Christophe **Van Neste**

Postdoctoral Researcher · Bioinformatician · Software Engineer

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"Philosopher and [bio]engineer in theory, visionary [bio]programmer in practice."

Education

Ghent University — *Ghent, Belgium*

Doctor of Pharmaceutical Sciences — *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 — *Venice, Italy*

Master of Philosophy — *Sep. 2008 - Nov. 2010*

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

Ghent University — *Ghent, Belgium*

Bachelor of Philosophy — *Okt. 2005 - Sep. 2008*

- Completed the bachelor with distinction.

Ghent University — *Ghent, Belgium*

Master of Bioscience Engineering — *Okt. 2002 - Sep. 2005*

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

Ghent University — *Ghent, Belgium*

Bachelor of Bioscience Engineering — *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 — *Ghent, Belgium*

Postdoctoral researcher & Bioinformatician — *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.
- 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.

Laboratory for pharmaceutical biotechnology — *Ghent, Belgium*

Forensic researcher — *Jun. 2015 - Nov. 2015*

- 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.

Illumina — *San Diego, USA*

Bioinformatics intern — *Mar. 2014 - May. 2014*

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

Laboratory for pharmaceutical biotechnology *Ghent, Belgium*

PhD student *May. 2011 - Jun. 2015*

- 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 trancriptomics. Mass spec data experience for proteomics.
- Programming laboratory robot for automated forensic sample processing
- System and network administration.

several organizations *Ghent, Belgium*

Webmaster *2005 - PRESENT*

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

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)

Publications

Peer-reviewed papers

Broeckx, Bart et al. (2013). "The prevalence of nine genetic disorders in a dog population from Belgium, the Netherlands and Germany". eng. In: *PLOS ONE* 8.9, p. 8. ISSN: 1932-6203. URL: http://dx.doi.org/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". eng. In: *GENERAL AND COMPARATIVE ENDOCRINOLOGY* 212, pp. 163–177. ISSN: 0016-6480. URL: http://dx.doi.org/10.1016/j.ygcen.2014.06.016.

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". eng. In: *CLINICAL CANCER RESEARCH* 19.24, pp. 6924–6934. ISSN: 1078-0432. URL: http://dx.doi.org/10.1158/1078-0432.CCR-13-1631.

Soetaert, Sandra et al. (2013). "Differential transcriptome analysis of glandular and filamentous trichomes in Artemisia annua". eng. In: *BMC PLANT BIOLOGY* 13, p. 14. ISSN: 1471-2229. URL: http://dx.doi.org/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". eng. In: *ONCOTARGET* 7.18, pp. 25241–25250. ISSN: 1949-2553. URL: http://dx.doi.org/10.18632/oncotarget.8308.

Van Bel, Michiel et al. (2013). "TRAPID: an efficient online tool for the functional and comparative analysis of de novo RNA-Seq transcriptomes". eng. In: *GENOME BIOLOGY* 14.12, p. 10. ISSN: 1465-6906. URL: http://dx.doi.org/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". eng. In: *FORENSIC SCIENCE INTERNATIONAL-GENETICS* 19, pp. 243–249. ISSN: 1872-4973. URL: http://dx.doi.org/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®-application”. eng. In: *FORENSIC SCIENCE INTERNATIONAL-GENETICS* 15, pp. 2–7. ISSN: 1872-4973. URL: http://dx.doi.org/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”. eng. In: *CELLULAR ONCOLOGY* 40.3, pp. 293–297. ISSN: 2211-3428. URL: http://dx.doi.org/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”. eng. In: *FORENSIC SCIENCE INTERNATIONAL-GENETICS* 20, e1–e3. ISSN: 1872-4973. URL: http://dx.doi.org/10.1016/j.fsigen.2015.09.006.

Van Neste, Christophe, Filip Van Nieuwerburgh, et al. (2012). “Forensic STR analysis using massive parallel sequencing”. eng. In: *FORENSIC SCIENCE INTERNATIONAL-GENETICS* 6.6, pp. 810–818. ISSN: 1872-4973. URL: http://dx.doi.org/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”. eng. In: *FORENSIC SCIENCE INTERNATIONAL-GENETICS* 9, pp. 1–8. ISSN: 1872-4973. URL: http://dx.doi.org/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”. eng. In: *SCIENCE & JUSTICE* 54.5, pp. 369–372. ISSN: 1355-0306. URL: http://dx.doi.org/10.1016/j.scijus.2014.05.009.

Vossaert, Liesbeth et al. (2013). “Reference loci for RT-qPCR analysis of differentiating human embryonic stem cells”. eng. In: *BMC MOLECULAR BIOLOGY* 14, p. 7. ISSN: 1471-2199. URL: http://dx.doi.org/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”. eng. In: *FORENSIC SCIENCE INTERNATIONAL-GENETICS* 26, E14–E16. ISSN: 1872-4973. URL: http://dx.doi.org/10.1016/j.fsigen.2016.10.020.

Willems, Sander, Maarten Dhaenens, et al. (2017). “Flagging false positives following untargeted LCMS characterization of histone PTM combinations”. eng. In: *JOURNAL OF PROTEOME RESEARCH* 16.2, pp. 655–664. ISSN: 1535-3893. URL: http://dx.doi.org/10.1021/acs.jproteome.6b00724.

Conferences/proceedings

Claeys, Shana et al. (2017). “The HBP1 tumour suppressor is a negative epigenetic regulator of MYCN-driven neuroblastoma through interaction with the PRC2 complex: poster & abstract.” In: Leuven, Belgium,

Lambertz, Irina et al. (2016). “Sensing mutant ALK: Capicua and ETV5 as executors of aberrant ALK-driven MAPK signaling”. eng. In: *Advances in Neuroblastoma Research, Congress abstracts*. Cairns, QLD, Australia.

Mus, Liselot et al. (2017a). “The ETV5 oncogene is a target of activated ALK signaling in neuroblastoma”. eng. In: *f-Tales, Abstracts*. Leuven, Belgium.

– (2017b). “The ETV5 oncogene is a target of activated ALK signaling in neuroblastoma”. eng. In: *OncoPoint, 5th Research seminar, Abstracts*. Ghent, Belgium.

– (2017c). “The ETV5 oncogene is a target of activated ALK signaling in neuroblastoma”. eng. In: *Research Day Faculties of Medicine and Health Sciences, and Pharmaceutical Sciences, Abstracts*. Ghent, Belgium.

Stewart, Grant et al. (2015). “Effect of sunitinib treatment on mutations and methylation in metastatic renal cancer”. eng. In: *JOURNAL OF CLINICAL ONCOLOGY*. Vol. 33. 7, suppl. Orlando, FL, USA.