

Marco van Zwetselaar

Bioinformatician / Software Developer

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Bioinformatician with a decade of experience in whole genome sequencing and high-performance computing. Twenty years prior experience as an IT professional, from board level consulting down to the bits and the iron. Open source software developer since the dawn of personal computing. GNU/Linux expert. Academic origins in geography, AI computing, modelling and statistics.

CURRENT **Self-employed** at Zwets IT. Independent contractor in IT and bioinformatics. On-site and remote bioinformatics software development; HPC design and construction; on-demand genomic analyses; bioinformatics mentoring & training.

PREVIOUS **Lead Bioinformatician** at Kilimanjaro Clinical Research Institute (KCRI, KCMC, Moshi, Tanzania), Aug 2012 – Feb 2023

- Construct the analysis pipelines for genomics at KCRI; design and perform bespoke analyses of genomic data for numerous projects.
- Design, build and manage the high-performance cluster at KCRI; build the HPC at Noguchi Memorial Institute for Medical Research, Accra.
- Train post-doc, PhD and MSc students; supervise interns; teach bioinformatics and programming courses.
- Project coordination of the Fleming Fund SeqAfrica project: establish a reference sequencing lab for antimicrobial resistance at KCRI.

Enterprise architect at Atos, Aug 2005 – Aug 2012

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

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

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

Software architect at Fortis, 1998 – 2004

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

Scientific programmer at Utrecht University, 1990 – 1994

EDUC- **MSc Human Geography**, Utrecht University, 1992

ATION *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

**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 6KVJTG283MK
**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

**TEACH-
ING** **Advanced CLI Bioinformatics**, NMIMR, Accra, Oct 2022
Command-line Bioinformatics, NMIMR, Accra, Sep 2021
Bioinformatics 101, KCMUCo MSc, Moshi, Jun 2021
Introduction to Bioinformatics, Fleming Fund, online, Mar 2021

**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

**RECENT
PAPERS**

Mziray SR, van Zwetselaar M, Kayuki CC, *et al.* Whole-genome sequencing of SARS-CoV-2 isolates from symptomatic and asymptomatic individuals in Tanzania. *Frontiers in Medicine*. 2023;9. doi:10.3389/fmed.2022.1034682.

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.

Sadiq AM, Mariki DE, Gundah CM, Assey EV, Zwetselaar M van, *et al.* Feeling the price tag of magnetic resonance imaging claustrophobia. *Journal of Magnetic Resonance Imaging*. 2021;54. doi:10.1002/jmri.27512.

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.
