STEPHANE WENRIC, Ph.D.

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SUMMARY

Experienced computational biologist and team lead with a strong scientific and technical background including expertise in genomics/transcriptomics, clinical data analysis, machine learning, statistics and software engineering & devops methodologies.

WORK EXPERIENCE

Tempus Labs

Principal Scientist - Computational Systems Biology — *March 2022 – Present*

Led the implementation of an externally licensed **RNASeq based subtyping algorithm** for pancreatic cancer (PurIST) on the Tempus platform, including technical transfer, **retrospective clinical validation study using RWE data**, manuscript and regulatory submissions, leading to a **new commercially available test for patients** (first and only test available for pancreatic cancer) and the **first PLA code granted by the American Medical Association for an algorithm-only analysis**. Led **collaborations with biotech and pharma** companies (subtyping based trial enrollment, RWE). Managed three direct reports.

Senior Computational Systems Biologist — *April 2021 – March 2022*

Led several R&D projects (prognostic and therapy response models) making use of Tempus' large-scale molecular (**RNASeq**, **DNA**) and clinical database. **Collaborated with biotech/pharma companies** to help them leverage Tempus' data in the context of their own R&D projects. Managed two direct reports.

Computational Oncology Scientist — *August 2019 – April 2021*

Led **R&D projects spanning multiple cancer types and data modalities** (**genomics**, **transcriptomics**) making use of advanced **machine learning** techniques, focusing on applying machine learning to improve subtyping and prognostic models in cancer. I mostly used **Python**, **R**, and **SQL**.

Icahn School of Medicine at Mount Sinai

Postdoctoral Research Fellow — *September 2017 – August 2019*

Contributed to several **high-impact research projects** making use of Mount Sinai's biobank, presented results at international conferences, took part in grants writing, and mentored students and junior lab members. Used **mixed linear model-based association tests** on ancestrally diverse populations, performed **network analysis** on large-scale identity-by-descent data for ancestry estimation, and contributed to various analytical pipelines. Worked with **genotyping**, **exome**, and **EHR** data, and addressed biomedical questions related to **pharmacogenomics**, **genetic ancestry**, and **CNVs**.

University of Liege

Research Fellow - GIGA-Research, Unit of Human Genetics — *July 2013 – August 2017*

Co-supervised by the head of the department of medical oncology and the director of the department of genetics, 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. Employed several **machine learning**, data mining, and **software engineering** techniques. Designed a non-invasive **breast cancer diagnostic** tool based on **circulating microRNAs** and machine learning. Studied the global disruption of **antisense long non-coding RNAs in breast cancer**, using stranded RNA-Seq and novel **gene prioritization** methods. Demonstrated the use of pooled samples as virtual reference to detect **somatic CNVs in multiple myeloma** patients using exome data.

Research Engineer - GIGA-Research, Unit of Human Genetics *April 2012 – June 2013*

Set up the software environment for **next-generation sequencing data analysis** at the university hospital genetic diagnostic center. Worked with **microarray** data (CGH & SNP, case-control and family-based studies) and **exome** sequencing data (mapping, variants calling and annotation), mainly for family-based cases.

DNAVision

Bioinformatician *November 2010 – April 2012*

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). Design and development of multiple IT projects (**integration of analysis pipelines with in-house LIMS**, development of a cross-platform archiving system, development of an automatic report creation system).

EDUCATION

University of Liege

Ph.D., Biomedical Sciences (cancer genomics) *2017*

Thesis: 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

SELECTED PUBLICATIONS

Real-world data validation of the PurIST pancreatic ductal adenocarcinoma gene expression classifier and its prognostic implications. **medRxiv**. 2023.

Toward a fine-scale population health monitoring system. **Cell**. 2021

Rapid response to the alpha-1 adrenergic agent phenylephrine in the perioperative period is impacted by genomics and ancestry. **The Pharmacogenomics journal**. 2020

Using Supervised Learning Methods for Gene Selection in RNA-Seq Case-Control Studies. **Frontiers in Genetics**. 2018

Transcriptome-wide analysis of natural antisense transcripts shows their potential role in breast cancer. **Scientific Reports**. 2017

Circulating microRNA-based screening tool for breast cancer. **Oncotarget**. 2015

SKILLS

Bioinformatics - Computational Biology - Machine Learning - Data Science - RNASeq - Cancer Genomics - Systems Biology - R - Python - Statistical Analysis - Algorithms - DNA - RNA - Transcriptomics - Population Genetics - Statistical Genetics - GWAS - Pharmacogenomics - SQL - Bash - Unix - Devops - EHR - RWE - RWD - Survival Analysis - Statistics - Oncology - AI