

13–16 August 2018 Cape St Francis Resort, Cape St Francis, Eastern Cape





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PROGRAMME

MONDAY, 13 AUGUST 2018

CAPE ST FRANCIS RESORT, EASTERN CAPE

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Objectives: Official welcome and national context for Foundational Biodiversity Information generation and management

Time Session title Presenter

12:00–13:00 Registration

13:00-14:00 Lunch

PLENARY SESSION

venue:	The Space	
Facilitator:	Prof. Ramagwai Sebola	
14:00–14:20	Official welcome and introduction by SANBI CEO	Dr Moshibudi Rampedi, CEO SANBI
14:20–14:40	Opening address by the Department of Science and Technology	Dr Yonah Seleti, DST
14:40–15:00	Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services (IPBES)	Mr Kiruben Naicker, DEA

15:00–15:20 National Research Foundation's support for Human Capital Initiatives Representative, NRF

15:20–16:00 Coffee/tea & group photo

16:00–17:30 Biodiversity and global change: National programmes for biodiversity assessment and monitoring

The National Biodiversity Assessment: preliminary assessment of data gaps and challenges
 Assessing and monitoring genetic diversity
 Information into action: municipalities as data users and generators
 Ensuring sustainable utilisation of internationally traded species though a NDF process
 Leveraging foundational biodiversity information for observing environmental change
 Lara Atkinson & Jasper Slingsby

Questions and discussion

17:30–18:30 Poster and networking session

TUESDAY, 14 AUGUST 2018 CAPE ST FRANCIS RESORT, EASTERN CAPE

Day 2 Objectives:

Explore various methods and approaches for generating the foundational biodiversity information required for biodiversity assessment and monitoring

Time	Session title	Presenter
PLENARY SES	SSION	
Venue: Facilitator:	The Space Rob Slotow	
08:30-09:00	Camera trapping for assessment and monitoring of species and populations Invited speaker: The Snapshot – Africa project	Dr Marco Willi, University of Minnesota
09:00-10:15	Presentations	
	• Snapshot Safari – South Africa: Contemporary applications of camera traps to monitor mammal communities in South African protected areas	Jan Venter
	Camera trapping in a mixed urban-agriculture mosaic landscape: the value of a well-designed survey regime	YVETTE EHLERS-SMITH
	Big brother is watching: detecting elusive species interactions through the use of camera traps	RUTH COZIEN
	• The ecological and conservation significance of camera-trap bycatch data: a case study of two reclusive, forest-specialised bird species from the Indian Ocean Coastal Belt Forest	David Ehlers-Smith
	Moving toward an integrated data management approach for camera trapping research	Ross Pitman

Questions and discussion

10:15-10:45 Coffee/tea

PLENARY SE	SSION	
Venue:	The Space	
Facilitator:	Theresa Sethusa	
10:45–11:15	DNA Barcoding Invited speaker: The International Barcode of Life: second phase and meta-barcoding projects for bio-surveillance	DR EVGENY ZAKHAROV, Associate Director, Genomics, Center for Biodiversity genomics, University of Guelph, Canada
11:15–11:50	Presentations	
	Bugging Around: An Overview of the Kruger Park Malaise Program	Ryan Rattray
	• DNA barcoding of KwaZulu-Natal Afromontane forest <i>Parmelia</i> (Parmeliaceae) species: A molecular approach to accurate specimen identification. (Speed presentation)	NQOBILE NDHLOVU

Time	Session title	Presenter
	• Barcoding of parasitoid wasps (Braconidae and Chalcidoidea) associated with wild and cultivated olives in the Western Cape of South Africa. (Speed presentation)	CHANTE POWELL
	Questions and discussion	
11:50–13:25	Biodiversity surveys in South Africa: addressing critical data gaps	
	The Karoo BioGaps Project making big strides for the Karoo	SILVIA KIRKMAN
	• Five years onwards, filling the 'Transkei gap': an updated checklist of the herpetofauna found in the Eastern Cape forest and adjacent grasslands	Werner Conradie
	Soil Fusarium survey in grassland	Riana Jacobs
	Approaches to data generation for monitoring and assessment of biodiversity	
	Developing a long-term biodiversity monitoring framework for the eThekwini Municipality	Mathilde van Rooyen
	A foundational biodiversity map of the terrestrial microbiome of a sub-Antarctic island	Venkatachalan Siddarthan
	Re-surveying the insectivorous bats of northern Kruger National Park, South Africa (speed presentation)	ERIN BRINKLEY
	• Assessments of road impacts on the conservation of wildlife biodiversity in the Kruger to Canyon Biosphere Reserve: Case study of Skukuza, Kruger National Park, South Africa (speed presentation)	Talifhani Brilliant Mashao
	Questions and discussion	
13:25-14:20	Lunch	

PARALLEL SESSION 1: Generating foundational biodiversity data for describing, monitoring and assessing biodiversity	PARALLEL SESSION 2: Citizen science initiatives for biodiversity data generation	
Venue: The Space Facilitator: Caswell Munyai Time: 14:20–16:00	Venue: The Chapel Facilitator: Michelle Hamer Time: 14:20–15:05	
Approaches to data generation for monitoring and assessment of biodiversity (continue)	Human capital development for citizen science programmes	
 The use of Collembola as bio-indicators – Charlene Janion-Scheepers Using Passive Integrated Transponders (PITs) in the Endangered African 	• The impact of citizen scientists in long-term surveying of SA's plants of conservation concern: a case study of the CREW Programme – Suvarna Рагвноо-Монах	
Penguin to monitor populations and movement – Katta Ludynia • The response of taxonomic and functional bird diversity to forest product	 CASABIO.org – A powerful and efficient citizen science platform for scientific observations of plants and animals including camera traps – DAVID GWYNNE-EVANS 	
harvesting in the Eastern Cape, South Africa – Jessica Leaver	iNaturalist – southern Africa's new citizen science platform – Tony Rebelo	
 Biodiversity of mycorrhizal fungi in South Africa – progress and challenges – JOANNA DAMES 	Questions and discussion	
Marine microbial community dynamics as a tool for measuring the response Approximate assumptions of the property of t	Venue: The Chapel Facilitator: Tony Rebelo Time: 15:05–16:00	
of sub-Antarctic ecosystems to climate change (speed presentation) – Nasipi Mtsi	Workshop: Introduction to iNaturalist	
Efficacy of point counts and mist-netting for species detection of forest- utilising birds in Eastern Cape forests (speed presentation) – JAKE MULVANEY	This workshop is an introduction to the philosophy behind iNaturalist: how it is designed ar works. We will explore the main components: Observations, Species (taxa), Places, Projects, Guidand People. Look at what makes an observation, the dictionary and links and extracting ar showcasing data. This will be interspersed with practical coursework: uploading observation	
Unravelling cryptic diversity	editing observations (including bulk edits); customising your interface – using your dashboard	
 Phylogenetic relationship in the slug-eater snakes, <i>Duberria</i> (Lamprophiidae) SHELLEY EDWARDS 	and managing your account. Time permitting; we will explore creating places and species lists Creating Projects and managing data; Creating Guides and ID apps; Reviewing IDs and contributing identifications.	
 Molecular data reveals potential cryptic lineages in two forest-dwelling reptile species along the east coast of South Africa (speed presentation) – THEO BUSSCHAU Questions and discussion 	 Please bring to the course: Your computer (laptop, tablet – or cell phone, smartphone or equivalent, but these are tricky and not ideal – with Wifi or Bluetooth capabilities), and power cord. Between 10 and 20 digital pictures (any size: 1 MB is ideal for the course, cropped and upright) of 	
	 1–10 different organisms. If you are into checklists and guides, please bring along a checklist to your nature reserve, farm or garden of any group. Just the names without authors. Yourself, with lots of questions. 	
	Please sign up before you come to the course: www.inaturalist.org . Please make sure that you are registered and remember your login: there won't be time at the course.	
	For more please see our Facebook page: https://www.facebook.com/iNatureZA	
16:00–16:30: Coffee/tea	16:00–16:30: Coffee/Tea	

PARALLEL SESSION 1: Generating foundational biodiversity data for describing, monitoring and assessing biodiversity			PARALLEL SESSION 2: Citizen science initiatives for biodiversity data generation		
Venue: The Space	Facilitator: Victor Rambau	Time: 16:30–17:15	Venue: The Chapel	Facilitator: Tony Rebelo	Time: 16:30–17:15
Speed presentatio	ns – documenting genetic div	versity:	Continuation of wo	rkshop: Introduction to iNati	uralist
Genetic structuri snake genus – Ch	ing in <i>Psammophylax</i> (Fitzinger _{HAD} KEATES	1843), a widespread African			
	y of the forest dwelling <i>Myoso</i> tus in Eastern Cape – E mmanuel I		•		
Comparison of G Forests – Monika	genetic structure of two fores Moir	st bats across Eastern Cape			
Speed presentatio	ns – DNA barcoding:		-		
DNA barcoding of	of South African red seaweed sp	ecies – Jamie Julies			
	of native and non-native succule ustry – Future Machate	nt plants in the South African			

Questions and discussion

POSTGRADU	POSTGRADUATE STUDENT FORUM		
Venue: Facilitator:	The Space Leigh Richards		
Time	Session title	Presenter	
17:15–19:30	 Career development for taxonomists Typical skills that are necessary to build a career in taxonomy. 	Tshifhiwa Mandiwana-Neudani	
	Science communication workshop:	FORTHMATE PHAKA & THILLA 7 CE CURE	

 Science communication workshop: TV production versus scientific publishing; the ever-growing online platform; science communication – do's and

WEDNESDAY, 15 AUGUST 2018 CAPE ST FRANCIS RESORT, EASTERN CAPE

Day 3 Objectives:

- Parallel session 1 Camera trap workshop: An open workshop to develop a national strategy for managing camera trap data
- Parallel sessions 2 & 3 Presentations: Updates on the FBIP activities; Information Systems and Architecture; Data management and data standards; Using foundational biodiversity data to address issues of global change; and Unravelling microbial diversity

Time Session title Presenter

Parallel session 1: Camera Trap workshop

Venue: The Chapel **Facilitator:** Rob Slotow

08:30–16:00 Camera trap data management workshop

Presentations, discussion and strategy development

- Camera trap data management workshop: input on systems being used for camera trap data management
- Camera trap data standards existing documentation review and agreement on standards
- Principles for a national camera trap data management system
- Development of plan for establishing a camera trap data management system

Parallel session 2: Presentations

Venue: The Space **Facilitator**: Carol Simon

08:30-9:15 Update on FBIP grants and calls; data submitted and communication strategy

Overview of the FBIP funding approach and grants awarded	Lita Pauw
FBIP generated data: an assessment of taxonomic and spatial spread	Mahlatse Kgatla
The FBIP communication strategy	DANE MACDONALD

Questions and discussion

Time	Session title Se	Presenter
09:15-10:45	Foundational biodiversity information management: systems and standards	
	National Biodiversity Information System (NBIS) update	Brenda Daly
	Developing collection data management services as part of the NBIS	Brenda Daly
	Biodiversity data curation: South Africa goes online	WILLEM COETZER
	A review of global data sharing trends and the case for open data	IAN ENGELBRECHT
	FBIP data challenges: the need to address quality standards	Mahlatse Kgatla
	SANBI coordinating the development of policies for managing foundational animal work in South Africa	RETHABILE MOTLOUNG
	Questions and discussion	
10:45-11:15	Coffee/Tea	

Parallel sessi	on 2: Presentations (continued)	
Venue: Facilitator:	The Space Kirstin Williams	
11:15–12:55	Collection specimen data management	
	• Development of a sustainable solution for biodiversity data management and curation: Case study of a 10-year academic collection at the African Centre for DNA Barcoding.	RONNY KABONGO
	• Challenges and progress with mobilising biodiversity data in the Iziko South African Museum entomology collection	SIMON VAN NOORT
	• Southern African Marine Mammal database: assessment and review of national museum collections, with the goal to consolidate existing specimen data, facilitate access to research collections and standardise curation	Keshni Gopal
	Conversion of East London Museum Malacology database to Specify6 (speed presentation)	Mary Cole
	What's in a name?	
	Using taxon concepts to reconcile the meanings of names in a collection context	IAN ENGELBRECHT
	• The inconsistent application of common and species names to polychaete worms used as bait can affect management	CAROL SIMON
	Names for South African frogs and aspects of folk taxonomy, a Zululand case study (speed presentation)	FORTUNATE PHAKA
	Questions and discussion	
12:55–14:00	Lunch	

Parallel session 2 (continued):		Parallel session 3:		
Venue: Facilitator: Time:	The Space Joanna Dames 14:00–15:00	Fa	enue: acilitator: ime:	The Franklin Room Tshifhiwa Mandiwana-Neudani 14:00–15:00
Unravelling microbial diversity		U	Using foundational biodiversity information for addressing global change challenges	
 Screening of ectomycorrhizal and other associated fungi in South African forestry nurseries – Veronique Chartier FitzGerald 		•	Biodiversity PHOLOSHI MA	and impacts of plant feeding mites on tea plant (<i>Camellia sinensis</i>) in South Africa –
 Root fungal diversity associated with three <i>Disa</i> species (speed presentation) Nondumiso Khambule 		•	Fire and Inv	asive Species Control Programme with eThekwini Municipality – Bongani Zungu
		•	The import	ance of herbaria distribution records in the study of gene flow likelihood from
 Marion Island vegetation and root associated fungal diversity (speed presentation) – Jahman Thabede 			sugarcane (<i>Saccharum</i> hybrids) to wild and weedy relatives in eastern South <i>P</i> presentation) – D ENNIS K OMAPE	
• Diversity of rhizobia associated with root nodulation in pigeon pea (<i>Cajanus cajan</i>) from South Africa (speed presentation) – Francina Bopape		•	Investigatio	ns into a new invasive worm in the Knysna Estuary (speed presentation) – H ENDRE
A plethora o – Mudzuli M	of Fusarium species in grassland biome soils (speed presentation) avhunga	•	•	ant communities to woody plant expansion at Hluhluwe–iMfolozi Parks, KwaZuluderesentation) – Nomathamsanga Mkhize
Questions and discussion		Q	uestions and	discussion
15:00–15:30 Coffee/tea				

Parallel session 2 (continued):				
Venue: Facilitator:	The Chapel Pholoshi Maake			
Time	Session title	Presenter		
15:30-17:00	Speed presentations: Assessing biodiversity in different habitats			
	Ant communities along an elevational transect, Udzungwa Mountain in Tanzania	CAROLINE KUNENE		
	• Investigating population demographics, breeding system and principle pollinator of Protea curvata	Precious Mabuza		
	The role of competition in structuring ant communities in selected grasslands and forest habitat	Nokubonga Thabethe		
	• Floristics of three Northern Coastal Forests in a global biodiversity hotspot: A comparison across patches of contrasting disturbance history	OLIVIER KAMBAJ		
	Checklist of epigaeic ants in Buffelsdraai Landfill Conservancy, South Africa	SBONGISENI XOLO		
	Ant and spider community response to alien invasive plant species (Chromolaena odorata)	Sinenhlahla Mntambo		

Time	Session title	Presenter
	Speed presentations: Taxonomy	
	• A taxonomic study of the planktonic freshwater free-living copepods in Turfloop Dam, Limpopo Province	PERAL MNISI
	• A taxonomic revision of the <i>Brevipalpus phoenicis</i> and <i>Brevipalpus obavatus</i> species complexes (Acari: Tenuipalpidae) in South Africa	RISUNA NDZERU
	• Phylogeny of the terrestrial snail genus Gittenedouardia (Mollusca: Gastropoda: Cerastidae)	EVELYN RAPHALO
	Questions and discussion	
17:00–17:15	Key outcomes, reflections and closure	JEFF MANUEL

CONTINUATION OF POSTGRADUATE STUDENT FORUM		
Venue: Facilitator:	The Space Leigh Richards	
Time	Session title	Presenter
17:30-19:00	Postgraduate Student Forum	
	Continuation of science communication workshop	FORTUNATE PHAKA & THULA ZEE CUBE

• Election of representatives for the FBIP Postgraduate Student Association

THURSDAY, 16 AUGUST 2018 CAPE ST FRANCIS RESORT, EASTERN CAPE

Day 4

Objectives: Training sessions and workshops to improve skills in biodiversity data management

08:00-13:00	08:00-13:00	08:00-13:00	
Parallel session 1:	Parallel session 2:	Parallel session 3:	
Camera trap data management – using existing systems for storing and working with camera traps data. A large number of projects in South Africa are currently generating camera trap data. A national system for archiving and sharing the data generated from these projects will ensure that a national resource can be developed for future use in research and decision-making.	Barcode of Life Database – using BOLD for DNA barcode data analysis and identification of material. This workshop will illustrate some of the key functionalities of the Barcode of Life Database (BOLD).	SANBI-GBIF Georeferencing Training: SANBI-GBIF will be hosting a georeferencing training event, to build skills in improving data quality. New approaches in georeferencing skills will be presented.	
Presenter: Marco Willi (University of Minnesota), YVETTE EHLERS-SMITH & ROB SLOTOW	Presenter: Evgeny Zakharov , Associate Director, Genomics, Center for Biodiversity genomics, University of Guelph, Canada	Presenters: Fhatani Ranwashe, Burgert Muller, Sherwyn Mack & Albe Bosman	
13:00–14:00: Lunch			

ABSTRACTS: MONDAY, 13 AUGUST 2018 - PLENARY SESSION

Biodiversity and global change: National programmes for biodiversity assessment and monitoring

Information into action: municipalities as data users and generators

Natasha Govender

Environmental Planning and Climate Protection Department, eThekwini Municipality; Natasha.Govender@durban.gov.za

We live in an increasingly urban world and the threats to natural systems are likewise intensifying. It is estimated that 70% of the global population will be urbanised by 2050, representing the fastest period of urban expansion in history. The bulk of this growth will take place in cities of the global south, such as Durban. As a result of these pressures, local government environmental practitioners involved in land-use decision-making require strong arguments supported by robust scientific information to firstly, motivate, if warranted, for the protection of certain conservation-worthy areas against alternative, competing land-uses; and secondly, to identify priority areas for conservation action to proactively secure a representative conservation area network. This requires an in-depth knowledge of the biodiversity features and ecological processes as well as the pressures and opportunities challenging its existence. The eThekwini Municipality's Environmental Planning and Climate Protection Department has identified important biodiversity areas in Durban through the use of Systematic Conservation Planning methodology. In doing so, Durban's environmental practitioners sourced data from various technical specialists within the municipality and also used in-house expertise to generate key datasets. The Systematic Conservation Assessment and its implementation provides useful lessons regarding data requirements for local, provincial and national government decision makers as well as how municipalities can be repositories and generators of important technical information.

Leveraging foundational biodiversity information for observing environmental change

Jasper Slingsby^{1,2}, Lara Atkinson¹, Johan Pauw¹

¹South African Environmental Observation Network (SAEON); <u>jasper@saeon.ac.za</u>,

²Centre for Statistics in Ecology, Environment and Conservation, Department of Biological Sciences, University of Cape Town

SAEON was created to aid sustainable development in South Africa by addressing the lack of reliable long-term data at scales that are relevant to informing policy, and to aid integration between various sources of information on the environmental, social and economic elements of sustainability. The vision is one of a sustained, coordinated, responsive and comprehensive in situ network that delivers long-term reliable data for scientific research and informs decision-making for a knowledge society and improved quality of life. As such, much of our work focuses on issues of global change, discerning anthropogenic impacts on the environment from natural variability, identifying current and potential drivers of change and their implications for societal benefits, and disseminating and mainstreaming our findings to inform policy and management decisions. While biodiversity monitoring is not our core function, biodiversity information is foundational to understanding the state and trajectory, function and societal benefits that can be derived from ecosystems. Here we present some of SAEON's projects relating to long term monitoring of biodiversity, how they depend on and/or feed into SANBI programmes, and their relevance for environmental policy and management.

ABSTRACTS: TUESDAY, 14 AUGUST 2018 - PLENARY SESSION

Camera trapping for assessment and monitoring populations

Snapshot Safari – South Africa: Contemporary applications of camera traps to monitor mammal communities in South African protected areas

Jan A. Venter¹, Mika M. Vermeulen¹, Craig Packer², Rob Slotow³, Colleen Downs³, Michael Somers⁴, Mike Peel⁵, Lourens Swanepoel⁶, Nokubonga Mgqatsa⁷, Hervé Fritz⁸, Sandi Willows-Munro³, Mark Keith⁹, Dan Parker¹⁰, Aliza le Roux¹¹

- ¹ School of Natural Resource Management, George Campus, Nelson Mandela University; Venter: <u>Jan.Venter@mandela.ac.za</u>
- ²College of Biological Sciences, University of Minnesota, United States of America
- ³ School of Life Sciences, University of KwaZulu-Natal
- ⁴Mammal Research Institute, University of Pretoria
- ⁵ Animal Production Institute, Agricultural Research Council
- ⁶Department of Zoology, University of Venda
- ⁷ Department of Zoology and Entomology, Rhodes University
- ⁸ Sustainability Research Unit, Nelson Mandela University
- ⁹Centre for Wildlife Management, University of Pretoria
- ¹⁰ School of Biology and Environmental Sciences, University of Mpumalanga
- ¹¹ Department of Zoology and Entomology, University of the Free State

The use of camera traps, especially since the mid 1990s, has helped improve our understanding of the ecological relationships and population dynamics displayed by animals in the wild. Improved technology has increased the popularity of camera traps and allowed for their application in wildlife research to become widespread. The purpose and application of cameras traps in wildlife ecology has evolved over time. Originally, camera traps were used to investigate simple measures of presence and absence; today, researchers are using data from camera traps in far more complex studies, to solve questions on wild animal spatial, behavioural and temporal patterns. The advantages of using camera traps in understanding animal ecology is that the researcher does not need to handle, be present or directly observe interactions for ecological data to be recorded.

Here we introduce Snapshot Safari – South Africa, which will include an unprecedented network of camera trap grids in dozens of protected areas and expansion areas in South Africa. Eventually hundreds of cameras will provide continuous monitoring of population sizes and trends of mammal species at each site. Some of the participating focus areas are managed as conservancies and stewardship areas, some are privately owned, some are state-run and others are under communal tenure. With the help of accurate camera trap censuses and innovative mapping approaches, we will be able to identify which sites are being managed successfully – and hence which conservation strategies should be incorporated into a toolbox for effective wildlife management.

Camera trapping in a mixed urban-agriculture mosaic landscape: the value of a well-designed survey regime

Yvette C. Ehlers Smith, David A. Ehlers Smith, Colleen T. Downs School of Life Sciences, University of KwaZulu-Natal; yvetteehlers@hotmail.com

Researchers have found that because of inappropriate census techniques, the demise of small species may go unnoticed until remedial action is no longer possible. Camera-trapping survey techniques can be considered the best survey method for cryptic and elusive species and are ideally suited to dense habitats such as forest and thicket. Using a systematically collected camera-trap dataset consisting of 250 individual camera trap stations across 157 distinct habitat patches, we assessed: 1) the influence of habitat characteristics; 2) landscape scale factors; 3) anthropogenic disturbance; 4) predation pressures; and 5) the effects of seasonality on the on the spatio-temporal distribution of vulnerable blue duiker (Philantomba monticola) within the coastal belt of southern KwaZulu-Natal. For blue duiker we highlighted habitat-specific associations, lower occupancy within nature reserves and a shift in activity patterns responding to anthropogenic disturbances, which would not have been possible without the camera-trap technology. Our results highlight the importance of a well-planned, georeferenced and integrated database that can aid in species-specific management plans for Protected Areas, and the multiple applications pertinent to conservation, ecology and landscape management that a single camera-trap dataset can provide.

Big brother is watching: detecting elusive species interactions through the use of camera traps

Ruth Cozien, Dr Timo van der Niet, Prof. Steve Johnson School of Life Sciences, University of KwaZulu-Natal; ruthcozien@gmail.com

Knowledge of species interactions such as those between plants and animal pollinators is critical both for answering fundamental questions about the evolution of biodiversity, as well as for conservation of contemporary mutualisms. However, identification of mutualistic partners may be challenging if interactions are elusive because they occur extremely infrequently or unpredictably, or are relatively inaccessible. Research work done in the pollination lab at the University of KwaZulu-Natal has included the use of camera traps to make several breakthroughs and change long-standing ideas about animal behaviour. Motion trigger cameras enabled identification of pollinators of a Critically Endangered species, after a decade of conventional observations failed, and recently helped document a pollination system previously unknown in continental Africa, in the Drakensberg. Camera trap data have also been used to identify fine scale pollinator movement patterns and distinguish between nectar robbers and legitimate pollinators, and revealed that bias in human rather than insect behaviour underlies the long accepted idea that pollinating moths are active primarily in the evening. Through such applications, motion trigger cameras have become an indispensable part of the pollination ecologist's toolkit, and over the past decade have greatly advanced our understanding of the 'who', 'what' and 'how' of plant-pollinator interactions.

The ecological and conservation significance of camera-trap bycatch data: a case study of two reclusive, forest-specialised bird species from the Indian Ocean Coastal Belt Forest

David A. Ehlers Smith, Yvette C. Ehlers Smith and Colleen T. Downs School of Life Sciences, University of KwaZulu-Natal; smithd1@ukzn.ac.za

Bycatch data from camera-trap surveys (i.e. species recorded that were not the target species of the survey) have significant value for informing ecological and conservation research, if camera-trap placement allows for adequate detection of bycatch species. Here, we present a case study in which the occupancy, habitat preference and tolerance to disturbance of two reclusive and cryptic forest-dependent bird species was sufficiently described from the bycatch of a camera-trap survey designed for forest mammals. The spotted ground thrush (Zoothera guttata; SGT) is a globally endangered forest specialist whose distribution is poorly understood in the critically endangered Indian Ocean Coastal Belt Forest biome, while the lemon dove (Aplopelia larvata) is a widespread, but elusive forest specialist present in coastal and Afrotemperate forests. We conducted camera-trap surveys in 82 forest patches of various sizes across a gradient of land-use types in the IOCBF during the winter seasons of 2014–2016 to establish occupancy (Ψ) of SGT, and repeat surveys in summer and winter seasons of the same years for lemon doves. We used occupancy modelling and incorporated forest microhabitat characteristics and surrounding land-use classifications to compare sites and efficiently describe distribution across the habitat mosaic, tolerance to disturbance and habitat preference.

Moving toward an integrated data management approach for camera trapping research

Ross Tyzack Pitman^{1,2}, Gareth Mann^{1,2}, Gareth Whittington-Jones¹, Rob Pickles¹, Chris Hallam¹, Joleen Broadfield^{1,2}, Hugh Robinson¹, Joe Smith¹, Luke Hunter¹, Guy A Balme^{1,2}

Panthera, 8 W 40th Street 18th Floor, New York, NY 10018, U.S.A; <u>RPitman@panthera.org</u>

Institute for Communities and Wildlife in Africa, Department of Biological Sciences, University of Cape Town, South Africa

International conservation by its very nature implies that data are collected, held and analysed by different individuals, across multiple countries, and in different formats – diluting the power of the data and hindering optimal decision-making. In conservation, decisions must be based on the best available information. Complicating matters further, analytical methods are constantly evolving, making it difficult for scientists to remain current. There exists an urgent need to standardise data collection, data processing and data management in one centralised location. Furthermore, there is a need to democratise even the most sophisticated analytical methods. Solving these two issues would allow conservation practitioners to efficiently share data, collaborate and easily use rigorous scientific analytical methods to make informed decisions.

Panthera is currently pioneering the development of a software program to address many of the limitations inherent in the conservation field. Called Panthera Integrated Data Systems, or PantheralDS for short, this local- and cloud-based computer platform leverages the latest technology and computational methods to help fight the rising tide of species decline and habitat degradation. PantheralDS provides a unique and intuitive combination of data management and analytical tools to cater to the growing needs of field ecologists and conservation scientists.

DNA Barcoding

Bugging around: an overview of the Kruger National Park malaise programme

Ryan D. Rattray¹, Michelle D'Souza², Michelle van der Bank¹, Paul D. N. Hebert²

African Centre for DNA Barcoding, Department of Botany, University of Johannesburg; ryanr@uj.ac.za Centre for Biodiversity Genomics, University of Guelph, Guelph, Ontario, Canada

Arthropods are the most diverse group of terrestrial life on earth and play a significant role in the diversity of many ecosystem services. A recent study indicates a decline in insect biomass in Europe; however, information is scare surrounding the distributions and diversity of arthropods in Africa as well as the impacts global change may have on these communities. The current project will focus on addressing the lack of knowledge in one of the world's most important national parks, providing a model that we anticipate seeing adopted in many other settings across the country and the world. This project aims to develop a comprehensive inventory of Malaise-trappable arthropod species in the Kruger National Park through DNA barcoding efforts. Twenty-five Malaise traps have been deployed at sites across the Kruger National Park and through this passive sampling method we expect to document the presence of at least 10 000 arthropod species, providing detailed information on their distributions and seasonal occurrence patterns. Furthermore, this data will provide an invaluable baseline for monitoring future change within the Kruger National Park.

DNA barcoding of KwaZulu Natal Afromontane forest *Parmelia* (Parmeliaceae) species: A molecular approach to accurate specimen identification

(speed presentation)

Nqobile Ndhlovu, Richard P. Beckett, Sandi Willows-Munro

School of Life Sciences, Department of Botany, University of KwaZulu-Natal; nqoohndhlovu@gmail.com or 216071059@stu.ukzn.ac.za

Accurate species identification is challenging, especially in groups with subtle taxonomic diagnostic characters such as lichens. The use of DNA barcodes can provide an effective alternative for consistent species identification. Molecular-based techniques have been shown to be a valuable tool for accurate specimen identification in fungi; in particular the internal transcriber spacer (ITS) region has been shown to successfully discriminate a broad range of fungal species. For this study we investigate the utility of the ITS DNA barcode for a cosmopolitan lichen-forming fungus, Parmelia (Parmeliaceae). Sixty ITS sequences generated from specimens collected from five sites around the province of KwaZulu-Natal were analysed. Phylogenetic analysis indicates that unlike European Parmelia species that form strong monophyletic clades, Parmelia species in KZN are paraphyletic or polyphyletic. This suggests that the taxonomy of Parmelia lichens in South Africa needs to be thoroughly revised. The molecular data presented in this study provides evidence of previously hidden species-level diversity in Parmelia and as such makes a contribution to the knowledge and understanding of the biodiversity of lichenised fungi in South Africa.

Barcoding of parasitoid wasps (Braconidae and Chalcidoidea) associated with wild and cultivated olives in the Western Cape of South Africa

Chanté Melissa Powell¹, Virgilio Caleca², Martina Sinno³, Michaela van Staden¹, Simon van Noort⁴, Clint Rhode¹, Elleunorah Allsop⁵, Barbara van Asch¹

¹Stellenbosch University Faculty of AgriSciences, Genetics; 17615054@sun.ac.za or chantepowell4@gmail.com

²University of Palermo, Department of Agricultural and Forestry Sciences

³University of Naples Federico II, Department of Agricultural Sciences

⁴Iziko South African Museum, Department of Natural History ⁵Agricultural Research Council, Infruitec- Nietvoorbij

While the international olive industry is threatened by the olive fly (Bactrocera oleae) – a pest causing great economic loss – South African commercial crops are less affected. The presence of native parasitoid wasp species may contribute to maintain olive fly populations at low levels. Additionally, seed wasps seem to be the main threat to cultivated olives. Olive flies, olive seed wasps and parasitoid wasps use wild and cultivated olives as hosts. This study aimed at compiling a list of wasp species associated with wild and cultivated olives in the Western Cape and their DNA barcoding sequences. A dual approach using morphological and molecular methods was applied for species identification of adult wasps reared from wild and cultivated olives. Four Braconidae (Bracon celer, Psyttalia humilis, Psyttalia lounsburyi and Utetes africanus) and six Chalcidoidea (Eupelmus spermophilus, Eurytoma oleae, Eurytoma varicolor, Sycophila aethiopica, Neochrysocharis formosa and Ormyrus sp.) were morphologically identified. In all cases, the morphological identification showed a strong correlation with patterns of phylogenetic clustering and genetic distances. These results can aid in early detection of olive infestations, and further explore the biology and ecology of wasps associated with wild and cultivated olives in South Africa.

The Karoo BioGaps Project making big strides for the Karoo

Silvia Kirkman and Theresa Sethusa South African National Biodiversity Institute; silviakirkman@gmail.com, T.Sethusa@sanbi.org.za

The Karoo BioGaps Project is a three-year, SANBI-led collaborative project funded by the FBIP, with over 20 collaborating institutions participating in the project. The aim of the project is to gather Karoo biodiversity data for 14 key taxonomic groups (plants, mammals, fish, birds, reptiles, amphibians, bees, dragonflies, grasshoppers, scorpions, butterflies, spiders, fungi and nematodes) in the poorly surveyed, but developmentally important region, to inform decision-making and development in the Karoo. Data are being collected via field surveys for key taxa in at least 30 pre-selected sites across the study region, which have resulted in new species being discovered, as well as data supporting range extensions of some taxa. Historical data for these taxa residing in museums and herbaria are also being mobilised through digitisation (imaging and transcribing) and georeferencing. Citizen scientists are contributing photographic data through two online portals. Taxonomic studies and updates are also being undertaken through genetic analyses of specimens collected in the field. Mobilised data are being analysed using geo-spatial modelling methods. The outputs will include a comprehensive database of data gathered during the project (~200 000 records), species pages and Red Listing of selected taxa, and species distribution maps and richness analyses.

Five years onwards, filling the 'Transkei gap': an updated checklist of the herpetofauna found in the Eastern Cape forest and adjacent grasslands

Werner Conradie

Port Elizabeth Museum (Bayworld), Humewood & School of Natural Resource Management, George Campus, Nelson Mandela University; werner@bayworld.co.za

From 2011 to 2013 we surveyed six forests along the Wild Coast of the Eastern Cape Province, South Africa, to determine the general herpetofaunal diversity. We then recorded a total of 22 amphibian and 37 reptile species. During the recent FBIP-funded Eastern Cape Forest project (2016–2018) we expanded on these results by surveying eight different forests. Of these, three were previously surveyed (Mkambati, Dwessa, Manubi) and five were new surveyed (Mboyti, Isidenge, Fort Fordyce, Baziya, Ngadu). We recorded a total of 26 amphibian and 39 reptile species. A number of those represented previously unknown populations of threatened species, as well as the expansion of known species distributions. Here we will provide an updated checklist to the reptiles and amphibians occurring in and around the highly fragmented Eastern Cape forests.

Soil *Fusarium* survey in the grassland biome of South Africa

A.Jacobs¹, M. Muvhunga¹,³, BA Summerell ², E. Venter³
¹ARC-Plant Health and Protection; <u>JacobsR@arc.agric.za</u>
²Royal Botanic Gardens Sydney, Australia
³Department of Botany and Plant Biotechnology, University of Johannesburg

Species in the genus Fusarium are characterised by significant variation in morphological characters, enabling the use of these characters for species identification. However, some species proved very difficult to identify based on morphology alone, and, therefore, extensive phylogenetic protocols were developed to aid in species identifications and descriptions. During the current Fusarium soil survey, an integrated approach is being used to demarcate species obtained from undisturbed soils in the grassland biome of South Africa. To date, ca. 1 200 isolates have been obtained from seven nature reserves and DNA barcode sequence data generated. The barcoded isolates represent new host reports for known species, new species and new haplotypes in some known species complexes. This survey serves as a crucial baseline study on the species richness of the fusaria in the grassland biome of South Africa.

Approaches to data generation for monitoring and assessment of biodiversity

Developing a long-term biodiversity monitoring framework for the eThekwini Municipality

L. van Rooyen^{1,2}, S. O'Donoghue², C. Downs³, R. Boon², E. Douwes²

¹School of Agricultural, Earth and Environmental Sciences, University of KwaZulu-Natal;

<u>Pretorius.lulu@gmail.com</u>

²Environmental Planning and Climate Protection Department, eThekwini Municipality, Durban ³School of Life Sciences, University of KwaZulu-Natal

Through the Durban Research Action Partnership (D'RAP) between the eThekwini Municipality and UKZN, the Environmental Planning and Climate Protection Department (EPCPD) of the Municipality endeavours to develop a long-term biodiversity-monitoring programme. The aim of such a programme would be to track the effect of environmental changes (such as climate change) on the City's biodiversity, to inform management and policy decisions. Although the role of the Post-Doc (appointed to work as an 'embedded researcher' in the Municipality) is to drive and facilitate the process, the programme is being co-developed by UKZN and Municipal staff members through a collaborative, transdisciplinary effort. Thus far a robust, adaptive framework has been developed, which will include a set of scientifically defendable biodiversity monitoring variables, as well as management indicators to reflect the implementation success of the EPCPD's Biodiversity Strategy. Through this undertaking it has emerged that one of the most urgent interventions required within the EPCPD is a properly designed biodiversity information management system to capture and host current and future datasets. The current challenge is to understand what is required to design, implement and host such a database.

A foundational biodiversity map of the terrestrial microbiome of a sub-Antarctic island

Siddarthan Venkatachalam¹, djRobert Pienaar¹, Gwynneth Matcher¹, Nasipi Mtsi¹, Peter le Roux², Michelle Greve², ³Bettine Jansen van Vuuren, ³Sudharshan Sekar, ¹Rosemary A Dorrington

¹Department of Biochemistry and Microbiology, Rhodes University; venkateshbiotech@gmail.com

²Department of Plant and Soil Sciences, University of Pretoria

³Department of Zoology, University of Johannesburg

The sub-Antarctic Prince Edward Islands (PEIs), located within the Indian sector of the Southern Ocean, have been the focus of ecological research for more than 50 years, providing important scientific data on the functioning of sub-Antarctic ecosystems and their response to climate change. Marion Island forms part of the Prince Edward Island system and supports six habitat complexes across 21 habitats that contain distinct groups of native and invasive plant species, providing different microclimates for microbial communities that play a critical role in biogeochemical processes of the island ecosystem. This study forms part of an FBIP Biodiversity survey of invertebrates and microbial communities of the PEIs. The aim was to map microbial community diversity across different habitat complexes, with an emphasis on interactions with keystone indigenous and invasive plant species. Around 180 soil samples were collected during March/April of 2015 and 2016. We used Next Generation Sequencing of amplicon libraries to characterise bacterial and fungal diversity. The data provide insights into the diversity and distribution of the soil microbiota, plant–microbe interactions, and the role of the microbiota in supporting the functioning of sub-Antarctic terrestrial ecosystems.

Re-surveying the insectivorous bats of northern Kruger National Park, South Africa

(speed presentation)

Erin R. Brinkley¹, Daniel M. Parker^{1,2}, and Peter J. Taylor³

¹Wildlife and Reserve Management Research Group, Department of Zoology and Entomology, Rhodes University; erinbrinkley95@gmail.com

²School of Biology and Environmental Sciences, University of Mpumalanga

³School of Mathematical and Natural Science, University of Venda

Insectivorous bats comprise ca. 20% of the mammalian diversity in South Africa's Kruger National Park (KNP). The work of Rautenbach (1984, 1985) was the last reliable assessment of the bats of northern KNP. We revisited the Rautenbach's (1984, 1985) sites to resurvey the insectivorous bat populations of northern KNP using both live-capture and passive acoustic monitoring. Sites were split into two regions, located within and around the northern rest camps – Pafuri and Punda Maria/Shingwedzi. We captured ten species from five different families within the two regions. With the addition of passive acoustic monitoring, we have detected at least twenty-four species – two of which are unknown – from five different families between Pafuri and Punda Maria/Shingwedzi. In both regions, the Molossidae dominated both the live-captures and the acoustic data. Importantly, our results compare favourably with those of Rautenbach (1984, 1985) and although we are yet to record five of the species that Rautenbach (1984, 1985) did, we have definitively identified at least two species that have not been previously recorded for KNP. Our data shows that more bats can be detected with the addition of bioacoustics and this provides a better overall understanding of bat diversity in northern KNP.

Assessments of road impacts on the conservation of wildlife biodiversity in the Kruger to Canyon Biosphere Reserve: Case study of Skukuza, Kruger National Park, South Africa

(speed presentation)

Talifhani Brilliant Mashao
Department of Geography, Environmental Sciences, University of Venda;
mashaobrilliant@gmail.com

Roads promote high levels of animal–vehicle collisions and have one of the most visible manmade impacts on wildlife. In South Africa, very few ecological studies have focused on the impacts from roads on wildlife in the national parks. In this study, the following procedure will be followed: The observer (the driver) will drive along a selected 100 km transect, each day for 30 days in each of the cold–dry, hot–wet and hot–dry seasons, for 1.5 hours after sunrise (after gate opening time) and again for 1.5 hours before sunset (before gate closing time). Both paved and unpaved roads will be included in the study. Paved roads will be driven at 50 km/hour and unpaved ones at 40 km/hour. For each carcass, a photograph will be taken and the position on the road and GPS coordinates will be recorded to avoid recounts. The outcome of the study will be a hotspot risk area map, indicating hotspots for road-kills inside the Kruger National Park and aiming to protect biodiversity by ensuring proper conservation with relevant mitigation measures. ArcGIS will be used to analyse the data and produce the maps, tables and graphs for data presentations.

ABSTRACTS: TUESDAY, 14 AUGUST 2018 - PARALLEL SESSION 1

Generating foundational biodiversity data for describing, monitoring and assessing biodiversity Approaches to data generation for monitoring and assessment of biodiversity (continue)

The use of Collembola as bio-indicators

Charlene Janion-Scheepers Iziko South African Museum; cscheepers@iziko.org.za

South Africa is a biodiversity hotspot for many soil groups. Soil organisms such as Collembola (springtails) have proven to be useful model organisms worldwide. Despite their global importance, Collembola remain notably species poor when compared to other insect groups. Also, due to their small size and the taxonomic expertise needed for identification, many biodiversity and agricultural studies exclude Collembola from their results. However, their response to change makes them ideal for use as bio-indicators. In Europe, Collembola are widely used in biodiversity assessments, ecotoxicology studies and as indicators of soil health and pollution. In South Africa, endemic species often represent a large proportion on the total assemblage and are thought to be more vulnerable to loss of natural habitat than non-endemic species. Thus, they can be used to assess the effect of global changes such as climate change and invasive species, change and habitat disturbance. In addition, due to the high endemism of this group, they can also be included in conservation plans. I will illustrate some of these examples and show how the accurate identification of species is the first step in exploring the usefulness of this group as soil health indicators.

Using Passive Integrated Transponders (PITs) in the Endangered African Penguin to monitor populations and movements

Katta Ludynia, Barbara J Barham, Richard Sherley Southern African Foundation for the Conservation of Coastal Birds (SANCCOB); katta@sanccob.co.za

Metal flipper bands were used to mark and individually identify African Penguins from the 1960s until they were discontinued in the early 2000s after potentially detrimental effects were shown in other penguin species. Several attempts were made to introduce other longterm marking techniques, such as silicone rubber bands and the use of individual spot patterns but these proved to be of limited use in the field. Passive Integrated Transponders (PITs) were adopted as a nation-wide marking system for African Penguins in 2013, initially as part of a study to assess the success of hand rearing of abandoned chicks at SANCCOB and later as a long-term monitoring system. A percentage of breeding African Penguin adults and fledglings in the main breeding colonies in South Africa are currently fitted with PITs each year as well as all rehabilitated African Penguins before release back into the wild. Birds are re-sighted in the colonies using hand-held and automated ground readers. Data obtained is used to update survival estimates for this endangered species, to understand movements between colonies and to assess iuvenile recruitment. Results will be fed into conservation management as per the Biodiversity Management Plan, i.e. to advise on translocation, establishment of new colonies and population modelling.

The response of taxonomic and functional bird diversity to forest product harvesting in the Eastern Cape, South Africa

Jessica Leaver, Jake Mulvaney, Michael I. Cherry Department of Botany and Zoology, Stellenbosch University; jes.leaver@gmail.com

Forests are of socio-economic significance as millions of impoverished households rely on forest resources to meet basic needs and derive cash incomes. Ecologically, forests depend on the persistence of bird diversity, given the vital ecological roles of birds. However, the impact of forest product harvesting on birds is poorly understood. This study thus aimed to assess the response of taxonomic and functional measures of bird diversity to prevalent forest product harvesting activities in state-managed forests in the Eastern Cape, South Africa. Four forest ecotypes were sampled using 0.04 ha circular plots (n = 64) in which harvest intensities, habitat structure and bird communities were recorded. Results of linear mixed models indicate that bird responses to harvesting activities vary depending on the aspect of diversity considered, and the nature and extent of harvesting. Thus, while taxonomic diversity showed positive and negative responses to bark and pole harvesting respectively, metrics of functional diversity, affected by pole and timber harvesting, were consistently negatively impacted. This suggests that current pole and timber harvest regimes negatively affect forest ecosystem functioning. Furthermore, results indicate that factors beyond harvest-driven structural modification, such as changes in food availability, may be important drivers of observed declines in functional bird diversity.

Biodiversity of mycorrhizal fungi in South Africa – progress and challenges

Joanna Dames

Department of Biochemistry and Microbiology, Rhodes University; <u>j.dames@ru.ac.za</u>

For over 500 million years fungi have associated with the roots of terrestrial plants forming a symbiotic relationship, which aids in nutrient acquisition and survival of the majority of plant species. Distinct types of these mycorrhizal associations are based on the fungi and plant species involved as well as the symbiotic structures formed within or around plant roots. Ectomycorrhizal (ECM) fungi have generally been introduced with exotic trees, while the South African vegetation is mainly arbuscular-mycorrhizal (AM) with the exception of the members of the Ericales, which are ericoid-mycorrhizal. Using next generation sequencing, ericoid-fungal root associates were predominantly from the Ascomycota, although Basidiomycota and Glomeromycota (AM fungi) were also detected. AM fungal diversity associated with a salt pan (Eastern Cape) and semi-arid environment in the Northern Cape were found to be dominated by species in the Ambispora, Glomus and Paraglomus genera with a rare component represented by species in the Redeckera, Archaeospora and Geosiphon genera. Although common in all ecosystems, mycorrhizal biodiversity in South African soils and plants have received little attention. Research conducted suggests that not only are our mycorrhizal populations fairly diverse, but they are also negatively affected by some agricultural management practices.

Marine microbial community dynamics as a tool for measuring the response of sub-Antarctic ecosystems to climate change

(speed presentation)

Mtsi Nasipi, Siddarthan Venkatachalam, Gwynneth Matcher and Rosemary Dorrington Department of Biochemistry and Microbiology, Rhodes University; nasipi.mtsi@gmail.com/ g17m4576@gmail.com

Ecosystems in Antarctica and the Southern Ocean are sentinels of global change, highly sensitive to changes in climate. The Southern Ocean acts as a carbon-dioxideand-heat-sink for the planet and plays a critical role in mitigating the effects of climate change. Situated within the sub-Antarctic are the Prince Edward Islands (PEIs); they are important terrestrial breeding grounds for large populations of seabirds and marine mammals that are critically dependent on the ecosystem services of the surrounding marine environment. Therefore, the terrestrial and marine habitats are closely linked. This study is part of a foundational biodiversity survey of invertebrates and microbial communities (bacteria and fungi) of the PEIs' terrestrial and marine system. Our study focuses on the diversity of marine microbiota, phytoplankton and bacterial communities and their role in supporting the PEIs ecosystem. We used Next Generation Sequencing analysis to characterise bacterial and phytoplankton diversity in the water column (near-shore, offshore, open ocean) of the PEIs. The data reveal a strong correlation between the microbial species diversity and climate-driven oceanographic variability. Our study highlights the need to collect baseline information on microbial communities as a tool for studying the response of ecosystems to climate change in the sub-Antarctic.

Efficacy of point counts and mist-netting for species detection of forest-utilising birds in Eastern Cape forests

(speed presentation)

Jake Mulvaney and Michael Cherry
Department of Botany and Zoology, Stellenbosch
University; jakem@sun.ac.za

Elucidating the limitations of point counts and mist-netting as survey techniques promotes better implementation of these methods for avian biodiversity monitoring. Occupancy modelling can highlight functional traits and environmental conditions most influencing species detection by these methods, though parameter applicability may be site-specific. To this end, sixty duplicate point count stations and thirty 180 m mist-net transects were equally distributed among six scarp and mist-belt forest fragments in the Eastern Cape. The forest bird communities were similarly structured, derived from a regional assemblage of 172 forest-utilising species. Both methods performed consistently between forests. Point counts better represented community structure than mist-nets (69.2% vs 32.0% total diversity), and better estimated the total avian diversity. Detection outcome did not vary between forests, highlighting instead the influences of survey method, as well as species body size, foraging stratum and habitat specialisation. Forest interiors were dominated by forest-dependent species and were canopy-oriented. Forest edge was more speciose overall as 63% of forest avian diversity is sourced from surrounding matrices, mostly restricted to forest edge interactions. However, a forest interior had better representation. Although forestdependent species are indicators of forest condition, holistic representation of forest communities requires accurate detection of forest edge-utilising species as well, as these facilitate forest landscape ecological processes.

Unravelling cryptic diversity

Phylogenetic relationship in the slug-eater snakes, *Duberria* (Lamprophiidae)

Shelley Edwards¹, Werner Conradie^{2,3}, Chris Kelly¹, Eli Greenbaum⁴

¹Zoology and Entomology Molecular Lab (ZEML), Department of Zoology and Entomology, Rhodes University; s.edwards@ru.ac.za

²Port Elizabeth Museum

³School of Natural Resource Management, George Campus, Nelson Mandela University

⁴Department of Biological Sciences, The University of Texas at El Paso

Slug-eater snakes, of the genus *Duberria*, are a fairly unique group as their specialised diet of molluscs is one that is rarely found in snakes. The genus, comprising four species, is distributed across the eastern regions of Africa stretching from Ethiopia down into South Africa, with each of the five subspecies of *Duberria lutrix* occupying isolated distributional ranges. We investigated the taxonomic level of the four currently described species (*D. lutrix*, *D. rhodesiana*, *D. shirana* and *D. variegata*) and subspecies of *D. lutrix* (*D. l. abyssinica*, *D. l. atriventris*, *D. l. basilewskyi*, *D. l. currylindahli* and *D. l. lutrix*). We produced phylogenetic trees from a concatenated dataset of two mitochondrial genes and one nuclear gene, and used Maximum Likelihood and Bayesian Inference to construct two trees. We assessed species level delineations using sequence divergence values, bGMYC methods and a program called 'Species Identifier'. From the analyses, we investigate whether currently described *D. lutri* subspecies should be raised to species level.

Molecular data reveals potential cryptic lineages in two forestdwelling reptile species along the east coast of South Africa

(speed presentation)

Theo Busschau, Savel Daniels, Werner Conradie
Department of Botany and Zoology, Stellenbosch University; theob@sun.ac.za

The contraction and subsequent fragmented nature of South African forests are generally thought to be the main driver of speciation in forest-living species. However, forest-living fauna in South Africa appear to be largely understudied. This is especially true for forest-living reptiles. This study assesses the genetic structure of two co-distributed forest-living reptile species; the forest thread snake (*Leptotyphlops sylvicolus*) and the Pondo flat gecko (*Afroedura pondolia*), across their distribution in the Eastern Cape and KwaZulu-Natal provinces of South Africa. By obtaining genetic and morphological data the aim is to examine the biogeographic history of these forest living reptiles and delineate species boundaries. Preliminary analyses of the molecular sequence data (ND4, Cytb, Prolactin and RAG1) for both species indicate that there are cryptic lineages present. In *A. pondolia* there are four clades in the mitochondrial tree topology and two in *L. sylvicolus*. Further population-level analyses as well as morphological analyses will provide additional support for the presence of cryptic species within these taxa. Divergence time estimates may provide insight to the biogeographic history of the fragmented forests where these taxa occur.

Speed presentations – documenting genetic diversity

Genetic structuring in *Psammophylax* (Fitzinger, 1843), a widespread African snake genus

Keates C.¹, Conradie W.^{2,3} and Edwards, S.¹

¹Zoology and Entomology Molecular Lab (ZEML), Department of Zoology and Entomology, Rhodes University;

<u>chadkeates97@gmail.com</u>

²Port Elizabeth Museum (Bayworld)

³School of natural Resource Management, George Campus, Nelson Mandela University

Psammophylax (Fitzinger, 1843) is a widespread southeast African genus of snakes that is currently under studied, both taxonomically and genetically. Skaapstekers are small- to medium-sized snakes that are most commonly found in moist savanna and grassland, and are often characterised as being terrestrial, diurnal, active foragers. The phylogeny of Psammophylax was estimated using genetic information from five of the six currently described species in the genus. The study utilised multiple phylogenetic and distance-based methods to elucidate the relationships within the genus. Phylogenetic analyses recovered a similar topology to past studies, but with increased resolution and support. Psammophylax acutus was recovered as sister to the other members within the genus and was found to be deeply divergent from other species within the genus. Increased sampling along the east coast resulted in the recovery of a paraphyletic clade that was missed by previous studies. The study resulted in the recognition of both a new species and a new genus. Although terrestrial, the study found substantial genetic structuring within the genus, the inclusion of samples from the more remote parts of Africa may result in the recovery of further genetic diversity within *Psammophylax*.

Genetic diversity of the forest dwelling Myosorex cafer and the generalist Rhabdomys dilectus in Eastern Cape

Matamba E¹, LR Richards², Cherry MI¹ and Rambau RV¹

¹Department of Botany and Zoology, University of
Stellenbosch; ematamba@sun.ac.za

²Department of Mammalogy, Durban Natural Science
Museum

The Eastern Cape forests are broadly divided into coastal scarp, dune forests and inland Afromontane mistbelt forests. The evolutionary history of taxa that utilise these forests is not fully understood. In this study we used barcodes of the mtDNA COI (630 bp) to investigated genetic diversity in the generalist four-striped mouse, Rhabdomys dilectus, and the dark-footed forest shrew, Myosorex cafer, which is strictly confined to forests. A total 42 specimens of R. dilectus and 34 of M. cafer were collected from eight forests encompassing the coastal scarp (Transkei Coastal Scarp) and inland Afromontane mistbelt forest (Amathole , Transkei and Eastern misbelt forest). The striped mouse has 22 haplotypes (h=0.9605) that are shared among all the localities that differ from each other by sequence divergences ranging from 0.059 to 0.91. On the other hand, M. cafer has 23 haplotypes (h=0.9483), with high site fidelity (they are not shared between sites) and separated by sequence divergences ranging from 0.05 to 1.75%. Myosorex data strongly suggests that movement of animals between forests is generally restricted, whereas R. dilectus data indicates higher connectivity between forest patches. Overall, the genetic data suggest recent population size expansions and validates the utility of COI barcodes.

Comparison of genetic structure of two forest bats across Eastern Cape forests

Monika Moir¹, Leigh Richards², Michael Cherry³, Victor Rambau⁴

- ¹ Department of Botany and Zoology, Stellenbosch University; monikam@sun.ac.za
- ² Durban Natural Science Museum
- ³ Department of Botany and Zoology, Stellenbosch University
- ⁴Department of Botany and Zoology, Stellenbosch University

The dusky pipistrelle bat, Pipistrellus hesperidus, and Swinnyi's horseshoe bat, Rhinolophus swinnyi, are small, insectivorous bats that occur across coastal (scarp) and Afromontane (mistbelt) forests in South Africa. Pipistrellus hesperidus is a forest-associated clutter-edge forager, while R. swinnyi is a forest-dependent clutter forager. Both species exhibit low wing loading, which is typically inversely related to dispersal ability, their differing forest dependence may result in genetic sub-structuring across their ranges. To test this, neighbour-joining trees (NJ) and haplotype networks were constructed using cytochrome b (1140bp) of P. hesperidus (n=45) and R. swinnyi (n=16) from 13 localities across scarp and mistbelt forests in the Eastern Cape. Neighbour-joining of P. hesperidus retrieved one monophyletic clade with shallow sequence divergence values (0.01-1.3%), twenty haplotypes diversity ($h = 0.906 \pm 0.026$), and low nucleotide diversity ($\pi =$ 0.00423 ± 0.00032). In contrast, two clades were retrieved for R. swinnyi: mistbelt forest clade and a weakly supported scarp clade. Rhinolophus swinnyi exhibited low seguence divergence (0.01–0.7%), eight haplotypes (h = 0.7 \pm 0.127), and nucleotide diversity (π = 0.00167 \pm 0.00057). Gene-flow appears high across all sites for P. hesperidus, while low level structuring was obtained for R. swinny reflecting reduced dispersal owing to its forest dependence.

Speed presentations – DNA barcoding

DNA barcoding of South African red seaweed species

Jamie Julies¹, Rouvay Roodt-Wilding¹, John Bolton², Rob Anderson²

- Molecular Breeding and Biodiversity Group, Department of Genetics, Stellenbosch University; 18265332@sun.ac.za
- ² Department of Biological Sciences, University of Cape Town

Red macro-algae (Rhodophyta) dominate the seaweed flora of South Africa and represent approximately two-thirds of the seaweed diversity. Species identification of marine macro-algae, especially the Rhodophyta, is very difficult and inconsistent due to elementary morphology and anatomy, and phenotypic plasticity. The latter limits and creates uncertainty on the taxonomic position of several genera. Accordingly, algal systematics has become more reliant on molecular tools to resolve and identify species. DNA barcoding has proven a powerful tool that has aided in species identification, discovery of cryptic species or new records of macro-algae globally. This approach will be utilised in the current study to increase foundational biodiversity knowledge in the form of DNA barcodes and species occurrence records specifically for red macro-algae occurring in the species-rich Port Alfred region on the south coast of South Africa. This region has the highest number of seaweed species, and the highest number of species endemic to South Africa.

DNA barcoding of native and non-native succulent plants in the South African horticultural industry

Machate F.H.¹ Bezeng B.S.² van der Bank M.¹

¹African centre for DNA barcoding, University of Johannesburg; futuremachate@gmail.com
²BirdLife South Africa

The horticultural trade has been identified as a key pathway through which non-native species are introduced into new environments globally. Among the non-native-species, succulent plants have been increasingly prioritised in trade, despite the negative ecological and economic impacts they pose to native diversity. Although strict laws exist in South Africa governing the trade of these species, they still are being sold. This is due to challenges in species identification, and the lack of standards with which traded species can be compared. Here, we seek to use the core DNA barcode regions to create a reference library of traded succulent species in South Africa to facilitate rapid and accurate identification. Of the 73 succulent plant species commonly listed in trade in South Africa, 33% had DNA barcode data available on the Barcode of Life Data System (BOLD). To complement this list, DNA barcode data were additionally generated for succulents on our list. Furthermore, we found that 3% of the species have been formally categorised as invasive. Our results show the efficacy of DNA barcoding as a tool to correctly assign traded unknown succulents to species. We recommend the use of this technique to ensure traders comply with legislature.

ABSTRACTS: TUESDAY, 14 AUGUST 2018 - PARALLEL SESSION 2

Citizen science initiatives for biodiversity data generation Human capital development for citizen science programmes

The impact of citizen scientists in long-term surveying of South Africa's plants of conservation concern: a case study of the CREW Programme

Suvarna Parbhoo-Mohan, Ismail Ebrahim, Vathiswa Zikishe Custodians of Rare and Endangered Wildflowers (CREW) Citizen Science Programme, South African National Biodiversity Institute; s.parbhoo@sanbi.org.za

The Custodians of Rare and Endangered Wildflowers (CREW) citizen science programme bridges the gap between science and society. CREW is a partnership between the government agency, the South African National Biodiversity Institute (SANBI), and the non-governmental organisation (NGO), the Botanical Society of South Africa, which brings botanists and the general public together to help conserve South Africa's most threatened plants. Furthermore, the CREW programme feeds into several targets of South Africa's National Plant Conservation Strategy.

We survey plants of conservation concern across the country while working closely with NGOs, conservation agencies and landowners to create awareness and strengthen plant distribution data. With 25% of South Africa's plant species listed as Threatened, the CREW programme is becoming increasingly important for the conservation of our exceptionally rich botanical heritage. The programme is regionally-based, ensuring citizen scientists receive hands-on training to ensure specific information is collected over a long-term.

This paper shall illustrate the activities of the CREW citizen scientists who are vital for the functioning of this national programme. The help that these remarkable individuals provide to the programme is instrumental for the identification of areas in need of conservation. With government conservation agencies experiencing ongoing loss of capacity and funding, the contribution of CREW citizen scientists to the conservation of South Africa's flora is invaluable. Examples of how the data collected are used to update existing information on plant species of conservation concern and feeds into land use planning and decision-making at the different tiers of government shall be described. The success of the CREW programme is directly linked to the passionate people who volunteer their time and resources to assist in national conservation efforts.

CASABIO.org – a powerful and efficient citizen science platform for scientific observations of plants and animals including camera traps

David Gwynne-Evans Casabio; <u>capebio@gmail.com</u>

CASABIO.org currently has over 40 000 observations and over 80 000 pictures of plants and animals. These have largely been acquired in the last year due to the maturation of the platform. Besides the efficient workflow that allows images to be readily converted to data that is useful for conservation, education and research purposes, it is the numerous outputs that are enticing to scientists and casual users alike. The flagship output is an automatically generated field guide that provides images of the organism, descriptions, etymologies, red-list status and a distribution map. The simple workflow for uploading camera trap observations that allows not just species, but individuals to be identified and mapped, is also demonstrated.

iNaturalist - southern Africa's new citizen science platform

Tony Rebelo South African National Biodiversity Institute; t.rebelo@sanbi.org.za

There are several natural history virtual museums available to scientists and citizen scientists in southern Africa. Until recently, the South African National Biodiversity Institute (SANBI) supported iSpot Nature, but following security upgrades which have compromised the site, SANBI has migrated to iNaturalist. iNaturalist offers the most versatility, providing not only a superb modern interface for uploading data – such as drag-and-drop uploading and smartphone apps, but also cutting-edge artificial intelligence identification tools, and versatile and adaptable filters and data access tools. It also interfaces other data providers such as wiki, EoL and GBIF, providing simultaneous access to many data resources.

After polling iSpotters, SANBI decided on iNaturalist above alternative virtual museums. Permission was granted by users to copy 85% of iSpot data to iNaturalist, and the migration is nearly complete, with just some data from July to September 2017 still to be migrated. No data have been compromised in the transfer, and several new tools activated in the process.

iNaturalist also offers superb data summaries and filters, with place, project, checklist and field guide tools. The dictionary is easily maintained, and incorporates our latest southern African plant and animal lists. An identification tool allows taxonomical specialists to rapidly curate their taxa online. Data users can easily download their own tailor-made filtered data at any time.

The next stage is to create a community on iNaturalist for the southern African community, so that SANBI can best serve the needs of the region. To this end, negotiations for a memorandum of understanding with iNaturalist regarding software, data and development are underway.

ABSTRACTS: WEDNESDAY, 15 AUGUST 2018 - PARALLEL SESSION 2

Update on FBIP grants and calls; data submitted and communication strategy

Overview of the FBIP funding approach and grants awarded

Lita Pauw South African National Biodiversity Institute; l.pauw@sanbi.org.za

Sustainable use and management of South Africa's biodiversity require a solid knowledge base and access to relevant information. However, a number of challenges have limited the use of the data and knowledge generated through research for decision-making. Therefore the Department of Science and Technology (DST) established the Foundational Biodiversity Information Programme (FBIP) in 2013 to fill the large gaps in our knowledge by means of a strategic approach and to unblock the value chain for foundational biodiversity data generation. Research grantmaking is one of the main mechanisms for achieving the objectives of the FBIP. The FBIP provides grants for the generation of knowledge related to documenting South Africa's biodiversity, mobilisation of species occurrence or distribution data, generation of DNA barcode data that will allow identification of biological material, and compilation of descriptive information on species. The grants must result in the release of data to the FBIP / South African National Biodiversity Institute (SANBI) for archiving, integration, management and dissemination.

The DST provides core funding for the programme as part of the Global Change Grand Challenge and it is jointly managed by the National Research Foundation (NRF) and SANBI. SANBI is responsible for managing the implementation of the programme and the NRF manages the project proposal review and grant allocation through a competitive process.

FBIP generated data: an assessment of taxonomic and spatial spread

Mahlatse Maropeng Kgatla South African National Biodiversity Institute; M.Kgatla@sanbi.org.za

Proper planning for biodiversity conservation requires the support of quality and reliable primary data. The Foundational Biodiversity Information Programme (FBIP) has been funding research specifically for generating primary data, including observation and specimen data. Accurate identification of specimens is a critical aspect of data and so DNA barcoding and taxonomic research are also supported. All data generated through the FBIP-funded projects have to be provided to SANBI and the datasets must be made openly accessible. To date, the FBIP has funded four large projects: the SeaKeys project, which generated more than 145 589 records, BioGaps which is involved in surveys of the Karoo as well as mobilisation of data from specimens in collections, a survey of animals in the forests of the Eastern Cape, and the latest project is Snapshot Safari which will generate and coordinate a large number of mammal records from camera traps. FBIP has also funded more than 100 small projects. In total the number of occurrence records generated to date is more than 273 977 and more records of data is anticipated as projects provide their datasets. These can help improve spatial planning for species conservation and Red List assessments.

The FBIP Communication Strategy

Dane McDonald South African National Biodiversity Institute; <u>d.mcdonald@sanbi.org.za</u>

The Foundational Biodiversity Information Programme (FBIP) communications drive was initiated at the 2017 FBIP Forum. A year later, the programme is reaching its primary and secondary audiences on a variety of platforms including social media. These audiences are showing steady growth. The FBIP's communications strategy has developed organically and places a high value on simplicity and focus. The goal is simple: making FBIPlinked primary literature and project activities accessible for the FBIP audience and stakeholders in an era of TMI (too much information). An effective workflow has been established which ensures that the FBIP's newsfeed is always ticking over and the communication style is distinctively 'newsy'. In terms of media framing and news values, the FBIP communications takes their lead from Maze et al. (2016) which suggests that the biodiversity sector should change its approach to communications from a 'doomand-gloom' message, to a positive message that includes a clear value proposition for biodiversity that will inspire action. A science communications strategy document has been formulated in collaboration with the South African Agency for Science and Technology (SAASTA) and is currently under review.

Foundational biodiversity information management: systems and standards

National Biodiversity Information System (NBIS)

Brenda Daly

South African National Biodiversity Institute; B.Daly@sanbi.org.za

This presentation reports on progress on the proposed data sharing architecture for a National Biodiversity Information System (NBIS) currently being developed by the South African National Biodiversity Institute (SANBI). The Open Group Architecture Framework (TOGAF) approach for planning, designing and governing an enterprise information technology architecture was followed and SANBI now has a detailed roadmap for a comprehensive information system (including SANBI-supported biodiversity community priorities) having completed Phase 1: Scoping and Design of the Architecture of the project.

As SANBI launches into implementation (Phase 2) this presentation will provide details of the underlining infrastructure to be applied, recommendations for design and exciting functionality and components that end-users can expect. A single user interface called the Biodiversity Advisor will be launched under the pre-existing Biodiversity Advisor brand.

Developing a collection data management service as part of the NBIS

Brenda Daly

South African National Biodiversity Institute; B.Daly@sanbi.org.za

This presentation looks ahead to the development of a national botanical and zoological collections data management service in South Africa. The South African National Biodiversity Institute (SANBI) and all participating museums and herbaria will push data to a central national data store, exposing what is available as a collective, however, ensuring that each institution holds full ownership, attribution and management control over their data.

The proposed way forward is explained, with possible suggestions and solutions to manage processes, workflow, systems and technologies as SANBI and its data partners work towards the data aggregation of collections. These services are envisaged as enabling components of the Natural Sciences Collections Facility (NSCF).

Biodiversity Data Curation: South Africa Goes Online

Willem Coetzer¹, Alex Holland², Ian Engelbrecht³

¹South African Institute for Aquatic Biodiversity; W.Coetzer@saiab.ac.za

²Albany Museum

³South African National Biodiversity Institute

The South African Institute for Aquatic Biodiversity (SAIAB) operates several research platforms, which may be used by the broader South African research community (e.g. a marine research vessel and a remotely operated underwater vehicle). SAIAB's Enterprise-grade data centre, along with expertise in systems administration and biodiversity information management, allow the institute to offer a biodiversity information management platform.

Data hosted by SAIAB is replicated across three data centres, with each centre being at least 250 m apart and operating independently. Infrastructure at two data centres replicates in real time, forming a high availability cluster. The third data centre is dedicated to storing backups. High-capacity tape backup will be added in the near future. As an additional measure, cloud storage is used to store daily extracts of Specify databases, which are retained for one year.

In the first instance, the platform aims to provide SAIAB researchers and associates with biodiversity data curation services. This begins with support for the SAIAB Collections Division, to ensure that voucher specimens, tissue samples and associated media are accurately catalogued and can be easily retrieved. Biodiversity data curation is broader than this. It also means that any biodiversity data/metadata (records of species, events, occurrences/observations and traits) can potentially be curated using Specify Software, and standardised and published (subject to relevant policies) to the GBIF Data Portal using the GBIF Integrated Publishing Toolkit. The use of Specify Software to curate biodiversity data that do not represent voucher specimens (e.g. underwater images and video) is a new research project within SAIAB, which has the potential to be extended beyond SAIAB.

A new national initiative, the Natural Science Collections Facility (NSCF), was launched in 2017 to reinvigorate natural science museums across the country, to halt deterioration of specimens and improve capacity for specimen and data curation.

In support of the NSCF, the SAIAB platform is offered to natural science museums in South Africa (excluding herbaria, which are all part of or affiliated with SANBI, and therefore accommodated by a different system). Each museum will be provided with a webserver, Specify 7 database, Specify web portal and IPT server.

In offering this platform to the broader South African Biodiversity Science community, SAIAB is primarily motivated by the potential for collaborative research in capacity development for biodiversity data curation / information management, using Specify Software. The first research project will examine participating museums' capacity to use the Specify Workbench sustainably, to import new voucher/occurrence records generated by fieldwork. The requisite training to enhance this potential will be provided.

The Natural Science Collections Facility (NSCF) is an important collaborator in the context of enhancing the general state of South Africa's specimen collections, and the Specify Collections Consortium is an important collaborator, specifically for support.

A review of global data sharing trends and the case for open data

lan Engelbrecht
South African National Biodiversity Institute; ianicus.za@gmail.com

Open access to biodiversity data is increasingly seen as essential to meeting sustainable development goals and fostering research towards those goals globally. The rapid expansion of information technology and the data sharing platforms enabled by the internet has brought about a quantum change in the way we do science. Data sharing and integration platforms are enabling new kinds of research at scales never before possible. For many scientists, sharing data is a new cultural paradigm, and while funding agencies and journals are incentivising this practice, there remains resistance. This presentation will provide an overview of insights gained into the dynamics of this new paradigm from a short review of the key literature on data sharing in the natural and biodiversity sciences. The benefits of data sharing are not as clear as many of us would like to believe, and the concerns of those reticent to share data must be given due consideration. The South African National Biodiversity Institute (SANBI) needs to position itself appropriately as a key role player in the biodiversity data sharing landscape, and I will advocate for an experimental, complex systems-based approach to fulfilling that role.

FBIP data challenges: the need to address quality standards

Mahlatse Maropeng Kgatla South African National Biodiversity Institute; M.Kgatla@sanbi.org.za

As one of the world's megadiverse countries, South Africa needs good quality and reliable primary data to conserve and sustainably utilise its biodiversity. For the past five years, the Foundational Biodiversity Information Programme (FBIP) has funded research and data mobilisation projects aimed at generating primary data, including, but not limited to, specimen, observation and DNA barcoding data. All data generated and compiled through FBIP grants has to be made publicly accessible, and it is reguired that it is submitted to the FBIP for checking before being loaded on to the FBIP website and submitted to GBIF. The FBIP requires researchers to use a Darwin Core adapted data template to compile the primary data generated from the funded projects. Darwin Core is a system of defined fields used to compile, manage and share biodiversity data. The Darwin Core also ensures data consistency and enables data to be easily shared. Good quality primary data need to be accurate to effectively support biodiversity conservation. The FBIP has identified common mistakes made when compiling data. These mistake affect the quality, accuracy and usefulness of the data. Addressing these problems may increase the value of the data being submitted to FBIP, and therefore the value of the programme, to ensure its continued funding.

SANBI coordinating the development of policies for managing foundational animal work in South Africa

Rethabile F. Motloung, Pholoshi A. Maake Biosystematics & Research Collections, South African National Biodiversity Institute; R.Motloung@sanbi.org.za and A.Maake@sanbi.org.za

The lack of foundational information and taxonomic expertise is a serious barrier to sound management of biodiversity, improved decision-making in conservation, sustainable use and equitable sharing of the benefits derived from biodiversity. It is for that reason that the Convention of Biological Diversity (CBD) instituted the Global Taxonomy Initiative as the main body to address lack of taxonomic information and expertise issues at the global level. In South Africa, the South African National Biodiversity Institute (SANBI) coordinates foundational information and reports on expertise required to provide such information for both animals and plants. To that account, SANBI developed the National Strategy for Zoological Taxonomy 2013–2020 (Hamer 2013) and Biosystematics Research Strategy for the algae, animals, bacteria and archaea, fungi and plants of South Africa 2013–2018 (Victor, Hamer & Smith 2013). For animals, however, there are no policies guiding compilation of foundational information i.e. species page information (e-Fauna project), taxonomic backbone (checklist) and expansion of information base (occurrence records). These policies are important as guidelines to promote consistency and provide point of reference in decision-making for the development and dissemination of foundational animal information. The Zoological Systematics division of SANBI, in collaboration with selected taxa expert groups, are embarking on developing the policies for e-Fauna project, creating and managing the animal taxonomic backbone and the expansion of the South African animal information base.

Collection specimen data management

Development of a sustainable solution for biodiversity data management and curation: Case study 10 years academic collection at the African Centre for DNA Barcoding

Ronny M. Kabongo¹, Willem Coetzer² and Michelle van der Bank¹

¹African Centre for DNA Barcoding, University of Johannesburg; ronnym@uj.ac.za

²South African Institute for Aquatic Biodiversity

DNA banking is one of the central capabilities on which modern genetic research rests. The DNA-banking system plays an essential role in the flow of genetic data from scientists to the application of genetic research. Recently, the housing of significant collections of biodiversity data (i.e. voucher specimens, tissue materials and DNA extracts) has become common practice in many academic institutions. To date, the African Centre for DNA Barcoding based at the University of Johannesburg has contributed some 24 000 records to the global barcode initiative, encompassing 67 orders, 266 families, 2 368 genera, 7 973 species represented by 24 853 specimens. A significant resource that may prove reliable in improving and refining field cost challenges, sampling gaps and taxonomic ambiguities. However, such collections remain in the obscurity without the parallel adaptation of biodiversity informatics tools and skills necessary.

Therefore, as recipient of the 2017 Global Genome Biodiversity Network-Global Genome Initiative Awards (GGBN-GGI), we present the implementation of a sustainable data management solution for biodiversity data curation and global discoverability through the GGBN data portal of over 13 000 genetic records. Addressing implementation of necessary tool and processes overlooking biodiversity specimen storage, database management, webserver publication and mapping to GGBN Data Standards.

Challenges and progress with mobilising biodiversity data in the Iziko South African Museum entomology collection

Simon van Noort

Department of Research & Exhibitions, Iziko South African Museum; svannoort@iziko.org,za

The Iziko South African Museum Entomology collection is both historically important (specimens date back to the 1850s) and an actively expanding collection. Curated holdings have tripled over the last 28 years. Digitisation commenced in 1990, and prior to the first funded SABIF digitisation project in 2006, collection staff had digitised 124 657 catalogue records into SAMDAT. The database was converted to Specify6 during 2011 and currently (as at 15 June 2018) contains 374 009 catalogue records. The digitisation process includes imaging of specimens and associated data labels using a Leica multi-focus stacking imaging system. In excess of 20 000 images have been captured including many type specimens. Digitisation of the curated collection has provided a dataset that will enable analyses and interpretation of biodiversity data of an economically and ecologically important group of organisms. However, ongoing inventory surveys in poorly sampled areas of South Africa are producing valuable, but hyper-diverse baseline data resulting in a processing bottleneck. A major challenge lies with the curation and digitisation of the estimated 10 million specimen backlog. Mobilisation of this data will provide critical input to applied scientific disciplines and will allow for informed conservation management decisions, which historically have excluded invertebrate data.

Southern African Marine Mammal database: assessment and review of national museum collections, with the goal to consolidate existing specimen data, facilitate access to research collections and standardise curation

Keshni Gopal¹, Simon Elwen², Wayne Florence¹

¹Iziko South African Museums; <u>kgopal@iziko.org.za</u>

²University of Pretoria, Mammal Research Institute (MRI)/Sea Search Africa

Museum collections are an invaluable data source, if properly accessible and available to the local and global research community. The predicament is that the marine mammal collection and associated databases do not meet international practice; and thus is currently being ameliorated and catalogued according to international Darwin Core standards before any scientific research, particularly DNA barcoding, can be carried out. The compilation of the cetacean inventory will make information easily accessible to researchers and the public, and will provide a way to ensure that samples are available from a wide variety of locations – a strategy especially important given that some species could be difficult to sample depending on their distribution or if highly threatened in the wild. Data verification and quality control of the tissue collection will promote genetic research as well as generate DNA barcodes on species that have not been submitted to IBOL/BOLD. Scientific knowledge will be generated, thus answering a wide range of questions on taxonomy, population genetic structure, phylogeography, and cryptic speciation that will add value to current and future conservation management strategies and the development of marine policies.

Conversion of East London Museum Malacology database to Specify6

(speed presentation)

Mary Cole

East London Museum; marybursey@elmuseum.za.org

The East London Museum received a small grant from the FBIP programme for data in the Malacology (mollusc) collections to be cleaned and migrated from an Access database to Specify. 18 267 dry collection and 3 965 wet collection records were supplied to the South African National Biodiversity Institute (SANBI). Most of the grant went towards the services of a consultant who put much thought into designing the way the data would be entered and retrieved, so it was not just a matter of migration. The value of the data has been improved due to efficient ways of extracting information. Many operations which used to be done one record at a time, are now handled in bulk. A thorough job of cleaning was done which greatly improved the accuracy of the data. As the Specify database began to be used, aspects which needed modification came to light, and these were done immediately. The transition from our old system to Specify was very smooth. This was due to the grant from FBIP for the services of an experienced consultant who paid meticulous attention to detail, necessary for the objectives of digitisation to be fulfilled.

Using taxon concepts to reconcile the meanings of names in a collection context

Ian Engelbrecht, Marianne le Roux, Ronell R. Klopper South African National Biodiversity Institute; <u>ianicus.za@gmail.com</u>

Taxon names are the standard means of communicating about taxa, but names in themselves are often imperfect specifiers of the taxa that they refer to. The meanings of names can change over time as scientific insights improve, or the same name may be used in differing or even conflicting perspectives, depending on the classification of a group of organisms. Taxon concepts aim to address this problem by including the authority of a concept when the name is used. Differing and imprecise use of names is particularly problematic for biodiversity data aggregation projects, since it cannot be assumed that the same name refers to the same taxonomic entity in different datasets, a problem that cannot simply be addressed by resolving synonyms. Recent developments in the use of taxonomic concepts are beginning to make it feasible to address this problem in a meaningful way in biodiversity informatics platforms. These include a standard approach for mapping the relationships between taxon concepts, and software to support the mapping process. This presentation will describe these developments, illustrated with a South African plant example, and the experience gained in applying these approaches to this taxon in the context of the National Herbarium.

The inconsistent application of common and species names to polychaete worms used as bait can affect management

Carol A. Simon, Alheit N. du Toit, Caveshlin Naidoo, Hendré van Rensburg and Conrad Matthee Department of Botany and Zoology, Stellenbosch University; csimon@sun.ac.za

Polychaetes are frequently used as bait for fishing. However, a lack of consensus among anglers and the literature regarding the application of common to scientific names of popularly used bait hampers their effective management. The aims of this study were therefore to determine which species are collected and common names applied to them, and generate COI barcodes for them. Participating anglers donated 12 species. Their identifications, supplemented by those by participants in an online survey, showed that individual common names are frequently applied to more than one species, but usually to species within the same family. However, multiple common names used for Nereidid and Sabellarid polychaetes, the collection of which is prohibited, is problematic since alternative common names appear on prohibited and permitted lists as specified by the Department of Agriculture, Forestry and Fisheries (DAFF). Furthermore, molecular analyses suggest that Lycidice natalensis, Gunnarea gaimardi and Lumbrineris tetraura may represent species complexes locally and globally. These results indicate that names of bait worms must be specified more clearly by DAFF to avoid confusion and that further taxonomic work needs to be conducted to clarify the identities of some species.

Names for South African frogs and aspects of folk taxonomy, a Zululand case study

(speed presentation)

Fortunate M. Phaka¹, Edward C. Netherlands^{1,2}, Donnavan J.D. Kruger³, Louis H. du Preez^{1,4}

- ¹African Amphibian Conservation Research Group, Unit for Environmental Sciences and Management, North-West University; <u>mafetap@gmail.com</u>
- ²Laboratory of Aquatic Ecology, Evolution and Conservation, University of Leuven, Belgium
- ³Faculty of Education, North-West University
- ⁴South African Institute for Aquatic Biodiversity

Humans use taxonomy to organise the world into recognisable units. Folk taxonomy deals with how humans name and classify organisms through culture. Unlike its scientific counterpart, folk taxonomy is mostly undocumented, it is not regulated by international rules and the resulting names are often specific to each culture. Vernacular names can be an instrument to increase participation of non-scientists in biodiversity matters. In South Africa, great strides have been made in standardising and increasing relatability of vernacular amphibian names in English and Afrikaans. This creates a need to achieve the same with the country's remaining nine languages which are indigenous languages used by the majority of the country's population. This study pilots methods of investigating and standardising indigenous frog names through a folk taxonomy case study on isiZulu frog names in the Zululand region of KwaZulu-Natal. Furthermore, use of indigenous knowledge systems is promoted and a contribution made to development of an indigenous language. Overlaps in folk and scientific taxonomy provide a basis for increasing universality of indigenous names and allows these names to be scientifically acceptable while staying true to their folk taxonomy roots.

Screening of ectomycorrhizal and other associated fungi in South African forestry nurseries

Veronique Chartier FitzGerald¹, Greer Hawley², Joanna Dames¹

¹Department of Biochemistry and Microbiology, Rhodes University; <u>v.chartierfitzgerald@ru.ac.</u>

<u>Za</u>

²EOH Coastal and Environmental Services, East London

The South Africa forestry industry, covering 1.3 million hectares, is dependent on exotic pine and eucalyptus species. Nursery seedlings are not inoculated with ectomycorrhizal (ECM) fungi or other beneficial microbes. The purpose of this investigation was to assess levels of naturally occurring ECM colonisation and associated fungi in South African nurseries. Pinus patula seedlings from 10 different South African nurseries were assessed for ECM colonisation using a grid line intersect method, and molecularly identified using morphological and next-generation Illumina sequencing. Colonisation of seedlings in production nurseries was low (2–21%). Morphologically the ECM fungi Thelephora terrestris, Suillus sibiricus, and the genera Russula, Pseudotomentella were identified. Molecularly the ECM fungi *T. terrestris*, *Inocybe jacobi* and the genus *Sphaerosporella* and several other ECM containing families were identified along with many saprotrophic/endophytic fungi belonging to genera such as *Penicillium*, **Ramasonia** and *Talaromyces*. This study provided an initial view of the microbiome fungal community found on South African seedlings, which must be taken into account when inoculating with beneficial microbes. It also determined that ECM fungal root colonisation levels are very low demonstrating the need for ECM fungal use within these nurseries, which can increase seedling growth, viability and resistance to pathogens.

Root fungal diversity associated with three *Disa* species

(speed presentation)

Nondumiso Khambule¹, Joanna Dames¹, Craig Peter²

¹Department of Biochemistry and Microbiology, Rhodes University; vnkhambule@gmail.com

²Department of Botany, Rhodes University

The family Orchidaceae is well represented on the African continent although the African orchid flora is rather poor when compared to that of tropical America or Asia. Orchids associate with fungi forming a special mycorrhizal interaction. The fungi provide nutrients and water to their host plant but, unlike other mycorrhizal interactions, they also supply carbon as various stages during orchid growth. Orchid mycorrhizal associations have not been well studied in South Africa, despite the wealth of wild orchid species occurring in various habitats. This study aimed to investigate the fungal communities associated with the roots of Disa cornuta, D. bracteata and D. polygonoides. Fungi were isolated and cultured from roots of the orchid plants. Fungal isolates obtained were identified via amplification of the ITS region, after sequencing comparisons were made using the GenBank database. Several *Penicillium*, *Trichoderma* and *Oidiodendron* species were identified. Of these, Oidiodendron is a known mycorrhizal fungus forming a relationship with ericoid roots. The presence of other fungal root endophytes is not surprising. Root staining did. however, confirm the presence of mycorrhizal pelotons inside orchid root cells, indicating a mycorrhizal symbiosis. To confirm diversity and presence of orchid mycorrhizal fungi, DNA was extracted from roots and amplicons where cloned into pGEM-T vector for blue/ white screening. The sequence results are pending. This study will expand the current knowledge on orchid mycorrhizal associations and fungal diversity, which is essential for continued conservation efforts.

Marion Island vegetation and root associated fungal diversity

(speed presentation)

Jahman Thabede, Robert Pienaar, Gwynneth Matcher, Joanna Dames, Rosemary Dorrington Department of Biochemistry and Microbiology, Rhodes University; g14t1480@campus.ru.ac.za

Endophytic fungi are defined as being able to colonise internal plant tissue without causing apparent harm to the host plant and are found in varied ecosystems. The purpose of this study was to determine the presence and diversity of arbuscular mycorrhizal (AM) fungi and dark septate endophytes (DSE), associated with the roots of selected plant species on Marion Island. Roots of Agrostis magellanica, Azorella selago, Poa cookie, Blechnum pennamarina, Acaena magellanica and Cotula plumose were stained to microscopically assessed the percentage colonisation of both AM and DSE fungi. Colonisation ranged from 41% to 96% and 0.83% to 52%, for AM and DSE fungi respectively. Root segments of Crassula moschata, Azorella selago, Cotula plumose and Sagina were surface sterilised and placed on Malt Exact Agar (MEA) plates. Twentysix endophytic fungal isolates were molecularly identified and were predominantly members of the Ascomycota with genera such as Antarctomyces, Elaphocordyceps, Tolypocladium and Penicillium being represented. This dominance of Ascomycota from identified sequences was confirmed in root samples sent for Illumina sequencing, which was followed by OTUs belonging to the Basidiomycota, Blastocladiomycota, Glomeromycota (notably Claroideoglomeraceae, Archaeosporaceae, Acaulosporaceae) and Mortierellomycota. These results highlight the fungal diversity able to thrive in the harsh environment of Marion Island.

Diversity of rhizobia associated with root nodulation in pigeonpea (*Cajanus cajan*) from South Africa

(speed presentation)

F.L. Bopape¹, A. I. Hassen¹, E.T. Gwata²

¹Agricultural Research Council, Plant Protection Research
Institute (ARC-PPRI); phalanef@arc.agric.za

²University of Venda

Pigeonpea (Cajanus cajan) is an important grain legume, in many African countries largely used for human consumption. It contributes to the improvement of soil fertility through biological nitrogen fixation. However, the productivity of pigeonpea is low, compared to other tropical legumes. The objectives were to collect rhizobial strains by soil trapping that are associated with root nodulation in pigeonpea; and molecular characterisation of the rhizobia from diverse locations in South Africa isolated with pigeonpea. Indigenous rhizobial isolates were collected from diverse locations across South Africa and trap isolated using five pigeonpea genotypes. Two-hundredand-eighty possible new pigeonpea rhizobial isolates were isolated from 40 soil samples in nine provinces of South Africa. The isolates were deposited to the South African Rhizobium Culture Collection (SARCC) based on their growth characteristics. DNA was extracted from all the isolates and 16S RNA PCR conducted. PCR products were sequenced. Only 55 isolates had sequence similarity to rhizobia when BLASTN, with majority belonging to Rhizobium, Bradyrhizobium and one to Phyllobacterium and Paraburkholderia each. The study generated novel information regarding the diversity of indigenous rhizobia associated with pigeonpea in South Africa, which could lead to future improvement of the growth and yield of pigeonpea genotype cultivation.

A plethora of *Fusarium* species in grassland biome soils

(speed presentation)

Mudzuli Mavhunga¹, Adriaana Jacobs¹, Eduard Venter², Brett. A. Summerell³

¹ARC-Plant Protection Research; <u>murendwa0306@gmail.com</u>
²Department of Botany and Plant Biotechnology, University of Johannesburg

³Royal Botanic Gardens & Domain Trust Sydney, Australia

The grassland biome is a rich source of fauna and flora biodiversity, vet little is known in South Africa and across the globe on the diversity of naturally occurring fusaria within the grassland biome. The genus Fusarium comprises some of the world's most economically important species that occur as saprophytes, plant pathogens and antagonists. The rapid urbanisation and subsequent conversion of the grassland biome in South Africa for agriculture and human uses increasingly threatens fungal species biodiversity. We use morphological and molecular techniques to study the diversity of ca. 1 000 Fusarium species isolated from soils collected at five nature reserves. The DNA barcodes generated from the translation elongation factor 1-alpha (TEF-1α) locus shows diversity among Fusarium species found in grassland soils, among them F. incarnatum-equiseti species complex, F. fujikuroi species complex, F. oxysporum species complex, F. chlamydosporum species complex, and F. solani species complex. The grassland biome houses a wide variety of Fusarium species that are important both medically and agriculturally. These findings further enhances our understanding of the genus Fusarium. Data gathered thus far ties in with other global surveys of this biome, enabling us to map biogeographical distribution patterns of these fungi.

Speed presentations: assessing biodiversity in different habitats

Ant communities along an elevational transect, Udzungwa Mountain in Tanzania

C. Kunene¹, S.H. Foord², T.C. Munyai¹
¹School of Life Sciences, University of KwaZulu-Natal; carolkt37@gmail.com
²SARChl-Chair on Biodiversity Value and Change, Department of Zoology, School of Mathematical and Natural Science, University of Venda

The Udzungwa Mountain is a biodiversity hotspot. It is a centre of mammal endemism and is recognised for its outstanding biodiversity importance and ecosystem services. However, climate change, land degradation and biodiversity loss has resulted in the Udzungwa Mountain being listed amongst the 17 most threatened tropical forest ecosystems of the world. There is a great demand for conservation strategies in this area, yet the species proven to be great indicators of change are understudied, viz. invertebrates. Invertebrates are a powerful tool in monitoring the environment. They are valuable indicators of changes in an ecosystems biological integrity. Amongst the most diverse and abundant groups of invertebrates are ants. Ants are a model organism used to predict the response of organisms to change and provide information on how to conserve ecosystems. Therefore, this study will provide checklist of ant species along the Udzungwa Mountain. It will enhance our understanding on the response of fauna to change on the Udzungwa Mountain by; describing how ant assemblages differ between the forest types and altitudinal zones and by describing how functional diversity vary along the forest types and altitudinal zones on the Udzungwa Mountain. The latter will be used to implement conservation strategies in this area.

Investigating population demographics, breeding system and principle pollinator of *Protea curvata*

Precious Mabuza, Kevin Balkwill
Animal, Plant and Environmental Science, University of Witwatersrand; mabuzapg@gmail.com

The study aimed to assess reproductive success in the vulnerable species, *Protea curvata*. Assessments were made on the demographics, breeding system and animal pollinators of a *Protea curvata* population. Great concern emerges from the finding that the population lacks juveniles. Seedling establishment is limited by fire management on the site as well as the species' lack of canopy seed-storage and serotiny. The species was found to be self-compatible. However, autonomously self-pollinated flowers had fewer viable seeds than geitonogamously selfed flowers and outcrossed flowers. *Protea curvata* nectar attracted both specialist and opportunistic nectarivores. Bird visits were more effective pollinators than bees. Nevertheless, bees were frequent visitors of *Protea curvata*. Other insect visits, although less common than bee visits, may also contribute to *Protea curvata* pollination. These findings will help formulate a conservation approach for the species.

The role of competition in structuring ant communities in selected grasslands and forest habitat

Nokubonga Thabethe¹, Stefan Foord², Caswell Munyai¹
¹School of Life Science, University of KwaZulu-Natal; nokubongafthabethe@gmail.com
²South African Research Chair on Biodiversity Value and Change and Centre for Invasion Biology, School of Mathematical & Natural Science, University of Venda

Competitive interactions are mechanism that play an important role in structuring natural communities. In ant ecology, competition has been cited as one of the most contentious issues. The main objective of the study is to determine the role of competition in controlling ant species co-existence in grassland and forest habitats. This will be achieved by performing ant baiting and setting out pitfall traps (open for five days) in March/April 2018 and September/October 2018 at three different sites (bluegum plantations, natural forest and grassland) on Wakefield farm, Pietermaritzburg, KwaZulu-Natal. Each site will be replicated three times. Ant activities will be observed at four bait types (cat food, cotton wool soaked in sugar water, oil, and a peanut-jam mixture), 45 m long transect, with 10 baiting stations, 5 m apart. Ground surface temperature will be recorded for each baiting station as a representative of the environmental conditions for foraging, while representative specimens will be collected and placed in 70% ethanol. Functional traits related to resource use by ants, and functional diversity of ants will be determined. Habitat complexity will be measured by determining the vertical and horizontal distribution of vegetation for both wet and dry seasons.

Floristics of three Northern Coastal Forests in a global biodiversity hotspot: A comparison across patches of contrasting disturbance history

Olivier Kambol Kambaj, Sershen Naidoo, Syd Ramdhani, Yanadayalan Govender School of Life Sciences, University of KwaZulu-Natal; oliverkambaj@gmail.com

The impacts of disturbance history on the floristics of Northern Coastal Forest (NCF), more specifically KwaZulu-Natal Coastal Forest within the Maputaland-Pondoland-Albany biodiversity hotspot (South Africa), are unknown. This study compared the floristics of three remnant patches of NCF (viz. Hawaan, Umdoni and Twinstreams in KwaZulu-Natal, South Africa) with contrasting disturbance histories: a primary forest with low levels of disturbance (Hawaan), a primary forest with high levels of disturbance (Umdoni) and a secondary forest (Twinstreams) that was rehabilitated with presently low disturbance levels. Transects and quadrats were used to assess species composition and diversity at each site. Collectively, 688 species, 394 genera and 111 families were found, but only 21.95% of the species were shared by the three forests. The most speciose family was Fabaceae followed, in order of decreasing number of species, by Asteraceae, Rubiaceae and Euphorbiaceae. The number of species was highest at the disturbed primary forest and notably lower at the primary forest. Diversity indices exhibited a similar trend. Cluster analyses and non-metric multidimensional scaling (NMDS) ordinations indicated that the secondary forest was intermediate between the two primary forests, with the disturbed primary forest and secondary forest being more similar. All forests had <50% similarity. Despite these differences, the disturbed and secondary forests maintained a NCF floristic affinity. The dissimilarity between Hawaan and other forests is most likely the product of differing disturbance histories and rehabilitation efforts. The findings suggested that NCF patches are likely to be different in richness but not in structure, signature taxa and affinity. Anthropogenic related pressures and disturbance appears to be a major cause of floristic differences among patches. This leads to higher levels of richness by accommodating opportunistic, atypical and alien species. In NCF patches, disturbance and rehabilitation may lead to the creation of novel ecosystems in which NCF signature taxa are likely to persist.

Checklist of epigaeic ants in Buffelsdraai Landfill Conservancy, South Africa

S. Xolo¹, S.H. Foord², R. Slotow¹, T.C. Munyai¹
¹School of Life Sciences, University of KwaZulu-Natal; sbongisenixolo@gmail.com
²SARChl-Chair on Biodiversity Value and Change, Department of Zoology, School of Mathematical and Natural Science, University of Venda

Deforestation of natural forests is considered a global threat to biodiversity. Management of protected and the restoration of degraded ecosystems are essential for protection of both biodiversity and ecosystem services. Although invertebrates, and ants in particular, have been used as indicators of forest recovery, most research focus on vegetation dynamics, neglecting dominant components of an ecosystem.

The current study will assess the success of habitat restoration practices in Buffelsdraai landfill site at eThekwini Municipality, KwaZulu-Natal Province. The study will focus on ants (Formicidae: Hymenoptera) as they comprise a significant component of invertebrate diversity and are probably a keystone in the terrestrial ecosystems. The current study describe ant diversity and the fundamental environmental variables along a reforestation gradient. Ants will be sampled at five sites which include sugarcane, newly, intermediate and long-term restored sites, grassland sites and Afromontane forest sites. The study predicted to find peaks of ant diversity in more open habitats comprised of generalists ant species and less ant diversity in forested sites with some specialists. Results from this work should address whether the landfill site is a success in terms of biodiversity restoration and recovery in the reforested landscapes, and whether ant assemblages inhabiting reforested sites are ideal to assess the success of reforestation practices.

Ant and spider community response to alien invasive plant species (*Chromolaena odorata*)

S.P. Mntambo¹, S.H. Foord², R. Slotow¹, T.C. Munyai¹
¹School of Life Sciences, University of KwaZulu-Natal; mntambosnenhlahla@gmail.com
²SARChI-Chair on Biodiversity Value and Change, Department of Zoology, School of Mathematical and Natural Science, University of Venda

Invasive alien plants have been a major threat to South Africa's native biodiversity for over two decades. There are numerous known ecological effects associated with the presence of invasive plant species. Since arthropods are more sensitive, they may suffer greater effects of invasive plants than any other group of organisms. This study proposes the use of arthropods that are known to be highly sensitive to environmental change, ants and spiders, to measure the response of fauna to invasion by *Chromolaena odorata* at Buffelsdraai Landfill Conservancy. Within the conservancy five sites will be chosen, each replicated four times. In each replicate, there will be vegetation structure profiling and, for ant and spider sampling, the Conservation Oriented Biodiversity Rapid Assessment for Tropical Forest (COBRA-TF) sampling protocol will be applied. The results of the study should answer, (1) how do ant and spider diversity patterns vary along a gradient of invasion by *Chromolaena odorata*?; and (2) how does ant and spider assemblage structure differs along a gradient of invasion by *Chromolaena odorata* in Buffelsdraai Landfill Conservancy?

Speed presentations: Taxonomy

A taxonomical study of freshwater free-living copepods in Turfloop Dam, Limpopo Province, South Africa

Peral Mnisi, Susan Dippenaar Department of Biodiversity, University of Limpopo; <u>peral.</u> <u>periologistmnisi@gmail.com</u>

Copepoda is the most abundant crustacean group encountered in zooplankton. They are found in most water bodies containing fresh, estuarine and marine water. As part of the zooplankton in freshwater ecosystems, copepods contribute a major portion to the aquatic productivity and biomass. Their general omnivorous habits make them important in the energy transfer of aquatic environments. Copepods also serve as a food source for aguatic organisms such as fish. Currently there are about 11 434 species, belonging to 10 orders, known worldwide. Most free-living species reported from freshwater bodies of southern Africa belong to the orders Calanoida (family Diaptomidae) and Cyclopoida (family Cyclopidae). Zooplankton was collected from Turfloop Dam, using a plankton net (100 µm) and preserved in 70% ethanol. Copepods were isolated and studied under stereo- and light microscopes, using the wooden slide technique. Collected copepods were dissected and morphological features drawn, using drawing tubes. in order to identify them. Examined specimens were identified as members of the orders Cyclopoida and Calanoida representing the genera Mesocyclops, Microcyclops, Thermocyclops, Paradiaptomus, Lovenula and Metadiaptomus. Specimens were further identified to species level based on their specific morphological characters. This study marks the first record of freshwater freeliving copepods in the Limpopo Province.

A taxonomic revision of the Brevipalpus phoenicis and Brevipalpus obavatus species complexes (Acari: Tenuipalpidae) in South Africa

R. Ndzeru^{1,2}, P.A. Maake², O. Thekisoe¹, P. Theron¹
¹Biosystematics Division, ARC – Plant Protection Research;
<u>NdzeruR@arc.agric.za</u> or <u>rndzeru@icloud.com</u>
²Unit for Environmental Sciences and Management, North-West University

The overall aims of this study is to review the taxonomy and systematics of the flat mites (Acari: Tenuipalpidae) Brevipalpus phoenicis and Brevipalpus obavatus species complexes to clarify systematic inconsistencies previously reported for South Africa, and explore the relative importance of morphological and genetic traits for the systematics of these mites. These flat mites represent some of the most economically important plant feeding mite species in the world. They poses a significant threat to agriculture in many countries as a high risk exotic pest, due to wide host range and destructive potential, on crops such as on pistachio, citrus, pomegranates, walnuts, grapes and various ornamentals. Their importance has also increased significantly over the past 40 years because of their association with plant viruses. This confusion could indicate that decades of host association and distributional data could be erroneous, complicating species identification and the separation of closely related species. This has indeed caused problems to South African exportations and to the interception of quarantine species at the entry points. This study aims to compare voucher specimens from various localities in South Africa. freshly collected in this study and specimens deposited in NCA, with type specimens of the suspected synonyms, where possible, using several microscopy techniques and molecular genetics.

Phylogeny of the terrestrial snail genus *Gittenedouardia* (Mollusca: Gastropoda: Cerastidae)

Raphalo Evelyn Mokgadi¹, Savel Daniels¹, Mary Cole²
¹Department of Botany and Zoology, Stellenbosch
University; evelynr@sun.ac.za
²East London Museum

South African terrestrial molluscs are taxonomically poorly studied including the genus Gittenedouardia, Bank and Menskhorst, 2008. Gittenedouardia is the most speciesrich genus of the family Cerastidae in South Africa. The overall aim of this study is twofold: firstly, to investigate the phylogenetic relationships among Gittenedouardia species in South Africa using molecular markers; secondly, to undertake a comparative phylogeography study of two forest dwelling species. The preliminary phylogenetic tree of eight out of 13 species, inferred from COI gene sequences supports the monophyly of the genus, with several clades separated into different taxa that are geographically confined. Three species G. spadicea, G. arenicola and G. natalensis exhibit very clear genetic substructure and marked sequence divergence suggesting the possible presence of cryptic lineages. The current molecular phylogeny is inconsistent with the morphological phylogenetic relationships of the genus. Further analyses using mitochondrial 16S rRNA and selected nuclear DNA loci will shed more light on evolutionary relationships and divergence time among Gittenedourdia species.

ABSTRACTS: WEDNESDAY, 15 AUGUST 2018 - PARALLEL SESSION 3

Using foundational biodiversity information for addressing global change challenges

Biodiversity and impacts of plant feeding mites on tea plant (*Camellia sinensis*) in South Africa

Pholoshi A. Maake¹, Edward A. Ueckermann²

¹ South African National Biodiversity Institute, Biosystematics & Research Collections; A.maake@sanbi.org.za

²School of Biological Sciences/Zoology, North-West University; <u>edalbert@lantic.net</u>

Mites are the most serious pests of tea in almost all tea producing countries. The vast expanse of the tea plantation ecosystem provides a stable, favourable microclimate, uninterrupted food supply, and suitable sites for the reproduction and survival of pests. Annual surveys of mites in South Africa were carried out between 1959 and 1990 for the National Collection of Arachnida (NCA), but most of the focus was on natural ecosystems. Mites in tea plantations were neglected and the diversity is unknown. The purpose of this study was to document the diversity, symptoms and impacts of economically important mite groups in tea plantations. Three functional estates were surveyed between 2015 and 2017 with mites collected using various methods to maximise capture. Over 250 slide mounted specimens have been prepared and lodged in the NCA. These represent mites belonging to 10 families, 16 genera and at least 20 species. The ongoing morphological study of the material indicated that at least six new species belonging to three families and five genera, Tetranychidae (Schizotetranychus and Myxonichus), Tenuipalpidae (Brevipalpus and Obuloides) and Tuckerellidae (Tuckerella) have been discovered. In most of the sections in the tea estates, the mite population remained fairly high with an estimated 30 to 100 mites per leaf. In these sections there was considerable defoliation due to the infestation. The farm managers reported that there was a clear correlation between infestation level and yield quality, eventually affecting pruning times. This is because where phytophagous mites were found in high numbers, the leaves looked red at the sites of attack. As the population increased, the infested leaves become darker, took a scorched appearance and a general reduction in size of the new leaves was common. Eventually these resulted in low tea production and even death of the plants in some cases.

Fire and Invasive Species Control Programme with eThekwini Municipality

Bongani Zungu¹, Errol Douwes^{1,2}

¹Environmental Planning and Climate Protection Department, eThekwini Municipality; Bongani.Zungu@durban.gov.za

²School of Life Sciences, University of KwaZulu-Natal

A new geologic time period, referred to as the Anthropocene, is widely accepted to have resulted from recent human domination of various earth system processes. Nowhere is this more apparent than in cities. Indeed, cities are mooted as being proxies for global change, and understanding the challenges that cities face can help in planning and design of sustainability interventions for broader application. eThekwini Municipality (Durban, South Africa) has for almost 20 years worked at ensuring better biodiversity conservation, through the development of a Durban Metropolitan Open Space System (D'MOSS), the management of which is underpinned by a suit of conservation planning, policy-based and management tools. Evidence now exists that some habitats and species within urban areas, for example, have already undergone changes due to altered climatic conditions as a results of increased CO₂ emissions. This has triggered a need for a more considered and focused approach to the management of threatened ecosystems. One such ecosystem, the Critically Endangered (CR) KwaZulu-Natal Sandstone Sourveld (KZNSS), is characterised both by its high forb diversity, and its low levels of formal protection. The development of a dedicated Fire and Invasive Species Control (FISC) Programme, within the municipality, has helped to optimise management of extant grasslands such as the KZNSS, not only through control of invasive species and fire application, but also through rigorous data collection and analysis. Annual Veld Condition Assessments (VCAs), for example, monitor the efficacy of the open space management practices, through the capture of site-specific diversity and fuel-load data. Analysis of such data has helped to improve management practices, with the outcome of reducing some of the climate-driven changes previously noted. It is, however, clear that better data management will be required over many years, if the long-term effects resulting from changes to climate and other earth systems, can be verified and meaningfully addressed.

The importance of herbarium distribution records in the study of gene flow likelihood from sugarcane (*Saccharum* hybrids) to wild and weedy relatives in eastern South Africa

(speed presentation)

Dennis Mmakgabo Komape¹, Stefan John Siebert¹, Johnnie van den Berg¹, Dirk Cilliers¹, Sandy Jane Snyman^{2,3}, Dyfed Lloyd Evans^{2,3}

*Unit for Environmental Sciences and Management, North-West University; dkomape@yahoo.co.uk

²Crop Biology Resource Centre, South African Sugarcane Research Institute

³School of Life Sciences, University of KwaZulu-Natal

Biosafety studies are necessary to evaluate the risks associated with cultivating a genetically modified (GM) sugarcane, since hybridisation may occur between crop plants and wild relatives if certain barriers to gene flow are crossed. Field surveys, herbarium distribution records and literature were used to assess likelihood factors. Spatial and temporal assessments of Saccharum wild relatives were conducted based on prevalence, spatial overlap, proximity, distribution potential and flowering times. A total of 815 herbarium specimens were sourced from 11 suitable herbaria. Imperata cylindrica, Sorghum arundinaceum and Miscanthidium capense scored the highest likelihood for prevalence, flowering and spatial overlap with sugarcane cultivation. The presence of 11 wild relatives was confirmed in sugarcane growing regions even though species from Cleistachne, Microstegium, Sarga and Sorghastrum were not found in close proximity to sugarcane plantations. Imperata cylindrica and Miscanthidium junceum scored the highest for distribution potential. Miscanthidium species ranked higher than others for gene flow potential in addition to Sorghum species. The highest likelihood for potential gene flow was associated with the coastal and southern-inland of KwaZulu-Natal. Future work should therefore include aspects influencing gene flow such as cytological compatibility.

Investigations into a new invasive worm in the Knysna estuary

(speed presentation)

H. van Rensburg, C. A. Simon Department of Botany and Zoology, University of Stellenbosch; 15684504@sun.ac.za

A recent survey of baiting activity within the Knysna Estuary identified the moonshine worm as the second most popular bait worm after the bloodworm, Arenicola loveni. However, proper management of this species is inhibited by confusion over its identification. Morphological and molecular evidence confirm that the moonshine worm is a member of the genus *Diopatra*. However, confusion still exists over exact species. Species within the genus are usually 17-20% different from each other based on COI analysis, but there is a less than 5% difference between the moonshine worms in Knysna estuary and three other species on Genbank. None of these species are native to South Africa; Diopatra neapolitana is from the Mediterranean while *Diopatra aciculata* and *Diopatra dentata* are from Australia. This confirms that the moonshine worms in Knysna estuary is alien, although further study is reguired to determine species identification. Furthermore, worms are distributed throughout most of the estuary with densities reaching as high as 51 worms/m² and our conservative population estimate suggests at least 20 million worms currently inhabit the estuary. Given its large size, growing up to 800 mm in length with a 12 mm width, and estimated abundance, it may be expected to have significant impacts on the trophic and ecological structures within the estuary.

Response of ant communities to woody plant expansion at Hluhluwe-iMfolozi Parks, KwaZulu-Natal

(speed presentation)

Nomathamsanqa Mkhize¹, Rob Slotow¹, Stefan Foord², T.C. Munyai¹

School of Life Sciences, University of KwaZulu-Natal; Nomathamsanqa.mkhize@yahoo.com
SARChl-Chair on Biodiversity Value and Change, Department of Zoology, School of Mathematical and Natural Science, University of Venda

Bush encroachment is transforming savanna ecosystem to woody dominated systems. This has a negative impact on biodiversity. Animals responsible for the functioning of the ecosystem are expected to suffer. Ants were used as a model organism to predict the response of biodiversity to such changes in the savanna. Ants respond fast to environmental changes and they dominate in terms of richness, abundance and often biomass. This study aimed at documenting which environmental variables underlie differences in ant assemblages and specificity of species in existing systems, identify indicator ant species associated with existing savanna and encroached systems. A total of 61 008 ants, making up 82 species, 25 genera and five subfamilies, were collected during January 2017 (wet season) and October 2017 (dry season). Most species (85%) were collected in the open habitat and during the wet season (82 species). Myrmicinae (47 species and 8 genera), was the most diverse subfamily followed by Ponerinae (18 species and 8 genera) and Formicinae (16 species and 6 genera). Tetramorium (22 species), Monomorium (10 species), Camponotus (6 species), Lepisiota and Pheidole (5 species) were the most diverse genera. The genera Cardiocondyla, Nylanderia, Paltothyreus, Plagiolepis and Pseudoponera were exclusively in the open habitat while only Anochetus was exclusively in the closed habitat.

POSTER ABSTRACTS

Foundational biodiversity in entomology at the Albany Museum – collecting dust?

Terence Bellingan¹, Alexandra Holland², Helen Barber-James^{2,4}, Musa Mlambo², Rose Prevec^{3,5}

¹Department of Entomology and Arachnology, Albany Museum; t.bellingan@am.org.za

²Department of Freshwater Invertebrates, Albany Museum

³Department of Earth Sciences, Albany Museum

⁴Department of Zoology and Entomology, Rhodes University

⁵Department of Botany, Rhodes University

The Albany Museum, founded in 1855, is the oldest museum in the Eastern Cape and the second oldest in South Africa. It has a wealthy history of entomology and a very exciting, rapidly growing palaeoentomology division. The oldest and most substantial collections consist of terrestrial and freshwater insects, with specimens dating back well over a century in both departments. The terrestrial entomology collection is in need of databasing and although the freshwater invertebrate collection has been growing at an unprecedented rate over the last three years, this year a shortage of manpower slowed down this process. The newer PEATS research programme in the Earth Sciences Department is making enormous strides in building up and accessioning recently discovered insect fossil specimens. This poster gives an overview of the state of each of these collections as foundational biodiversity tools, and aims to make an assessment on their usefulness to local and international researchers. Problems in making foundational biodiversity more accessible are highlighted and solutions are proposed.

A phylogenetic analysis and study of the pollination systems within *Wurmbea* (Colchicaceae) species in South Africa

Sachin Shaney Doarsamy, Steven Johnson, Benny Bytebier

University of KwaZulu-Natal; sachindoarsamy@gmail.com

Plant evolutionary biology requires the understanding of sexual systems and the mechanism responsible for such changes and phylogenetic studies enable insight into hidden evolutionary processes and reveal important taxonomic events in the speciation of a species. Wurmbea (Colchicaceae) is a small bulb genus distributed between Africa and Australia with 21 species occurring in South Africa. The genus has a bimodal distribution in South Africa with two distinctive regions of diversity with a further three subspecies occurring in the high altitude regions of Africa. In addition to this, preliminary work on Wurmbea elatior showed that the species mimics the scent of dung to attract flies to pollinate the flowers. Limited information is available for the remaining 20 species. An analysis of the scent chemistry and observed pollinators will help to understand the radiation and use of scent in the genus between the regions. Furthermore, the phylogeny will provide clear species delimitations and reveal cryptic species. Lastly, distribution maps, red list statuses and habitat information will be updated to provide an accurate description for each species.

Three new species of the sac spider genus *Planochelas* Lyle & Haddad, 2009 (Araneae, Trachelidae) from Central and Southern Africa

Thembile T. Khoza¹, Robin Lyle²

¹South African National Biodiversity Institute, Biosystematics Division; T.Khoza@sanbi.org.za

²Agricultural Research Council – Plant Protection Research, Biosystematics Division

Members of the recently described Afrotropical genus *Planochelas* (Araneae: Trachelidae) are very small and arboreal. They are mainly collected by canopy fogging in tropical forest and savanna. In this study, three new species of trachelids are described namely: *P. haddadi* sp. nov., *P. jocque* sp. nov. and *P. neethlingi* sp. nov. from central and southern Africa, together with the updated key. The material examined in the current study was collected from Mikebo (Democratic Republic of the Congo), Ndumo Game Reserve and Isimangaliso Wetlands Park (South Africa).

The description of genus *Centrobolus* (Spirobolida:Pachybolidae): taxonomical characters

Raesetsa Portia Mailula^{1,2}, C. Munyai¹, M. Hamer²
¹Department of Biological Sciences, School of Life Sciences,
University of KwaZulu-Natal; R.Mailula@sanbi.org.za
²South African National Biodiversity Institute

There are about 450 millipede species described from South Africa, but there are many more undescribed species, there are taxonomic problems for many groups and the distribution of most species is not well known. A revision of the genus *Centrobolus*, which is endemic to southern Africa, is required. About 39 species have been described in this genus, however, there are still gaps in the information because some descriptions are without detailed illustrations or descriptions of the main characters. With the aim of understanding the taxonomy of Centrobolus, material in museum collections is being examined and the main taxonomic characters are being investigated using light and scanning electron microscopy. The results have shown the challenges with the taxonomy of the group, where colour is different but the main characters, the anterior and posterior gonopods, are the same. DNA analyses are needed to resolve these problems.

A phylogeny-based comparative study of the phytochemical and pharmacological characteristics of *Croton* species occurring in KwaZulu-Natal, South Africa.

Tanya Mathe, B. Bytebier, J.F. Finnie, J. van Staden School of Life Sciences, University of KwaZulu-Natal; tanyamathe@gmail.com

Extracts from six Croton species C. gratissimus, C. sylvaticus, C. menyhartii, C. pseudopulchellus, C. steenkampianus and C. rivularis collected from KwaZulu-Natal, South Africa, were screened for antibacterial activities using the microdilution technique. In addition, the phenolic profiles of aqueous (50%) methanol extracts obtained from the plants were assessed using the Folin Coicalteu (Folin C), butanol-hydrochloric acid and aluminium chloride assays. Methanol plant extracts were ran using thin layer chromatography and the plates were later stained with the Dragendorff reagent to determine the presence of alkaloids. The most potent antibacterial activity was exhibited by the dichloromethane (DCM) extracts of C. steenkampianus leaves and the petroleum ether (PE) extracts of C. pseudopulchellus stems which yielded a minimum inhibition concentration value (MIC) of 0.04 mg/ml against E. faecalis. The DCM stem bark and leaf extracts, as well as the PE twig extracts of C. pseudopulchellus, also exhibited noteworthy activities against S. aureus (MIC value of 0.08 mg/ml). The total phenolic content in the tested plants ranged from 1.84±0.13 to 23.8±1.94 mg GAE/g DW. The plants contained varying quantities of condensed tannins (0.27±0.003 to 31.3±0.23) and flavonoids (1.31±0.05 to 31.2±2.99). Alkaloids were also detected in C. gratissimus, C. menyhartii, C. sylvaticus and C. rivularis. The current findings validate the use of *Croton* species in African folk medicine.

Digitisation at Schonland Herbarium to feed into the bigger BioGaps Karoo Project

Someleze Mgcuwa Schonland Herbarium, Albany Museum; mgcuwas@gmail.com

The Karoo BioGaps Project collaborated with the Selmar Schonland Herbarium in Grahamstown to digitise the six families of plants that most commonly occur in the Karoo (Aizoaceae, Asteraceae, Crassulaceae, Euphorbiaceae, Iridaceae and Poaceae). This collaboration aims to advance the scientific understanding of valuable Karoo ecosystems to support decision-making around development in the Karoo area. Digitisation entailed databasing some of the plant specimens directly into BRAHMS (6 400 records). However, most specimens were imaged with their labels (around 50 000 records), and then uploaded onto SANBI's online Transcribe portal whereby transcribers digitise the information found on the labels. This process helps to make specimen data available for georeferencing and finally for research and conservation analyses. Not only is this collaboration contributing valuable information to the Karoo BioGaps Project, but the herbarium has gained skills and techniques to strengthen digitising and databasing of specimen data so that it becomes more useful to science.

The rural citizen scientist birding project increasing biodiversity awareness and positively affecting lives of youth in Limpopo Province

Dikobe Karen Molepo¹, Mamadi Theresa Sethusa¹¹South African National Biodiversity Institute, Zoological Systematics Division; <u>D.Molepo2@sanbi.org.za</u> and <u>T.Sethusa@sanbi.org.za</u>

There is an urgent need to mobilise Informative Essential Biodiversity Variables (EBVs) for under-collected areas targeted for development. These areas are predominantly deep rural and historically under-developed. With development projects accelerated in rural areas in attempts to bring resources to the people, increasing biodiversity pressures are introduced in areas previously minimally impacted. The pace at which the development projects are rolled-out far supersedes the collection efforts by taxonomists and scientists. Joining efforts with rural communicates through citizen science initiatives and training para-ecologists, provides a possible solution to the problem. The rural citizen scientist birding project recruited 15 out-of-school youth in Letaba (5 Giyani and 5 Tzaneen) and Tubatse (5 Burgersfort). The youth received training in bird identification and recordal, a taxonomic group used successfully as a biodiversity surrogate. We report on the impact of the project on the youth, focusing on developed skills (identification and recordal proficiencies), biodiversity awareness and commitment to continue contributing to biodiversity recordal. About 60% of the youth is confident in using identification tools and are able to identify common birds to species level, although still prefers atlasing in groups. About 25% occasionally record lifers and attempt atlasing alone, with 15% still struggling. On average, a total of 30–40 species are reported per trip (2–4 hours). Comparing voluntary (pre-project) and prompted (after-project) biodiversity interest and awareness, only 13% indicated voluntary interest and awareness, and after prompting, about 87% are biodiversity conscious and committed to the project. Of the 87%, 33% would continue atlasing beyond the duration of the project (without subsistence allowance) and are currently submitting longer species lists per trip, and are consistent in atlasing. The youth continue to gain experience in bird identification and atlasing, which provides them with an opportunity to be employed as bird guides in the ever increasing tourism sector in South Africa.

Phylogeographic pattern of a polymorphic southern African species, the Southern boubou *Laniarius ferrugineus* (Gmelin, 1788)

Dikobe K. Molepo¹, Tshifhiwa G. Mandiwana-Neudani¹, Jérôme Fuchs². Rauri C.K. Bowie³
¹Department of Biodiversity, University of Limpopo; molepodikobe@gmail.com

²Muséum National d'Histoire Naturelle, Paris, France

³University of California, Berkeley, California, United States of America

Some species of birds show no geographical variation while others present widespread complex geographical variation morphologically rendering them polytypic in nature. The Southern boubou Laniarius ferrugineus (Gmelin, 1788), a southern African endemic, is one such species with prominent geographic variation and unknown genetic structure. Despite the traditional way of relying on morphology and patterns of distribution ranges to understand intraspecific variation and its origin, this study explores the geographic structure of genetic, morphological and vocal variation across the distribution range of L. ferrugineus. One mitochondrial marker (ATP6) and three nuclear introns (FGB5, MUSK, TGFb2) from historical and modern samples, morphometric and vocal data were explored. The Bayesian phylogenies point to a strongly supported divergence within L. ferrugineus forming two major distinct lineages. These are represented by the southern (ferrugineus/natalensis/pondoensis) and the northern (transvaalensis/tongensis/savensis) lineages. The 95% parsimony networks show two differentiated haplotype lineages (not well-recovered for nuclear loci). The genetic and morphometric evidence demonstrate strong support for the divergence within L. ferrugineus. These findings will have implications on the taxonomic circumscription, our general perspective on geographical variation, conservation and the biogeography of this species.

Epischoenus (Schoeneae, Cyperaceae): taxonomic revision and phylogenetic studies

Ngalirendwe Muthaphuli^{1,2}, Tammy Elliot^{1,3}, Samson Chimphango^{1,3}, A. Muthama Muasya^{1,3} ¹Bolus Herbarium, Department of Biological Sciences, University of Cape Town; <u>murendwarendwa@gmail.com</u>

The Cape Core Region (CCR) has continued to fascinate naturalists since early explorers in the 16th century. Though the region has guite a long history of floristic studies, there are still large gaps in our knowledge on species occurrences and tens of new plant species are described annually. Among the diverse groups are the Cyperaceae. a family of monocotyledonous plants comprising perennials or annual herbs, occurring frequently in the fynbos biome and especially prominent in post fire habitats. The family is known to pose taxonomic difficulties, especially in identification and classification, as the Cyperaceae possess very small flowers whose morphology is often obscure, with their inflorescence morphology difficult to interpret. Among the least studied Cyperaceae taxa is the CCR endemic genus Epischoenus which was last studied in the 1950s as part of the Flora of the Cape Peninsula. The main aim of this study was to revise the taxonomy of Epischoenus and to infer their phylogenetic relationships. We recognise seven previously described taxa as distinct species and have identified four species to be new to science based on morphological and ecological data. Based on molecular phylogenetic results, Epischoenus is now included in the widespread genus Schoenus, but one of the Epischoenus species has been moved into Tetraria.

'For Pete's sake, it's a collection: what is the data management that you speak of?'

Jofred Opperman, Aisha Mayekiso Iziko South African Museums; <u>jopperman@iziko.org.za</u> and <u>amayekiso@iziko.org.za</u>

Collections form the backbone of any museum. The Iziko Museums of South Africa house a vast variety of natural. social and art history collections. The Iziko South African Museums aim to maintain these collections to supports scientific research for those in government, industry, academia and the public. As custodians of collections, museums not only have a moral and legal responsibility to curate and manage these collections, but they also have to maintain and curate the associated data. The Iziko Museums of South Africa have incorporated the Specify database in their workflow of curation of natural history collections. Specify is very useful in digitisation, managing and tracking of specimens in terms of loans/storage location and linking images/document to specimens. In light of this, a survey is currently being conducted amongst Iziko Museums of South Africa's collection staff to establish the challenges that staff face in managing the scientific data. Furthermore recommendations will be presented in terms of human capacity development.

An automated approach to amphibian diversity surveys: a case study for northern Zululand

Wentzel W. Pretorius¹, Donnavan J.D. Kruger¹, Edward C. Netherland¹, Louis H. Du Preez¹

¹African Amphibian Conservation Research Group, Unit for

African Amphibian Conservation Research Group, Unit for Environmental Sciences and Management, North-West University; <u>wentzel.pretorius93@gmail.com</u>

Most animal species have the ability to produce speciesspecific vocal signals with unique acoustic patterns. This enables scientists to monitor animals based on their acoustic behaviour. Literature on the anuran diversity of northern KwaZulu-Natal is outdated, with the last comprehensive survey conducted more than 30 years ago. Six localities were used to conduct Passive Acoustic Monitoring (PAM) via automated recorders. The recorders were equipped with a solar panel and 12V rechargeable Lead-Acid batteries. This ensured long term recordings over more than a year. Recorders recorded 10 minutes out of each hour from 18:00 to 07:00. During the study 69% (29/42) of the expected species were recorded. Anuran activity peaked in early mornings. Two species: Leptopelis mossambicus and Ptvchadena anchietae were recorded at all of the sites. The highest frog diversity was found in St Lucia with 16 species. Due to El Niño, observed rainfall patterns were not typical for this area. All of the chosen localities for this study are located in protected areas, which highlight the importance of such reserves. Using automated recorders, PAM proved to be a practical method for medium- to long-term non-invasive biodiversity estimates.

SANBI citizen science platform now on iNaturalist

Tony Rebelo
South African National Biodiversity Institute; <u>t.rebelo@sanbi.org.za</u>

The South African National Biodiversity Institute (SANBI) has moved their virtual museum citizen science platform from iSpot to iNaturalist at www.inaturalist.org. Migration of data from observers who granted permission is now complete. Some 263 366 observations of 20 965 taxa of animals, plants and fungi were migrated. Some 378 users opted to migrate amounting to 84% of the southern African data on iSpot. All ancillary data have also been migrated. Unfortunately, projects could not be migrated, but iNaturalist has various projects, places and filters that access this data. The major advantage of iNaturalist is that data can be easily filtered and exported in a variety of formats by users. Other advantages are being able to load multiple observations, manage projects with journals, downloads and use projects with filters to refine data selection, the easy development of checklist and field guides, and efficient identification and curation tools. Courses are underway to train users – please contact the author to arrange a course for your institution. iNaturalist is geared for teaching, coursework and running citizen science projects – see the online tutorials and guidelines for more details.

Investigating the herpetological diversity of the Karoo – a report from the Biogaps Project

J. Weeber, K. Tolley

South African National Biodiversity Institute; wbrjosh@gmail.com and K.Tolley@sanbi.org.za

The Karoo boasts a wide variety of unique flora and fauna, yet the region is still poorly surveyed for biodiversity. This lack of knowledge is true for all taxonomic groups, but none more so than reptiles. For example, only 3.5% of South Africa's reptile records have been obtained from the Karoo despite the region making up more than 30% of the country's total land mass and offering exceptional habitat for many of our reptile species. The Karoo has also been identified as an important development area for South Africa. Large scale international development projects such as shale gas drilling, uranium mining and the Square Kilometre Array, in conjunction with renewable energy infrastructure and continued farming will require responsible and informed planning. Here presented is a detailed account of the herpetological surveys conducted by the South African National Biodiversity Institute (SANBI) as part of the Karoo Biogaps Project, made possible by a grant from the Foundational Biodiversity Information Programme (FBIP), and offer preliminary investigations into the herpetological diversity of this unique region.



BIMF-FBIP Forum, 14–17 August 2017 Salt Rock Hotel and Beach Resort, Durban