

Emmanuel Noutahi

PH.D. CANDIDATE IN BIOINFORMATICS · UNIVERSITÉ DE MONTRÉAL

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Research Interest

Genome Evolution - Comparative Genomics - Computational Phylogenetics - Sequence Analysis - Machine Learning - Structural Bioinformatics

Education

Ph.D. in Bioinformatics

UNIVERSITÉ DE MONTRÉAL (UDEM)

Montréal, Qc

Since 2014

Advisor : Dr Nadia El-Mabrouk

Title : Méthodes et algorithmes pour l'amélioration de l'inférence des gènes orthologues

Expected thesis defense date : Summer 2018

Certificate in Machine Learning

COURSERA

Montréal, Qc

2013

Online course by Andrew Ng

B.S. in Bioinformatics

UNIVERSITÉ DE MONTRÉAL (UDEM)

Montréal, Qc

2011 - 2014

Graduated on the dean's honors list

Teaching experience

IFT1065 - Discrete Mathematics for Computer Science

TEACHING ASSISTANT

Université de Montréal

Winter 2015, 2016, 2017

Introduction to writing proofs, Combinatorics, Graphs, Analysis of algorithm complexity, etc

BCM 2002 - Molecular Biology and Bioinformatics

TEACHING ASSISTANT

Université de Montréal

Fall 2014, 2016, 2017

Introduction to linux and biological databases, Sequencing, Genome assembly and annotation, RNA secondary structure prediction.

IFT 3295 - Algorithms in Bioinformatics

TEACHING ASSISTANT

Université de Montréal

Fall 2015, 2016, 2017

Dynamic programming in Bioinformatics (sequence alignment, motif searching, etc), Pattern matching, Methods and algorithms for phylogenetic inference, Genome rearrangements, LCA reconciliation, etc

Work experience

Research assistant

LABORATOIRE DE BIOLOGIE INFORMATIQUE ET THÉORIQUE (LBIT) - UDEM

Montréal, Qc

Jan-Aug 2014

Supervisor : Prof. Nadia El-Mabrouk

Development of **profileNJ**, a new method for gene tree correction, using information from both species evolution and sequence alignment.

Research Intern

LABORATOIRE ZENKLUSEN, DÉPARTEMENT DE BIOCHIMIE - UDEM

Montréal, Qc

May-Dec 2013

Supervisors : Sandra-Rima Imrazene & Prof. Daniel Zenklusen

Development of matlab tools for RNA quantification and localization in 2D and 3D, using data from single molecule fluorescent *in situ* hybridization.

Research Intern

CENTRE ROBERT-CEDERGREN - UDEM

Supervisors : Dr. Sandrine Moreira & Prof. Gertraud Burger

In silico modeling and validation of the 3D structure of an RNA ligase in *Diplonema papillatum*.

Montréal, Qc

May-Aug 2012

Scholarships & Awards

2014-2016	DIRO Excellence Scholarships , Département d'Informatique et de Recherche Opérationnelle - UDEM	Montréal, Qc
2015-2016	International Fee Exemptions , Faculté des Études Supérieures et Postdoctorales - UDEM	Montréal, Qc
2014-2016	FESP Scholarships for direct passage to doctorate , Faculté des Études Supérieures et Postdoctorales - UDEM	Montréal, Qc
2012-2014	FAS Dean's honor list , Faculté des arts et des sciences - UDEM	Montréal, Qc
2011-2015	Benin Excellence Scholarships , Direction des Bourses et Secours Universitaires du Bénin	Cotonou, Bénin
2011	Vallet Fondation Excellence Scholarships , Fondation Vallet France-Bénin	Cotonou, Bénin

Extracurricular activities and Social involvement

Bioinformatics Students Association of UDEM

Montréal, Qc

DOCTORAL STUDENT REPRESENTATIVE

2014 - 2016

Represent and advocate for graduate students at Faculty meetings
Participate in initiatives to improve the quality of graduate education.

VICE PRESIDENT COMMUNICATION

2016 - 2017

Organizing committee of the 1st and 2nd bio-hackathon at Université de Montréal.
Organization of networking events between students, principal investigators and bioinformatics professionals.

Conference Organizing Committee

Montréal, Qc

14TH RECOMB COMPARATIVE GENOMICS SATELLITE WORKSHOP

Oct 2016

Internship Supervision

Montréal, Qc

ANNA THIBERT

Jan-May 2018

Master student in Bioinformatics from Toulouse

KYLIAN BERREBI

Jun-Aug 2017

Engineer student in Computer Science from Toulouse

Reviewer Activity for Conferences and Journals

BMC BIOINFORMATICS

MGAG (MOLECULAR GENETICS AND GENOMICS)

RECOMB & RECOMB-CG (INTERNATIONAL CONFERENCE ON RESEARCH IN COMPUTATIONAL MOLECULAR BIOLOGY)

APBC (ASIA PACIFIC BIOINFORMATICS CONFERENCE)

GLBIO (GREAT LAKES BIOINFORMATICS CONFERENCE)

SPIRE (INTERNATIONAL SYMPOSIUM ON STRING PROCESSING AND INFORMATION RETRIEVAL)

ISMB (INTERNATIONAL CONFERENCE ON INTELLIGENT SYSTEMS FOR MOLECULAR BIOLOGY)

GIW (INTERNATIONAL CONFERENCE ON GENOME INFORMATICS)

Community Involvement

MEMBER OF THE INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY (ISCB)

Since 2018

MEMBER OF THE INTERNET SOCIETY

Since 2016

Advocating for an open internet for everyone.

REVIEWER AT ReScience

Since 2016

Peer reviewing of replications and open-source implementations of published computational research.

MEMBER OF AJEB BÉNIN

Since 2013

Promoting academic excellence in Benin.

Selected Presentations

Symposium Annuel de Physique pour un Avenir en Recherche et en Industrie (SAPHARI 2018)

Montréal, Qc

INVITED TALK

Mar 2018

Étudier l'évolution des génomes avec la bioinformatique.

16th Asia Pacific Bioinformatics Conference (APBC 2018)

Yokoyama, Japan

ACCEPTED MANUSCRIPT PRESENTATION

Jan 2018

GATC : A Genetic Algorithm for gene Tree Construction under the Duplication-Transfer-Loss model of evolution.

Noutahi E. and El-Mabrouk N.

14th RECOMB Comparative Genomics Satellite Workshop (RECOMB-CG 2016)

Montréal, Qc

POSTER PRESENTATION

Oct 2016

CoreTracker, a new sequence-based method to predict codon reassignments.

Calderon V., Noutahi E., Blanchette M., El-Mabrouk N., and Lang B.F.

POSTER PRESENTATION

Oct 2016

A simple genetic algorithm to correctly label the leaves of a reconciled gene tree.

Noutahi E., and El-Mabrouk N.

27th Annual Symposium on Combinatorial Pattern Matching (CPM 2016)

Tel Aviv, Israel

ACCEPTED MANUSCRIPT PRESENTATION

Jun 2016

Efficient non-binary gene tree resolution with weighted reconciliation cost.

Lafond M., Noutahi E., and El-Mabrouk N.

Montreal Bioinformatics User Group (MonBUG)

Montréal, Qc

CONTRIBUTED TALK

Oct 2015

Phylogenetic tree exploration and visualization made easy with ETE.

Refereed Publications

Noutahi E., & El-Mabrouk N. (2018). GATC : A Genetic Algorithm for gene Tree Construction under the Duplication-Transfer-Loss model of evolution. In *16th Asia Pacific Bioinformatics Conference (APBC 2018)*. *BMC Genomics*, 19(S2),102. doi :10.1186/s12864-018-4455-x.

Noutahi E., Calderon V., Blanchette M., Lang B.F., & El-Mabrouk N. (2017). CoreTracker : accurate codon reassignment prediction, applied to mitochondrial genomes. *Bioinformatics*, 33(21), 3331-3339.

Rahman S., Zorca C.E., Traboulsi T., Noutahi E., Krause M.R., Mader S., & Zenklusen D. (2017). Single-cell profiling reveals that eRNA accumulation at enhancer-promoter loops is not required to sustain transcription. *Nucleic acids research*, 45(6), 3017-3030.

Sabir J.S., Jansen R.K., Arasappan D., Calderon V., Noutahi E., Zheng C., Park S., Sabir M.J., Baeshen M.N., Hajrah N.H., & Khiyami M.A. (2016). The nuclear genome of *Rhazya stricta* and the evolution of alkaloid diversity in a medically relevant clade of Apocynaceae. *Scientific reports*, 6, p.33782

Noutahi E., Semeria M., Lafond M., Seguin J., Boussau B., Guéguen L., El-Mabrouk N., & Tannier E. (2016). Efficient Gene Tree Correction Guided by Genome Evolution. *PLoS ONE* 11(8) : e0159559. doi : 10.1371/journal.pone.0159559.

Lafond M., Noutahi E., & El-Mabrouk N. (2016). Efficient non-binary gene tree resolution with weighted reconciliation cost. In *27th Annual Symposium on Combinatorial Pattern Matching (CPM 2016)*, Leibniz International Proceedings in Informatics (LIPIcs), vol. 54, pp. 14 :1–14 :12. Schloss Dagstuhl-Leibniz-Zentrum fuer Informatik, Dagstuhl, Germany.

Moreira S., Noutahi E., Lamoureux G., & Burger G. (2015). Three dimensional structure model and predicted ATP interaction rewiring of a deviant RNA ligase 2. *BMC structural biology*, 15(1), 20.

Skills

COMPUTER SCIENCE

I am experienced in algorithm development and data analysis, including complex data visualisation. I am also familiar with machine learning in python and have experience in both back-end (Django, Flask) and front-end (Vue.js, D3.js Bootstrap, etc) web application development. I am passionate about open source software and try to share and actively contribute to open source projects on GitHub.

Programming & Web Proficient in : Python - Java - C - Matlab - Perl - JavaScript - HTML5 - CSS3
Familiar with : R - PHP - C#
Database MySQL - SQLite - Object-relational mapping tools
OS & Softwares Linux/Unix (shell, awk, sed, etc) - Microsoft Windows - Git - \LaTeX - Inkscape - Gimp

BIOINFORMATICS

I regularly use modern bioinformatic methods and softwares for genome assembly, annotation, molecular phylogeny, comparative genomics and structure prediction; and have an extensive knowledge about their underlying algorithms. I am also the main developer of several bioinformatic tools (some listed below) and have contributed to a few public bioinformatic projects.

GATC A genetic algorithm for gene trees construction under the DTL reconciliation framework.
CoreTracker A package for prediction of sense-to-sense codon reassignments and analysis of genetic code deviation.
ProfileNJ Fast and accurate polytomy resolution and gene tree correction under the DL reconciliation framework.
PyPhylo Automated pipeline for phylogenomic data preparation and phylogenetic trees inference.
ARNquant Quantification of RNA expression from 2D “single-molecule fluorescence *in situ* hybridization” data

LANGUAGES

French (native language) - English (good) - Fon - Yoruba