

Christophe Van Neste

BIOENGINEER · BIOINFORMATICIAN · SOFTWARE ENGINEER

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Education

Ghent University

DOCTOR OF PHARMACEUTICAL SCIENCES

Ghent, Belgium

May. 2011 - June. 2015

- Porting forensic DNA analysis to deep sequencing

For my doctoral thesis, I explored the possibilities of massively parallel sequencing in the field of forensics.

'Ca Foscari University

MASTER OF PHILOSOPHY

Venice, Italy

Sep. 2008 - Nov. 2010

- Completed cum laude
- Specialization in philosophy of science.
- Thesis: *Evolutionary epistemology and the problem of ignorance*

Ghent University

BACHELOR OF PHILOSOPHY

Ghent, Belgium

Okt. 2005 - Sep. 2008

- Completed the bachelor with distinction.

Ghent University

MASTER OF BIOSCIENCE ENGINEERING

Ghent, Belgium

2002-2005 (courses), 2007-2008 (thesis)

- Specialization in cellular and genetic biotechnology
- Thesis: *Possibilities of low-field nuclear magnetic resonance in fat crystallization research*

Ghent University

BACHELOR OF BIOSCIENCE ENGINEERING

Ghent, Belgium

Okt. 2000 - Sep. 2002

- Completed the bachelor with distinction.

Skills

Programming Python, R, Node.JS, Typescript, C/C++, Perl, JAVA, SQL, LaTeX

Web Django, Flask, React, Angular, Firebase, HTML5, LESS, SASS

Languages Dutch, English, Italian, French, German, Russian

Experience

Center for Medical Genetics Ghent

POSTDOCTORAL RESEARCHER & BIOINFORMATICIAN

Ghent, Belgium

Dec. 2015 - PRESENT

- Researching DNA secondary structures and replicative stress in neuroblastoma and pan-cancer.
- Researched classification algorithms (decision trees, neuronal networks) to improve outcome prediction of neuroblastoma patients.
- Multivariate ranking of biomarkers for patient stratification.
- Built and deployed overall bioinformatics platform utilizing Docker container, focusing on high-availability, ease of use, and auto-scaling.
- Implementing a network analysis tool with random restart walk in collaboration with UGent systems biology team.
- Supervising PhD students. Assisting them in constructing research hypotheses, experimental design, and data analysis.
- Assisting in bioinformatics course for graduate students.
- Data processing experience with ChIP seq, ATAC seq, shallow whole genome sequencing.
- Preparing applications for ethics commission.

Computational Bioscience Research Center, KAUST

POSTDOCTORAL FELLOW

Thuwal, Saudi Arabia

Jul. 2018 - Jun. 2020

- Applying text mining and natural language processing to the medical literature, to extract knowledge for the advancement of medical research, with special attention to cancer research.
- Extracting useful information from big data in biomedicine through use of machine learning and deep neural networks.
- Using graph methods on the knowledge graphs we generate, to derive novel insights.
- Supervising master and PhD-students, coordinating scientific projects.
- Teaching assistant in the course "AI in bioinformatics."
- Teaching assistant for the 5-day workshop "Women Machine Learning Bootcamp 2019."
- Fire warden and qualified first-aider.

Laboratory for pharmaceutical biotechnology

FORENSIC RESEARCHER

- Working on massively parallel sequencing projects.
- Discussing the minimal nomenclature requirements within the forensic DNA commission.
- Setting up international collaborations in the field of forensics.
- Assisting the initiation of a pharmacogenomics project.

Ghent, Belgium

Jun. 2015 - Nov. 2015

Illumina

BIOINFORMATICS INTERN

- Developing apps for the BaseSpace platform.
- Collaborating with core BaseSpace developers to improve their platform.
- Experience with Docker, D3, scrum, test driven development.

San Diego, USA

Mar. 2014 - May. 2014

Laboratory for pharmaceutical biotechnology

PHD STUDENT

- Developed software tools to assist forensic community transitioning to use of sequencing for DNA profiling
- Implemented a RESTful API server for forensic allele nomenclature.
- Data processing experience with Roche 454, Illumina, IonTorrent, Nanopore for genomics, methylomics, and transcriptomics. Mass spec data experience for proteomics.
- Programming laboratory robot for automated forensic sample processing.
- System and network administration for accredited forensic laboratory.

Ghent, Belgium

May. 2011 - Jun. 2015

several organizations

WEBMASTER

- Learning different web languages: PHP, JavaScript, HTML, CSS.
- Implementing the content management system Drupal.

Ghent, Belgium

2005 - PRESENT

General Interests

PROFESSIONAL

- data analysis
- web design and app creation
- software design

PERSONAL

- chess
- cooking
- philosophy
- running

Scientific Committees

2015-2016 **Member**, DNA commission of the International Society for Forensic Genetics (ISFG)

Honors & Awards

2016-2020 **Postdoctoral Fellowship**, Research Foundation - Flanders (FWO)

Flanders, Belgium

Publications

Peer-reviewed papers

- Albalawi, Fahad et al. (2019). "Hybrid model for efficient prediction of poly(A) signals in human genomic DNA". In: *METHODS* 166.SI, 31–39. ISSN: 1046-2023. DOI: {10.1016/j.ymeth.2019.04.001}.
- Bajic, Vladan P. et al. (2019). "Glutathione "Redox Homeostasis" and Its Relation to Cardiovascular Disease". In: *OXIDATIVE MEDICINE AND CELLULAR LONGEVITY*. ISSN: 1942-0900. DOI: {10.1155/2019/5028181}.
- Broeckx, Bart J. G. et al. (2013). "The Prevalence of Nine Genetic Disorders in a Dog Population from Belgium, the Netherlands and Germany". In: *PLOS ONE* 8.9. ISSN: 1932-6203. DOI: {10.1371/journal.pone.0074811}.
- Christiaens, Olivier et al. (2015). "Differential transcriptome analysis of the common shrimp *Crangon crangon*: Special focus on the nuclear receptors and RNAi-related genes". In: *GENERAL AND COMPARATIVE ENDOCRINOLOGY* 212, 163–177. ISSN: 0016-6480. DOI: {10.1016/j.ygcen.2014.06.016}.

- Claeys, Shana et al. (2019). "ALK positively regulates MYCN activity through repression of HBP1 expression". In: *ONCOGENE* 38.15, 2690–2705. ISSN: 0950-9232. DOI: {10.1038/s41388-018-0595-3}.
- Decaestecker, Bieke et al. (2018). "TBX2 is a neuroblastoma core regulatory circuitry component enhancing MYCN/FOXM1 reactivation of DREAM targets". In: *NATURE COMMUNICATIONS* 9. ISSN: 2041-1723. DOI: {10.1038/s41467-018-06699-9}.
- Essack, Magbubah et al. (2019). "Literature-Based Enrichment Insights into Redox Control of Vascular Biology". In: *OXIDATIVE MEDICINE AND CELLULAR LONGEVITY*. ISSN: 1942-0900. DOI: {10.1155/2019/1769437}.
- Kordopati, Vasiliki et al. (2018). "DES-Mutation: System for Exploring Links of Mutations and Diseases". In: *SCIENTIFIC REPORTS* 8. ISSN: 2045-2322. DOI: {10.1038/s41598-018-31439-w}.
- Parson, Walther et al. (2016). "Massively parallel sequencing of forensic STRs: Considerations of the DNA commission of the International Society for Forensic Genetics (ISFG) on minimal nomenclature requirements". In: *FORENSIC SCIENCE INTERNATIONAL-GENETICS* 22, 54–63. ISSN: 1872-4973. DOI: {10.1016/j.fsigen.2016.01.009}.
- Sharpe, Kevin et al. (2013). "The Effect of VEGF-Targeted Therapy on Biomarker Expression in Sequential Tissue from Patients with Metastatic Clear Cell Renal Cancer". In: *CLINICAL CANCER RESEARCH* 19.24, 6924–6934. ISSN: 1078-0432. DOI: {10.1158/1078-0432.CCR-13-1631}.
- Soetaert, Sandra S. A. et al. (2013). "Differential transcriptome analysis of glandular and filamentous trichomes in *Artemisia annua*". In: *BMC PLANT BIOLOGY* 13. ISSN: 1471-2229. DOI: {10.1186/1471-2229-13-220}.
- Stewart, Grant D. et al. (2016). "Dynamic epigenetic changes to VHL occur with sunitinib in metastatic clear cell renal cancer". In: *ONCOTARGET* 7.18, 25241–25250. DOI: {10.18632/oncotarget.8308}.
- Stewart, Grant et al. (2015). "Effect of sunitinib treatment on mutations and methylation in metastatic renal cancer." In: *JOURNAL OF CLINICAL ONCOLOGY* 33.7, S. Genitourinary Cancers Symposium, Orlando, FL, FEB 26-28, 2015. ISSN: 0732-183X. DOI: {10.1200/jco.2015.33.7_suppl.492}.
- Van Bel, Michiel et al. (2013). "TRAPID: an efficient online tool for the functional and comparative analysis of de novo RNA-Seq transcriptomes". In: *GENOME BIOLOGY* 14.12. ISSN: 1474-760X. DOI: {10.1186/gb-2013-14-12-r134}.
- Van Neste, Christophe, Dieter Deforce, and Filip Van Nieuwerburgh (2015). "Effect of multiple allelic drop-outs in forensic RMNE calculations". In: *FORENSIC SCIENCE INTERNATIONAL-GENETICS* 19, 243–249. ISSN: 1872-4973. DOI: {10.1016/j.fsigen.2015.08.001}.
- Van Neste, Christophe, Yannick Gansemans, et al. (2015). "Forensic massively parallel sequencing data analysis tool: Implementation of MyFLq as a standalone web- and Illumina BaseSpace (R)-application". In: *FORENSIC SCIENCE INTERNATIONAL-GENETICS* 15, 2–7. ISSN: 1872-4973. DOI: {10.1016/j.fsigen.2014.10.006}.
- Van Neste, Christophe, Alexander Laird, et al. (2017). "Epigenetic sampling effects: nephrectomy modifies the clear cell renal cell cancer methylome". In: *CELLULAR ONCOLOGY* 40.3, 293–297. ISSN: 2211-3428. DOI: {10.1007/s13402-016-0313-5}.
- Van Neste, Christophe, Wim Van Criekinge, et al. (2016). "Forensic Loci Allele Database (FLAD): Automatically generated, permanent identifiers for sequenced forensic alleles". In: *FORENSIC SCIENCE INTERNATIONAL-GENETICS* 20, E1–E3. ISSN: 1872-4973. DOI: {10.1016/j.fsigen.2015.09.006}.
- Van Neste, Christophe, Filip Van Nieuwerburgh, et al. (2012). "Forensic STR analysis using massive parallel sequencing". In: *FORENSIC SCIENCE INTERNATIONAL-GENETICS* 6.6, 810–818. ISSN: 1872-4973. DOI: {10.1016/j.fsigen.2012.03.004}.
- Van Neste, Christophe, Mado Vandewoestyne, et al. (2014). "My-Forensic-Loci-queries (MyFLq) framework for analysis of forensic STR data generated by massive parallel sequencing". In: *FORENSIC SCIENCE INTERNATIONAL-GENETICS* 9, 1–8. ISSN: 1872-4973. DOI: {10.1016/j.fsigen.2013.10.012}.
- Van Nieuwerburgh, Filip et al. (2014). "Retrospective study of the impact of miniSTRs on forensic DNA profiling of touch DNA samples". In: *SCIENCE & JUSTICE* 54.5, 369–372. ISSN: 1355-0306. DOI: {10.1016/j.scijus.2014.05.009}.
- Vanhauwaert, Suzanne et al. (2018). "In silico discovery of a FOXM1 driven embryonal signaling pathway in therapy resistant neuroblastoma tumors". In: *SCIENTIFIC REPORTS* 8. ISSN: 2045-2322. DOI: {10.1038/s41598-018-35868-5}.
- Vossaert, Liesbeth et al. (2013). "Reference loci for RT-qPCR analysis of differentiating human embryonic stem cells". In: *BMC MOLECULAR BIOLOGY* 14. ISSN: 1471-2199. DOI: {10.1186/1471-2199-14-21}.
- Willems, Sander, Senne Cornelis, et al. (2017). "RMNE calculation in forensic profiles with a high number of loci and allelic drop-outs using polynomial expansion". In: *FORENSIC SCIENCE INTERNATIONAL-GENETICS* 26, E14–E16. ISSN: 1872-4973. DOI: {10.1016/j.fsigen.2016.10.020}.
- Willems, Sander, Maarten Dhaenens, et al. (2017). "Flagging False Positives Following Untargeted LC-MS Characterization of Histone Post-Translational Modification Combinations". In: *JOURNAL OF PROTEOME RESEARCH* 16.2, 655–664. ISSN: 1535-3893. DOI: {10.1021/acs.jproteome.6b00724}.