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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

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

**2012-2015** Editorial Board member Microbiome

**2014-present** CRC College of Reviewers

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

**2015-present** Associate 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)**

*1)*Gregory B Gloor, Jean M Macklaim, Michael Vu, and Andrew D Fernandes. Compositional uncer- tainty should not be ignored in high-throughput sequencing data analysis. *Austrian Journal of Statistics*, accepted, 2016.

*2)*Gregory B Gloor and Gregor Reid. Compositional analysis: a valid approach to analyze microbiome high-throughput sequencing data. *Can J Microbiol*, pages 1–12, Apr 2016.

*3)*GregoryBGloor,JiaRongWu,VeraPawlowsky-Glahn,andJuanJoséEgozcue.It’sallrelative:ana- lyzing microbiome data as compositions. *Ann Epidemiol*, 26(5):322–9, May 2016.

*4)*Sarah Lynn Martz, Mabel Guzman-Rodriguez, Shu-Mei He, Curtis Noordhof, David John Hurlbut, Gregory Brian Gloor, Christian Carlucci, Scott Weese, Emma Allen-Vercoe, Jun Sun, Erika Chiong Claud, and Elaine Olga Petrof. A human gut ecosystem protects against c. difficile disease by targeting tcda. *J Gastroenterol*, Jun 2016.

*5)*CamillaUrbaniak,GregoryBGloor,MurielBrackstone,LeslieScott,MarkTangney,andGregorReid. The microbiota of breast tissue and its association with tumours. *Appl Environ Microbiol*, Jun 2016.

*6)*JordanEBisanz,PraemaSuppiah,WMurrayThomson,TrudyMilne,NigelYeoh,AnitaNolan,Grace  Ettinger, Gregor Reid, Gregory B Gloor, Jeremy P Burton, Mary P Cullinan, and Simon M Stebbings. The oral microbiome of patients with axial spondyloarthritis compared to healthy individuals. *PeerJ*, 4:e2095, 2016.

*7)*Camilla Urbaniak, Michelle Angelini, Gregory B Gloor, and Gregor Reid. Human milk microbiota profiles in relation to birthing method, gestation and infant gender. *Microbiome*, 4:1, 2016.

*8)*Gregory B. Gloor, Jean M. Macklaim, and Andrew D. Fernandes. Displaying variation in large datasets: a visual summary of effect sizes. *Journal of Computational and Graphical Statistics*, http://dx.doi.org/10.1080/10618600.2015.1131161, 2016.

*9)*AmyMcMillan,StephenRulisa,MarkSumarah,JeanM.Macklaim,JustinRenaud,JordanE.Bisanz, Gregory B. Gloor, and Gregor Reid. A multi-platform metabolomics approach identifies highly spe- cific biomarkers of bacterial diversity in the vagina of pregnant and non-pregnant women. *Scientific Reports*, 5:14174 EP –, 09 2015.

*10)*Jordan E Bisanz, Megan K Enos, George PrayGod, Shannon Seney, Jean M Macklaim, Stephanie Chilton, Dana Willner, Rob Knight, Christoph Fusch, Gerhard Fusch, Gregory B Gloor, Jeremy P Bur- ton, and Gregor Reid. Microbiota at multiple body sites during pregnancy in a rural tanzanian popu- lation and effects of moringa-supplemented probiotic yogurt. *Appl Environ Microbiol*, 81(15):4965–75, Aug 2015.

*11)*Lee W Goneau, Thomas J Hannan, Roderick A MacPhee, Drew J Schwartz, Jean M Macklaim, Gre- gory B Gloor, Hassan Razvi, Gregor Reid, Scott J Hultgren, and Jeremy P Burton. Subinhibitory an- tibiotic therapy alters recurrent urinary tract infection pathogenesis through modulation of bacterial virulence and host immunity. *MBio*, 6(2), 2015.

*12)*Jean M Macklaim, Jose C Clemente, Rob Knight, Gregory B Gloor, and Gregor Reid. Changes in vaginal microbiota following antimicrobial and probiotic therapy. *Microb Ecol Health Dis*, 26:27799, 2015.

*13)*NStDenis,MGabriel,JPTurowec,GBGloor,SS-CLi,A-CGingras,andDWLitchfield.Systematic investigation of hierarchical phosphorylation by protein kinase CK2. *J Proteomics*, 118(6):49–62, Nov 2014.

*14)*ChantalleBrace,GregoryBGloor,MarkRopeleski,EmmaAllen-Vercoe,andElaineOPetrof.Micro- bial composition analysis of *Clostridium difficile* infections in an ulcerative colitis patient treated with multiple fecal microbiota transplantations. *J Crohns Colitis*, 8:1113–7, Feb 2014.



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GB Gloor Curriculum Vitae June 28, 2016



*15)*Thomas A McMurrough, Russell J Dickson, Stephanie M F Thibert, Gregory B Gloor, and David R Edgell. Control of catalytic efficiency by a coevolving network of catalytic and noncatalytic residues. *Proc Natl Acad Sci U S A*, 111(23):E2376–83, Jun 2014.

*16)*Kristin D Kernohan, Douglas Vernimmen, Gregory B Gloor, and Nathalie G Bérubé. Analysis of neonatal brain lacking ATRX or MeCP2 reveals changes in nucleosome density, CTCF binding and chromatin looping. *Nucleic Acids Res*, 42(13):8356–68, 2014.

*17)*GregorReid,NicholasNduti,WilbertSybesma,RemcoKort,TobiasRKollmann,RodAdam,Hamadi Boga, Eric M Brown, Alexandra Einerhand, Hani El-Nezami, Gregory B Gloor, Irene I Kavere, Johanna Lindahl, Amee Manges, Wondu Mamo, Rocio Martin, Amy McMillan, Jael Obiero, Pamela A Ochieng, Arnold Onyango, Stephen Rulisa, Eeva Salminen, Seppo Salminen, Antony Sije, Jonathan R Swann, William van Treuren, Daniel Waweru, and Steve J Kemp. Harnessing microbiome and probiotic re- search in sub-Saharan Africa: recommendations from an African workshop. *Microbiome*, 2(1):12, Apr 2014.

*18)*AndrewDFernandes,JenniferNsReid,JeanMMacklaim,ThomasAMcMurrough,DavidREdgell, and Gregory B Gloor. Unifying the analysis of high-throughput sequencing datasets: characteriz- ing RNA-seq, 16s rRNA gene sequencing and selective growth experiments by compositional data analysis. *Microbiome*, 2:15.1–15.13, 2014.

*19)*Camilla Urbaniak, Amy McMillan, Michelle Angelini, Gregory B Gloor, Mark Sumarah, Jeremy P Burton, and Gregor Reid. Effect of chemotherapy on the microbiota and metabolome of human milk, a case report. *Microbiome*, 2:24, 2014.

*20)*SRahat-Rozenbloom,JFernandes,GBGloor,andTMSWolever.Evidenceforgreaterproductionof colonic short chain fatty acids in overweight than lean humans. *Int J Obes (Lond)*, Mar 2014.

*21)*Xiaohong Tracey Gan, Grace Ettinger, Cathy X Huang, Jeremy P Burton, James V Haist, Venkatesh Rajapurohitam, James E Sidaway, Glynn Martin, Gregory B Gloor, Jonathan R Swann, Gregor Reid, and Morris Karmazyn. Probiotic administration attenuates myocardial hypertrophy and heart failure after myocardial infarction in the rat. *Circ Heart Fail*, 7(3):491–9, May 2014.

*22)*Mariana Rosenthal, Allison E Aiello, Carol Chenoweth, Deborah Goldberg, Elaine Larson, Gregory Gloor, and Betsy Foxman. Impact of technical sources of variation on the hand microbiome dynamics of healthcare workers. *PLoS One*, 9(2):e88999, 2014.

*23)*RussellJDicksonandGregoryBGloor.Bioinformaticsidentificationofcoevolvingresidues.*Methods Mol Biol*, 1123:223–43, 2014.

*24)*Jordan E Bisanz, Shannon Seney, Amy McMillan, Rebecca Vongsa, David Koenig, LungFai Wong, Barbara Dvoracek, Gregory B Gloor, Mark Sumarah, Brenda Ford, Dorli Herman, Jeremy P Burton, and Gregor Reid. A systems biology approach investigating the effect of probiotics on the vaginal microbiome and host responses in a double blind, placebo-controlled clinical trial of post-menopausal women. *PLoS One*, 9(8):e104511, 2014.

*25)*Jordan E Bisanz, Megan K Enos, Joseph R Mwanga, John Changalucha, Jeremy P Burton, Gregory B Gloor, and Gregor Reid. Randomized open-label pilot study of the influence of probiotics and the gut microbiome on toxic metal levels in Tanzanian pregnant women and school children. *MBio*, 5(5):e01580–14, 2014.

**C.1 Invited presentations**

2016, Invited speaker at Exploring Human Host-Microbiome Interactions in Health and Disease 2016, EBI, Cambridge, UK

2016, Invited workshop organizer at Exploring Human Host-Microbiome Interactions in Health and Dis- ease 2016, EBI, Cambridge, UK

2016, Invited workshop presenter, The Human Microbiome and Epidemiology, 2016 Epidemiology Congress of the Americas, Miami, USA

2016, Invited presentation/workshop, Infection, Inflammation and Immunity course, The Arctic Univer- sity of Norway, Tromso, NO

2016, Oral Presentation, Great Lakes Bioinformatics/Canadian Computational Biology Conference, Toronto, CA

2015, Invited speaker at Exploring Human Host-Microbiome Interactions in Health and Disease 2015, EBI, Cambridge, UK

2015, Invited paper at CoDaWork 2015, Girona, Spain

2015, Applying compositional data framework to microbiome datasets, Canadian Society of Microbiology workshop organizer 2015, Saskatoon, Canada

2015, Invited speaker, University of Guelph Bioinformatics group

2014, Invited seminar, Dept. of Biochemistry, University of Calgary

2014, Invited participant at NIH sponsored Microbiome Quality Control Initiative: only Canadian group invited, Rockville, MD, USA

**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**

**Developing molecular methods as diagnostic tools to identify biological factors contribut- ing to crop productivity and soil health** Agriculture and Agrifoods Canada, Agricultural Innovation Program, 2015-2017

*Investigators:* A&L Bioligicals led by Dr. George Lazarovitz (CSO), GLOOR, G academic co-applicant. *Keywords:* soil health, soil ecology, soil microbiology, soilborne disease, disease suppressive soil, ecol-

ogy, diagnostics, tomato, potato, bacteria, fungi, yield

*7.11.1 Total:600,000, direct to Gloor: 120000*

**Molecular covariation in protein families** Current NSERC Discovery grant, 2010-2015

*Investigators:* GLOOR,Gregory

*Keywords:* Proteins, molecular coevolution, computational biology, molecular biology, protein evolu- tion, epistasis, molecular evolution, mutual information, yeast genetics, phosphoglycerate kinase

*Total:155000, direct to Gloor: 155000*

**Role of intestinal microbiota in non-alcoholic fatty liver disease pre and post bariatric surgery:**

CIHR, 2013-2016

*Investigators:* ALLARD, Johane P (PI),COMELLI, Elena M; GLOOR, Gregory B; JACKSON, Timothy D; LOU, Wen-Yi W; OKRAINEC, Allan

*Keywords:* BARIATRIC SURGERY; DIET; INFLAMMATION; LIPOPOLYSACCHARIDE; MICROBIOTA; NON- ALCOHOLIC FATTY LIVER DISEASE; STEATOHEPATITIS

*7.1.1 Total:522169, direct to Gloor: 25000*

**Meta-transcriptome of high-yield corn endophytic microbiome** Ontario Centre of Excellence, 2014-2015

*Investigators:* GLOOR,GREGORY *Keywords:* Microbial ecology, plant endophytic organisms, microbial genomics, microbial metatran-

scriptomics, crop yield enhancement, maize microbiome, RNA-seq, metagenomics

*Total:25000, direct to Gloor: 25000*

**Exploiting the therapeutic effects of the fecal microbiome in bariatric care** CIHR Team grant in Bariatric Care (ranked first in competition), 2014-2019

*Investigators:* PIs: ALLARD, Johane P ; GAISANO, co-applicants:Herbert Y , BANKS, Kate; COMELLI, Elena M; GLOOR, Gregory B; HOTA, Susy S; JACKSON, Timothy D; LOU, Wen- Yi W; OKRAINEC, Allan; PHILPOTT, Dana J; POUTANEN, Susan M

*Keywords:* BARIATRIC SURGERY; DIET; INFLAMMATION; LIPOPOLYSACCHARIDE; MICRO- BIOTA; NON- ALCOHOLIC FATTY LIVER DISEASE; STEATOHEPATITIS

*Total:1,500,000, direct to Gloor: 80000*