



PERSONAL STATEMENT

I am currently a postdoctoral fellow and head of the Bioinformatics and Drug Resistance Group at the Center for Lung Infection and Immunity, University of Cape Town. My research focusses on the causative agent of tuberculosis, *Mycobacterium tuberculosis*: I apply a combination of wet work and bioinformatics to investigate genomic and transcriptional associates of drug resistance, clinical outcomes, and patient infectiousness.

I have investigated patient infectiousness, treatment outcomes and community based likely transmission of extensively drug resistant tuberculosis using clinical and genomic data, developed a novel technique to selectively sequence *M. tuberculosis* RNA directly from patient sputum, compared in silico to traditional strain typing methods, and developed bioinformatic analysis tools for non-bioinformaticians. I am also developing techniques to enable whole genome sequencing of *M. tuberculosis* directly from patient sputum and for the fully quantitative detection of drug resistance mutations in a minority of the bacterial population. I am involved in numerous secondary projects, including developing lung and blood specific transcriptomic signatures for vaccine efficacy, response to treatment and proteomic diagnosis using urine.

I am experienced in manuscript preparation and have been integral in the writing of numerous grant application (including several submission to NIH, MRC, EDCTP and Royal Society). I have informally co-supervise M.Sc. and Ph.D. candidates and am formally co-supervising a Ph.D. candidate who is investigating the impact of new anti-TB drugs on patient-important outcomes.

I trained as a molecular biologist but have an aptitude and passion for programming. In my current position, I conceptualize ideas, perform lab work and optimization of techniques and develop the necessary computational methods to analyze the data. I am practiced in many laboratory, statistical and bioinformatic techniques and am biohazard level 3 certified.

WORK EXPERIENCE

2 2017 – Present
Center for Lung Infection and Immunity
University of Cape Town

1 2011 – 2012
Internship
Cereal Genomics Laboratory
University of Stellenbosch

1 2017 (6 months)
Novartis-CRG mobility program
Centre for Genomic Regulation
Barcelona, Spain

EDUCATION

- 2017 - present
Postdoctoral fellow
Centre for Lung Infection and Immunity
University of Cape Town, Cape Town
- 2015 - 2017
PhD Med Medicine
University of Cape Town, Cape Town
Upgraded to PhD
- 2014 - 2015
MSc Med Medicine
University of Cape Town, Cape Town
- 2013 - 2014
BSc Honours Medical Molecular Biology
University of Stellenbosch, Cape Town
- 2008 - 2012
BSc Molecular Biology with Biotechnology
University of Stellenbosch, Cape Town

SHORT AND ONLINE COURSES COMPLETED AND RESEARCH VISITS

Course	Presenter, Location
Genetic data analysis using R	PRstatistics, Scotland
Bioinformatics Training (2 weeks)	LSHTM, London
Gene Expression Biomarker Masterclass	UCT, Cape Town
Next Generation Sequencing	CAF, Cape Town
Digital and RT-PCR	CAF, Cape Town
Good Clinical Laboratory Practice	HVTN, Cape Town
Machine Learning	Stanford University, Online
Writing in The Sciences	Stanford University, Online
Game Theory	Stanford University, Online
Deep Learning Specialization (4 courses)	Deeplearning.ai, Online
Data Science Specialization (10 courses)	Johns Hopkins University, Online
Genomic Data Science Specialization (8 courses)	Johns Hopkins University, Online
Statistical Reasoning for Public Health 1	Johns Hopkins University, Online
Statistical Reasoning for Public Health 2	Johns Hopkins University, Online
Statistical Inference	Johns Hopkins University, Online
Biostatistics in Public Health Specialization (4 courses)	Johns Hopkins University, Online
Phylogenetics: An Introduction	EMBL-EBI, Online
IBM Cognitive Class	Big Data University, Online
Epidemics - the Dynamics of Infectious Disease	Pennsylvania State University, Online

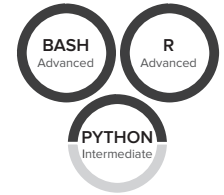
LABORATORY TECHNIQUES

- Technique
- Biohazard Level 3 certified
 - Mycobacterial, bacterial and yeast cell culture
 - DNA and RNA isolation (manual methods)
 - PCR and RT-PCR
 - Digital PCR
 - Cloning
 - Plasmid Isolation (manual methods)
 - SDS-PAGE
 - Protein Expression
 - Southern Blot
 - Western Blot
 - Zymogram
 - Scanning Electron Microscopy
 - Confocal Microscopy
 - Microtiter Assays

STATISTICAL TECHNIQUES

- Technique
- Basic Descriptive Statistics
 - Regression and Classification Analyses
 - Survival Models (Cox, Kaplan-Meier)
 - Genome Wide Association
 - Machine and Deep Learning Techniques
 - Population Genetics

PROGRAMMING LANGUAGE



SELECT AWARDS

Award	Awarder	Year
Best postgraduate publication	Faculty of Health Sciences, UCT	2018
Best oral presentation	SATS conference	2017

NOTABLE OUTPUTS | H-index=4 | Citations=90

Title and Authors
Long Term Bedaquiline-Related Treatment Outcomes in Patients with Extensively Drug Resistant Tuberculosis from South Africa <i>Olayanjun O*, Limberis JD*, Esmail A, Oelofse S, Gina P, Pieterzen E, Fadul M, Warren R, Dheda K</i>
Outcomes, infectiousness, and transmission dynamics of patients with extensively drug-resistant tuberculosis and home-discharged patients with programmatically incurable tuberculosis: a prospective cohort study <i>Dheda K*, Limberis JD*, Pieterzen E, Phelan J, Esmail A, Lesosky M, Fennelly K, te Riele J, Mastrapa B, Spiller P, Streicher E, Dolby T, Abdallah A, Ben Rached F, Simpson J, Smith L, Gumbo T, van Helden P, Sirgel F, McNeerney R, Theron G, Pain A, Clark T**, Warren M**</i>
Selected Questions and Controversies about Bedaquiline: A view from the field <i>Dheda K, Esmail A, Limberis JD, Maartens G</i>
Xpert MTB/RIF Results in Patients With Previous Tuberculosis: Can we distinguish true from false positive results? <i>Theron G, Venter R, Calligaro G, Smith L, Limberis JD, Meldrau R, Chanda D, Esmail A, Peter J, Dheda K</i>
Outcomes, Infectiousness And Transmission Dynamics Of Patients With Extensively Drug Resistant Tuberculosis And Home-Discharged Patients With Programmatically Incurable TB <i>Limberis JD, Pieterzen E, Phelan J, Esmail A, Lesosky M, Fennelly K, te Riele J, Mastrapa B, Spiller P, Streicher E, Dolby T, Abdallah A, Ben Rached F, Simpson J, Smith L, Gumbo T, van Helden P, Sirgel F, McNeerney R, Theron G, Pain A, Clark, Warren M, Dheda K</i>

Journal/ Conference, Year, IF	Contribution
European Respiratory Journal, 2018 IF=10.6 DOI: 10.1183/13993003.00544-2018	Co-first Author
Lancet Respiratory Medicine, 2017 IF=19.3 DOI: 10.1016/S2213-2600(16)30433-7	Co-first Author
International Journal of Tuberculosis and Lung Disease, 2016, IF=1.7 DOI: 10.5588/ijtld.16.0065	Co-author
Journal Clinical Infectious Disease, 2015 IF=8.9 DOI: 10.1093/cid/civ1223	Co-author
American Thoracic Society, 2017	Presenter

WEB APPLICATIONS (see SemiQuant.com)

Title	Description
DEAD: Diagnostic Estimates and Disease	Determine the performance of a diagnostic test(s)
HBHS: Sample Size Calculator	Calculate the required sample sizes or power of your study based on some priors
LinkTB: Visualize Variant Clustering	Interaction networks, phylogenetic trees, cluster analysis and drug resistance determination

SELECT PROJECT SUMMARIES

- Host and microbiological determinants of infectiousness in patients with drug sensitive-, multi- and extensively drug resistant tuberculosis (2014 – 2018; National Institutes of Health)**
My role: Project management and laboratory lead; development of new methods to interrogate and analyze the bacterial transcriptome in complex clinical samples; perform data analysis and interpretation.
- Are Mycobacterium tuberculosis bacilli in highly infectious tuberculosis patients in a different transcriptional state compared to those in patients with low infectiousness? (Jan 2017 – July 2017; Novartis)**
My role: My role as the principal investigator was to develop a method to enrich the complex clinical sample for *M. tuberculosis* RNA and develop the necessary bioinformatic methods to analyze the data.
- Diagnosis, spread, and management of incurable TB in the Western Cape Province of South Africa (2014 – 2017; Oppenheimer Foundation)**
My role: Project manager and laboratory lead; perform culture, DNA extraction, and analyze clinical and whole genome sequence data to determine the risk factors and transmission of incurable tuberculosis.
- TESA Networks of Excellence for the evaluation of new diagnostics and interventions for tuberculosis (TESA; 2017 – 2020; EDCTP)**
My role: Project manager. To coordinate exchange programmes and courses within the TESA network and to assist in the development of mentoring programmes.

REFERENCES

Supervisor	Mentor	Mentor	Mentor	Mentor
Prof. Keertan Dheda UCT Keertan.Dheda@uct.ac.za	Prof. Grant Theron SUN G.Theron@sun.ac.za	Prof. Rob Warren SUN RW1@sun.ac.za	Prof. Taane Clark LSHTM Taane.Clark@lshtm.ac.uk	Dr. Julia Ponomarenko CRG Julia.Ponomarenko@crgeu