

Maia Kaplan

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Work Experience	Streamline Genomics: April 2019 – Present Software Engineer (Bioinformatics). Responsible for: design, implementation, and iteration of analysis pipelines, internal biological database curation and maintenance. Develop: API endpoints, bioinformatic technical features, and biological validation.
	My Intelligent Machines November 2017 – April 2019 Bioinformatic Scientist: coordinated workflows, knowledge engineering, and optimization.
	McGill University September 2015 – April 2017 Teaching Assistant: Mathematical Models in Biology, Biology Lab, Genetics.
	University of British Columbia September 2010 – June 2012 Research Assistant in molecular immunology lab of Stewart Turvey.
Education and Publications	McGill University, Canada September 2015 – October 2017 <i>Master of Science: Biology (Bioinformatics).</i> Supervisors: T. Bureau and M. Blanchette. Characterizing recent intron gain events in <i>Arabidopsis lyrata</i> using phylogenetic inference.
	University of British Columbia, Canada September 2010 – May 2015 <i>Bachelors of Science: Biology with focus on Genetics and Evolution.</i>
	Université de Lausanne, Switzerland [Exchange] September 2012 – June 2013
	Publication: Ali, Salman <i>et al.</i> Functional genetic variation in NFKBIA and susceptibility to childhood asthma bronchopulmonary dysplasia. DOI: 10.4049/jimmunol.1201015.
Publication: Burki, Fabien <i>et al.</i> Untangling the early diversification of eukaryotes: a phylogenomic study of the evolutionary origins of Centrohelida, Haptophyta and Cryptista. DOI: 10.1098/rspb.2015.2802.	
Computer and Programming Skills	<i>Primary Setup:</i> Python, MySQL, docker, vim, git.
	<i>Operating Systems:</i> Linux, MacOS, Microsoft Windows.
	<i>Bioinformatic Tools:</i> Biopython, BLAST, BWA, GATK, RepeatMasker, Samtools, Trinity. <i>Other:</i> Atlassian, Agile, Bash, Make, SQL, R, OOP, pytest, HPC, HTML.
Research Experience	Variant calling and filtering for large datasets:
	Small single point changes and insertion/deletion identification in <i>c. elegans</i> . 2018
	Illumina Hi-Seq reads aligned to reference genome to identify variants, large structural changes as well as small indels. 2017
	Detecting and characterizing Transposable Elements (TEs):
	Applying HI-C data in novel machine learning models to predict TE position. 2017
	Applying machine learning techniques to expand on previous work that detected exapted, or domesticated, TEs within a genome. 2016
Computational methods related to molecular theory:	
Common amino acid changes affecting protein folding in experimental settings. 2016	
Phylogenetic analysis of novel protist species with P. Keeling and F. Burki. 2015	
Simulating evolutionary processes of allele fixation with J. Draghi and M. Whitlock. 2013	