AHMED DEBIT, Ph.D.

Senior Bioinformatician

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SUMMARY

Skilled computational biologist with a strong scientific and technical background, including experience in genomics/transcriptomics, data analysis, statistics, and machine learning.

WORK EXPERIENCE

Institut de Biologie ENS (IBENS), Paris, France 11/2020 - 12/2025

Postdoctoral Research Fellow

- Developed bioinformatics pipelines for RNA-seq data analysis, covering genomics and transcriptomics.
- Analyzed large-scale marine datasets such as MMETSP, Tara Oceans, and Phaeoexplorer.
- Developed a novel machine learning tool for lncRNA prediction in marine microbial species; this tool helped increase the reliability of long non-coding RNA (lncRNA) identification (https://gitlab.com/a.debit/votinglnc).
- Integrated RNA-seq and imaging satellite data.
- Implemented a SQL database containing approximately 2 million lncRNAs from 414 marine micro-organism species. This database is publicly accessible at (www.lncplankton.bio.ens.psl.eu).
- Collaborated with both national (Station Biologique de Roscoff, France) and international laboratories (Department of Bioscience, Kwansei Gakuin University, Japan).
- Presented results at international conferences, submitted manuscripts, and participated in grant writing.
- Mostly used R, Bash, Python, and SQL.
- Mostly worked on Linux, using HPC clusters (SLURM and HT-Condor), and source code tracking (GitLab).

Laboratory of Human Genetics (GIGA-Research), Liège, Belgium 02/2017 - 03/2020

Research Fellow

- Developed generic bioinformatics pipelines for RNA-seq data analysis generated using various library preparation kits, including Ovation SOLO, CATS Diagenode, BGI, and Illumina.
- Implemented a novel feature selection method (https://gitlab.com/a.debit/stabfs) to identify the most important and robust biotypes from large datasets.
- Implemented an optimized machine learning pipeline aimed at identifying short molecular biomarker signatures for cancer screening.
- Designed a circulating miRNA-based short biomarker signature for Breast Cancer (BC) screening in the Rwandan population (with an AUC = 0.86 on an independent cohort). This signature can serve as an alternative to mammography in clinics.
- Integrated bulk RNA-seq, circulating miRNA (RT-qPCR), and metabolite data to design an integrated signature for breast cancer screening in Belgian women.
- Designed a novel performance metric to measure the intrinsic stability of Random Forest methods using TCGA-Cancer datasets.
- Collaborated with an industrial partner (Diagenode, Liege) and an international laboratory (Hospital of Kigali, Rwanda).
- Primarily used R, Bash, and Python; worked on Linux and HPC clusters (SLURM) and managed source code with GitLab.

BIO3-Medical Genomics Unit (GIGA-Research), Liège, Belgium 11/2015 - 01/2017

Research Fellow

- Compared methods for RNA-seq normalization and correction of batch effects.
- Utilized co-expression networks and information flow methodologies as components of a comprehensive pipeline for the investigation of gene-gene interactions.
- Participated in national and international workshops on DNA-seq and RNA-seq bioinformatics data analysis.

EDUCATION

University of Liège, Belgium

10/2020

Ph.D., Bioinformatics (Cancer genomics and Machine learning)

University of Liège, Belgium

06/2015

Master, Bioinformatics

University of Tizi-Ouzou, Algeria

07/2008

Engineer, Computer Science

SELECTED PUBLICATIONS

Debit, A., Vincens, P., Bowler, C., & Cruz de Carvalho, H. (2025). LncPlankton: a comprehensive database of candidate lncRNAs from marine microbial eukaryotes. NAR Genomics and Bioinformatics, 7(4), lqaf159.

Debit, A., Poulet, C., Josse, C., Jerusalem, G., Azencott, C. A., Bours, V., & Van Steen, K. (2025). Assessing Random Forest self-reproducibility for optimal short biomarker signature discovery. Briefings in Bioinformatics, 26(4), bbaf318.

Denoeud, F., Godfroy, O., Cruaud, C., Heesch, S., Nehr, Z., Tadrent, N., …, Debit, A., …, & Cock, J. M. (2024). Evolutionary genomics of the emergence of brown algae as key components of coastal ecosystems. Cell, 187(24), 6943-6965.

Debit, A., Charton, F., Pierre-Elies, P., Bowler, C., & Cruz de Carvalho, H. (2023). Differential expression patterns of long noncoding RNAs in a pleiomorphic diatom and relation to hyposalinity. Scientific Reports, 13(1), 2440.

Uyisenga, J. P., Debit, A., Poulet, C., Freres, P., Poncin, A., Thiry, J., … & Josse, C. (2021). Differences in plasma microRNA content impair microRNA-based signature for breast cancer diagnosis in cohorts recruited from heterogeneous environmental sites. Scientific Reports, 11(1), 11698.

Onesti, C.E., Boemer, F., Josse, C., Debit, A., Poulet, C., Bours, V. and Jerusalem, G., (2021). Abstract PS17-01: A metabolomic signature as screening method for breast cancer diagnosis. Cancer Research, 81(4_Supplement), pp.PS17-01.

Uyisenga, J.P., Butera, Y., Debit, A., Josse, C., Ainhoa, C.C., Karinganire, E., Cyuzuzo, A.P., Umurungi, N., Kalinijabo, Y., Uwimana, S. and Mutesa, L., (2020). Prevalence of histological characteristics of breast cancer in Rwanda in relation to age and tumor stages. Hormones and Cancer, 11(5), pp.240-249.

Cataldo, D.D., Sepult, C., Vanwinge, C., Gillard, A., Duysinx, B., Maquoi, E., Poulet, C., Debit, A., Noel, A. and Bellefroid, M., (2020). Role of ADAM8 Protease in Malignant Pleural Mesothelioma Chemoresistance. In B71. PROGRESS IN MALIGNANT PLEURAL DISEASE (pp. A4206-A4206). American Thoracic Society.

Debit, A., 2019, October. Towards an accurate cancer diagnosis modelization: Comparison of Random Forest strategies. In IGES 28th Annual Meeting, October 12-14, 2019, Houston, TX, USA.

SOFTWARE AND TOOLS

Aurore,B., Thomas,D., Fabien,D., Olivier,G., Sandrine,L., Mark,C., Ahmed,D. and Helena,C. de C. (2025) SCANS: Assessing lncRNA conservation across species. In JOBIM2025_proceedings.

Debit, A. and de Carvalho,H.C. (2025) votingLNC: Identification of Long non-coding RNAs through majority voting ensemble learning. 10.6084/M9.FIGSHARE.24799632.V4.

Debit, A., & Poulet, C. (2023). Stable feature selection using random forest and stability measures. (Version 2). figshare. https://doi.org/10.6084/m9.figshare.24878646.v2

SKILLS

Hard Skills: R Programming (Advanced), Machine learning (Experienced), Statistical modeling (Experienced), Bash scripting (Experienced), Git (Experienced), HPC (Experienced).
Techniques: Predictive modeling, Data visualization, Tool development, Database (MySQL), Web development.
Bioinformatics databases: Ensembl, TCGA, GenePattern, NR-NT, RefSeq, Pfam, UniProt, UniRef.