Maia Kaplan

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Present Role and Interests

Streamline Genomics: April 2019 – Present
Software Engineer (Bioinformatics). Design, implement, and iterate on both the bioinformatic analysis pipelines and biological database. Calling variants in unstable (eg. cancerous) samples requires significant available knowledge for meaningful interpretation.

Public outreach: September 2016 – Jan 2020
Leading bio-info focus groups, speaking at Montreal meetups, and organizing seminars.

Continue to explore applications of statistical methods: May 2017 – Present
Differential gene expression, noise reduction in high-throughput data, and silly AI.

Education

McGill University, Canada September 2015 – October 2017
Master of Science: Biology (Bioinformatics). *Supervisors:* T. Bureau and M. Blanchette
Graduate-level courses: Computational Biology Methods & Research, Bioinformatics Seminar, Bioinformatics: Functional Genomics, Mining Biological Sequences.

University of British Columbia, Canada September 2010 – May 2015
Bachelors of Science: Biology with focus on Genetics and Evolution
Université de Lausanne, Switzerland [Exchange] September 2012 – June 2013

Masters Thesis

Characterizing recent intron gain events in *Arabidopsis lyrata* using phylogenetic inference: 2017
Overview of Masters thesis: Systematically detect novel introns by comparative genomics.
Methods used: Integrating publicly available data (such as raw RNA-seq, gene annotations, and genome alignments) to detect novel introns. Investigating likely causes of intron gains, and confirmation of computational findings through biological experiments.

Publications

Stewart Turvey Lab at Child and Family Research Institute: Ali, Salman *et al. Functional genetic variation in NFKBIA and susceptibility to childhood asthma, bronchiolitis, and bronchopulmonary dysplasia.* The Journal of Immunology 190, no. 8 (2013): 3949-3958. DOI: 10.4049/jimmunol.1201015.
Personal contributions: Cloning and measuring differential expression levels.

Patrick Keeling Lab at University of British Columbia: Burki, Fabien *et al.*. *Untangling the early diversification of eukaryotes: a phylogenomic study of the evolutionary origins of Centrohelida, Haptophyta and Cryptista.* In Proc. R. Soc. B, vol. 283, no. 1823, p. 20152802. The Royal Society, 2016. DOI: 10.1098/rspb.2015.2802.
Personal contributions: Transcriptome analysis, data curation, phylogenetic analyses.

Computer Skills

Programming Languages: Python, Perl, Bash.
Operating Systems: Linux, MacOS, Microsoft Windows.
Bioinformatic Tools: BLAST, BedTools, Bcftools, Biopython, BWA, Bowtie, Trinity Assembler, GATK, Picard, Samtools, HMMER, RepeatMasker, LiftOver, IGV.

Research Experience

Variant identification via WGS: 2017
Illumina Hi-Seq reads aligned to reference genome to identify variants, large structural changes as well as small indels.

Detecting exapted transposable elements: 2016
Applying machine learning techniques to expand on previous work that detected exapted, or domesticated, TEs within a genome.

Phylogenetic analysis of single celled eukaryotes: 2015
Exploring protist evolution and biodiversity through genome and transcriptome sequencing, with Dr. Patrick Keeling and Fabien Burki.

Undergraduate directed studies project 2013
Simulating evolutionary processes, with Drs. Jeremy Draghi and Michael Whitlock.

NSERC Undergraduate Student Research Award 2012
Updating curriculum for undergraduate math course with Dr. Fok-Shuen Leung.

Summer Studentship at B.C Clinical Genomics Network 2011
Constructing reporter plasmids for NFKBIA promoter to compare variants in promoter.

Projects and Collaborations

Applying HI-C data in novel machine learning models to predict TE position. Adding genome-wide contact frequency maps (representing 3D genomic space) in addition to typical biological features to predict Transposable Elements in the human genome.

Scientific collaborations with molecular biologist: Variant identification in *c. elegan* for candidates of mutant phenotype.

Scientific collaborations with biochemistry lab: Customization of multiple sequence alignment tool for in-house use of complex gene family.

Websites managed: Personal website, Public github repository
The Flat Bike Collective, McGill Biology Graduate Student Association

Past Work Experience

My Intelligent Machines November 2018 – April 2019
Bioinformatic Scientist: coordinated execution of method-centric workflows. Worked closely with knowledge engineering and optimization teams to provide modular pipelines.

McGill University September 2015 – April 2017
Teaching Assistant: BIOL309 - Mathematical Models in Biology, BIOL112 – Cell and Molecular Biology Lab, BIOL202 – Basic Genetics

Vancouver Student Homes August 2013 – April 2015
Managing rooms for young working professionals and students

University of British Columbia September 2010 – June 2012
Research Assistant in immunology lab of Stewart Turvey

City of Richmond and Rapids Swim Team April 2008 – July 2012
Lifeguard, swimming instructor, coach, swim meet organizer

Personal Activities

Serving dinners at Centre Mission Bon Accueil April 2015 – March 2017
Hosting activities at Telus World of Science: Body Works May 2014 – August 2015
Student representative for the UBC Science One Program September 2010 – April 2011
Sports – Biking, climbing, snowshoeing, swimming, skiing, and running