

# Marco van Zwetselaar

## Bioinformatician / Software Developer

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P.O. Box 2236 · Moshi, Kilimanjaro · Tanzania

Bioinformatician with research focus on whole genome sequencing and microbial genomics. Background in modelling and statistics. Thirty years work experience in all facets of the IT profession. Open source developer since the appearance of the personal computer.

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

- construct the analysis pipelines of the genomics unit at KCRI, and design and perform bespoke analyses of genomic data for various projects
- server management, data management, software development, analysis & visualisation for clinical and genomic studies at KCRI

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**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

**IT architect**: Fortis, 1998 – 2004

**Software architect**: RIVM, 1994 – 1998

**Scientific programmer**: Utrecht University, 1990 – 1994

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**LANG-**            **Spoken**: English, Dutch, Italian, German, French, some Swahili

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

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**RECENT**            **Specialization Probabilistic Graphical Models**

**COURSES**            **(Honours)**, Stanford (Coursera) Mar 2017, licence 6KVJTG283MK

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

**Classical Papers in Molecular Genetics**, University of Geneva  
(Coursera) Sep 2016, licence Y8WYEP2KQH2P.

**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

**Extremes of Life: Microbes and their Diversity**, Kyoto University (Coursera) Dec 2014, licence 2495a8d27d25416996af852e816cd78b

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**RECENT  
PUBLIC-  
ATIONS**

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.

Ostermann J, Vasudevan L, Van Zwetselaar M, Moses S, Engadaya E, Mfinanga S. Mobile Phone Assisted Reminder and Incentive System (mParis). *NIH Tech Showcase presentation 2018*.

Sonda T, Kumburu H, Zwetselaar M van, *et al.* Benchtop Whole-Genome Sequencing for Identification of Nosocomial Outbreaks in Tanzania. *Infect Control Hosp Epidemiol* 2016; 37: 622–3.

Sonda T, Kumburu H, van Zwetselaar M, *et al.* Meta-analysis of proportion estimates of Extended-Spectrum-Beta-Lactamase-producing Enterobacteriaceae in East Africa hospitals. *Antimicrobial Resistance & Infection Control* 2016; 5: 18.

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**RECENT  
SOFT-  
WARE**

[github.com/zwets](https://github.com/zwets) | [io.zwets.it](http://io.zwets.it)

- **unfasta** – command-line pipes and filters for genomic data
- **taxo** – offline command-line taxonomy browser
- **kcst** – k-mer counting sequence typing and species identification
- **sast** – simple assembly sequence typing
- **fastq-utils** – small utilities to manipulate fastq format files
- **gene-cutter** – template-based extraction of allele matches
- **blast-pcr** – test primers against all known genomes
- **phylo-utils** – utilities for Newick format files