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| **BIOGRAPHICAL SKETCH**  Provide the following information for the key personnel and other significant contributors. Follow this format for each person.  **DO NOT EXCEED FOUR PAGES.** | | | | |
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| NAME  Gloor, Gregort | | POSITION TITLE  Professor of Biochemistry | | |
| eRA COMMONS USER NAME  GGLOOR | |
| INSTITUTION AND LOCATION | DEGREE  *(if applicable)* | | YEAR(s) | FIELD OF STUDY |
| University of Western Ontario, Canada | B.Sc (Hons.) | | June 1983 | Genetics |
| University of Western Ontario, Canada | Ph.D. | | June 1988 | Biochemistry |
| University of Wisconsin-Madison | Postdoc | | 1988-1990 | Molecular Microbiology |

**A. Personal Statement**

My work focuses on computational biology and bioinformatics; with an interest in the use of high-throughput sequencing methods to study bacterial populations and a second interest in molecular evolution. Oddly enough these two research areas fit very nicely together as they both deal with very large numbers of data points and use very similar statistical analysis tools. I have found that the underlying tools in one domain translate rather well into the other. I also actively develop method to characterize microbiota samples using emerging sequencing platforms. We were the first to develop a method for the Illumina GA/HiSeq platform, developed 16S sequencing methods for the Ion Torrent, and recently l have developed a strategy for sequencing amplimers of arbitrarily low complexity on the Illumina MiSeq platform. My lab developed a novel statistical method for meta-RNA-seq that uses Baysian techniques coupled with the centred log-ratio transformation to conduct a consistency check on gene expression levels. The approach is compatible with and extends the compositional data analysis approaches that are widely used in other scientific domains. With this, we can identify gene expression changes that are not linked to organism abundance. This methodology provides a robust statistical framework that allows us to interrogate mixed microbial communities and find out what the constituent organisms are doing. With this, we showed that the organisms in the vaginal community demonstrate a remarkable consistency in their functional capacity, regardless of the community composition. This demonstrated that enumerating the constituents of an ecosystem may be providing less information regarding their functional impact than is generally believed.

The compositional data analysis approach developed for meta-RNA seq appears to be a generally sound one for the analysis of other high-dimensional sequencing experiments, and we have adapted it to characterize differential abundance generally for high throughput sequencing experiments. Additionally, I have adapted a number of other compositional analysis tools for use in high throughput sequencing and am making them available to the broader community.

**B. Positions and Honors**

* **1990-1992** Assistant Professor of Molecular Genetics, Memorial University of Newfoundland, Canada
* **1993-1997** Assistant Professor of Biochemistry, University of Western Ontario, Canada
* **1997-2002** Associate Professor of Biochemistry, University of Western Ontario, Canada
* **2002-** Professor of Biochemistry, University of Western Ontario, Canada
* **2019-** Chair, Department of Biochemistry

**Other experience and Professional Memberships**

**1998-2008** Medical Research Council of Canada: BMB/Genetics/Genomics invitee Peer Review

Panel Invitee, (one Peer Review Panel meeting each in 1998-2008)

**2006-2009** National Cancer Institute of Canada, Model Organisms Panel B2 Member

**2008-2013**  IODE Doctoral Scholarship committee, member

**2010-2016** Canadian Institutes of Health Research, Genetics Peer Review Panel Full Member

**2016-** Chair, Canadian Institutes of Health Research, Genomics Panel

**2012-2015** Editorial Board member Microbiome

**2014-present** CRC College of Reviewers

**2015** Ontario Genomics Institute: SPARC and Genome Canada review panel

**2015-2021** Associate Editor, Microbiome

**2021-** Consulting Editor, Microbiome

**Honors**

**2005** Schulich School of Medicine Teaching Award

**2007**  University Student's Council Teaching Honor Roll

**2009**  University Student's Council Teaching Honor Roll

**2011**  University Student's Council Teaching Honor Roll

**2011-2013** Faculty Scholar

**C. Peer reviewed Publications (last 3 years)**

* J.R.Wu,J.M.Macklaim,B.L.Genge,andG.B.Gloor,*FindingtheCentre:CompositionalAsymmetryin High-Throughput Sequencing Datasets*, pp. 329–346. Cham: Springer International Publishing, 2021.
* L. A. Grieves, G. B. Gloor, T. R. Kelly, M. A. Bernards, and E. A. MacDougall-Shackleton, “Preen gland microbiota of songbirds differ across populations but not sexes,” *J Anim Ecol*, vol. 90, pp. 2202– 2212, 09 2021.
* L. A. Grieves, G. B. Gloor, T. R. Kelly, M. A. Bernards, and E. A. MacDougall-Shackleton, “Preen gland microbiota of songbirds differ across populations but not sexes,” *J Anim Ecol*, vol. 90, pp. 2202– 2212, 09 2021.
* D. Nouri-Nejad, B. L. O’Donnell, C. S. Patil, R. E. Sanchez-Pupo, D. Johnston, S. Sayedyahossein, K. Jurcic, R. Lau, L. Gyenis, D. W. Litchfield, M. F. Jackson, G. B. Gloor, and S. Penuela, “Pannexin 1 mutation found in melanoma tumour reduces phosphorylation, glycosylation, and trafficking of the channel-forming protein,” *Mol Biol Cell*, p. mbcE19100585, 01 2021.
* Erb, G. B. Gloor, and T. P. Quinn, “Editorial: Compositional data analysis and related methods applied to genomics—a first special issue from NAR Genomics and Bioinformatics,” *NAR Genomics and Bioinformatics*, vol. 2, 12 2020. lqaa103.
* R. R. Cochrane, S. L. Brumwell, A. Shrestha, D. J. Giguere, S. Hamadache, G. B. Gloor, D. R. Edgell, and B. J. Karas, “Cloning of thalassiosira pseudonana’s mitochondrial genome in saccharomyces cerevisiae and escherichia coli,” *Biology (Basel)*, vol. 9, Oct 2020.
* K. F. Al, J. D. Denstedt, B. A. Daisley, J. Bjazevic, B. K. Welk, S. E. Pautler, G. B. Gloor, G. Reid, H. Razvi, and J. P. Burton, “Ureteral stent microbiota is associated with patient comorbidities but not antibiotic exposure,” *Cell Reports Medicine*, vol. 1, no. 6, p. 100094, 2020.
* S. Yang, G. Reid, J. R. G. Challis, G. B. Gloor, E. Asztalos, D. Money, S. Seney, and A. D. Bocking, “Effect of oral probiotic lactobacillus rhamnosus gr-1 and lactobacillusreuteri rc-14 on the vaginal microbiota, cytokines and chemokines in pregnant women,” *Nutrients*, vol. 12, Jan 2020.
* D. J. Giguere, J. M. Macklaim, B. Y. Lieng, and G. B. Gloor, “omicplotr: visualizing omic datasets as compositions,” *BMC Bioinformatics*, vol. 20, p. 580, Nov 2019.
* L. Grieves, G. Gloor, M. Bernards, and E. MacDougall-Shackleton, “Songbirds show odour-based discrimination of similarity and diversity at the major histocompatibility complex,” *Animal Be- haviour*, vol. 158, pp. 131 – 138, 2019.
* T.A.Hamilton,G.M.Pellegrino,J.A.Therrien,D.T.Ham,P.C.Bartlett,B.J.Karas,G.B.Gloor,and D. R. Edgell, “Efficient inter-species conjugative transfer of a crispr nuclease for targeted bacterial killing,” *Nat Commun*, vol. 10, p. 4544, Oct 2019.
* M. Laforet, T. A. McMurrough, M. Vu, C. M. Brown, K. Zhang, M. S. Junop, G. B. Gloor, and D. R. Edgell, “Modifying a covarying protein-dna interaction changes substrate preference of a site- specific endonuclease,” *Nucleic Acids Res*, vol. 47, pp. 10830–10841, Nov 2019.
* T. P. Quinn, I. Erb, G. Gloor, C. Notredame, M. F. Richardson, and T. M. Crowley, “A field guide for the compositional analysis of any-omics data,” *Gigascience*, vol. 8, Sep 2019.
* C. Elwood, A. Y. K. Albert, E. McClymont, E. Wagner, D. Mahal, K. Devakandan, B. L. Quiqley, Z. Pakzad, M. H. Yudin, J. E. Hill, D. Money, VOGUE Research Group, A. Bocking, T. Dumonceaux, G. Gloor, S. Hemmingsen, J. E. Hill, M. Links, D. Money, K. O’Doherty, G. Reid, J. van Schalkwyk, P. Tang, and M. H. Yudin, “Different and diverse anaerobic microbiota were seen in women living with hiv with unsuppressed hiv viral load and in women with recurrent bacterial vaginosis: a cohort study,” *BJOG*, Sep 2019.
* M. D. Berg, D. J. Giguere, J. S. Dron, J. T. Lant, J. Genereaux, C. Liao, J. Wang, J. F. Robinson, G. B. Gloor, R. A. Hegele, P. O’Donoghue, and C. J. Brandl, “Targeted sequencing reveals expanded ge- netic diversity of human transfer rnas,” *RNA Biol*, vol. 16, pp. 1574–1585, Aug 2019.
* Z. Awamleh, G. B. Gloor, and V. K. M. Han, “Placental micrornas in pregnancies with early onset intrauterine growth restriction and preeclampsia: potential impact on gene expression and patho- physiology,” *BMC Med Genomics*, vol. 12, p. 91, 06 2019.
* D. G. Wootton, M. J. Cox, G. B. Gloor, D. Litt, K. Hoschler, E. German, J. Court, O. Eneje, L. Keogan, L. Macfarlane, S. Wilks, P. J. Diggle, M. Woodhead, M. F. Moffatt, W. O. C. Cookson, and S. B. Gordon, “A haemophilus sp. dominates the microbiota of sputum from uk adults with non-severe community acquired pneumonia and chronic lung disease,” *Sci Rep*, vol. 9, p. 2388, Feb 2019.
* Almeida, A. L. Mitchell, M. Boland, S. C. Forster, G. B. Gloor, A. Tarkowska, T. D. Lawley, and R. D. Finn, “A new genomic blueprint of the human gut microbiota,” *Nature*, vol. 568, p. 499, Feb 2019.
* B.R. Joris and G. B. Gloor, “Unaccounted risk of cardiovascular disease: the role of the microbiome in lipid metabolism,” *Curr Opin Lipidol*, Jan 2019.
* M. D. Berg, J. Genereaux, Y. Zhu, S. Mian, G. B. Gloor, and C. J. Brandl, “Acceptor stem differences contribute to species-specific use of yeast and human tRNAser,” *Genes (Basel)*, vol. 9, p. 612, Dec 2018.
* T. A. McMurrough, C. M. Brown, K. Zhang, G. Hausner, M. S. Junop, G. B. Gloor, and D. R. Edgell, “Active site residue identity regulates cleavage preference of LAGLIDADG homing endonucleases,” *Nucleic Acids Res*, vol. 46, pp. 11990–12007, Oct 2018.
* M. I. Petrova, J. M. Macklaim, S. Wuyts, T. Verhoeven, J. Vanderleyden, G. B. Gloor, S. Lebeer, and G. Reid, “Comparative genomic and phenotypic analysis of the vaginal probiotic lactobacillus rham- nosus GR-1,” *Front Microbiol*, vol. 9, p. 1278, 2018.
* G.B.Gloor,R.G.Wong,E.Allen-Vercoe,V.Dinculescu,M.Pignanelli,C.Bogiatzi,G.Reid,andJ.D. Spence, “Data on the gut and saliva microbiota from a cohort of atherosclerosis patients determined by 16s rrna gene sequencing,” *Data Brief*, vol. 19, pp. 481–485, Aug 2018.
* M. Pignanelli, C. Bogiatzi, G. Gloor, E. Allen-Vercoe, G. Reid, B. L. Urquhart, K. N. Ruetz, T. J. Velenosi, and J. D. Spence, “Moderate renal impairment and toxic metabolites produced by the in- testinal microbiome: Dietary implications,” *J Ren Nutr*, vol. 29, pp. 55–64, Aug 2018.
* M.Pignanelli,C.Just,C.Bogiatzi,V.Dinculescu,G.B.Gloor,E.Allen-Vercoe,G.Reid,B.L.Urquhart, K. N. Ruetz, T. J. Velenosi, and J. D. Spence, “Mediterranean diet score: Associations with metabolic products of the intestinal microbiome, carotid plaque burden, and renal function,” *Nutrients*, vol. 10, Jun 2018.
* McMillan, S. Rulisa, G. B. Gloor, J. M. Macklaim, M. Sumarah, and G. Reid, “Pilot assessment of probiotics for pregnant women in rwanda,” *PLoS One*, vol. 13, no. 6, p. e0195081, 2018.
* J. M. Macklaim and G. B. Gloor, “From RNA-seq to biological inference: Using compositional data analysis in meta-transcriptomics,” *Methods Mol Biol*, vol. 1849, pp. 193–213, 2018.
* Bogiatzi, G. Gloor, E. Allen-Vercoe, G. Reid, R. G. Wong, B. L. Urquhart, V. Dinculescu, K. N. Ruetz, T. J. Velenosi, M. Pignanelli, and J. D. Spence, “Metabolic products of the intestinal micro- biome and extremes of atherosclerosis,” *Atherosclerosis*, vol. 273, pp. 91–97, Jun 2018.

**C.1 Invited presentations**

* 2020, Invited speaker, Genentech (Zoom presentation)
* 2020, Invited speaker and organiser, ISAPP Annual Meeting
* 2019, Invited workshop speaker, Computational and Methodological Statistics 2019, London, England
* 2019, Invited Participant/Speaker, Emerging Challenges in Microbiome Data Analysis, BIRS, Banff, Canada
* 2019, Invited Speaker, Barcelona Microbiome Debates, Barcelona, Spain
* 2019, Invited Speaker, Department of Bioinformatics, North Carolina State University, Charlotte
* 2019, Invited Speaker, Department of Biology, North Carolina State University,
* 2019, Invited Speaker, Program in Bioinformatics, Duke University,
* 2019, Invited Webinar Presenter, International Society for the Application of Probiotics and Probiotics (ISAPP)
* 2019, Invited Speaker, North American Microbiome Congress, Washington, USA 3
* 2018, Invited Webinar Presenter, International Life Sciences Institute (ILSI)
* 2018, Invited industrial speaker (KGK Biosciences), Supply Side West, Las Vegas, USA
* 2018, Invited speaker, Department of Physiology and Pharmacology, UWO
* 2018, Invited speaker, Department of Epidemiology, SUNY Buffalo, USA
* 2018, Invited speaker, EMBL-EBI, EBI Seminar Series, Hinxton, Cambridgeshire, UK
* 2018, Invited speaker, Gairdner Foundation Symposium on health through food and microbes, London, CA
* 2018, Invited speaker Gynecological Research Symposium, The Society of Gynecologic Oncology of Canada, Toronto, CA
* 2018, Workshop organizer and presenter, Compositional Data analysis methods, NGS’18, Barcelona, Cat- alonia

**C.2 Software**

ALDEx2 ALDEx tool to determine pairwise differences between groups in compositional high-throughput sequence data. Available on Bioconductor since 2014

CoDaSeq Compositional data analysis tools for exploration of compositional high-throughput sequence data. Available on github.com/ggloor/CoDaSeq

**D. Research support**

**Ongoing research support**

**NSERC Alliance Grant, 2022-2024:** Rapid scaling of viral spike protein production for SARS-CoV-2 test- ing using *Phaeodactylum tricornutum*

*PI: Edgell DR*, Co-PI Gloor GB, Karas B. Suncor total: $800000

**Mitacs Accelerate, 2020:** Rapid scaling of viral spike protein production for SARS-CoV-2 testing using *Phaeodactylum tricornutum*

*PI: Gloor GB*, Co-PI Edgell DR, Partner organization: Suncor total: $40000

**NSERC Alliance Grant 2020-2024:** Development and validation of rapid point of care food safety assays for Salmonella and Campylobacter - Rapid detection facilitated by CRISPR

*PI; Rieder, M*, Co-applicants Gloor, GB, Edgell, DR and Karas, B. Industrial Partner is International Point of Care Ray, D and Styba, G.

total: $730999 + 1:1 matching from IPOC

**Weston Family Microbiome Initiative 2020-2022:** A Jekyll and Hyde role for gut bacterial proteases in the regulation of pain

*Co-PI: Lomax, AEG, Reed, DE*, Co-applicants Gloor, GB, Vanner, SJ, Allen-Vercoe E, Reed, DE, Ross, AC, Sheth, P, Bercik, P, De Palma, G

Applied research into the microbial causes of pain in IBD patients. Gloor role is metagenomic and meta- transcriptomic profiling of patient microbiome samples.

total: $3213000

**CIHR Project Grant 2019-2022:** Metabolic and Metagenomic effects of repopulation of the intestinal mi- crobiome in patients with severe unexplained atherosclerosis (extended due to covid-19)

*PI: Spence, DJ*, Co-applicants Azarpazhooh, Mahmoud Reza; Burton, Jeremy P; Gloor, Gregory B; Silver- man, Michael; Urquhart, Bradley L

Clinical trial to determine the effect of stool transplant on progression of atherosclerosis in patients pre- disposed coronary artery disease. Gloor role is metagenomic and metatranscriptomic profiling of patient microbiome samples.

total: $200000

**CIHR Project Grant, 2019-2024:** Modulation of pain in IBD by microbial proteases

*PI: Lomax, AEG*, Co-PI Gloor, GB, Allen-Vercoe E, Reed, DE, Ross, AC, Vanner, SJ

Basic research into the microbial causes of pain in IBD patients. Gloor role is metagenomic and meta- transcriptomic profiling of patient microbiome samples.

total: $395990

**CIHR Project Grant, 2018-2023:** ConCRISPR:Conjugativec delivery of a hybrid CRISPR/Tev nuclease system for specific microbiota modulation in the mammalian gut

*PI: Edgell, DE*, Co-PI Gloor, GB and Karas B

Basic research into the technology platform to target and eradicate specific taxa or genetic components of the human gut microbiome.

total: $891000