Ahmed DEBIT, M.Sc./Ir

CONTACT INFORMATION

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EDUCATION

GIGA-University of Liege, Belgium

Ph.D. Thesis under preparation, GIGA-R / Faculty of Applied Sciences Uliege, Thesis defense expected April 2020

- Tentative Thesis Title: *Bioinformatics and Genomic Data Analysis for Personalized Medicine*
- Advisors: Prof. Vincent Bours and Prof. Kristel Van Steen

M.Sc., Bioinformatics and Modelling, June 2015

- Topic: *Machine Learning Based Tool for Automatic Quantification and Classification of Rare Objects in Histological Whole-slide Images*
- Advisors: Prof. Pierre Geurts and Raphaël Marée Ph.D
- Project website: http://www.student.montefiore.ulg.ac.be/ debit/project/

University of Tizi-Ouzou, Algeria

Computer Science Engineering, June, 2008

- Topic: *The design and Implementation of Multi-function Net Platform*

PROFESSIONAL EXPERIENCE

Research Fellow March 2017 to Present

GIGA-Research, Unit of Human Genetics, University of Liege
GIGA-Research, BIO3 Unit, University of Liege
Advisors: Prof. Vincent Bours and Prof. Kristel Van Steen

I worked mainly on Machine Learning ML and NGS data analysis. I contributed to the design of an optimized ML pipeline for short molecular signature discovery in the domain of human cancer. I applied the pipeline to identify best short signature(s) on different datasets (RNA-seq, miRNA expression, and metabolites) in the context of Breast Cancer BC. Those signatures are then used for BC screening and to predict a response to Neoadjuvant Chemotherapy NAC treatment in BC.
I was involved in many projects. I designed a flexible RNA-seq analysis pipeline including steps: QC and cleaning, mapping, QC mapping, UMI deduplication, summarization and vizualization.
I worked with RNA-seq data generated using different library kits: Ovation SOLO, CATS diagenode, and Illumina.

Research Fellow (part-time) November 2015 to February 2017

GIGA-Research, BIO3 Unit, University of Liege
Advisor: Prof. Kristel Van Steen

Under the supervision of the head of BIO3-Medical Genomics Unit Prof. Kristel Van Steen, my task was to use part of prior biological knowledge RNA-seq as a guidance of the gene x gene interaction analysis. I designed a pipeline for DE analysis containing different normalization methods for RNA-seq. Biological in-

sight can be gained by looking for patterns of expression changes within sets of genes. A co-expression network analysis has been inferred on basis of diferentially expressed genes using WGCNA method, and module information was then integrated as part of gene x gene interaction pipeline

System Administration June 2009 to September 2010

Directorate of Transmission, Algeria

I've been recruited as part of a project to computerize different administrative tasks like passport and national identity card. My tasks were mainly managing of the local network and databases, and writing technical reports for monitoring the process.

Other projects

Novel long intergenic non-coding RNAs discovery in mouse

I worked on a project in collaboration with the Laboratory of Tumors and Development Biology (LBTD-GIGA Cancer). The project aimed to identify three classes of novel long intergenic noncoding RNAs that are differentially expressed between cell types. I got stranded RNA-seq reads, and I performed all bioinformatics analysis of sequencing data including the reference-guided genome assembly and the prediction of novel lincRNAs.

Rank aggregated methods for Differential Expression DE analysis

The aim of the project was to enhance the accuracy and the stability of differential expression discovery by using an aggregated method. All DE methods mostly used in the literature for RNA-seq data have been included. Tests have been performed on 5 RNA-seq datasets of different settings, and the results are collected and analyzed.

Impact of RNA-seq normalization methods on the stability/performance of gene selection methods

In this project, I studied the impact of different RNA-seq normalization methods on the stability and the performance of gene selection methods. I demonstrated that statistical tests commonly used for differential expression like GLM-LRT test are less sensitive to normalization methods than random forest based feature selection.

Submitted Journal Publications as First Authors

1. **Assessing Random Forest Self Reproducibility and Self Stability for Optimal Short Biomaker Signature Discovery.** PNAS, "in press"
2. **Exploring and Evaluating the Reproducibility of Gene Selectors for RNA-seq Data.** BMC Bioinformatics, "in press"

Submitted Journal Publications as Co-Authors

1. **Molecular Characteristics of Breast Cancer in Rwanda in Relation to Age and Tumor Stages.** International Journal of Clinical Oncology IJCO, "in press"

Conferences, Workshops and Talks

Talks:

- *On the Reproducibility of Random Forest Techniques for Cancer Screening* International Genetic Epidemiology Society IGES, 28th Annual Meeting, Houston TX, USA, October 2019.
- *Biomarker Signatures Discovery to Support Cancer Diagnosis: Towards an Accurate and Robust Machine Learning Strategy* SAB Medical-Genomics, Liege, Belgium, February 5, 2019.
- *Algorithm Optimization for Diagnostic/Prognostic Signature Discovery in the Context of Breast Cancer* GIGA Cancer 2018, Liege, Belgium, November 30, 2018.
- *Towards an Accurate Cancer Diagnosis Modelization: Comparison of Random Forest Strategies* byteMal 2018, Liege, Belgium, October 5, 2018.

Poster Presentations:

- 19th BeSHG meeting Precision Medicine: Application of Genetics in Prevention and Treatment, Liege, March 2019
- byteMal Meeting, Liege, October 2018
- Joint meeting GIGA-Cancer Day 2018/EDT Cancerology, Liege, September 2018
- European Society of Human Genetics (ESHG 2017), Copenhagen, May 2017

Workshops

- Elixir-IIB Carpentry Software, University of Milano Bicocca, February 22-23, 2018
- Open Multiscale Systems Medicine (OpenMultiMed) COST Action CA15120, MC Meeting Porto, Portugal, 20-23 February 2017
- Multi-Omic Integrative Analysis of Gene Expression (MIAGE), CIPF Valencia (Spain), 23-27 January 2017
- WG2 COST Training Workshop on Interactions in Complex Disease Analysis, Antwerp, 27-28-29 April 2016
- NGS Data Analysis: Variant calling and RNA-Seq, 4 Days Workshop VIB Leuven (08/01, 15/01, 22/02, 26/02) 2016

Awards And Grants

1. FNRS Travel Grant 2017
2. COST Action OpenMultiMed Grant, CA15120 2017
3. COST Action Statictical Interactions/Interactome Grant, BM1204 2016

Memberships

- European/American Society of Human Genetics ESHG/ASHG
- Belgian Society of Human Genetics BeSHG
- International Genetic Epidemiology Society IGES
- European Cooperation in Science and Technology COST

Technical Skills

- **Programming & markup languages:** R, R Shiny, Bash, Python, Java, SQL, PHP, XML, HTML/CSS, LaTeX
- **Bioinformatics API:** Ensembl, TCGA, GenePattern, BIOJAVA
- **Frameworks:** Maven, Hibernate, Spring
- **Databases:** MySQL, SQLite
- **High performance computing**: Unix environment, HPC Cluster, Slurm, Parallel computing
- **Version control**: GitLab, sourceTree

Languages

- English — Professional proficiency
- French — Fluent
- Arabic — Fluent
- Kabylian — Native speaker

References

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Chloe-Agathe Azencott, PhD

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