Stephane Wenric, PhD

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Professional Experience

Senior Computational Systems Biologist April 2021 to Present
Tempus Labs

I led several R&D projects making use of Tempus' large-scale genomics, transcriptomics, and clinical database. I also collaborated with biotechnology and pharmaceutical companies to help them leverage Tempus' data in the context of their own R&D projects. I managed two direct reports.

Computation Oncology Scientist August 2019 to April 2021
Tempus Labs

I contributed to several R&D projects spanning multiple cancer types and data modalities (genomics, transcriptomics) making use of advanced machine learning techniques. I mostly used Python, R, SQL.

Postdoctoral Fellow September 2017 to August 2019
Icahn School of Medicine at Mount Sinai
Advisor: Dr. Eimear Kenny

I contributed to several high-impact research projects making use of Mount Sinai's patients biobank. I presented results at international conferences, took part in grants writing, and mentored a number of students and junior members in the lab.
I used mixed linear models to perform GWAS on ancestrally diverse populations, I performed network analysis on large-scale identity-by-descent data for ancestry estimation and I contributed to various analytical pipelines.
I worked both with genotyping and exome data, and addressed biomedical questions related to pharmacogenomics, genetic ancestry, CNVs.

Research Fellow July 2013 to August 2017
GIGA-Research, Unit of Human Genetics, University of Liege
Advisors: Prof. Vincent Bours and Prof. Guy Jerusalem

Co-supervised by the head of the department of medical oncology and the director of the department of genetics, I leveraged the integration of sequencing and biological data coming from various sources (exome, RNA-seq, miRNA expression, CGH) to tackle specific technical, biological, and clinical problems related to human cancer. To accomplish this, I employed several machine learning, data mining, and software engineering techniques.
I designed a non-invasive breast cancer diagnostic tool based on circulating microRNAs and machine learning, I studied the global disruption of antisense long non-coding RNAs in breast cancer, using stranded RNA-Seq and novel gene prioritization methods, and I demonstrated the use of pooled samples as virtual reference to detect somatic CNVs in multiple myeloma patients using exome data.

Research Engineer April 2012 to June 2013
GIGA-Research, Unit of Human Genetics, University of Liege & University Hospital

I set up the software environment for next-generation sequencing data analysis at the university hospital genetic diagnostic center. I worked with micro-array data (CGH

& SNP, case-control and family-based studies). I worked with exome sequencing data (mapping, variants calling and annotation), mainly for family-based cases.

Bioinformatician Nov 2010 to April 2012
DNAVision

I worked on the design and development of various bioinformatics pipelines (QC, assembly, metagenomics, mapping, annotation, variants calling) related to next-generation sequencing (Roche 454, Illumina HiSeq 2000, SOLiD 4).
I contributed to the design and development of significant IT projects (integration of analysis pipelines with the in-house LIMS, development of a cross-platform archiving system, development of an automatic report creation system).

Education

University of Liege, Belgium

Ph.D., Biomedical Sciences, 2017

- Thesis Topic: *Bioinformatics contribution to the analysis of omics data in the clinical, technical, and molecular domains of human cancer.*
- Advisors: Prof. Vincent Bours and Prof. Guy Jerusalem

Master, Biomedical Engineering, 2010

- Topic: *Completion of the OMIM network using machine learning techniques.*
- Advisors: Prof. Pierre Geurts and Prof. Louis Wehenkel
- *Cum Laude*

Bachelor, Engineering, 2007

- Major: *Computer Science*, Minor: *Biomedical Engineering*

Peer-reviewed Journal Publications as first author

1. **Rapid response to the alpha-1 adrenergic agent phenylephrine in the perioperative period is impacted by genomics and ancestry.**
   The Pharmacogenomics Journal. 2020
2. **Using supervised learning methods for gene selection in RNA-Seq case-control studies.**
   Frontiers in Genetics. 2018
3. **Transcriptome wide analysis of natural antisense transcripts shows their potential role in breast cancer.**
   Scientific Reports. 2017
4. **Exome Copy Number Variation detection: use of a pool of unrelated healthy tissue as reference sample.**
   Genetic Epidemiology. 2016
5. **Circulating microRNA-based screening tool for breast cancer.**
   Oncotarget. 2015

Peer-reviewed Journal Publications as co-author

1. **Toward a fine-scale population health monitoring system.**
   Cell. 2021
2. **EPS: Automated Feature Selection in Case-Control Studies using Extreme Pseudo-Sampling.**
   Bioinformatics. 2021

3. **VPS51 biallelic variants cause microcephaly with brain malformations: A confirmatory report.**
   European Journal of Medical Genetics. 2019

4. **Variations of circulating biomarkers during and after anthracycline-containing chemotherapy in breast cancer patients.**
   BMC Cancer. 2018

5. **Genomic Studies of Multiple Myeloma Reveal an Association between X Chromosome Alterations and Genomic Profile Complexity.**
   Genes, Chromosomes and Cancer. 2016

6. **Evaluation of BRCA1-related molecular features and microRNAs as prognostic factors for triple negative breast cancers.**
   BMC Cancer. 2015

Patents

1. European patent: EP2942399. **Method for the diagnosis of breast cancer**. 2015

2. International patent: WO2016150475. **Circulating microRNAs for the diagnosis of breast cancer**. 2015

Poster presentations

1.	Human Genetics in NYC Conference	2019
2.	American Society of Human Genetics Annual Meeting (ASHG)	2018
3.	Human Genetics in NYC Conference	2018
4.	American Society of Human Genetics Annual Meeting (ASHG)	2017
5.	European Conference of Human Genetics (ESHG)	2017
6.	GIGA Cancer	2015
7.	Belgian Medical Genomics Initiative	2014
8.	BeNeLux Bioinformatics Conference	2013
9.	Belgian Society of Human Genetics	2013

Awards and grants

1.	WBI.World Fellowship	2017-2019
2.	B.A.E.F. Henri Benedictus Fellowship	2017-2018
3.	Fonds Leon Frederic Travel Award	2017-2018
4.	F.R.S.-FNRS research fellow scholarship	2013-2017

Academic activities

1. American Society of Human Genetics — Member (2017-2019)
   (a) Platform session — Chair (2018)
   (b) DNA Day Essay contest — Judge (2018)
2. CREE Data Science Summer School for Computation Genomics
   (a) Teaching activity — (2018)
3. Frontiers in Genetics
   (a) Reviewer — (2019)

Languages

- English — Full professional proficiency
- French — Native speaker
- Dutch — Professional proficiency
- German, Hebrew, Spanish — Elementary proficiency

Technical Skills

- **Programming & markup languages**: Python, R, Perl, Bash, PHP, node.js, jQuery & javascript, XML, HTML/CSS, LaTeX
- **Bioinformatics API**: Ensembl, OMIM, TCGA, GEO
- **Databases**: MySQL, Redshift, MongoDB
- **High performance computing**: Unix environment, Slurm, SGE, Torque
- **Version control**: Git, SVN
- **Misc**: Machine learning, statistics