

Bioinformatics gone Wild!!

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Background

- *National Zoological Gardens of South Africa - NRF facility*
- *Evaluation of mandate by Minister*
- *Currently in transition to join SANBI (March 2018)*
- *Contribute and expand on animal aspects of diversity*

Aims

- *undertake, facilitate and coordinate interdisciplinary basic and applied research*
- *this is aggregated into core programs and knowledge hubs*
- *in partnership with zoological gardens, conservation agencies, academic and other institutions*
- *become a centre of research excellence in the biodiversity conservation landscape*



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Performance Indicators

1. Provide a platform for high quality research accessible to wider research community
2. Undertake high quality research and generate knowledge
3. Develop technology and pursue innovation
4. Grow human capital through research and technology development
5. Advancing science in society

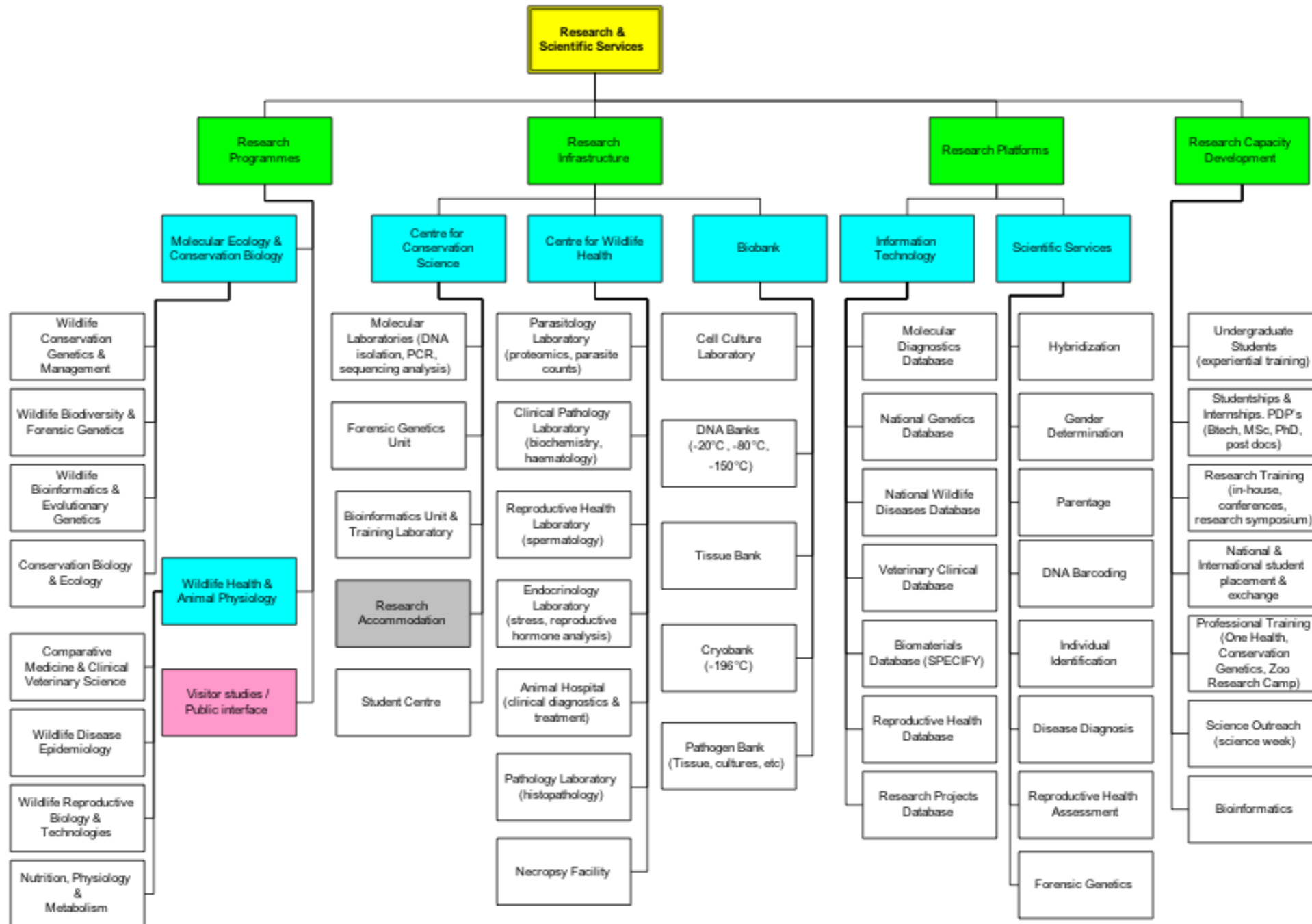


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Background



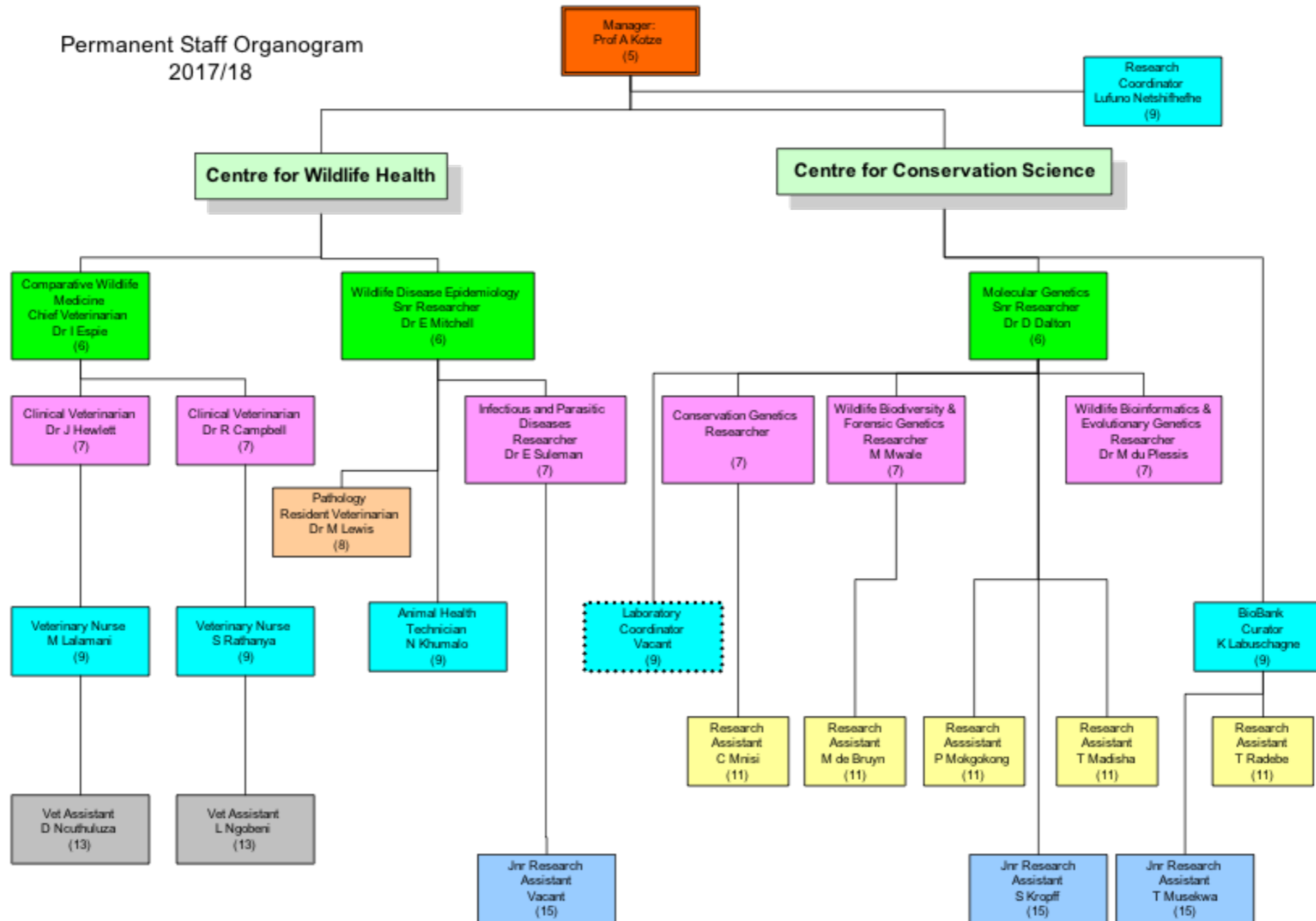
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NZG
National Zoological Gardens
of South Africa

Background



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NZG
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Bioinformatics at the NZG

Training

Research

Infrastructure

Resources

Bioinformatics training

Workshops

Student training

Mentorship

- *understanding the command line*
- *working with next generation sequencing data*
- *microsatellite development from NGS data*
- *assembly and mapping of NGS data*
- *microbiome analysis*



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Bioinformatics research

There is participation in the genomics research arena from across all of the researchers in the NZG

Pathogen genomes

Forensics of wildlife species

Evolutionary genomics

Microbiome analysis

Conservation genomics

Bioinformatics research

Pathogen genomes

Characterization of the genomes of Toxoplasma and Sarcocystis from clinically mixed samples

Mapping of total reads to host reference

Reduce number of overall reads

Map remaining reads to pathogen reference / generate de novo assembly



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NRF
National Research
Foundation

NZG
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Bioinformatics research

Forensics of wildlife species

Project on geo-locating origin of pangolin samples – confiscated

Extensive evidence of the poaching of pangolins based on confiscations

Currently less known about where exactly this happens

Aim is to develop a SNP marker based approach to be able to place samples at site of origin

RADseq - SNP discovery - Validation of polymorphic nature - Validation of accuracy to map to site of origin

Bioinformatics research

Evolutionary genomics

Understanding the evolutionary relationships among African pangolins

*Generate low pass genome sequence data for the African pangolins
(White bellied, Black bellied, Giant, Temmincks pangolin)*

Assembly of mitochondrial genomes

Conduct phylogenetic analysis based at the full mitochondrial genome level

Bioinformatics research

Microbiome analysis

Currently developing capacity to conduct host-microbiome interaction research across a number of species

Working on optimizing a number of pipelines incorporating either Qiime, Mothur along with downstream analysis

Microbiome of Pangolin (oral and fecal).

Microbiome of Bushbabies - response to change (seasonality and locality).

Microbiome of South African frog species.

Bioinformatics research

Microbiome of South African frog species.

Does the skin of frog species reflect the microbiome of their environment

Do frogs have genetic capacity to independently regulate skin microbiome

*Can we develop a model for predicting disease susceptibility in frogs
based on available skin microbiome data*

3 X Experiments



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Bioinformatics research

Develop model for predicting disease susceptibility based on microbiome data

Collect all available microbiome data re frog skin



Analyze and report on diversity



Categorise frog species on degree of susceptibility



Identify microbial species / combinations of species - association



Develop a model for predicting susceptibility



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Bioinformatics research

Conservation Genetics

Development of Microsatellite markers for understanding genetic

Diversity in populations

- *Utilize NGS data directly on a per read basis*
- *Generally considered error prone*
- *Relatively good outcomes to date – requires improvement*



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Conservation Genetics - NGS microsatelite development workflow

Generate low pass sequence data for spp. of interest

QC and filtering

Identify repetitive regions in sequence data

Validate to keep only perfect repeats

Filter to keep repeats of size of interest

Tag bases in sequences which have low quality scores

Develop primer sequences flanking repeats

Evaluate primers for amplification success and polymorphic nature

Implement on population of interest



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Bioinformatics research

Conservation Genetics - NGS microsatelite development workflow

Programs implemented in workflow

FastQC

Trimmomatic

Repeatsfinder

*Perfect_Repeat**

*Base_QC**

Primer3

*Good_Primer**



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Bioinformatics research

Next Generation Biodiversity Assessments

Advantages over traditional methods

- *huge capacity to utilise large sample sizes / sites*
- *reduction in field sampling time*

Utilises metabarcoding and / or metagenome sequencing

Target gene = dependent on species under investigation

*Experimental setup - sample sites in parallel – use traditional and next gen
– assess degree of variability in outcomes – derive mathematical models*

Bioinformatics infrastructure & resources

Via funding from the NRF the NZG acquired a compute server for day to day research activities (256 Gb)

*Additionally also a storage server with 10 TB storage capacity
(on main server and same on backup)*

In terms of data generation

- Ion S5 sequencer*
- QuantStudio 12K*

*Refurbished building to house Bioinformatics research team as well as
a 20 seater Bioinformatics training room*



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In summary

Ongoing successful partnership with CHPC has facilitated development of Bioinformatics Capacity at the NZG

- training of students*
- evaluation of pipelines*
- analysis of complex datasets*

Significant amount of work still in the pipeline for the organisation - rely on the continued support of the CHPC

Potential to develop the relationship to include new partners by virtue of the transition to SANBI



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Acknowledgements

- *NRF*
- *CHPC*
- *NZG Research Staff*
- *SANBI*
- *Collaborators*
- *Palesa Madupe (NZG) and Dane Kennedy (CHPC)*

