

# 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.

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**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

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**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

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**EDUCATION** **MSc Human Geography**, Utrecht University, 1992

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

**IB Diploma**, UWC of the Adriatic, 1986

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

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

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**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

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**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 surveillancee**, 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

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## RECENT WORK

[github.com/zwets](https://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
- **k cst** – 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*

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## 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/s12864-024-10115-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.

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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.

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