Gavin Murray Douglas

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Academic Positions

Assistant Professor (July 2025 – *Ongoing*)
Department of Biology, University of New Brunswick, Fredericton, NB, Canada

Postdoctoral Research Scholar (Jan. 2024 – June 2025)
Department of Biological Sciences & Bioinformatics Research Center, North Carolina State University, Raleigh, NC, USA | Supervisor: Dr. Louis-Marie Bobay

Postdoctoral Researcher (May 2021 – Dec. 2023)
Department of Microbiology & Immunology, McGill University, Montréal, QC, Canada
Supervisor: Dr. Jesse Shapiro

Education

PhD Microbiology and Immunology (Jan. 2017 – May 2021)
Dalhousie University, Halifax, NS, Canada | Supervisor: Dr. Morgan Langille
Thesis: Integrating functional and taxonomic data types for microbiome data analysis

MSc Ecology and Evolutionary Biology (Sept. 2013 – Nov. 2015)
University of Toronto, Toronto, ON, Canada | Supervisor: Dr. Alan Moses
Thesis: Investigating the evolutionary forces acting on mammalian transcription factor binding

BSc Specialist in Evolutionary Biology (Sept. 2009 – June 2013)
University of Toronto, Toronto, ON, Canada

Academic Awards

- Banting Postdoctoral Fellowship (2024 - 2025; Gov. of Canada; $140,000 / 2 years)
- NSERC Postdoctoral Fellowship (2021 – 2023; Gov. of Canada; $90,000 / 2 years)
- Globalink Research Award (2019; Mitacs Canada; $6,000)
- NSERC Michael Smith Foreign Study Supplement (2019; Gov. of Canada; $6,000)
- NSERC Alexander Graham Bell CGS Doctoral (2017 – 2020; Gov. of Canada; $105,000 / 3 years)
- Izaak Walton Killam Predoctoral Scholarship Level 2 (2017 – 2019; The Killam Trusts; Honorary)
- President's Award (2017-2019; Dalhousie University; Tuition / 3 years)
- Kathryn A. Weldon Travel Award (2018; Dalhousie Medical Research Foundation; $2,000)
- Early Career Scientist Bursary (2018; International Human Microbiome Consortium; €500)
- NSERC CGS Master's (2013 – 2014; Gov. of Canada; $17,500)
- NSERC Undergraduate Student Research Award (2012; Gov. of Canada; $5,625)

Peer-Reviewed Publications

**Joint first authors; †Joint senior authors*

Douglas GM and Shapiro BJ. 2024. Pseudogenes act as a neutral reference for detecting selection in prokaryotic pangenomes. *Nature Ecology and Evolution* 8:304-314. https://doi.org/10.1038/s41559-023-02268-6 (Related *News and Views* article)

El Chaar M, Khoury Y, **Douglas GM**, El Kazzi S, Jisr T, Soussi S, Merhi G, Moghnieh RA, Shapiro BJ. 2024. Longitudinal genomic surveillance of multidrug-resistant *Escherichia coli* carriage in critical care patients. *Microbiology Spectrum* 12:e03128-23. https://doi.org/10.1128/spectrum.03128-23

Douglas GM, Kim S, Langille MGI, Shapiro BJ. 2023. Efficient computation of contributional diversity metrics from microbiome data with FuncDiv. *Bioinformatics* 39:btac809. https://doi.org/10.1093/bioinformatics/btac809

Douglas GM, Hayes MG, Langille MGI†, Borenstein E†. 2022. Integrating phylogenetic and functional data in microbiome studies. *Bioinformatics* 38:5055-5063. https://doi.org/10.1093/bioinformatics/btac655

Migicovsky Z, **Douglas GM**, Myles S. 2022. Genotyping-by-sequencing of Canada's apple biodiversity collection. *Frontiers in Genetics* 13:934712. https://doi.org/10.3389/fgene.2022.934712

Wright AH, Shawkat A, Migicovsky Z, **Douglas GM**, Yurgel S, Bunbury-Blanchette A, Franklin J, Adamas SJ, Walker AK. 2022. A characterization of a cool climate organic vineyard's microbiome. *Phytobiomes* 6:69-82. https://doi.org/10.1094/PBIOMES-03-21-0019-R

Nearing JT*, **Douglas GM***, Hayes MG, MacDonald J, Desai DK, Allward N, Jones CMA, Wright RJ, Dhanani AS, Comeau AM, Langille MGI. 2022. Microbiome differential abundance methods produce different results across 38 datasets. *Nature Communications* 13:342. https://doi.org/10.1038/s41467-022-28034-z

Douglas GM and Langille MGI. 2021. A primer and discussion on DNA-based microbiome data and related bioinformatics analyses. *Peer Community Journal* 1:e5. https://doi.org/10.24072/pcjournal.2

Douglas GM and Shapiro BJ. 2021. Genic selection within prokaryotic pangenomes. *Genome Biology and Evolution* 13:evab234. https://doi.org/10.1093/gbe/evab234

Cook J, **Douglas GM**, Zhang J, Glick BR, Langille MGI, Liu K-H, Cheng Z. 2021. Transcriptomic profiling of *Brassica napus* responses to *Pseudomonas aeruginosa*. *Innate Immunity* 27: 143-157. https://doi.org/10.1177/1753425920980512

Douglas GM, Bielawski JP, Langille MGI. 2020. Re-evaluating the relationship between missing heritability and the microbiome. *Microbiome* 8:87. Podcast interview. https://doi.org/10.1186/s40168-020-00839-4

Douglas GM, Maffei VJ, Zaneveld J, Yurgel SN, Brown JR, Taylor CM, Huttenhower C, Langille MGI. 2020. PICRUSt2 for prediction of metagenome functions. *Nature Biotechnology* 38:685-688. https://doi.org/10.1038/s41587-020-0548-6

Nejman D*, Livyatan I*, Fuks G*, et al. 2020. The human tumor microbiome is composed of tumor type-specific intracellular bacteria. *Science* 368:973-980. https://doi.org/10.1126/science.aay9189

Palau M, Piqué N, Comeau AM, **Douglas GM**, Ramírez-Lázaro MJ, Lario S, Calvet X, Langille MGI, Miñana-Galbis D. 2020. Detection of *Helicobacter pylori* microevolution and multiple infection from gastric biopsies by housekeeping gene amplicon sequencing. *Pathogens* 9:97. https://doi.org/10.3390/pathogens9020097

Douglas GM and Langille MGI. 2019. Current and promising approaches to identify horizontal gene transfer events in metagenomes. *Genome Biology and Evolution* 11:2750-2766. https://doi.org/10.1093/gbe/evz184

Bolyen E*, Rideout JR*, Dillon MR*, et al. 2019. Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. *Nature Biotechnology* 37:852-857. https://doi.org/10.1038/s41587-019-0209-9

Yurgel SN, Nearing JT, **Douglas GM**, Langille MGI. 2019. Metagenomic functional shifts to plant induced environmental changes. *Frontiers in Microbiology* 10:1682. https://doi.org/10.3389/fmicb.2019.01682

Singh R et al. 2019. Enhancement of the gut barrier integrity by a microbial metabolite through the Nrf2 pathway. *Nature Communications* 10:89. https://doi.org/10.1038/s41467-018-07859-7

Nearing JT, **Douglas GM**, Comeau AM, Langille MGI. 2018. Denoising the Denoisers: An independent evaluation of microbiome sequence error-correction approaches. *PeerJ* 6:e5364. https://doi.org/10.7717/peerj.5364

Yurgel SN, **Douglas GM**, Dussault A, Percival D, Langille MGI. 2018. Dissecting community structure in wild blueberry root and soil microbiome. *Frontiers in Microbiology* 9:1187. https://doi.org/10.3389/fmicb.2018.01187

McElroy MS, Navarro AJR, Mustiga G, Stack C, Gezan S, Peña G, Sarabia W, Saquicela D, Sotomayor I, **Douglas GM**, Migicovsky Z, Amores F, Tarqui O, Myles S, Motamayor JC. 2018. Prediction of cacao (*Theobroma cacao*) resistance to *Moniliophthora* spp. diseases via genome-wide association analysis and genomic selection. *Frontiers in Plant Science* 9:343. https://doi.org/10.3389/fpls.2018.00343

Douglas GM*, Hansen R*, Jones C, Dunn K, Comeau AM, Bielawski JP, Tayler R, El-Omar EM, Russell RK, Hold GL†, Langille MGI†, Van Limbergen J†. 2018. Multi-omics differentially classify disease state and treatment outcome in pediatric Crohn's disease. *Microbiome* 6:13. https://doi.org/10.1186/s40168-018-0398-3

McClure KA, Gardner KM, **Douglas GM**, Toivonen PMA, Hampson CR, Song J, Forney CF, DeLong J, Rajcan I, Myles S. 2018. A genome-wide association study of fruit quality and historical scab resistance in an apple collection. *The Plant Genome* 11:170075. https://doi.org/10.3835/plantgenome2017.08.0075

Inkpen A, **Douglas GM**, Brunet T, Leuschen K, Doolittle F, Langille MGI. 2017. The coupling of taxonomy and function in microbiomes. *Biology and Philosophy* 32:1225-43. https://doi.org/10.1007/s10539-017-9602-2

Yurgel SN, **Douglas GM**, Comeau AM, Mammoliti M, Dussault A, Percival D, Langille MGI. 2017. Variation in bacterial and eukaryotic communities associated with natural and managed wild blueberry habitats. *Phytobiomes* 1:102-113. https://doi.org/10.1094/PBIOMES-03-17-0012-R

Comeau AM, **Douglas GM**, Langille MGI. 2017. Microbiome Helper: A custom and streamlined workflow for microbiome research. *mSystems* 2:e00127-16. https://doi.org/10.1128/msystems.00127-16

Douglas GM, Wilson MD, Moses AM. 2016. Decreased transcription factor binding levels nearby primate pseudogenes suggests regulatory degeneration. *Molecular Biology and Evolution* 33:1478-85. https://doi.org/10.1093/molbev/msw030

Khan T, **Douglas GM**, Patel P, Nguyen Ba AN, Moses AM. 2015. Polymorphism analysis reveals reduced negative selection and elevated rate of insertions and deletions in intrinsically disordered protein regions. *Genome Biology and Evolution* 7:1815-26. https://doi.org/10.1093/gbe/evv105

Douglas GM*, Gos G*, Steige KA*, Salcedo A, Holm K, Ågren JA, Hazzouri KM, Wang W, Platts AE, Josephs EB, Williamson RJ, Neuffer B, Lascoux M, Slotte T, Wright SI. 2015. Hybrid origins and the earliest stages of diploidization in the highly successful recent polyploid *Capsella bursa-pastoris*. *PNAS USA* 112:2806-11. https://doi.org/10.1073/pnas.1412277112

Book Chapters

Douglas GM, Comeau AM, Langille MGI. 2018. Processing a 16S rRNA sequencing dataset with the Microbiome Helper workflow. *Microbiome Analysis – Methods and Protocols* (Springer; Editors: Beiko RG, Hsiao RG, Parkinson J):131-141. https://doi.org/10.1007/978-1-4939-8728-3_9

Douglas GM, Beiko RG, Langille MGI. 2018. Predicting the functional potential of the microbiome from marker genes using PICRUSt. *Microbiome Analysis – Methods and Protocols* (Springer; Editors: Beiko RG, Hsiao RG, Parkinson J):169-177. https://doi.org/10.1007/978-1-4939-8728-3_11

Other Writing

Douglas GM. 2024. Policy considerations for Canada's open access publishing strategy. *Journal of Science Policy & Governance*. 25:07. https://doi.org/10.38126/JSPG250107

Douglas GM. 2022. Mutiny. Winner of the Federation of European Microbiological Societies' blog writing competition on "How Microbiology will Change our Future". Link to story. Podcast interview.

Oral Presentations

Characterizing the relationship between rates of co-occurrence and horizontal gene transfer across prokaryotic marine genomes. June 2024. American Society for Microbiology - Microbe Conference (Atlanta, USA).

Pseudogenes as a neutral reference for detecting selection in prokaryotic pangenomes. June 2023. The Canadian Society of Microbiologists Annual Conference (Halifax, Canada).

Strategies for efficiently writing a strong thesis. February 2023. Webinar by the McGill Microbiology & Immunology Graduate Student Association (Montréal, Canada).

POMS enables interpretation of functional differences between the stool microbiome of obese and control individuals. December 2022. McGill Centre for Microbiome Research Symposium: Emerging Breakthroughs in Microbiome Science (Montréal, Canada).

The need-to-know facts of microbiome research. July 2019. Continuing Medical Education: Gut flora and the answers your patients are looking for (Dartmouth General Hospital, Dartmouth, Canada).

Prediction of microbial genomes from 16S rRNA gene sequences and application for disease state classification. March 2019. Crossroads Interdisciplinary Health Research Conference (Halifax, Canada).

Posters *(*Presenter; my name in bold)*

El Chaar M, Mordorisissan JM, Abdallah B, **Douglas GM***, Shapiro BJ. June 2024. The composition of the microbiota in the full-term newborn's gut, and mother's colostrum and breastmilk: Evidence of early bacterial transmission. American Society for Microbiology - Microbe conference (Atlanta, USA).

Douglas GM*, Stott CM, Bobay L-M, Raymann K, Shapiro BJ. July 2023. Allelic diversity across honey bee gut microbiomes is consistent with niche-specific adaptation. Microbial Population Biology – Gordon Research Conference (Andover, USA).

Watts S*, Migicovsky Z, **Douglas GM**, Myles S. January 2022. Genome-wide association studies in Canada's Apple Biodiversity Collection. Plant & Animal Genome Conference XXIX (Virtual, organized in San Diego).

Nearing JT*, **Douglas GM**, Hayes M, MacDonald J, Desai D, Allward N, Jones CMA, Wright R, Dhanani A, Comeau AM, Langille MGI. June 2020. Microbiome differential abundance methods produce strikingly different results across 38 datasets. Symposium: "Having IMPACTT: Advancing Microbiome Research" (Held virtually, but organized at the University of Calgary, Canada).

Douglas GM*, Langille MGI, Borenstein E. October 2020. Identifying robust functional biomarkers in microbiome sequencing data with POMS. Cold Spring Harbor Laboratory Conference – Microbiome (Held virtually, but organized in Cold Spring Harbor, USA).

Douglas GM*, Langille MGI, Borenstein E. September 2020. Identifying robust functional biomarkers in microbiome sequencing data with POMS. Wellcome Genome Informatics Conference (Held virtually, but organized in Hinxton, UK).

Douglas GM*, Langille MGI. December 2019. Making sense of functional microbiome associations with POMS. Genomics in Medicine Conference (Dalhousie University, Canada).

Douglas GM*, Zaneveld J, Maffei VJ, Xu ZZ, Leuschen K, Brown JR, Huttenhower C, Langille MGI. June 2018. PICRUSt 2.0: Novel features for predicting functional potential. 7th International Human Microbiome Conference (Killarney, Ireland).

Douglas GM*, Zaneveld J, Maffei VJ, Xu ZZ, Leuschen K, Huttenhower C, Brown JR, Langille MGI. March 2018. PICRUSt 2.0: Novel features for predicting functional potential. Keystone Symposia: Microbiome, Host Resistance and Disease (Banff, Canada).

Stadnyk AW*, **Douglas GM**, Comeau AM, Jain U, Schaeble W, Stover C, Beiko R, Langille MGI. March 2017. Properdin deficiency does not impact the mouse response to DSS-induced colitis despite differences in colonic microbiome. Canadian Digestive Diseases Week (Banff, Canada).

Jones C*, **Douglas GM**, Comeau AM, Hansen R, Russell R, Hold G, Van Limbergen J, Langille MGI. November 2016. Assessing the relative contribution of genetics and micro-omics for predicting pediatric Crohn's Disease. International Human Microbiome Consortium (Houston, USA).

Jones C*, **Douglas GM**, Comeau AM, Hansen R, Russell R, Hold G, Langille MGI, Van Limbergen J. October 2016. An integrated microbiome and genetic analysis of pediatric Crohn's disease. World Congress of Pediatric Gastroenterology, Hepatology and Nutrition (Montréal, Canada).

Jones C, **Douglas GM***, Comeau AM, Hansen R, Russell R, Hold G, Langille MGI, Van Limbergen J. August 2016. Assessing the relative contribution of genetics and the microbiome for predicting pediatric Crohn's disease. International Soc. for Microbial Ecology (Montréal, Canada).

Comeau AC*, **Douglas GM**, Langille MGI. June 2016. Integrated Microbiome Resource: Developing an open and streamlined experimental and analysis pipeline for microbiomics research. American Society for Microbiology (Boston, USA).

Douglas GM*, Wilson MD, Moses AM. January 2015. Detecting selection on mammalian transcription factor binding sites. Stochastic Physics in Biology - Gordon Research Conference (Ventura, USA).

Douglas GM*, Wilson MD, Moses AM. June 2014. Degeneration of mammalian cis-regulatory modules. Society for Molecular Biology and Evolution Conference (San Juan, Puerto Rico).

Khan T, **Douglas GM***, Nguyen Ba AN, Moses AM. June 2014. Analysis of polymorphisms reveal constraints on amino acids and increased rates of insertions and deletions in intrinsically disordered regions. Society for Molecular Biology and Evolution Conference (San Juan, Puerto Rico).

Douglas GM*, Lascoux M, Holm K, Steige KA, Slotte T, Gos G, Hollister J, Wright SI. July 2013. Rapid relaxation of purifying selection in the young allopolyploid *Capsella bursa-pastoris*. Society for Molecular Biology and Evolution Conference (Chicago, USA).

Other Relevant Work Experience

- **Independent Contractor** (Sept. 2015 and Aug. 2020, remote work): I conducted paid bioinformatics tasks on an independent basis. I also contributed results and co-authored a consulting report on the genetic basis of carotenoid content in spinach.
- **Bioinformatician** (Sept. 2015 – Dec. 2016, Dalhousie University): I was responsible for building tools and pipelines for analyzing a variety of different bioinformatics datasets. My main focuses were (1) analyzing microbiome data (with Dr. Morgan Langille) and (2) associating mutations in the apple and cannabis genomes with agriculturally relevant phenotypes (with Dr. Sean Myles).

Supervisory Experience

- Sana Naderi (Feb. 2023 – Dec. 2023, McGill University): PhD student analyzing SARS-CoV-2 sequencing time-series data from Québec wastewater samples using population genetic approaches.
- Isabel Kim (Fall 2021 – Winter 2022, McGill University): Undergraduate student conducting an independent research project, which focused on developing and evaluating diversity metrics based jointly on taxonomic and functional microbial ecology data.
- Jocelyn MacDonald (Winter 2019, Dalhousie University): Undergraduate experiential learning student that compared methods for differential abundance tests applied to microbiome data.

Teaching Experience

Workshop Leader (July 2025, University College Dublin)

I volunteered as the leader for one week of a two-week bioinformatics workshop for 16 researchers (mainly graduate students in biomedical fields). I was the sole workshop leader and presenter for this week, which involved 27 hours of lectures and/or leading bioinformatics workshops, in addition to an exam on the final day. The content included R programming, analyzing RNA-seq data, variant calling, population structure, genome-wide association studies, metagenomics, and network biology. Attendees who passed received a certificate, and University College Dublin students counted this course towards their degree (VET40470).

Session Leader (Sept. 2022 – Oct. 2023, McGill University)

I lectured and led discussions in group meetings for McGill University medical students, which covered fundamental and clinical research approaches. This was part of Research Fundamentals 1 (INDS123).

Guest Lecturer (Oct. 2020 – Feb. 2025)

Guest lecturer for four courses, including both undergraduate and graduate courses, on topics related to molecular evolution and microbiome research. These courses were at separate institutions: Acadia University, Dalhousie University, McGill University, and North Carolina State University.

Workshop Instructor

- *Visitor at Sheba Medical Center, Tel Aviv, Israel* (May 16, 2019). I delivered a lecture and workshop on analyzing 16S rRNA gene sequencing data for a diverse group of microbiome and clinical researchers.
- *Volunteer Instructor* at Dalhousie University (Aug. 2018). I presented a series of four workshops to biology graduate students on “R programming for biologists”. I began each workshop with a lecture and then lead the students through in-class assignments to solidify the lecture content. All the resources I developed are openly available.
- *Canadian Bioinformatics Workshop* at the Ontario Institute for Cancer Research in Toronto (June 5 - 7, 2018). I presented a lecture on the major classes of bioinformatics tools used for taxonomic and functional profiling of shotgun metagenomics data and developed a tutorial to complement this lecture. I was also a teaching assistant for all tutorials presented over three days.
- *Module Instructor* at Dalhousie University (Nov. – Dec. 2016). I created and delivered a four-week graduate-level module entitled “Introduction to Python programming for biologists”. I lectured two classes each week and created all the quizzes and assignments (three quizzes and four assignments). This module was one of several modules offered as part of BIOL5705 (Graduate Modules class) in the Biology department. The resources I developed are available here.
- *Bioinformatics Tutorial Developer* (Sept. 2016 – Oct. 2017). While working as a bioinformatician in the Langille Lab at Dalhousie University I developed several online tutorials to teach researchers how to analyze microbiome data. These tutorials were presented at several international conferences to hundreds of trainees. These tutorials are available on the Microbiome Helper website.

Teaching Assistant

- *Laboratory Methods in Microbiology & Immunology (MICI2400)*, Dalhousie University (Winter 2020). I helped lead lab sessions and marked students' reports for this lab-based course that introduced aseptic technique and basic microbiology practices to students.
- *Adaptation and Biodiversity (BIO120)*, University of Toronto (Fall 2013 and 2014). I supervised laboratory classes, which were diverse workshops that introduced students to key themes in organismal and evolutionary biology.

Volunteer and Service Experience

Formatting Volunteer – Peer Community Journal (July 2024 – *Ongoing*)

Articles recommended by 'Peer Communities' (such as PCI Genomics, see below) are eligible for publication in the Peer Community Journal. Alongside other volunteers, I help format submissions correctly, check for mandatory information, and correct reference details prior to publication.

Managing Board Member – Peer Community In (PCI) Genomics (May 2023 – *Ongoing*)

PCI Genomics is a platform for reviewing and recommending preprints. As a board member, I approve new recommenders, evaluate recommenders' work and assessments, and deal with internal conflicts between authors, reviewers, and recommenders. I am also PCI Genomics' representative (as of Nov. 2023) to the broader PCI non-profit organization, where I vote on pertinent matters, such as proposals for the creation of new thematic PCIs (analogous to new journals), and PCI policies.

Peer Community in Genomics (PCI Genomics) Recommender (Apr. 2021 - *Ongoing*)

As a recommender, my role is like that of a traditional editor, except that I also write a short article recommending the preprint if it passes the review process (listed below).

- Positive selection acted upon cetacean ion channels during the aquatic transition. 2024. *Peer Community in Genomics*, 100256. https://doi.org/10.24072/pci.genomics.100256
- A unique and customizable approach for functionally annotating prokaryotic genomes. 2023. *Peer Community in Genomics*, 100233. https://doi.org/10.24072/pci.genomics.100233
- A workflow for studying enigmatic non-autonomous transposable elements across bacteria. 2023. *Peer Community in Genomics*, 100166. https://doi.org/10.24072/pci.genomics.100166
- EukProt enables reproducible Eukaryota-wide protein sequence analyses. 2022. *Peer Community in Genomics*, 100021. https://doi.org/10.24072/pci.genomics.100021

Volunteer – American National Science Policy Network (Dec. 2022 – Sept. 2024)

I contributed to this organization's Communication Committee through three initiatives. First, I helped write and edit science policy blog posts published monthly on the organization's website. Second, I volunteered as a member of the "Writer's Room", where I discussed draft manuscripts written by myself and other volunteers prior to them being submitted to formal science and policy venues. Last, I co-organized a panel discussion on open access science publishing with three experts that have divergent perspectives on this topic (held virtually on July 17, 2024).

Executive Member – McGill Association of Postdoctoral Fellows (May 2022 – Dec. 2023)

I held executive positions as Vice President Finance and Operations (May 2022 – May 2023), which involved managing all financial transactions, and Vice President Academic (June 2023 – Dec. 2023). In this latter role I organized an academic award series for McGill postdoctoral fellows. I also contributed in other ways, such as redesigning and maintaining the organization's website, representing our organization as a councillor on the Post-Graduate Students' Society council, and representing postdocs more generally at the annual Canadian Association of Postdoctoral Administrators meeting. This last event was held in Montréal from Oct. 31 to Nov. 1, 2022, where I was a panelist on a discussion panel entitled "Preparing postdocs for a diverse job market".

Co-President - Science & Policy Exchange (Dec. 2022 – Dec. 2023)

Science & Policy Exchange (SPE) is a volunteer-run, non-profit organization (based in Montréal) with the mandate of introducing next-generation researchers to Canadian science policy. I co-supervised over 30 volunteers as they conducted numerous initiatives, such as organizing forums, writing policy briefs, and consulting with policymakers. Beyond general managing, my specific contributions were:

1. Providing testimony to the House of Commons Standing Committee on Science & Research (May 9, 2023), regarding the value and number of federal awards for graduate students and postdoctoral scholars. My and other testimonies helped inform the Committee's recommendations.
2. Coordinating with the Canadian Association of Postdoctoral Scholars to analyze survey data and write a report on international postdoctoral scholars' work permit processing times in Canada.
3. Sitting on the advisory board for a new annual collection of publications organized by the University of Ottawa's Institute of Science, Society and Policy.
4. Co-authoring an editorial on the Canadian Science Policy Centre website.
5. Being a panelist at the Canadian Association of Postdoctoral Fellows Annual General Meeting (Nov. 16, 2023) on a panel discussion entitled 'Supporting Postdocs'.

Postdoctoral Representative (June 2022 – May 2023)

I represented postdoctoral fellows within the department of Microbiology and Immunology at McGill as part of the department's graduate student association. I was the first postdoctoral representative for this department, and I developed a standard operating procedure for future representatives to follow.

Graduate Studies Committee Member (Sept. 2019 – Aug. 2020)

I represented graduate students' perspectives in discussions related to graduate student program requirements, and funding. This was during my PhD in the Department of Microbiology and Immunology at Dalhousie University.

iGEM Mentor (May 2018 – Oct. 2018)

I supervised the bioinformatics work of the Dalhousie University undergraduate team for the 2018 International Genetically Engineered Machine (iGEM) competition. This involved helping students determine which hypotheses they should test and how to conduct the required statistical analyses. I also supervised the fundraising work for our team, which included creating a promotional video.

Peer-Reviewing *(Number of reviews, excluding revised versions)*

Animal Microbiome (1)
Annals NY Acad. of Sci. (1)
Bioinformatics (2)
BMC Genomics (1)
BMC Microbiology (1)
BMC Supplements (1)
Comp. and Struct. Bio. J. (1)
Environ. Sci. and Poll. Res. (1)
Frontiers in Bioinformatics (1)
Frontiers in Genetics (1)
Frontiers in Microbiology (1)
G3: Genes, Genomes, Gen. (1)
Genome Biology (1)
GigaScience (1)
Genome Bio. & Evolution (1)
Gut Microbes (1)
Horticulture Research (1)
ISME Communications (1)
J. Open Source Software (2)
Microbial Genomics (1)
Mol. Bio. and Evolution (2)
mSystems (6)
Nature Ecology & Evol. (1)
npj Biofilms and Micro. (1)
PCI Genomics (3)
PLOS Comp. Biology (2)
PLOS Genetics (1)
Proc. Nat. Acad. Sci. USA (1)
Scientific Reports (5)