Mathias VANDENBOGAERT

Life Sciences Bio-Informatics – Scientific Data A.I. Analyst

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EXPERIENCE

- Bio-informatics Scientist
  BioLizard N.V. 📅 2023 – present 📍 Ghent, Belgium.
  Bioinformatics Scientist & Technology Consultant as part of a data science consultancy company, involved in computational bulk and single-cell RNA, (meta-) genomics and proteomics data analyses.
- Bio-informatics Scientist
  Institut Curie 📅 2020 – 2023 📍 Paris, France
  Translational Immunotherapy Research. Integrative Functional Genomics of Cancer. Single-cell *scRNA-seq* & *scATAC-seq* data analysis. Proteomics: *immuno-peptidomics* mass-spectrometry data analysis.
- Bio-informatics Analyst
  Institut Pasteur 📅 2012 – 2020 📍 Paris, France.
  Pôle de Génotypage des Pathogènes (PGP) – Cellule d'Intervention de Biologie d'Urgence (CIBU) ; Unité de Recherche et Expertise « Environnement et Risques Infectieux » (URE-ERI). Microbial *meta-genomics* NGS data analysis.
- Bio-informatics Analyst
  Institut Pasteur 📅 2006 –2012 📍 Paris, France.
  Unité de Biologie Systémique – Proteomics: Analysis of LC-MS/MS high-throughput data; Genomics: DNA-chip data analysis.
- Post-doc Computational Biology ,
  Ecole Normale Supérieure 📅 2005 –2006 📍 Paris, France
  Dynamics and Organization of Genomes -- Center for Computational Biology: Comparative Genomics to Identify Gene Transcription Regulation.
- Post-doc Computational Biology
  University Basel 📅 2004 –2005 📍 Basel, Schweiz.
  Computational Systems Biology -- Biozentrum & Swiss Institute of Bioinformatics: Identification of Genome-Wide Functional Regulatory Networks.

EDUCATION

- Ph.D. Computational Biology 📅 2000 - 2004
  Laboratoire bordelais de Recherche en Informatique (LABRI, Université de Bordeaux I, France), and *Institut National de Recherche en Informatique et Automatique* (I.N.R.I.A. Rocquencourt, France).
- M.Sc. Computer Science for Biology 📅 2000
  Institut Pasteur, Paris, France.
- M.Sc. Biochemistry, 📅 2000
  Laboratory of "Protein Biochemistry and Protein Engineering"
  University Ghent, Belgium.
- B.Sc., Biology 📅 1997
  University Ghent, Belgium.

ACADEMIC & INDUSTRY EXPERTISE

Linux/Unix High-Performance Computing (HPC) & Data analysis & visualization

- Environments: Linux RedHat (CentOS), Unix FreeBSD 10.3/11.x, SunOS/OpenIndiana b151a9+.
- Programming languages: C, C++, Bash, Java, Perl, Python, Awk, R, GPU parallel programming with C/CUDA, OpenMPI.
- Cluster Management tools: PBS/SGE/Slurm, Pvfs2, Google cloud.
- Containers & Virtualization: Docker, Singularity.
- Software Design and development: Eclipse – Cvs, Svn, Git – MySql DB – Jupyter – Snakemake / NextFlow (from scratch & Nf-Core)

Single-cell data analysis, 10X Genomics.

- scRNA-seq: Seurat, Scanpy, Scirpy
- scATAC-seq: ArchR, Signac
- single-cell lineage tracing: monocle, Slingshot

High-throughput data analysis

- Meta-genomics: Illumina, Ion Torrent Proton, Oxford Nanopore – workflow & pipeline development to production-level instances.
- Bulk RNA-seq data analysis: R universe & python 3.12 – bio-statistics for client-intimate consultancy commitments.

Proteomics / mass-spectrometry data analysis

- DB Search engines: Mascot, Comet, MGSF+, MaxQuant Nf-core

Multi-omics data analysis

- 10X genomics: scRNA-seq / scATAC-seq
- Smart-seq2

A.I. Scientific data analysis:

- Large Language Models (LLM): Nucleotide Transformer (NT), DNABERT-2/S, HyenaDNA.

MOST SIGNIFICANT PUBLICATIONS IN THE LAST 5 YEARS

Hamy, Anne-Sophie, Judith Abécassis, Keltouma Driouch, Lauren Darrigues, Mathias Vandenbogaert, Cecile Laurent, Francois Zaccarini, et al. "Evolution of Synchronous Female Bilateral Breast Cancers and Response to Treatment." Nature Medicine 29, no. 3 (2023): 646–655. https://www.nature.com/articles/s41591-023-02216-8.

Balière, Charlotte, Elodie Calvez, Jean-Michel Thiberge, Somphavanh Somlor, Mathias Vandenbogaert, Marc Grandadam, and Valérie Caro. "A Six Years (2010–2016) Longitudinal Survey of the Four Serotypes of Dengue Viruses in Lao PDR." Microorganisms 11, no. 2 (January 18, 2023): 243. https://www.mdpi.com/2076-2607/11/2/243.

Vandenbogaert M, Kwasiborski A, Gonofio E, Descorps-Declère S, Selekon B, Nkili Meyong AA, Ouilibona RS, Gessain A, Manuguerra JC, Caro V, Nakoune E, Berthet N. Nanopore sequencing of a monkeypox virus strain isolated from a pustular lesion in the Central African Republic. Sci Rep. 2022 Jun 24;12(1):10768. doi: 10.1038/s41598-022-15073-1. PMID: 35750759; PMCID: PMC9232561.

Virginie Sauvage, Johanna Gomez, Laure Boizeau, Mathias Vandenbogaert, Léa Barbier, Claude Tayou Tagny, Aimée Olivat Rakoto Alson, Pascal Bizimana, Sekou Oumar Coulibaly, Mohamed Abdallahi Boullahi, Hadiza Soumana, Guy Mbensa, Valérie Caro, Syria Laperche. New insights into Human Pegivirus-1 (HPgV-1) genotypes diversity in sub-Saharan Africa. Infection, Genetics and Evolution, Volume 94, p. 104995, Oct 2021.

Ian Nunes Valença, Rafael dos Santos Bezerra, Kamila Chagas Peronni, Virginie Sauvage, Mathias Vandenbogaert, Valérie Caro, Wilson Araújo da Silva Junior, Dimas Tadeu Covas, Ana Cristina Silva-Pinto, Syria Laperche, Simone Kashima, Svetoslav Nanev Slavov. Deep sequencing applied to the analysis of viromes in patients with beta-thalassemia. Revista do Instituto de Medicina Tropical de São Paulo (vol. 63), May 2021.

Sauvage V, Boizeau L, Candotti D, Vandenbogaert M, Servant-Delmas A, Caro V, Laperche S. Early MinION™ nanopore single-molecule sequencing technology enables the characterization of hepatitis B virus genetic complexity in clinical samples. PLoS One. 2018 Mar 22;13(3):e0194366. doi: 10.1371/journal.pone.0194366. eCollection 2018.