska & Haddad, 2013		6	1
Heliophanus charlesi Wesołowska, 2003			1
Heliophanus nanus Wesołowska, 2003			
Heliophanus patellaris Simon, 1901?			
Heliophanus pistaciae Wesołowska, 2003	1	9	15
Hispo georgius (Peckham & Peckham, 1892)		11	
Hyllus dotatus (Peckham & Peckham, 1903)			2
Icius insolidus (Wesołowska, 1999)		5	5
Langona hirsuta Haddad & Wesołowska, 2011	2	4	2
Langona warchalowskii Wesołowska, 2007			
Menemerus rubicundus Lawrence, 1928			
Menemerus transvaalicus Wesołowska, 1999			
Menemerus sp. 3[†]			
Mexcala rufa Peckham & Peckham, 1902			
Natta horizontalis Karsch, 1879	4	15	1
Pellenes bulawayoensis Wesołowska, 1999			
Pellenes epularis (O. Pickard-Cambridge, 1872)			
Pellenes geniculatus (Simon, 1868)	2		1
Pellenes modicus Wesołowska & Russell-Smith, 2000			
Pellenes tharinae Wesołowska, 2006			
Phlegra bresnieri (Lucas, 1846)		5	
Phlegra etosha Wesołowska, 2006	1		

Family/species	Pitfalls	Litter	Beats
Phlegra karoo Wesołowska, 2006	5	6	
Pignus simoni (Peckham & Peckham, 1903)	5	8	37
Propiomarengo plana (Haddad & Wesołowska, 2013)			3
Psenuc dependens (Haddad & Wesołowska, 2011)	1	1	57
Rhene konradi Wesołowska, 2009			
Rhene lingularis Haddad & Wesołowska, 2011			
Thyene coccineovittata (Simon, 1885)			1
Thyene inflata (Gerstäcker, 1873)	1		72
Thyene natalii Peckham & Peckham, 1903			3
Thyene thyenioides (Lessert, 1925)			1
Tusitala barbata Peckham & Peckham, 1902		2	27
Selenopidae	0	0	0
Anyphops karrooicus (Lawrence, 1940)?			
Anyphops sp.[†]			
Selenops sp. indet			
Sparassidae	0	0	2/100.00/66.7
Palystes sp.			1
Olios correvoni Lessert, 1921			1
Pseudomicrommata longipes (Bösenberg & Lenz, 1895)			
Stasimopidae	0	0	0
Stasimopus sp. indet			
Symphytognathidae	0	0	1/100.0/100.0
Symphytognathidae sp. 1 indet			1
Tetragnathidae	0	0	0
Tetragnatha sp. imm			
Theraphosidae	1/100.0/100.0	0	0
Harpactira sp. indet	3		
Theridiidae	6/40.0/33.3	8/53.3/44.4	12/80.0/66.7
Anelosimus sp. indet	2	3	26
Enoplognatha molesta O.P.-Cambridge, 1904	7	15	173
Euryopis episinoides (Walckenaer, 1847)?		3	1
Euryopis funebris (Hentz, 1850)?	5	14	
Euryopis sp. 3 indet	2	16	
Histagonia sp. indet	1	1	1
Latrodectus geometricus C.L. Koch, 1841			2
Latrodectus renivulvatus Dahl, 1902			
Phoroncidia sp. indet			
Phycosoma sp. indet		1	4
Steatoda erigoniformis (O.P.-Cambridge, 1872)?	7		
Theridion purcelli O.P.-Cambridge, 1904			18
Theridion sp. 2 indet		2	106
Theridion sp. 3 indet			6
Theridion sp. 4 indet			156
Theridion sp. 5 indet			
Thymoites sp. indet			4
Tidarren sp. indet			3

Family/species	Pitfalls	Litter	Beats
Theridiosomatidae	0	1/100.0/100.0	1/100.0/100.0
Theridiosomatidae sp. indet		1	48
Thomisidae	3/23.1/14.3	7/63.6/33.3	11/84.6/52.4
Ansiae tuckeri (Lessert, 1919)			24
Diaea puncta Karsch, 1884			2
Firmicus abnormis (Lessert, 1923)			29
Heriaeus allenjonesi Van Niekerk & Dippenaar-Schoeman, 2013		1	3
Misumenops rubrodecoratus Millot, 1942			76
Monaeses pustulosus Pavesi, 1895			7
Oxytate sp. indet		1	3
Pherecydes tuberculatus O.P.-Cambridge, 1883		1	33
Simorcus lotzi Van Niekerk & Dippenaar-Schoeman, 2010	2	9	45
Stiphropus sp. indet			
Synema sp. indet			
Thomisops sulcatus Simon, 1895	9	29	
Thomisus australis Comellini, 1958			
Thomisus dalmasi Lessert, 1919			
Thomisus stenningi Pocock, 1900			
Thomisus kalaharinus Lawrence, 1936			
Thomisus schultzei Simon, 1910			
Thomisus sp. imm			34
Tmarus sp. indet		1	48
Xysticus natalensis Lawrence, 1938			
Xysticus sagittifer Lawrence, 1927	1	3	
Trachelidae	3/37.5/33.3	5/62.5/55.6	5/62.5/55.6
Afroceto africana (Simon, 1910)	4	9	12
Capobula montana Haddad et al., 2021			
Fuchibotulus sp.[†]		1	
Orthobula sp.[†]			1
Thysanina gracilis Lyle & Haddad, 2006	1	7	40
Thysanina sp. 2[†]		1	
Thysanina sp. 3[†]			1
Trachelas pusillus Lessert, 1923	1	1	
Trachelas sp. 2[†]			1
Uloboridae	0	1/100.0/50.0	1/100.0/50.0
Uloborus plumipes Lucas, 1846		1	2
Uloborus walckenaerius Latreille, 1806			
Zodariidae	7/87.5/70.0	7/87.5/70.0	0
Caesetius sp. indet	1	1	
Capheris sp. indet	9	28	
Cydrela sp. indet	1	1	
Diores femoralis Jocqué, 1990		1	
Diores poweri Tucker, 1920	11	5	
Diores triangulifer Simon, 1910			
Dusmadiores sp.?	1		

Family/species	Pitfalls	Litter	Beats
Heradida loricata Simon, 1893			
Mallinus nitidiventris Simon, 1893	10	1	
Ranops sp.[†]	4	1	
Total spider abundance	781	2144	2570
Student species richness	84	97	92

Data availability https://doi.org/10.5061/dryad.v15dv41w1.

Code availability Not applicable.

Declarations

Conflict of interest The author declares no conflict of interest with any party.

Ethical approval This research was conducted under permits 10/25209, NC.614/2017 and 201911000003852 of the Free State Department of Economic Development, Tourism and Environmental Affairs.

Consent to participate Not applicable.

Consent for publication Not applicable.

References

Barbier EB, Burgess JV, Dean TJ (2018) How to pay for saving biodiversity. Science 360:486–488. https://doi.org/10.1126/science.aar3454

Boetzl FA, Ries E, Schneider G, Krauss J (2018) It's a matter of design—how pitfall trap design affects trap samples and possible predictions. PeerJ 6:e5078. https://doi.org/10.7717/peerj.5078

Brennan KEC, Majer JD, Moir ML (2005) Refining sampling protocols for inventorying invertebrate biodiversity: influence of drift-fence length and pitfall trap diameter on spiders. J Arachnol 33:681–702

Buschke FT, Seaman MT (2011) Functional feeding groups as a taxonomic surrogate for a grassland arthropod assemblage. Afr Invert 52:217–228

Butler VP, Haddad CR (2011) Spider assemblages associated with leaf litter of three tree species in central South Africa (Arachnida: Araneae). Afr J Ecol 49:301–310. https://doi.org/10.1111/j.1365-2028.2011.01265.x

Cardoso P, Heikkinen L, Jalkanen J, Kohonen M, Leponiemi M, Mattila L, Ollonen J, Ranki J, Virolainen A, Zhou X, Pajunen T (2017) Standardized spider (Arachnida, Araneae) inventory of Hankoniemi, Finland. Biodivers Data J 5:e21010. https://doi.org/10.3897/BDJ.5.e21010

Chandler M, See L, Copas K, Bonde AM, López BC, Danielsen F, Legind JK, Masinde S, Miller-Rushing AJ, Newman G (2016) Contribution of citizen science towards international biodiversity monitoring. Biol Conserv 213:280–294

Chao A, Jost L (2012) Coverage-based rarefaction and extrapolation: standardizing samples by completeness rather than size. Ecology 93:2533–2547. https://doi.org/10.1890/11-1952.1

Chao A, Lee SM (1992) Estimating the number of classes via sample coverage. J Am Stat Assoc 87:210–217

Costello MJ (2015) Biodiversity: the known, unknown, and rates of extinction. Curr Biol 25:R368–R371. https://doi.org/10.1016/j.cub.2015.03.051

Cowling RM, Hilton-Taylor C (1994) Patterns of plant diversity and endemism in southern Africa: an overview. In: Huntley BJ (ed) Botanical Diversity in Southern Africa. Strelitzia 1. National Botanical Institute, Pretoria, pp 33–54.

Dikmenli M (2010) Biology student teachers' conceptual frameworks regarding biodiversity. Education 130:479–489

Dippenaar-Schoeman AS, Haddad CR, Foord SH, Lyle R, Lotz LN, Marais P (2015) South African National Survey of Arachnida (SANSA): review of current knowledge, constraints and future needs for documenting spider diversity (Arachnida: Araneae). Trans R Soc S Afr 70:245–275. https://doi.org/10.1080/0035919X.2015.1088486

Foord SH, Dippenaar-Schoeman AS, Haddad CR (2011) South African spider diversity: African perspectives on the conservation of a mega-diverse group. In: Grillo O, Venora G (eds) Changing diversity in changing environment. InTech Publishing, Rijeka, pp 163–182

Foord SH, Dippenaar-Schoeman AS, Haddad CR, Lyle R, Lotz LN, Sethusa T, Raimondo D (2020) The South African National Red List of spiders: patterns, threats, and conservation. J Arachnol 48:110–118. https://doi.org/10.1636/0161-8202-48.2.110

Fourie R, Haddad CR, Dippenaar-Schoeman AS, Grobler A (2013) Ecology of the plant-dwelling spiders (Arachnida: Araneae) of the Erfenis Dam Nature Reserve. South Africa Koedoe 55:1113. https://doi.org/10.4102/koedoe.v55i1.1113

Haddad CR, Butler VP (2018) Ground-dwelling spider assemblages in contrasting habitats in the central South African Grassland Biome. Koedoe 60:a1482. https://doi.org/10.4102/koedoe.v60i1.1482

Haddad CR, Dippenaar-Schoeman AS (2002) The influence of mound structure on the diversity of spiders (Araneae) inhabiting the abandoned mounds of the snouted harvester termite *Trinervitermes trinervoides* (Sjöstedt). J Arachnol 30:403–408. https://doi.org/10.1636/0161-8202(2002)030[0403:TIOMSO]2.0.CO;2

Haddad CR, Dippenaar-Schoeman AS (2005) Epigeic spiders (Arachnida: Araneae) in Nama Karoo grassland in the Northern Cape Province. Navorsinge Van Die Nasionale Museum, Bloemfontein 21:1–10

Haddad CR, Dippenaar-Schoeman AS, Foord SH, Lotz LN, Lyle R (2013) The faunistic diversity of spiders (Arachnida: Araneae) of the Grassland Biome in South Africa. Trans R Soc S Afr 68:97–122. https://doi.org/10.1080/0035919X.2013.773267

Haddad CR, Foord SH, Fourie R, Dippenaar-Schoeman AS (2015) Effects of a fast-burning spring fire on the ground-dwelling spider assemblages (Arachnida: Araneae) in a central South African grassland habitat. African Zoology 50:281–292. https://doi.org/10.1080/15627020.2015.1088400

Haddad CR, de Jager L, Foord SH (2019) Habitats and cardinal directions are key variables structuring spider leaf litter assemblages under *Searsia lancea*. Pedobiologia 73:10–19. https://doi.org/10.1016/j.pedobi.2019.01.002

Hammer Ø, Harper DAT, Ryan PD (2001) PAST – PAlaeontological STatistics. Palaeontol Electronica 4:1–9

Hochkirch A, Samways MJ, Gerlach J, Böhm M, Williams P, Cardoso P, Cumberlidge N, Stephenson PJ, Seddon MB, Clausnitzer V, Borges PAV, Mueller GM, Pearce-Kelly P, Raimondo DC, Danielczak A, Dijkstra KDB (2021) A strategy for the next decade to address data deficiency in neglected biodiversity. Conserv Biol 35:502–509. https://doi.org/10.1111/cobi.13589

Kaiser W, Avenant N, Haddad CR (2009) Assessing the ecological integrity of a grassland ecosystem: refining the SAGraSS method. Afr J Ecol 47:308–317. https://doi.org/10.1111/j.1365-2028.2008.00962.x

Kiljunen N, Pajunen T, Fukushima C, Soukainen A, Kuurne J, Korhonen T, Saarinen J, Falck I, Laine E, Mammola S, Urbano F, Macías-Hernández N, Cardoso P (2020) Standardised spider (Arachnida, Araneae) inventory of Kilpisjärvi, Finland. Biodivers Data J 8:e56486. https://doi.org/10.3897/BDJ.8.e56486

Lamarre GPA, Juin Y, Lapied E, Le Gall P, Nakamura A (2018) Using field-based entomological research to promote awareness about forest ecosystem conservation. Nat Conserv 29:39–56. https://doi.org/10.3897/natureconservation.29.26876

Lees AC, Pimm SL (2015) Species, extinct before we know them? Curr Biol 25:R177–R180. https://doi.org/10.1016/j.cub.2014.12.017

Lewandowski E, Specht H (2015) Influence of volunteer and project characteristics on data quality of biological surveys. Conserv Biol 29:713–723. https://doi.org/10.1111/cobi.12481

Lotz LN, Seaman MT, Kok DJ (1991) Surface active spiders (Araneae) of a site in semi-arid central South Africa. Navorsinge Van Die Nasionale Museum, Bloemfontein 7:529–540

Lovell SJ, Hamer ML, Slotow RH, Herbert D (2010) Assessment of sampling approaches for a multi-taxa invertebrate survey in a South African savanna-mosaic ecosystem. Austral Ecol 35:357–370. https://doi.org/10.1111/j.1442-9993.2009.02052.x

Magurran AE (2004) Measuring biological diversity. Blackwell, Bodmin

Mittermeier RA, Turner WR, Larsen FW, Brooks TM, Gascon C (2011) Global biodiversity conservation: the critical role of hotspots. In: Zachos FE, Habel JC (eds) Biodiversity hotspots. Springer, Berlin, pp 3–22.

Mokany K, Ferrier S, Harwood TD, Ware C, Di Marco M, Grantham HS, Venter O, Hoskins AJ, Watson JEM (2020) Reconciling global priorities for conserving biodiversity habitat. PNAS 117:9906–9911. https://doi.org/10.1073/pnas.1918373117

Mucina L, Rutherford MC (eds) (2006) The vegetation of South Africa, Lesotho and Swaziland. Strelizia 19. South African National Biodiversity Institute, Pretoria.

Mucina L, Hoare DB, Lotter MC, Du Preez PJ, Rutherford MC, Scott-Shaw R, Bredenkamp GJ, Powrie LW, Scott L, Camp KGT, Cilliers SS, Bezuidenhout H, Mostert TH, Siebert SJ, Winter PJD, Burrows JE, Dobson L, Ward RA, Stalmans M, Oliver EGH, Siebert F, Schmidt E, Kobisi K, Kose L (2006a) Grassland biome. In: Mucina L, Rutherford MC (eds) The vegetation of South Africa, Lesotho and Swaziland. Strelitzia 19. South African National Biodiversity Institute, Pretoria, pp 349–437.

Mucina L, Rutherford MC, Palmer AR, Milton SJ, Scott L, Lloyd JW, Van der Merwe B, Hoare DB, Bezuidenhout H, Vlok JHJ, Euston-Brown DIW, Powrie LW, Dold AP (2006b) Nama-Karoo Biome. In: Mucina L, Rutherford MC (eds) The vegetation of South Africa, Lesotho and Swaziland. Strelitzia 19. South African National Biodiversity Institute, Pretoria, pp 324–347.

Myers N, Mittermeier RA, Mittermeier CG, Da Fonseca GAB, Kent J (2000) Biodiversity hotspots for conservation priorities. Nature 403:853–858. https://doi.org/10.1038/35002501

Neethling JA, Haddad CR (2013) Arboreal spider assemblages associated with four tree species in the Grassland Biome of central South Africa (Arachnida: Araneae). Transactions of the Royal Society of South Africa 68:123–131. https://doi.org/10.1080/0035919X.2013.806374

Oberprieler SK, Andersen AN, Braby MF (2019) Invertebrate by-catch from vertebrate pitfall traps can be useful for documenting patterns of invertebrate diversity. J Insect Conserv 23:547–554. https://doi.org/10.1007/s10841-019-00143-z

Robertson MP, Cumming GS, Erasmus BFN (2010) Getting the most out of atlas data. Divers Distrib 16:363–375. https://doi.org/10.1111/j.1472-4642.2010.00639.x

Soukainen A, Pajunen T, Korhonen T, Saarinen J, Chichorro F, Jalonen S, Kiljunen N, Koskivirta N, Kuurne J, Leinonen S, Salonen T, Yrjölä V, Fukushima C, Cardoso P (2020) Standardised spider (Arachnida, Araneae) inventory of Lammi, Finland. Biodivers Data J 8:e50775. https://doi.org/10.3897/BDJ.8.e50775

Supriatna J, Leo S, Anugra BG, Dwiyahreni AA, Winarni NL, Margules C (2020) Lessons learned from training students to conduct primate surveys. Primate Conserv 34:217–225

Theobald EJ, Ettinger AK, Burgess HK, Debey LB, Schmidt NR, Froehlich HE, Wagner C, Hillerislambers J, Tewksbury J, Harsch MA, Parrish JK (2015) Global change and local solutions: tapping the unrealized potential of citizen science for biodiversity research. Biol Conserv 181:236–244. https://doi.org/10.1016/j.biocon.2014.10.021

Tolley KA, Weeber J, Maritz B, Verburgt L, Bates MF, Conradie W, Hofmeyr MD, Turner AA, Da Silva JM, Alexander GJ (2019) No safe haven: protection levels show imperilled South African reptiles not sufficiently safe-guarded despite low average extinction risk. Biol Conserv 233:61–72. https://doi.org/10.1016/j.biocon.2019.02.006

Triplehorn CA, Johnson NF (2005) Borror and DeLong's introduction to the study of insects, 7th edn. Thompson Brooks/Cole, Belmont

Victor JE, Smith GF, Van Wyk AE (2015) A method for establishing taxonomic research priorities in a megadiverse country. Phytotaxa 203:55–62. https://doi.org/10.1590/sajs.2013/1182

Work TT, Buddle CM, Korinus LM, Spence JR (2002) Pitfall trap size and capture of three taxa of litter-dwelling arthropods: implications for biodiversity studies. Environ Entomol 31:438–448. https://doi.org/10.1603/0046-225X-31.3.438

World Spider Catalog (2021) World Spider Catalog. Version 22.5. Natural History Museum Bern. http://wsc.nmbe.ch. Accessed 11 Aug 2021.

Yang LH, Gratton C (2014) Insects as drivers of ecosystem processes. Curr Opin Insect Sci 2:26–32. https://doi.org/10.1016/j.cois.2014.06.004

Yli-Panula E, Jeronen E, Lemmetty P, Pauna A (2018) Teaching methods in biology promoting biodiversity education. Sustainability 10:3812. https://doi.org/10.3390/su10103812