Marco van Zwetselaar

Bioinformatician / Software Developer

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Bioinformatician with research focus on whole genome sequencing and microbial genomics. Thirty years work experience as an IT professional, from board level consulting down to the bits and the iron. Appreciated for his ability to work across the business-IT divide. Open source software developer since the dawn of personal computing who still loves coding. Academic background in geography, modelling and statistics.

CURRENT

Lead Bioinformatician at Kilimanjaro Clinical Research Institute (KCMC, Moshi, Tanzania), Aug 2012 – present

- Build the analysis pipelines of the genomics unit at KCRI, and design and perform bespoke analyses of genomic data for numerous projects

- Train and supervise one post-doc, two PhD, two MSc students, four interns; teach bioinformatics courses

- Design, build and manage the high-performance cluster at KCRI

- Project coordination of the Fleming Fund SeqAfrica project: establish a reference sequencing lab for antimicrobial resistance at KCRI

PREVIOUS

Enterprise architect: Atos, Aug 2005 – Aug 2012

Lead architect: Delta Lloyd OHRA (through Atos), 2011 – 2012

Consultant: a.s.r. verzekeringen (through Atos), 2008 – 2011

IT architect: Achmea (through Atos Origin), 2005 – 2009

Software architect: Fortis, 1998 – 2004

Software developer: Nat. Inst. Public Health & Env (RIVM), 1994 – 1998

Scientific programmer: Utrecht University, 1990 – 1994

EDUC-ATION

MSc Human Geography, Utrecht University, 1992

Cap. sel. **Artificial Intelligence**, Utrecht University, 1992

IB Diploma, UWC of the Adriatic, 1986

LANG-UAGES

Spoken: English, Dutch, Italian, German, French, some Swahili

Computing: C++, C, Python, Haskell, awk/bash, R, Java, SQL, JavaScript, Scheme & LISP, Erlang, Smalltalk, Prolog

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RECENT COURSES

Mathematics for Machine Learning, Imperial College (Coursera), July 2020, licence 4CHZR56VKCFG

Real-time Virus Genome Sequencing, Nanopore sequencing & bioinformatics for viral outbreak response, ARTIC Network, Accra, Dec 2018

Specialization Probabilistic Graphical Models (Honours), Stanford (Coursera) Mar 2017, licence 6KVJTGM283MK

Specialization Bioinformatics Algorithms (Distinction), UCSD (Coursera) Apr 2016, licence UQQK6D5JX8DV

High-dimensional Data Analysis, PH525.4.x (edX), Apr 2016, licence fd79ffa5aaed4e829401a42a1c548b9d

Statistical Inference for High-throughput Experiments, PH525.3.x (edX), Mar 2016, licence aec1b523e2d2418cbc0ab47d8ab5b35b

Algorithms for DNA sequencing, Johns Hopkins (Coursera), Jan 2016, licence GMWNE2NMP8

TEACHING

Advanced CLI Bioinformatics, NMIMR, Accra, Sep 2021

Bioinformatics 101, KCMUCo MSc, Moshi, Jun 2021

Introduction to Bioinformatics, Fleming Fund, online, Mar 2021

RECENT PAPERS

Sengeruan LP, van Zwetselaar M, Kumburu HH, *et al.* Plasmid characterization in bacterial isolates of public health relevance in a tertiary healthcare facility in Kilimanjaro, Tanzania. *J Global Antimicrob Resistance.* 2022. doi:10.1016/j.jgar.2022.06.030.

Nkya S, Mwita L, Mgaya J, Kumburu H, van Zwetselaar M, Menzel S, *et al.* Identifying genetic variants and pathways associated with extreme levels of fetal hemoglobin in sickle cell disease in Tanzania. *BMC Med Genet.* 2020;21:125.

Kumburu HH, Sonda T, van Zwetselaar M, *et al.* Using WGS to identify antibiotic resistance genes and predict antimicrobial resistance phenotypes in MDR Acinetobacter baumannii in Tanzania. *J Antimicrob Chemother.* 2019 doi:10.1093/jac/dkz055.4

Sonda T, Kumburu H, Zwetselaar M van, *et al.* Molecular epidemiology of virulence and antimicrobial resistance determinants in Klebsiella pneumoniae from hospitalised patients in Kilimanjaro, Tanzania. *Eur J Clin Microbiol Infect Dis* 2018; 1–14

Sonda T, Kumburu H, van Zwetselaar M, *et al.* Whole genome sequencing reveals high clonal diversity of Escherichia coli isolated from patients in a tertiary care hospital in Moshi, Tanzania. *Antimicrobial Resistance & Infection Control* 2018; 7.

Van Zwetselaar M, Nyombi B, Sonda T, *et al.* Aeromonas caviae mimicking Vibrio cholerae infectious enteropathy in a cholera-endemic region with possible public health consequences: two case reports. *Journal of Medical Case Reports* 2018; 12.

Sonda T, Kumburu H, Zwetselaar M van, *et al.* Prevalence and risk factors for CTX-M gram-negative bacteria in hospitalized patients at a tertiary care hospital in Kilimanjaro, Tanzania. *Eur J Clin Microbiol Infect Dis* 2018; 1–10.

RECENT WORK

github.com/zwets | github.com/kcri-tz

- **unfasta** – command-line pipes and filters for genomic data
- **gene-paths** – determine gene order from assembly graphs
- **kcri-cge-bap** – open source bacterial analysis pipeline
- **taxo** – offline command-line NCBI and GTDB taxonomy browsers
- **kcst** – k-mer counting sequence typing and species identification
- **picoline** – simplistic workflow & job control for on-machine pipelines
- **fastq-utils** – small utilities to manipulate fastq format files
- **hpc.kcri.it** – documentation website for KCRI high-performance cluster

Access to internal bioinformatics analysis repositories provided on request