

# Scientific Writing

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African Leadership University  
Kigali, Rwanda  
October 2021

SCCS Conference  
Tihány, Hungary  
August 2020

# Scientific Writing

# Scientific Writing

- One of the most important skills for scientists, but largely overlooked

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- Cover the basics of scientific writing



# Scientific Writing

- One of the most important skills for scientists, but largely overlooked
- Cover the basics of scientific writing
  - Scientific papers but largely applicable to grants and other forms of writing and even presentations!



Perspective

## Setting the Terms for Zoonotic Diseases: Effective Communication for Research, Conservation, and Public Policy

Julie Teresa Shapiro <sup>1,\*</sup>, Luis Viquez-R <sup>2</sup>, Stefania Leopardi <sup>3</sup>, Amanda Vicente-Santos <sup>4</sup>, Ian H. Mendenhall <sup>5</sup>, Winifred F. Frick <sup>6,7</sup>, Rebekah C. Kading <sup>8</sup>, Rodrigo A. Medellín <sup>9</sup>, Paul Racey <sup>10</sup> and Tigga Kingston <sup>11,\*</sup>

Heliyon 7 (2021) e06563



Contents lists available at [ScienceDirect](#)

**Heliyon**

journal homepage: [www.cell.com/heliyon](http://www.cell.com/heliyon)



Research article

Influence of sugarcane growth stages on bird diversity and community structure in an agricultural-savanna environment

Sifiso M. Lukhele <sup>a,d,\*</sup>, Julie Teresa Shapiro <sup>c</sup>, Them'b'alilahlwa A.M. Mahlaba <sup>a</sup>, Muzi D. Sibiya <sup>a,e</sup>, Robert A. McCleery <sup>e</sup>, Robert J. Fletcher Jr. <sup>e</sup>, Ara Monadjem <sup>a,b</sup>

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<sup>b</sup> Mammal Research Institute, Department of Zoology and Entomology, University of Pretoria, Private Bag 20, Hatfield, 0028, Pretoria, South Africa

<sup>c</sup> CIRI, Centre International de Recherche en Infectiologie, Université de Lyon, Inserm U1111, Université Claude Bernard Lyon 1, CNRS UMR5308, Ecole Normale Supérieure de Lyon, 46 Allée d'Italie, Lyon, 69007, France

<sup>d</sup> Department of Biological Sciences, University of Cyprus, P O Box 20537, Nicosia, 1678, Cyprus

<sup>e</sup> Department of Wildlife Ecology and Conservation, University of Florida, Gainesville, FL, 32611-0430, USA



Where to start???

# Where to start???

- Remember your goal: to tell a story by conveying your results

# Scientific Writing Style

# Scientific Writing Style

- Use simple, direct, short sentences. Avoid long sentences with many subsections / clauses.

# Scientific Writing Style

- Use simple, direct, short sentences. Avoid long sentences with many subsections / clauses.
  - May differ from other languages where complex sentences are preferred.

# Scientific Writing Style

- Use simple, direct, short sentences. Avoid long sentences with many subsections / clauses.
- Scientific writing takes practice

# Scientific Writing Style

- Use simple, direct, short sentences. Avoid long sentences with many subsections / clauses.
- Scientific writing takes practice
- Make sure others read drafts of your work



# Scientific Writing Style

- Use simple, direct, short sentences. Avoid long sentences with many subsections / clauses.
- Scientific writing takes practice
- Make sure others read drafts of your work
- Kudos to everyone for whom English is not your first language, you're amazing!

Where to start???

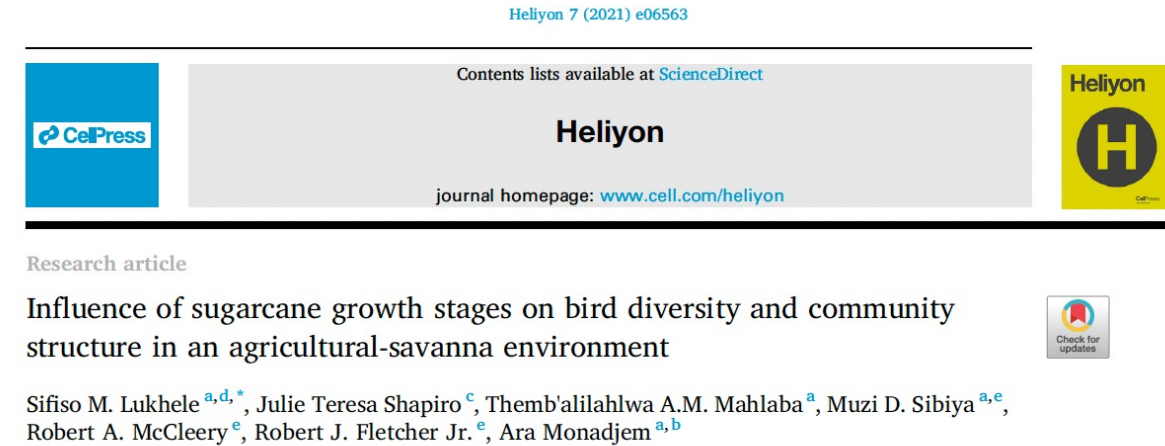
# Where to start???

Sections of a scientific article:

# Where to start???

## Sections of a scientific article:

### 1. Abstract



#### ABSTRACT

Agricultural intensification is a threat to terrestrial ecosystems around the world. Agricultural areas, especially monocultures, create homogenous landscapes for wildlife. However, certain crops, such as sugarcane, are harvested in phases, creating a mosaic of fields in different stages of growth. We investigated changes in avian communities across four different sugarcane growth stages: emerging, short, medium and tall sugarcane, as well as control sites that represented native savanna habitat in northeast Eswatini prior to conversion to agriculture. In total, we sampled nine sites in sugarcane fields (at different growth stages) and three in native savanna. We conducted bird counts at 5-week intervals along 200m line transects over both the breeding and non-breeding seasons. We recorded a total of 124 bird species belonging to 58 families. Bird species richness and diversity were higher in savannas compared to any stages of growth in sugarcane. In contrast, functional beta diversity and uniqueness were higher in sugarcane than in savanna. Community composition was also different between the two land-uses. While there was overlap in bird species composition between different sugarcane growth stages, there was high beta diversity and high turnover between sites, indicative of the high temporal and spatial variability in bird communities in sugarcane fields. We demonstrated that the spatial and temporal variability created by the different growth stages of sugarcane promotes the occurrence of species with different traits, which may contribute to ecosystem functioning and promote the conservation of bird species as sugarcane fields can provide resource complementation for species with different needs.

# Where to start???

## Sections of a scientific article:

### 1. Abstract

- Summary of the paper, including short versions of all parts of the paper

#### A B S T R A C T

Agricultural intensification is a threat to terrestrial ecosystems around the world. Agricultural areas, especially monocultures, create homogenous landscapes for wildlife. However, certain crops, such as sugarcane, are harvested in phases, creating a mosaic of fields in different stages of growth. We investigated changes in avian communities across four different sugarcane growth stages: emerging, short, medium and tall sugarcane, as well as control sites that represented native savanna habitat in northeast Eswatini prior to conversion to agriculture. In total, we sampled nine sites in sugarcane fields (at different growth stages) and three in native savanna. We conducted bird counts at 5-week intervals along 200m line transects over both the breeding and non-breeding seasons. We recorded a total of 124 bird species belonging to 58 families. Bird species richness and diversity were higher in savannas compared to any stages of growth in sugarcane. In contrast, functional beta diversity and uniqueness were higher in sugarcane than in savanna. Community composition was also different between the two land-uses. While there was overlap in bird species composition between different sugarcane growth stages, there was high beta diversity and high turnover between sites, indicative of the high temporal and spatial variability in bird communities in sugarcane fields. We demonstrated that the spatial and temporal variability created by the different growth stages of sugarcane promotes the occurrence of species with different traits, which may contribute to ecosystem functioning and promote the conservation of bird species as sugarcane fields can provide resource complementation for species with different needs.



# Where to start???

Sections of a scientific article:

1. Abstract
2. Introduction

## 1. Introduction

The expansion and intensification of agriculture is one of the principal threats to biodiversity, especially in tropical and sub-tropical regions of the world (Foley et al., 2005; Laurance et al., 2013). Crop agriculture typically involves clearing native vegetation (Matson et al., 1997), which homogenizes the environment both in terms of fine-scale vegetation structure and broad-scale variation across landscapes (Altieri, 1999). Recent studies have demonstrated that homogenization of vegetation structure in African savannas results in the decline of species diversity (Ke et al., 2018; McCleery et al., 2018)

# Where to start???

## Sections of a scientific article:

1. Abstract
2. Introduction
  - Background and context

### 1. Introduction

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# Where to start???

## Sections of a scientific article:

1. Abstract
2. Introduction
  - Background and context
  - Start to reference others for support

### 1. Introduction

The expansion and intensification of agriculture is one of the principal threats to biodiversity, especially in tropical and sub-tropical regions of the world (Foley et al., 2005; Laurance et al., 2013). Crop agriculture typically involves clearing native vegetation (Matson et al., 1997), which homogenizes the environment both in terms of fine-scale vegetation structure and broad-scale variation across landscapes (Altieri, 1999). Recent studies have demonstrated that homogenization of vegetation structure in African savannas results in the decline of species diversity (Ke et al., 2018; McCleery et al., 2018).



# Where to start???

Sections of a scientific article:

1. Abstract
2. Introduction
3. Materials and Methods

## 2. Methods

### 2.1. *Materials and methods*

#### 2.1.1. *Study area*

Our study was conducted in the Lowveld physiographic region of Eswatini, a low-lying region situated between the northern Drakensberg Escarpment in the west and the Lubombo Mountain range to the east; the Lowveld is the warmest and the driest region in the country ([Figure 1](#)). The region experiences hot, wet summers and cool, dry winters with mean daily temperatures of 26 °C and 18 °C, respectively. This area receives a mean annual rainfall of 574 mm and about 80% of the rain is

# Where to start???

Sections of a scientific article:

1. Abstract

2. Introduction

3. Materials and Methods

- What you did. Study site, data collection, data processing, statistical analysis / models.

## 2. Methods

### 2.1. Materials and methods

#### 2.1.1. Study area

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1. Abstract

2. Introduction

3. Materials and Methods

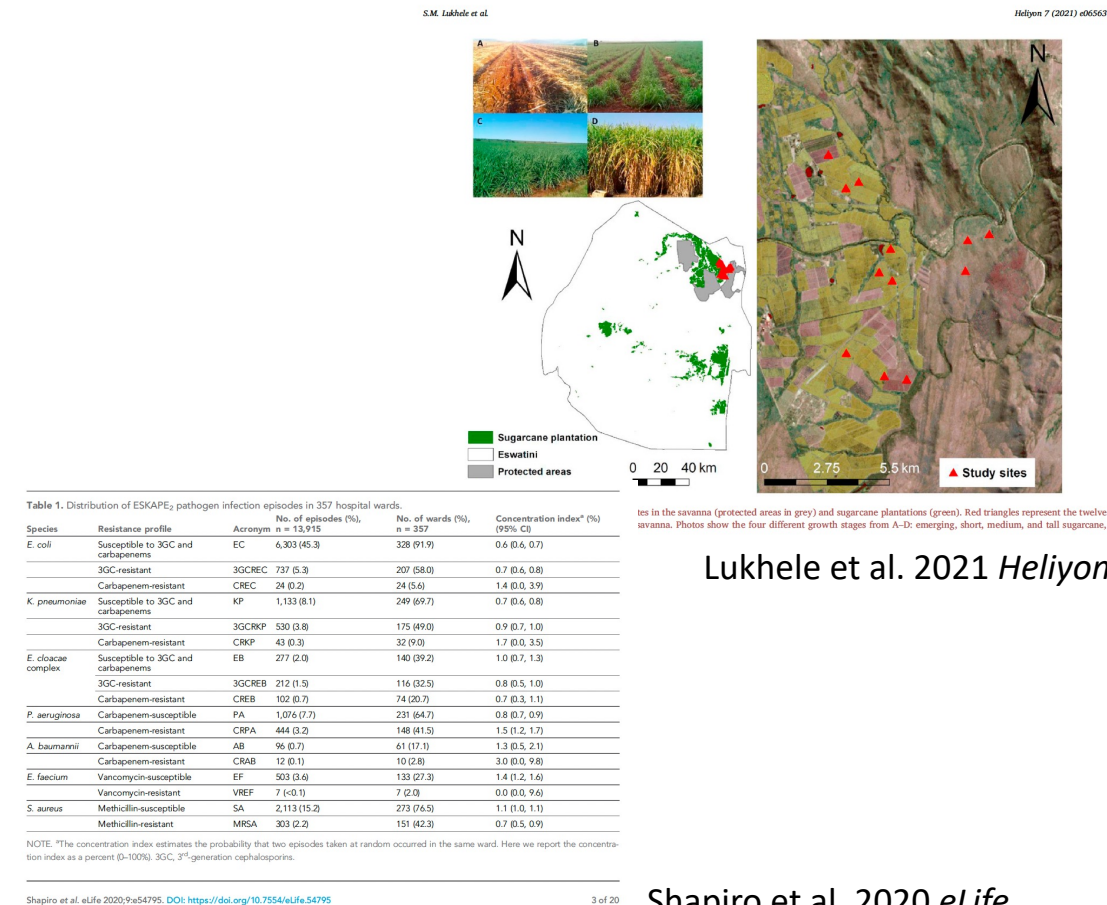
- What you did. Study site, data collection, data processing, statistical analysis / models.
- May include figures or tables (maps, sites, etc)

## 2. Methods

### 2.1. Materials and methods

#### 2.1.1. Study area

Our study was conducted in the Lowveld physiographic region of Eswatini, a low-lying region situated between the northern Drakensberg Escarpment in the west and the Lubombo Mountain range to the east; the Lowveld is the warmest and the driest region in the country (Figure 1). The region experiences hot, wet summers and cool, dry winters with mean daily temperatures of 26 °C and 18 °C, respectively. This area receives a mean annual rainfall of 574 mm and about 80% of the rain is



# Where to start???

Sections of a scientific article:

1. Abstract
2. Introduction
3. Materials and Methods
4. Results

## 3. Results

### 3.1. *Species richness and diversity*

We recorded a total of 7,350 detections of birds belonging to 124 species and 58 families. Of these, 103 species from 52 families were recorded in savanna compared with 55 species from 31 families in sugarcane. The species accumulation curve for sugarcane (overall) was approaching the asymptote whereas that for savanna was still rising, although the rate of increase appeared to be decreasing and had passed the inflection point (Figure 2a). The species accumulation curves for each sugarcane growth stage did not appear to have reached an asymptote suggesting that the entire community was not detected (Figure 2b). The



# Where to start???

## Sections of a scientific article:

1. Abstract
2. Introduction
3. Materials and Methods
4. Results
  - What you found, text, tables figures

### 3. Results

#### 3.1. Species richness and diversity

We recorded a total of 7,350 detections of birds belonging to 124 species and 58 families. Of these, 103 species from 52 families were recorded in savanna compared with 55 species from 31 families in sugarcane accumulation curve for sugarcane (overall) was an asymptote whereas that for savanna was still rising, the rate of increase appeared to be decreasing and had passed its inflection point (Figure 2a). The species accumulation curves for each growth stage did not appear to have reached an asymptote (Figure 2b). The entire community was not detected (Figure 2b). The

Lukhele et al. 2021 *Heliyon*

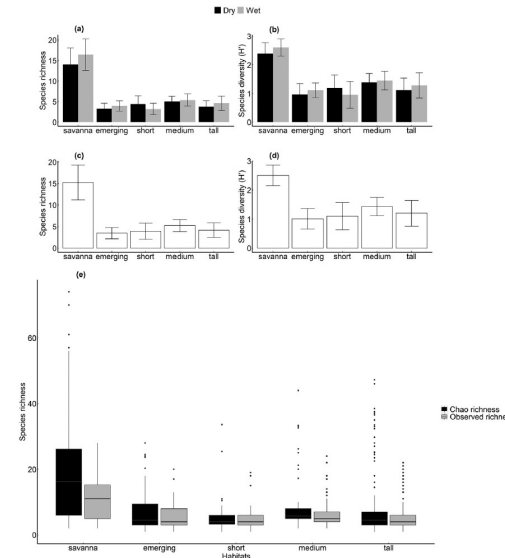


Figure 3. Mean number of: (a) species; and (b) Shannon diversity index recorded per transect in the two land-uses in the dry and wet season. Mean number of: (c) species; and (d) Shannon diversity recorded per habitat across all sessions. Error bars represent standard error. Boxplot showing: (e) a comparison of the observed species richness and estimated species richness (Chao estimator) for the savanna and sugarcane sites, with "emerging", "short", "medium", and "tall" represent the different growth stages in the sugarcane.

eLife Research article

Ecology | Microbiology and Infectious Disease

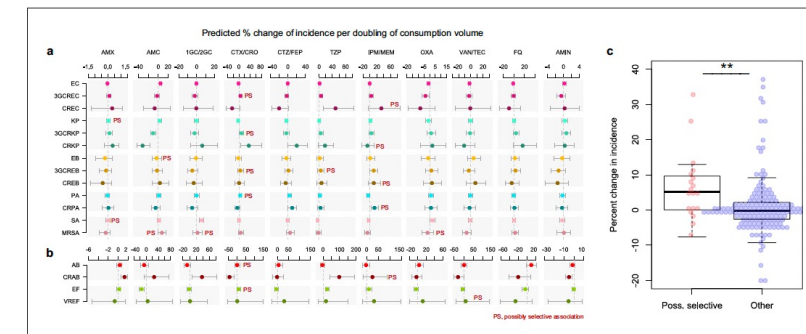


Figure 2. Possibly selective associations between the use of specific antibiotics and the incidence of infection with ESKAPE<sub>2</sub> pathogen variants. Shown are the predicted percent changes in incidence (points) with 95% confidence interval (bars) for each variant in each ward (n = 357) for every doubling in the consumption volume of 11 antibiotic groups, based on multivariable quasi-Poisson regression models of the incidence of each variant in each ward (n = 357) that included the connectivity and incidence control covariates (see Materials and methods). Associations classified as possibly selective (n = 19) are indicated by a 'PS' mark. Models involving *A. baumannii* and *E. faecium*, which exhibited larger 95% confidence intervals due to smaller incidence of the resistant variants, are shown with separate scales (panel b) for readability. (c), possibly selective associations had higher coefficients compared to other associations. The center line indicates the median; box limits indicate the upper and lower quartiles; whiskers indicate the 1.5x interquartile range; points indicate the individual coefficients. \*\*p<0.01, two-sided Mann-Whitney U-test. Acronyms of pathogen variants and antibiotics are listed in Tables 1 and 2, respectively.

Shapiro et al. 2020 *eLife*

# Where to start???

Sections of a scientific article:

1. Abstract
2. Introduction
3. Materials and Methods
4. Results
5. Discussion

## 4. Discussion

We examined bird communities in sugarcane fields of different growth stages and compared these with the communities in neighbouring native savanna. We recorded more bird species in the savanna than in any of the growth stages of sugarcane. However, despite the presumed homogeneity of monocultures, our study demonstrated that the different growth stages of sugarcane created spatial and temporal variability, thus allowing distinctly different bird communities to persist in this agricultural landscape. This is the first study to show such heterogeneity in avian communities in a monoculture crop (due to variation in growth stages), although such a pattern has previously been reported in North American grasslands that were burned in patches, creating a similar mosaic to that seen in Eswatini sugarcane plantations ([Coppedge et al., 2008](#); [Farneda](#)

# Where to start???

Sections of a scientific article:

1. Abstract
2. Introduction
3. Materials and Methods
4. Results
5. Discussion
  - Contextualizing your results, compare to other studies, offer possible explanations, suggest future directions

## 4. Discussion

We examined bird communities in sugarcane fields of different growth stages and compared these with the communities in neighbouring native savanna. We recorded more bird species in the savanna than in any of the growth stages of sugarcane. However, despite the presumed homogeneity of monocultures, our study demonstrated that the different growth stages of sugarcane created spatial and temporal variability, thus allowing distinctly different bird communities to persist in this agricultural landscape. This is the first study to show such heterogeneity in avian communities in a monoculture crop (due to variation in growth stages), although such a pattern has previously been reported in North American grasslands that were burned in patches, creating a similar mosaic to that seen in Eswatini sugarcane plantations ([Coppedge et al., 2008](#); [Farneda](#)

# Where to start???

Sections of a scientific article:

1. Abstract
2. Introduction
3. Materials and Methods
4. Results
5. Discussion
6. Conclusion (Optional)

## 5. Conclusion

Our study demonstrates that while native savanna has greater richness and diversity of birds and supports a distinct avian community from

Lukhele et al. 2021 *Heliyon*



# Where to start???

Sections of a scientific article:

1. Abstract
2. Introduction
3. Materials and Methods
4. Results
5. Discussion
6. Conclusion (Optional)
  - Wrap up, emphasize the significance of your study

## 5. Conclusion

Our study demonstrates that while native savanna has greater richness and diversity of birds and supports a distinct avian community from

Introduction

Big Problem

Identify the  
gap

Your  
Project

Discussion

Your  
Methods

Your Results

Context

Revisit the big picture

How to start writing???

# How to start writing???

- Materials and Methods (while they're still fresh!)

# How to start writing???

- Materials and Methods (while they're still fresh!)
  - Be as detailed as possible

# How to start writing???

- Materials and Methods (while they're still fresh!)
  - Be as detailed as possible
  - Where the study was conducted, information on the site

# How to start writing???

- Materials and Methods (while they're still fresh!)
  - Be as detailed as possible
  - Where the study was conducted, information on the site
  - For how long

# How to start writing???

- Materials and Methods (while they're still fresh!)
  - Be as detailed as possible
  - Where the study was conducted, information on the site
  - For how long
  - How you collected the data



# How to start writing???

- Materials and Methods (while they're still fresh!)
  - Be as detailed as possible
  - Where the study was conducted, information on the site
  - For how long
  - How you collected the data
  - How you analyzed the data

# How to start writing???

- Methods (while they're still fresh!)
- Results

# How to start writing???

- Methods (while they're still fresh!)
- Results
  - Should mirror the Methods

# How to start writing???

- Methods (while they're still fresh!)
- Results
  - Should mirror the Methods
  - For each Method summarize a result

# Where to start???

- Methods (while they're still fresh!)
- Results
  - Should mirror the Methods
  - For each Method summarize a result
    - Method: We trapped bats for two weeks in each season
    - Result: We caught 20 bats belonging to two species in the dry season and 40 bats belonging to four species in the wet season.

# How to start writing???

- Methods (while they're still fresh!)
- Results
- Discussion

# How to start writing???

- Methods (while they're still fresh!)
- Results
- Discussion
  - Write a list of each major result

# How to start writing???

- Methods (while they're still fresh!)
- Results
- Discussion
  - Write a list of each major result
  - Build a paragraph for each → Context, comparison, explanations



# How to start writing???

- Methods (while they're still fresh!)
- Results
- Discussion
  - Write a list of each major result
  - Build a paragraph for each → Context, comparison, explanations
  - Include caveats / cautions

# How to start writing???

- Methods (while they're still fresh!)
- Results
- Discussion
  - Write a list of each major result
  - Build a paragraph for each → Context, comparison, explanations
  - Include caveats / cautions
  - Conclude with importance and potentially future directions

# How to start writing???

- Methods (while they're still fresh!)
- Results
- Discussion
- Introduction

# How to start writing???

- Methods (while they're still fresh!)
- Results
- Discussion
- Introduction
  - Pick your broad context

# How to start writing???

- Methods (while they're still fresh!)
- Results
- Discussion
- Introduction
  - Pick your broad context
  - Narrow down to your specific project

# How to start writing???

- Methods (while they're still fresh!)
- Results
- Discussion
- Introduction
- Abstract

# Alternatively...

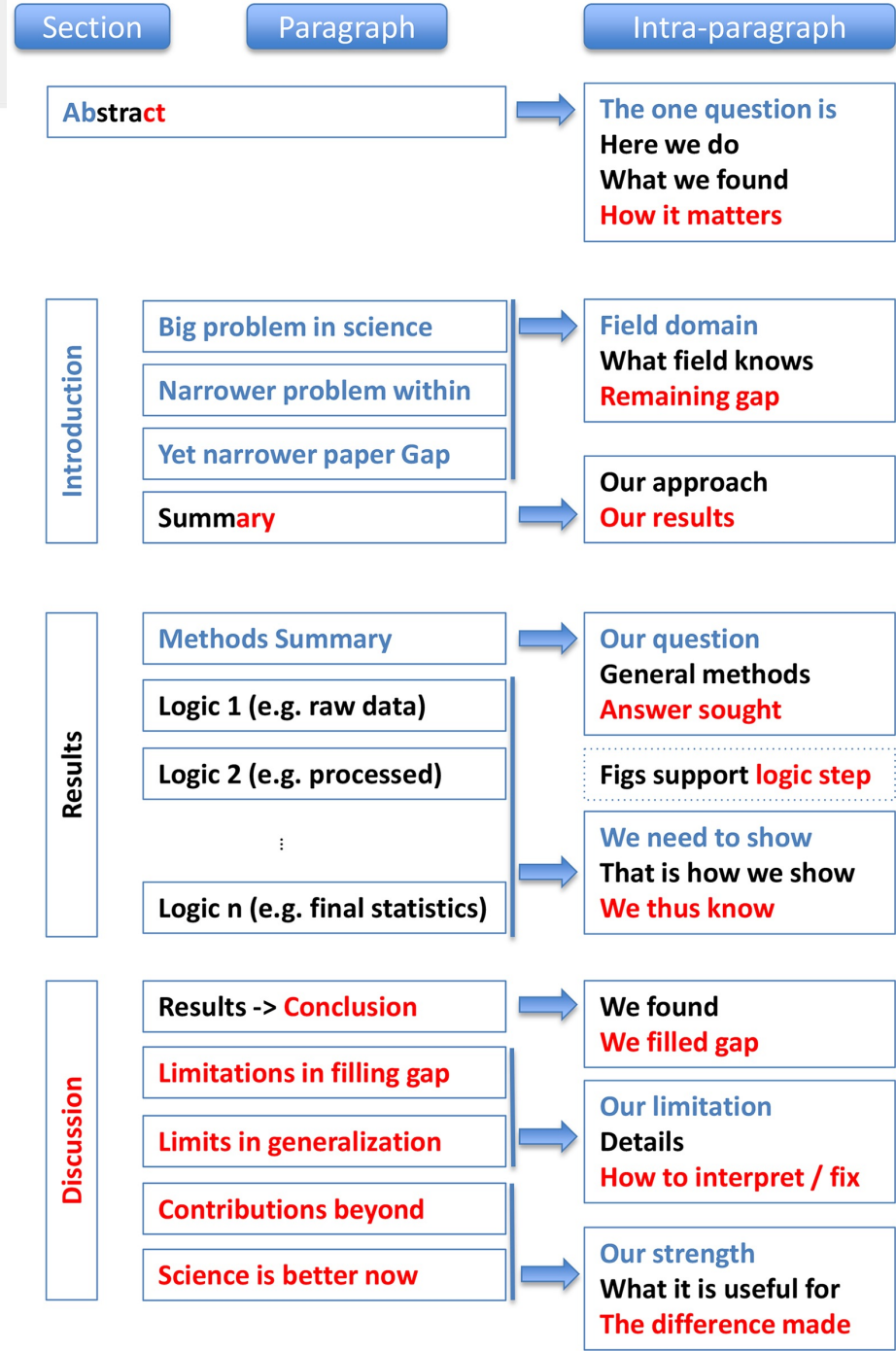
- Start with Figures and build around them
- For some people Figures help figure out the story
- Ideally have Figures based on results / analysis when you start writing

# Ten simple rules for structuring papers

Brett Mensh, Konrad Kording

Published: September 28, 2017 • <https://doi.org/10.1371/journal.pcbi.1005619> • >> See the preprint

Article	Authors	Metrics	Comments	Media Coverage
⌵				





# Exercise – How to structure Introduction & Discussion

Fungal Ecology xxx (2015) 1–4



Contents lists available at [ScienceDirect](#)

Fungal Ecology

journal homepage: [www.elsevier.com/locate/funeco](http://www.elsevier.com/locate/funeco)



Short communication

## Characterization of fungi associated with the nasal hairs of Molossid bats

[Julie Teresa Shapiro](#)<sup>a,\*</sup>, [Thiago Mateus Rocha dos Santos](#)<sup>a,b</sup>, [Clarice Rossato Marchetti](#)<sup>c</sup>,  
[Aline Pedroso Lorenz-Lemke](#)<sup>d</sup>, [Emília Delarmelina](#)<sup>e</sup>, [Marcelo Oscar Bordignon](#)<sup>a</sup>

# Exercise – How to structure Introduction

## 1. Introduction

Mycoses are rapidly becoming one of the leading threats to wildlife ([Daszak et al., 2001](#); [Fisher et al., 2012](#)). A number of emerging fungal pathogens have reduced populations of diverse taxa including sea corals ([Geiser et al., 1998](#)), reptiles ([Thomas et al., 2002](#); [Bowman et al., 2007](#); [Allender et al., 2011](#)), and amphibians ([Daszak et al., 1999](#); [Briggs et al., 2010](#)). In 2006, bats in the northeastern United States were reported with white fungus on their nose and wings ([Blehert et al., 2009](#)). The pathogen, which invades the dermal tissue, has devastated the bat populations of the region ([Blehert et al., 2009](#); [Frick et al., 2010](#)). The novel fungus, *Pseudogymnoascus destructans* ([Minnis and Lindner, 2013](#)), has also been reported in bats in Europe, although it does not appear pathogenic there ([Wibbelt et al., 2010](#); [Puechmaille et al., 2011](#)).

# Exercise – How to structure Introduction

## 1. Introduction

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Shapiro et al. 2015 *Acta Tropica*

## 1. Mycoses are a threat to wildlife, including bats.



# Exercise – How to structure Introduction

The mycobiota of bats in Brazil is largely unknown. We observed the presence of filamentous fungi among the hairs between the snout and upper lip of three species of Molossid bats, *Cynomops planirostris*, *Molossus molossus*, and *Molossus rufus* (Fig. 1). Worldwide, there are approximately 90 species of Molossid bats, which can be found on every continent ([Wilson and Reeder, 2005](#)). These bats are small to medium size insectivores characterized by a free tail extending beyond the uropatagium, narrow wings, dark, velvety fur, and an internal keel ([Gregorin and Taddei, 2002](#)). Brazil is home to 29 species of Molossid bats ([Nogueira et al., 2014](#)), 14 of which can be found in Mato Grosso do Sul state ([Cáceres et al., 2008](#); [Bordignon et al., 2011](#); [Santos and Bordignon, 2011](#)).

Shapiro et al. 2015 *Acta Tropica*

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# Exercise – How to structure Introduction

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Shapiro et al. 2015 *Acta Tropica*

1. Mycoses are a threat to wildlife, including bats.

**2. Mycobiota of Brazilian bats is unknown but we have observed fungus on specific species**

# Exercise – How to structure Introduction

These fungi on the nasal hairs of Molossid bats have not been previously reported or described. The objective of this study was to identify these fungi. We also compared the species richness and composition of fungi isolated from the different bat species and from the two different habitat types.

Shapiro et al. 2015 *Acta Tropica*

1. Mycoses are a threat to wildlife, including bats.
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# Exercise – How to structure Introduction

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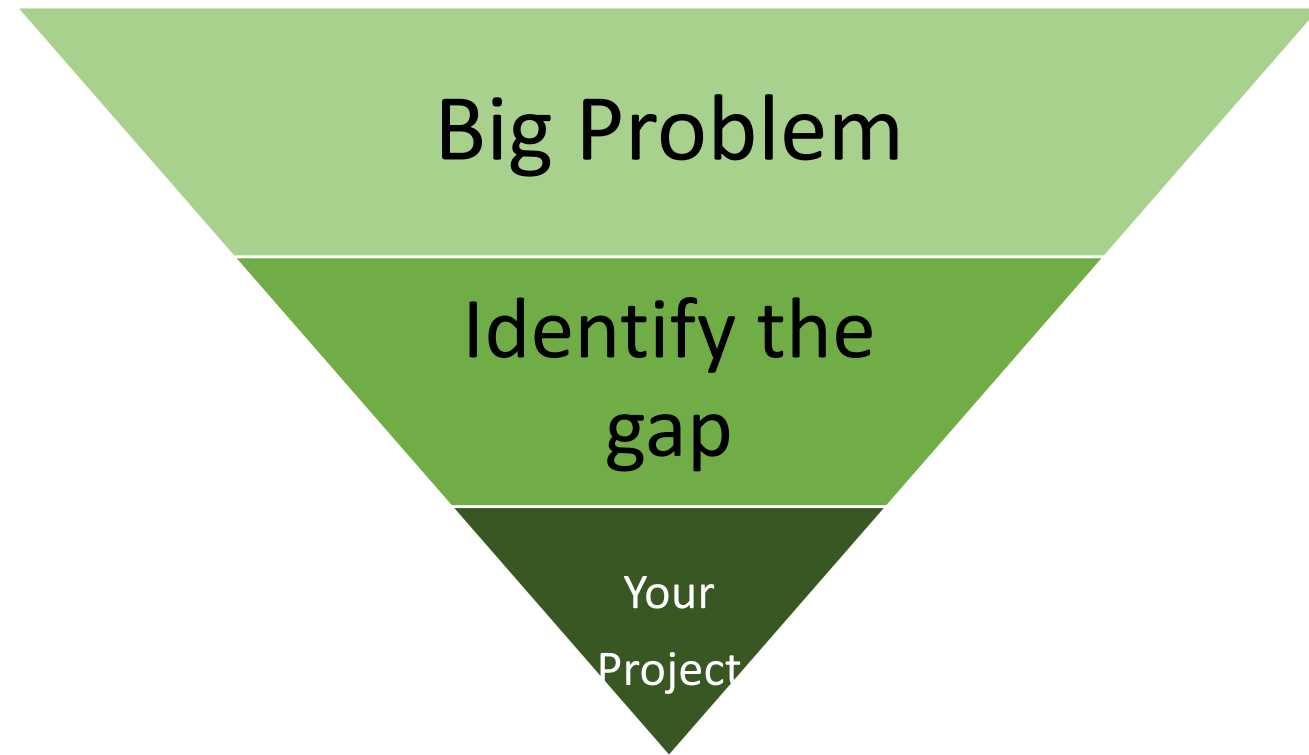
Shapiro et al. 2015 *Acta Tropica*

1. Mycoses are a threat to wildlife, including bats.
2. Mycobiota of Brazilian bats is unknown but we have observed fungus on specific species

## 3. Objective of the study

# Exercise – Structuring the Introduction

1. Mycoses are a threat to wildlife, including bats.
2. Mycobiota of Brazilian bats is unknown but we have observed fungus on specific species
3. Objective of this study





# Exercise – Methods

## 2. Materials and methods

### 2.1. Study site

We collected bats from around Mato Grosso do Sul, southwest Brazil between April 2012 and January 2013 in both the Cerrado and Pantanal. The Cerrado is a large seasonal xeromorphic plant formation located on the plateau of Central Brazil, commonly called “Brazilian Savanna” ([Eiten, 1972](#)). The Pantanal is an extensive, unpredictable wetland, influenced by the vegetation classes that border it, such as the Cerrado, Amazonian forest, and Chaco, favoring a great variety of vegetation types ([Pott et al., 2011](#)). In the Cerrado, bats were collected on rural properties outside of Campo Grande and within the city of Campo Grande. Trapping in the Pantanal occurred around the Negro River and Miranda River ([Table 1](#)).

### 2.2. Bat capture and fungus isolation

We captured bats of three species for this study: *Cynomops planirostris*, *Molossus molossus*, and *Molossus rufus*. In the study area, only bats of the genera *Cynomops* and *Molossus* have the nasal hairs which appear to host fungi. Other Molossid bats have wrinkled upper lips and therefore no hairs on the muzzle. To capture bats, mist nets were placed near roosts, small water bodies, and possible flyways. Bats were removed from mist-nets using latex gloves and placed in sterilized cloth bags. The bats were identified to species level according to [Gregorin and Taddei \(2002\)](#). Forceps were sterilized in a flame and then dipped in alcohol. Visible fungus filaments were removed with forceps and placed in Petri dishes on sterile potato dextrose supplemented with chloramphenicol ( $100\text{ }\mu\text{g ml}^{-1}$ ) and gentamicin ( $50\text{ }\mu\text{g ml}^{-1}$ ) to prevent bacterial contamination. Each Petri dish was then capped and sealed with plastic tape immediately after placing the filament on the agar. When filaments were not visible, the sterilized forceps were passed over the nasal hairs and pressed onto the agar. These plates were closed and then sealed with plastic film.

Cultures were left to grow at room temperature in sealed Petri dishes. There was no significant variation in room temperature during the incubation period, which lasted approximately 15 d. When there was more than one morphotype on a dish, each was placed onto a different plate. This was done in a sterilized laminar flow hood using sterile forceps to prevent any contamination.



# Exercise – Methods

## 2.3. Molecular methods

To more accurately identify fungal cultures, the rRNA internal transcribed spacer region (ITS1, 5.8S, and ITS2; ca. 600 pb) was sequenced. DNA was extracted from circular fragments of mycelium with a diameter of approximately 0.5 cm following a modified CTAB protocol ([Doyle and Doyle, 1987](#)). The isolated material was quantified using NanoDrop 2000 (Thermo Scientific) and its quality was assessed using 1% agarose gel electrophoresis. Amplifications were performed using primers ITS1F ([Gardes and Bruns, 1993](#)) and ITS4 ([White et al., 1990](#)). Each PCR reaction contained 0.2 mM of dinucleotide triphosphate (dNTPs), 0.2 µM of each primer (ITS1F and ITS4), 1X GoTaq buffer (Promega), 1 U of GoTaq DNA polymerase (Promega), and 1 µl of genomic DNA. The final volume of amplification was 25 µl. PCR reactions were amplified in an Applied Biosystems Veriti 96-Well Thermal Cycler using the following parameters: 5 min at 94 °C followed by 30 cycles of 1 min at 94 °C, 45 s at 55 °C, and 1 min at 72 °C, and then a final elongation of 10 min at 72 °C. After PCR, an aliquot of 2 µl from each sample was checked by horizontal electrophoresis in 1% agarose gel. PCR products were cleaned with PEG 20% ([Dunn and Blattner, 1987](#)) and sequenced according to the protocols of Macrogen Inc. (Seoul, South Korea).

Sequencing reads were assembled and edited using Geneious® 7.1.7 (<http://www.geneious.com>; [Kearse et al., 2012](#)). High-quality consensus sequences of each isolate were compared to the NCBI GenBank database with BLAST ([Altschul et al., 1990](#)). Each sequence was compared to the first 30 matches in GenBank. If at least 20 of the first 30 sequences matched the same genus or species, the isolate was identified as belonging to that genus or species.

All sequences were submitted to GenBank under accession numbers **KR610358 – KR610373**.

**Table 1**

Fungal isolates and identification from each individual bat. All sequences have been submitted to GenBank (BankIT ID 1822184).

Bat species	Bat ID	Biome	Coordinates	Visible fungal filaments	Genus/Species/Isolate
<i>Cynomops planirostris</i>	2	Cerrado	20°30'21"S 54°32'44"W	Yes	Fungal sp. isolate 2.1 <sup>a</sup> <i>Cladosporium</i> sp. isolate 2.1 <i>Penicillium</i> sp. isolate 2.3 <i>Aspergillus</i> sp. isolate 4.1
	4	Cerrado	20°30'21"S 54°32'44"W	No	
	5	Cerrado	20°30'21"S 54°32'44"W	No	<i>Aspergillus</i> sp. isolate 5.1
	6	Cerrado	20°30'21"S 54°32'44"W	No	<i>Penicillium</i> sp. isolate 6.1
	7	Cerrado	20°30'21"S 54°32'44"W	No	<i>Penicillium</i> sp. isolate 7.1 Fungal sp. isolate 7.2 <sup>a</sup>
	8	Cerrado	20°47'57"S 54°50'45"W	No	Fungal sp. isolate 8.1 <sup>a</sup> <i>Penicillium</i> sp. isolate 8.2
	<i>Molossus molossus</i>	Cerrado	20°28'00"S 57°34'11"W	Yes	<i>Aspergillus terreus</i> isolate 1.1 <i>Penicillium</i> sp. isolate 1.2 <i>Aspergillus terreus</i> isolate 1.3 Fungal sp. isolate 1.4 <sup>a</sup>
					<i>Penicillium</i> sp. isolate 10.1 <i>Paecilomyces</i> sp. isolate 10.2 <i>Penicillium</i> sp. isolate 11.1
<i>Molossus rufus</i>	3	Pantanal	19°19'35"S 57°02'00"W	Yes	<i>Aspergillus terreus</i> isolate 3.1 Fungal sp. isolate 3.2 <sup>a</sup>
	9	Pantanal	19°34'37"S 57°00'42"W	Yes	Fungal sp. isolate 9.1 <sup>a</sup>
	12	Pantanal	19°34'37"S 57°00'42"W	No	<i>Aspergillus</i> sp. isolate 12.1 <i>Penicillium</i> sp. isolate 12.2

<sup>a</sup> Adequate sequences for identification were not obtained.

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# Exercise – Structuring the Discussion

## 3. Results and discussion

A total of 22 ascomycete colonies were cultured from 12 individual bats of three different bat species: *Cynomops planirostris* (n = 6), *Molossus molossus* (n = 3), and *Molossus rufus* (n = 3) (Table 1, Fig. 2). Five bats were captured near the Negro River and Miranda River, in the Pantanal. Within the Cerrado, six bats were collected on rural properties and one was collected within the city of Campo Grande. Of the 22 isolates cultured, adequate sequences for identification were obtained from 16 of them, and they were identified to the level of genus or species (Table 1). From the 16 isolates, eleven unique ITS sequence types were obtained from different species in four genera. At the species level, *Aspergillus terreus* (three isolates with identical sequences) was identified from three cultures from two different bats. Two additional sequence types of *Aspergillus* were also identified, one sequence type of *Cladosporium*, one sequence type of *Paecilomyces*, and eight sequence types of *Penicillium*. The divergence among the different sequence types of *Aspergillus* was about 10% while in *Penicillium*, divergence ranged from 1 to 6.5%. *Penicillium* sp. isolate 6.1 was the most different from the other isolates, diverging 6.5% from other *Penicillium* spp. sequence types. The other seven *Penicillium* spp. isolates diverged <2% from each other.

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## 1. Summarize the different fungi isolated from the bats

# Exercise – Structuring the Discussion

Some fungal isolates appeared to be common across bat species and the two biomes, Cerrado and Pantanal. Seven similar *Penicillium* isolates (divergence <2%) were cultured from seven individuals of all three bat species in both the Cerrado and Pantanal. *A. terreus* was also cultured from multiple bats, *M. molossus* (Bat 1, Cerrado) and *M. rufus* (Bat 3, Pantanal) (Table 1). Other fungi may be more specific or less common in the environment. Several fungal isolates were found in only a single individual, such as *Aspergillus* sp. isolate 12.1, *Cladosporium* sp. isolate 2.1, *Paecilomyces* sp. isolate 10.2, and *Penicillium* sp. isolate 6.1. These fungi might come from more specific sources that these individual bats were in contact with.

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1. Summarize the different fungi isolated from the bats

**2. Compare specificity of fungi with bats and offer an explanation (how common fungi are in the environment)**

# Exercise – Structuring the Discussion

Our results point to the possibility that the fungi associated with the Molossid bats of southwest Brazil are diverse and may vary significantly between individuals, species, and biomes. Studies of bats' mycobiota in caves have also found *Cladosporium* spp. and *Penicillium* spp. ([Voyron et al., 2011](#); [Johnson et al., 2013](#)). In particular, *Penicillium* sp. isolate 1.2 and *Penicillium* sp. isolate 10.1, both from *M. molossus*, had close matches to fungi isolated from Vespertilionid bats in Indiana, USA ([Johnson et al., 2013](#)). Although these fungi identified by [Johnson et al. \(2013\)](#) were psychrophilic or psychrotolerant from cave-dwelling bats, we have no evidence that the bats we captured roost in caves or in cool climates. We captured five *C. planirostris* exiting a roost in a tree while several captured *M. molossus* and *M. rufus* were exiting roosts located under the roofs of buildings. It is possible that fungi such as *Penicillium* spp. or *Cladosporium* spp. might colonize a wide variety of bat species and are not cave-specific, but come from other environmental sources, perhaps the soils or dust in a wide variety of roosts including caves, trees, and artificial structures.

1. Summarize the different fungi isolated from the bats
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# Exercise – Structuring the Discussion

We did not culture the same fungal isolate from different bats presenting fungal filaments. Although morphologically similar to the naked eye, these filaments do not appear to be a unique fungal species across individuals. Multiple fungal morphotypes were cultured from nearly all bats presenting these fungal filaments. How or why the filaments form on the nasal area of Molossid bats remains unclear. Although we observed no indication that these fungi are pathogenic to the bats from which we were cultured, some, such as *A. terreus* and species from the genera *Cladosporium* and *Paecilomyces*, may cause opportunistic infection in other organisms ([Perfect and Schell, 1996](#); [Foley et al., 2002](#); [Woolhouse and Gowtage-Sequeria, 2005](#)). Several isolates, such as the *A. terreus* (from *M. molossus* and *M. rufus*) and *Aspergillus* sp. isolates 4.1 and 5.1 (from *C. planirostris*), had close matches to pathogenic specimens in GenBank, which may give some cause for concern. Across the world, a growing number of fungi, both opportunistic or introduced species, have been implicated in emerging infections of various wildlife species ([Geiser et al., 1998](#); [Daszak et al., 2001](#); [Drew Harvell et al., 2002](#); [Fisher et al., 2012](#)), including bats ([Blehert et al., 2009](#); [Frick et al., 2010](#)). Such pathogens have the potential to spread to and unexpectedly devastate more susceptible populations, for example in the case of White Nose Syndrome (WNS; [Blehert et al., 2009](#); [Frick et al., 2010](#)). Currently, *C. planirostris*, *M. molossus*, and *M. rufus* are considered species of “Least Concern” by the IUCN ([Barquez and Diaz, 2008](#); [Barquez et al., 2008a,b](#)), due to their extensive geographic distributions, ranging from Mexico to Argentina. Population trends for *M. rufus* are stable ([Barquez et al., 2008a](#)), while they are unknown for *C. planirostris* ([Barquez and Diaz, 2008](#)) and *M. molossus* ([Barquez et al., 2008b](#)). Nonetheless, the case of WNS in particular has shown the potential of mycoses to cause devastating population crashes and local extinctions of previously abundant species ([Frick et al., 2010](#)).

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# Exercise – Structuring the Discussion

Our results indicate the need for further research into the potential effects these fungi may have on Molossid bats in Brazil. Sequencing additional genetic markers may yield more precise identifications of these isolates at the species level and further enhance our understanding of them. The variability of species richness and composition of fungi cultured from Molossid bats, even among individuals of the same species, all within a small geographic area, points to a potentially complex and species-rich mycobiota associated with these particular bat species in this region of Brazil.

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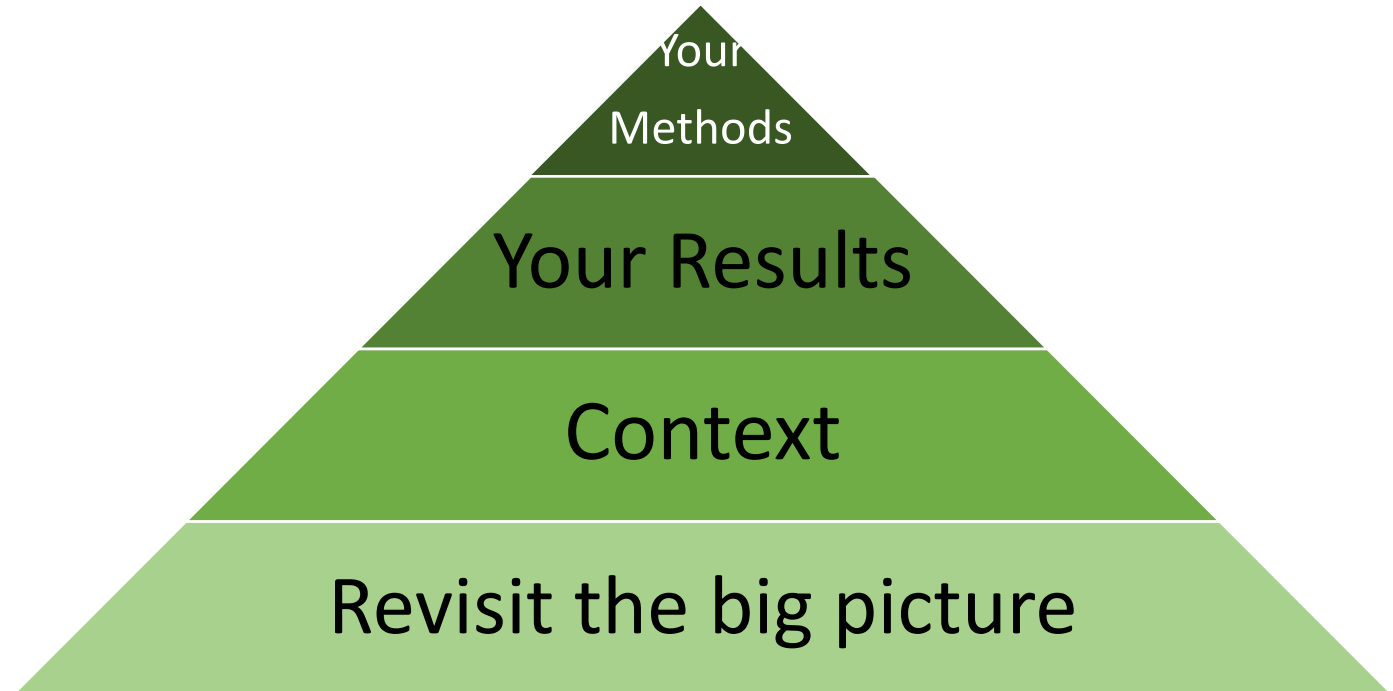
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# Structuring An Abstract – Your Paper in Miniature

## A B S T R A C T

Fungal pathogens have become a serious threat to wildlife, threatening populations of even once common, abundant species. We describe the mycobiota associated with the nasal hairs of three Molossid bat species, *Cynomops planirostris*, *Molossus molossus*, and *Molossus rufus*, in southwest Brazil. Bats were captured in the Cerrado and Pantanal biomes. We cultured 22 fungal isolates from twelve individual bats. Sixteen sequences of the ITS region were obtained, yielding 11 unique sequence types from the genera *Aspergillus*, *Cladosporium*, *Paecilomyces*, and *Penicillium*. No obvious detrimental effects on the bats from the fungi were observed, although some species or genera that we identified are known pathogens in other species. This is the first report of such fungi associated with the nasal hairs of Molossid bats. Our results indicate the need for further research on the biodiversity, ecological role, and potential effects of this mycobiota on Molossid bats.

Shapiro et al. 2015 *Acta Tropica*

1. Problem: Fungal pathogens are a threat to wildlife.
2. Methods & Results: Bat species studied, location, molecular methods, ID of fungi
3. Implications and importance of the study

# Examples from Reading

Paper 1 - “Characterization of fungi associated with the nasal hairs of Molossid bats (Gervais 1856), Mato Grosso do Sul, Southwest Brazil”

What was missing from the “draft” version?

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  - Too much repetition of results in the Discussion, not enough Discussion


# Titles – The Hardest Part?

First record of *Leishmania braziliensis* presence detected in bats, Mato Grosso do Sul, southwest Brazil

[Julie Teresa Shapiro](#)<sup>a,\*</sup>, [Manoel Sebastião da Costa Lima Junior](#)<sup>b</sup>,  
[Maria Elizabeth Cavaleiros Dorval](#)<sup>c</sup>, [Adriana de Oliveira França](#)<sup>d</sup>,  
[Maria de Fatima Cepa Matos](#)<sup>e</sup>, [Marcelo Oscar Bordignon](#)<sup>a</sup>

## Ebola spillover correlates with bat diversity

Check for  
updates

[Julie Teresa Shapiro](#)<sup>1,2,3</sup>  • [Adia R. Sovie](#)<sup>2</sup> • [Chelsey R. Faller](#)<sup>2,4</sup> • [Ara Monadjem](#)<sup>5,6</sup> • [Robert J. Fletcher Jr](#)<sup>1,2</sup> •  
[Robert A. McCleery](#)<sup>1,2,6</sup>


Accurate accounting: How to balance ecosystem services and disservices

[Julie Shapiro](#)<sup>1</sup>, [András Báldi](#)<sup>\*</sup>

*MTA Centre for Ecological Research, Lendület Ecosystem Services Research Group, Hungary*

# Titles – For Creative Types

Leaf me alone: visual constraints on the ecology of social group formation

Elliott P. Steele<sup>1,2</sup> • Mark E. Laidre<sup>1,2</sup> 

7. A mathematical model of Bieber Fever:  
The most infectious disease of our time?

Valerie Tweedle<sup>1</sup> and Robert J. Smith?<sup>2</sup>

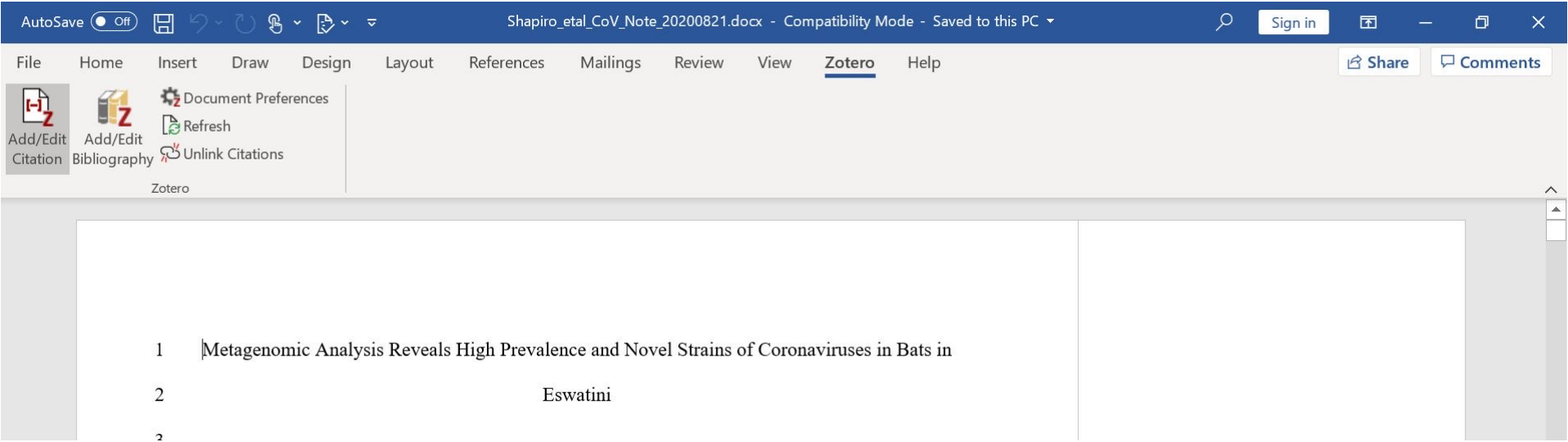
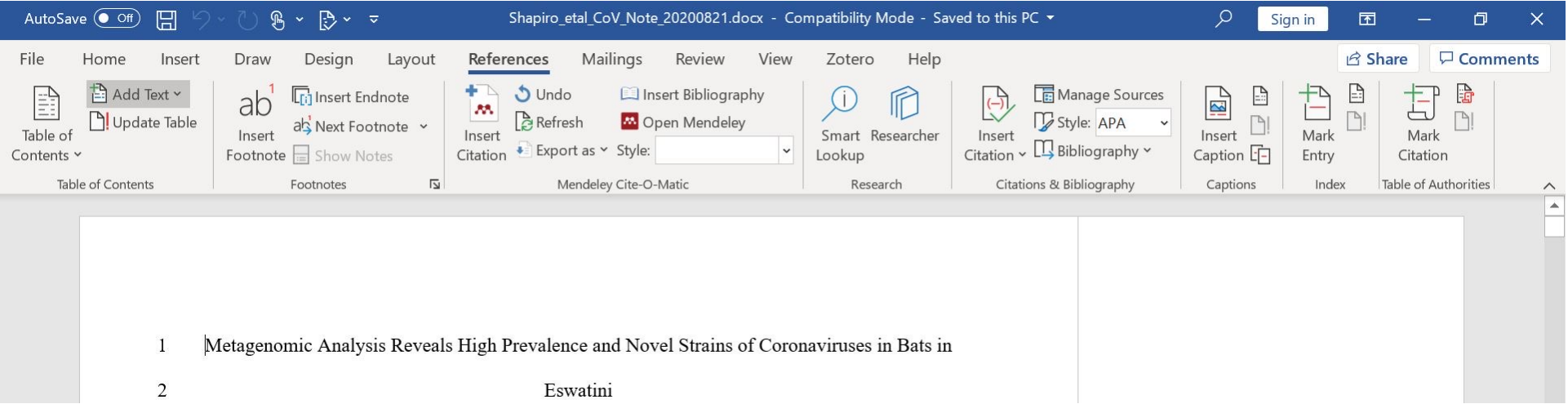
Snakes on a Spaceship—An Overview of  
Python in Heliophysics

A. G. Burrell , A. Halford, J. Klenzing,  
R. A. Stoneback, S. K. Morley ... [See all authors](#) >

# Reference managers

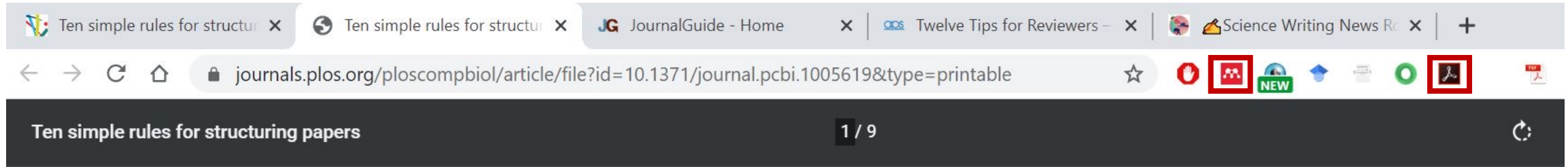


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  - Applied vs. Theoretical framing; Public Health vs. Ecology

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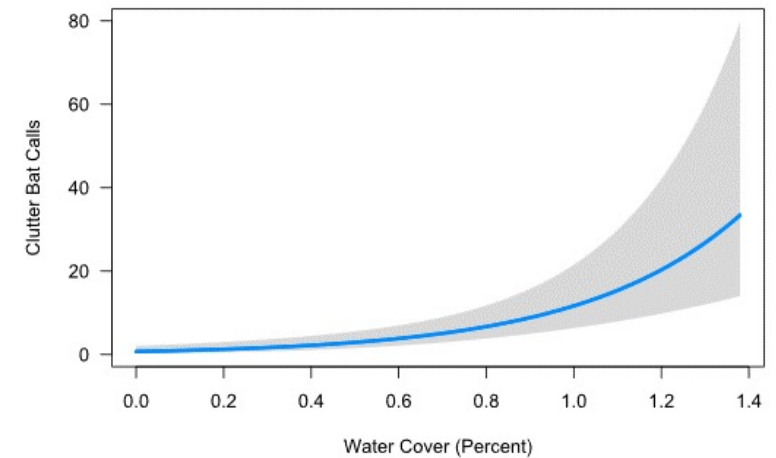
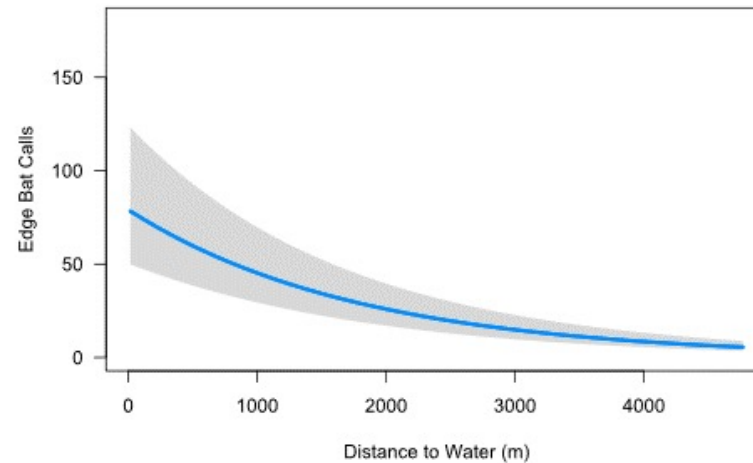
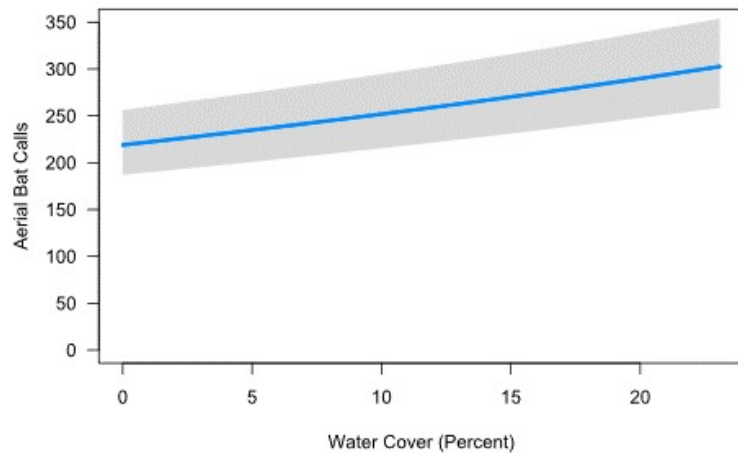
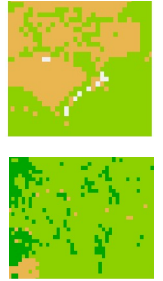
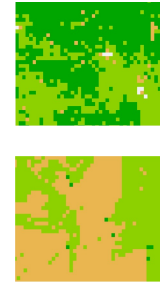
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What Have I Forgotten To Talk About???

Bonus slides

# An Example – Effects of Land-Cover on Bat Activity in a Savanna in Eswatini



# Exercise – Structuring the Introduction



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Response of bat activity to land cover and land use in savannas is scale-, season-, and guild-specific



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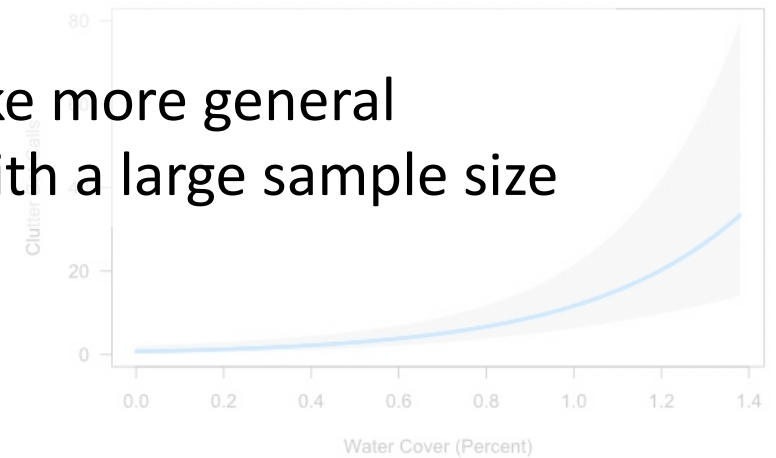
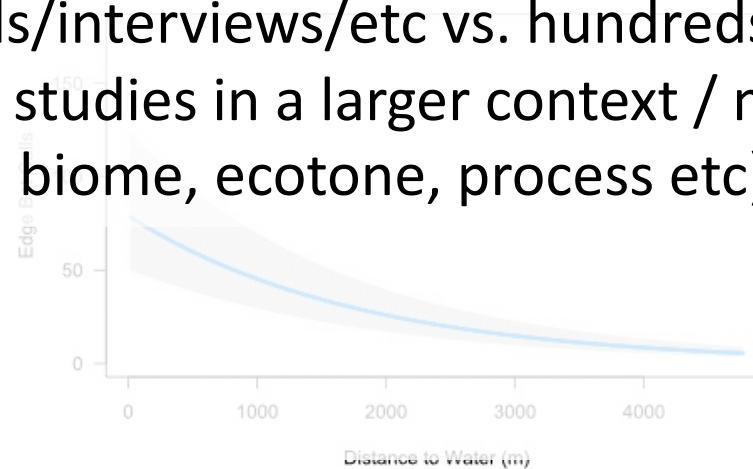
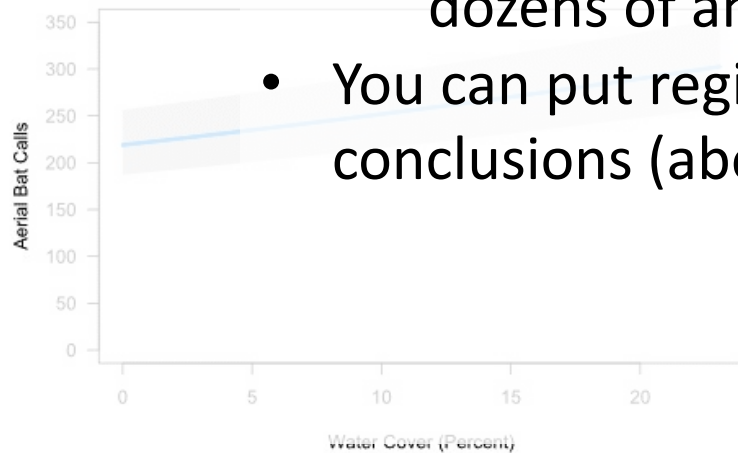
Chiroptera

Landscape ecology

Savanna

# What Context Would You Pick?

- Remember - It also depends on your sample size and the extent of sampling
  - Your conclusions (and context) will be more limited with 3 sites vs 30 or dozens of animals/interviews/etc vs. hundreds
- You can put regional studies in a larger context / make more general conclusions (about a biome, ecotone, process etc) with a large sample size



# Exercise – Structuring the Introduction

## 1. Introduction

Tropical savannas are biomes of global importance for people and wildlife (Bond and Parr, 2010; Murphy et al., 2016; Parr et al., 2014). They contain high levels of biodiversity, provide essential habitat for endemic and endangered species (Murphy et al., 2016), account for a large amount of terrestrial net primary productivity, and store carbon (Parr et al., 2014). Savannas also provide essential resources to people, such as pasture for livestock, firewood, thatching materials, and medicinal plants (Egoh et al., 2009; Fensham et al., 2005; Hoffmann et al., 2012; Parr et al., 2014; van der Werf et al., 2010).

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## 1. Savannas are important



# Exercise – Structuring the Introduction

## 1. Savannas are important

Despite their importance, tropical savannas are generally under-appreciated, understudied and under-protected (Laurance et al., 2014; Parr et al., 2014), with less than 13 % under any kind of official protection (Jenkins and Joppa, 2009). Globally, one of the principal threats to tropical savannas is land-cover change, particularly the conversion of savanna to agriculture, including both low-intensity croplands and high intensity commercial production (Aleman et al., 2016; Laurance et al., 2014).

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1. Savannas are important

2. Savannas are threatened, especially by land cover change

# Exercise – Structuring the Introduction

Land-cover change has profound, often negative impacts on wildlife (Foord et al., 2018; Reynolds et al., 2018; Sala et al., 2000). At fine spatial scales, land-cover change alters the type and structure of vegetation, eliminating foraging habitat or shelter (Fahrig et al., 2011; Goodwin et al., 2002; Tscharntke et al., 2012). On larger scales, landscape composition (the different types of land cover) and configuration (the spatial pattern of land cover) affect wildlife through different mechanisms: changes in landscape composition typically lead to reductions in native vegetation or other habitats and the loss of resources located in them (Fischer and Lindenmayer, 2006; Tscharntke et al., 2012), while changes in landscape configuration, regardless of the amount of cover, affect wildlife through edge effects, patch isolation, and loss of connectivity across the landscape (Fahrig, 2003).

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1. Savannas are important
2. Savannas are threatened, especially by land cover change

## 3. How land-cover change threatens savannas

# Exercise – Structuring the Introduction

Bats are the second most diverse order of mammals (Burgin et al., 2018) and provide important ecosystem services such as pest control, pollination, and seed dispersal (Boyles et al., 2011; Kunz et al., 2011; Maas et al., 2013; Taylor et al., 2017; Williams-Guillén et al., 2008). They may also serve as bioindicators (Jones et al., 2009). There is growing evidence that in savannas in particular, some bat species exhibit strong preferences for agricultural landscapes (Noer et al., 2012; Toffoli and Rughetti, 2017) where they play an important role in consuming pest insects (Bohmann et al., 2011; Puig-Montserrat et al., 2015; Taylor et al., 2013a, 2013b, 2018, 2017).

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2. Savannas are threatened, especially by land cover change
3. How land-cover change threatens savannas



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1. Savannas are important
2. Savannas are threatened, especially by land cover change
3. How land-cover change threatens savannas

4. Introduce bats and their importance

# Exercise – Structuring the Introduction

The role of the entire landscape mosaic is increasingly recognized as essential for effective species conservation (Hansson and Angelstam, 1991; Hobbs, 1994; Wiens, 2009). Conserving bats, and thus maintaining the ecosystem services and functions that they provide therefore requires an understanding of how they use the mosaics of various land covers and land uses increasingly found in modified landscapes. Understanding how bats respond to the composition and configuration of these different land covers can then inform conservation planning by indicating key elements (e.g. size or shape of native vegetation patches) in the landscape necessary for maintaining or promoting bat activity. Without this understanding, conservation planning may be ineffective due to missing key elements of the landscape or preserving habitat at the wrong spatial scale (Hansson and Angelstam, 1991; Hobbs, 1994; Wiens, 2009).

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2. Savannas are threatened, especially by land cover change
3. How land-cover change threatens savannas
4. Introduce bats and their importance

5. Why it's important to understand to understand bats' response to land-cover change



# Exercise – Structuring the Introduction

Bats can respond to variation in both fine-scale vegetation structure and landscape-scale composition and configuration (Brigham et al., 1997; Fuentes-Montemayor et al., 2013; Gehrt and Chelsvig, 2003; Mendes et al., 2017b; Monadjem and Reside, 2008). Their response to land cover varies greatly between regions, biomes, seasons (Ferreira et al., 2017; Klingbeil and Willig, 2010; Mendes et al., 2014; Monadjem et al., 2018a), and species or guilds (Gorresen et al., 2005; Klingbeil and Willig, 2009; Mendes et al., 2017a; Müller et al., 2012).

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3. How land-cover change threatens savannas
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6. What we know so far about bats and land-cover change in general



# Exercise – Structuring the Introduction

To date, most research on the impacts of land-cover change on bats has been conducted in forest biomes (Estrada-Villegas et al., 2010; Ferreira et al., 2017; Pinto and Keitt, 2008; Williams-Guillén and Perfecto, 2011), limiting our ability to generalize patterns. Our understanding of how land-cover change affects bats in savannas, particularly in Africa, is far more limited (Meyer et al., 2016; Monadjem and Reside, 2008; Mtsetfwa et al., 2018; Weier et al., 2018). Studies from North American pine savannas and South American Cerrado savannas show land-cover modification and reduced canopy cover (land cover composition), not configuration, reduce bat diversity metrics (Bailey et al., 2019; Pereira Ramos et al., 2018). However, these responses are often species-specific, varying by foraging guild or other traits (Bailey et al., 2019; Mendes et al., 2017b; Muylaert et al., 2016; Pereira Ramos et al., 2018).

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7. Gaps in our knowledge → savanna habitats



# Exercise – Structuring the Introduction

In southern African savannas, changes in land cover and land use may impact bats by eliminating their foraging habitat, destroying their roosts, or reducing populations of their insect prey. This could be an especially grave threat to clutter foraging bats, which rely on dense vegetation for foraging, and edge foraging bats, which use edge habitats between dense and open vegetation (Cooper-Bohannon et al., 2016; Monadjem et al., 2010). There is evidence that high intensity agriculture can negatively affect some bat species (Mtsetfwa et al., 2018), but remnant natural and semi-natural vegetation (Mtsetfwa et al., 2018; Weier et al., 2018) and wetlands (Sirami et al., 2013) in such landscapes may promote bat activity. However, the role of landscape configuration has not been considered. In addition, the relative effects of fine-scale vegetation compared to landscape composition and configuration have not been directly compared. Finally, studies in this region have only compared the effects of savanna and commercial agriculture on bats (Mtsetfwa et al., 2018; Sirami et al., 2013; Weier et al., 2018), while the role of rural areas and villages has been largely neglected, despite comprising a large, and growing component of the landscape (Bailey et al., 2015).

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8. Hypotheses regarding how land-cover change might affect bats based on current knowledge (include gaps)



# Exercise – Structuring the Introduction

In order to understand the effects of land cover and land use on bats in tropical savannas, we measured guild-level responses in bat activity across the wet and dry seasons to both vegetation structure and land-cover composition and configuration across northeastern Eswatini (formerly Swaziland). This region is part of the Maputaland-Albany-Pondoland biodiversity hotspot (Steenkamp et al., 2005) and undergoing rapid land-cover change, primarily as a result of agricultural expansion and intensification (Bailey et al., 2015). Our objectives were to: 1) quantify the response of bats to variation in fine-scale vegetation structure and landscape-scale land-cover composition and configuration; 2) compare the variation in responses by foraging guild; 3) determine the most relevant spatial scale of the response for each guild; and 4) ascertain how responses vary by season.

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## 9. Specific goals of this study that fill the gaps

# Exercise – Structuring the Introduction

We expected to see guild-specific responses to both fine- and landscape-scale characteristics. Previous studies have found that guilds respond to different characteristics at different spatial scales depending on their ecology (Ferreira et al., 2017; Fuentes-Montemayor et al., 2013; Pereira Ramos et al., 2018; Pinto and Keitt, 2008). We expected clutter bats that use denser vegetation and fly shorter distances to respond more strongly to fine-scale vegetation structure because they rely on dense vegetation immediately around them for foraging, while edge and aerial bats that forage in open areas and fly longer distances were expected to respond more strongly to landscape-scale characteristics since they fly and forage above vegetation (Cooper-Bohannon et al., 2016; Monadjem et al., 2010). In general, we expected to see a greater effect of landscape composition than configuration on bats, as has been reported in previous studies (Arroyo-Rodríguez et al., 2016; Meyer and Kalko, 2008). We also expected to see strong seasonal variation in response from all guilds, because this has been observed in previous studies in the region (Monadjem and Reside, 2008; Mtsetfwa et al., 2018; Taylor et al., 2013a, 2013b), likely due to the scarcity of resources, such as water or insect prey in the dry season (Fukui et al., 2006; Hagen and Sabo, 2012; Salsamendi et al., 2012).

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## 10. Hypotheses