

Marco van Zwetselaar

Bioinformatician / IT Professional

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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 software development
- Bioinformatics consultancy and pipeline development
- HPC design, construction and management
- Advanced Linux systems management
- Bioinformatics training & mentoring

PREVIOUS **Lead Bioinformatician** at KCRI (Moshi, Tanzania), Aug 2012 – Feb 2023

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- 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, awk/bash, R, Java, SQL, Haskell,
JavaScript, Scheme & LISP, Erlang, Smalltalk, Prolog

RECENT COURSES	Move to modern C++ / Progress to C++17 , Udemy, August 2024
	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

RECENT TEACHING	Building Workflows and Pipelines , on-line, Oct 2025
	Linux Container Technologies , on-line, Sep 2025
	Git, GitHub and Workflows , Tanzania (on-line), Aug 2025
	Bioinformatics for AMR surveillance , on-line, Aug 2025
	Bioinformatics Introduction , CIDRZ, Lusaka, June 2025
	Bioinformatics for AMR surveillance , CHSU, Lilongwe, Mar 2025
	Bioinformatics Refresher , FAO/NMIMR, Accra, May 2023
	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

- **unfasta** – command-line pipes and filters for genomic data
- **gene-paths** – determine gene order from assembly graphs
- **amr-trinity** – run the big three AMR tools in one go
- **cge-bap** – 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

Access to internal bioinformatics analysis repositories provided on request

RECENT PAPERS

Zwetselaar M van, Ostermann J, Beti M, *et al.* Design of an Automated Mobile Phone-Based Reminder and Incentive System: Application in a Quasi-Randomized Controlled Trial to Improve the Timeliness of Childhood Vaccinations in Tanzania. *JMIR Formative Research*. 2025;9: e65150. doi:10.2196/65150

Mapunda L, *et al.* Co-existence of two blaNDM-5 and blaOXA-181 on distinct plasmids in a carbapenem-resistant *Klebsiella pneumoniae* from a tertiary hospital, Tanzania. *Journal of Global Antimicrobial Resistance*. 2025;41: 173–180. doi:10.1016/j.jgar.2024.12.011

Jaswant G, *et al.* Molecular characterisation of human rabies in Tanzania and Kenya: a case series report and phylogenetic investigation. *Infectious Diseases of Poverty*. 2024;13: 79. doi:10.1186/s40249-024-01245-w

Sarenje KL, van Zwetselaar M, Kumburu H, *et al.* Antimicrobial resistance and heterogeneity of *Neisseria gonorrhoeae* isolated from patients attending sexually transmitted infection clinics in Lusaka, Zambia. *BMC Genomics*. 2024;25: 290. doi:10.1186/s12864-024-101155-y

Mbwambo GA, van Zwetselaar M, Sonda T, *et al.* Complete genome sequence of *Brucella abortus* isolated from a human blood culture sample in Tanzania. *Microbiology Resource Announcements*. 2024;13: e00930-23. doi:10.1128/mra.00930-23

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.

Kumburu HH, Shayo M, Zwetselaar M van, *et al.* Nanopore sequencing technology for clinical diagnosis of infectious diseases where laboratory capacity is meager: A case report. *Heliyon*. 2023;9. doi:10.1016/j.heliyon.2023.e17439

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.

Zwetselaar M van, 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.
