

Annual Report
Centre for Comparative Genomics & Evolutionary Bioinformatics (CGEB)
July 1, 2012 - June 30, 2013

SECTION 1 - OVERVIEW OF C/I AND ITS MISSION

1.1 C/I MISSION STATEMENT

The CGEB Centre was officially approved by the Dalhousie Senate in June, 2008 with the mission to foster collaborations amongst ten comparative genomics/bioinformatics and microbial evolution researchers at Dalhousie. The main focus of the Centre's research is understanding how microbial genomes evolve and diversify, however the research programs collectively span computational biology, biological oceanography, computer science, statistical modeling and comparative genomics, with a strong focus on method and theory.

Specifically, the CGEB Centre's goals are to: 1) recruit top-notch postdoctoral fellows and Ph.D. students to CGEB labs through the provision of Tula Foundation fellowships and research allowances; 2) maintain a CGEB seminar series to attract world-class speakers to interact with CGEB principal investigators and trainees; 3) fund CGEB trainees to attend and present their work at national and international scientific meetings; and 4) provide an intellectual forum that promotes collaborations between CGEB members and facilitates applications for external research funding. For each of the last five years, we have met or exceeded all of these goals.

1.2 CURRENT YEAR'S ACTIVITIES

A. CGEB Seminar Series

The seminar series has successfully hosted several well-attended seminars this past year, all sponsored by funding from the Tula Foundation.

- Dr. Trevor Lawley, Wellcome Trust Sanger Institute, U.K., June 2013. "*Emergence and global spread of healthcare-associated Clostridium difficile*"
- Dr. Vamsi Mootha, Harvard Medical School, April 2013. "*Comparative mitochondrial physiology*"
- Dr. James McNerney, National University of Ireland, December 2012. "*Shedding light on eukaryote origins: New approaches and new data*"
- Dr. Josh Neufeld, University of Waterloo, July 2012. "*Exploring the uncharted microbial frontier through targeted recovery of taxonomic novelty*"
- Dr. Maureen O'Malley, University of Sydney, July 2012. "*Prokaryote evolution: Is there something special about it?*"

B. Sponsorship of International Meeting Symposia

CGEB financially supported the following symposia through our Seminar Series funds from the Tula Foundation:

- a symposium at the **14th International Congress for Protistology (ICOP XIV)**, Vancouver, (2013)
- a symposium at the **12th International Colloquium on Endocytobiology and Symbiosis**, Dalhousie University (2013)

C. CGEB Journal Clubs

The *CGEB Journal Club* (started in 2007) is open to all CGEB lab trainees and faculty members. The group meets bi-weekly throughout the year. Participants select and present a current research paper for analysis and discussion, most often outside their own immediate research area. Many of our trainees have stated that this activity is invaluable and an integral part of their overall training.

A more specialized *Microbiome Journal Club* meets weekly in Computer Science, and involves faculty and trainees from several CGEB labs. This focuses more specifically on methods of metagenomic and bioinformatic analysis, as these apply to human (microbiomic) and environmental microbial communities. Recently, such discussion formed the foundation of a major review article (Boon *et al.*, 2013).

D. CGEB Lab Meetings

In addition to weekly lab meetings of the Roger/Archibald/Slamovits/Simpson/Gray/Doolittle labs, we also hold monthly CGEB ‘joint lab meetings’ that include all ten CGEB lab faculty members, trainees, lab personnel and associates. The purpose of these meetings is to introduce CGEB faculty and trainees to the ever-expanding group of trainees in the various labs and to initiate collaborative projects between departments. Faculty members and/or their trainees provide an overview of their research in a seminar-style format, with adequate time allotted for questions, constructive criticism, and open discussion.

E. Publications and Presentations

During the reporting period, CGEB faculty and trainees have published 64 papers and 10 book chapters (*see Section 2.2.1*), including contributions in high impact journals such as *Nature*, *Current Biology*, *Proceedings of the National Academy of Sciences USA*, and *PLoS Biology*. The international profile of CGEB researchers is further demonstrated by the 28 invited presentations given at international conferences or invited seminars (*see Section 2.3*). In addition, CGEB trainees collectively contributed to 53 presentations at domestic and international events (*see Section 2.4*).

F. CGEB Developed Software

A large portion of CGEB research efforts is directed at development of computer software tools for evolutionary modeling analyses and bioinformatics. Since 2007, CGEB has produced 33

bioinformatics software tools (*see Section 2.9 for new software, 2012-2013*). These are ‘open-source’ software tools (or suites of tools) for analysis of genomic data that have been created, published and made available (or soon will be) to the international scientific community through free web access.

G. External Funding

CGEB researchers have been extremely successful in attracting external funding, collectively garnering a total of ~\$1,986,580 of external grant support over 2012-2013 from NSERC, CIHR, CFI, Canada Research Chairs, the Canadian Institute for Advanced Research, NSHRF, and the Tula Foundation (*see Section 3.2.1*).

1.3 COMING YEAR’S ACTIVITIES

The main core activities that have really sustained the productivity of the CGEB Centre to date (see above descriptions) will continue in the next year. These include:

- weekly lab meetings and monthly joint lab meetings
- bi-weekly CGEB Journal club, and weekly Microbiome Journal Club
- CGEB Seminar Series (invited speakers)
- continued sponsorship of student travel/presentations at domestic and international events
- meetings of CGEB PIs to discuss Centre business (annual meetings, plus occasional *ad hoc* meetings)

In addition to the above regular activities, in the coming year we plan to host several special events that will be partially sponsored by CGEB (using the CGEB New Opportunities fund; Section 3.1 – III, pg. 22). The first is a one-day meeting (Dec. 7th, 2013) entitled ‘Death of evidence: fashion-driven distortion in science publishing’ in which several high-profile speakers will be presenting, including Dr. Sarah Richardson (Harvard), Dr. Rosemary Redfield (UBC) and Dr. Florian Maderspacher (Elsevier publishing). The second meeting, still in the early planning stages, would be a microbiomics meeting to which both local CGEB community and non-CGEB scientists and high-profile international researchers will be invited. This would occur in the summer of 2014.

SECTION 2 – DETAILED DESCRIPTION OF C/I ACTIVITIES

2.1 CORE GROUP OF PERSONNEL AFFILIATED WITH THE C/I

Summary of C/I Personnel (2012-13)

Position	Number
Faculty Members	10
Administrative Staff	1
Technical Staff	6
Research Associates	1
Other Associate Members	5
Postdoctoral Fellows	20
Doctoral Students	13
Master's Students	6
Other (i.e. Undergraduates / Honours students)	11
Total:	73

2.1.1 List faculty attached to the C/I involved in research (*include name, rank, affiliation*)

1. Dr. Andrew Roger, Professor and Tier I Canada Research Chair, Biochemistry and Molecular Biology
2. Dr. W. Ford Doolittle, Professor Emeritus, Biochemistry and Molecular Biology
3. Dr. John Archibald, Professor, Biochemistry and Molecular Biology
4. Dr. Claudio Slamovits, Assistant Professor, Biochemistry and Molecular Biology
5. Dr. Michael Gray, Professor Emeritus, Biochemistry and Molecular Biology
6. Dr. Joseph Bielawski, Associate Professor, Biology
7. Dr. Alastair Simpson, Associate Professor, Biology
8. Dr. Robert Beiko, Assistant Professor and Tier II Canada Research Chair, Computer Science
9. Dr. Christian Blouin, Associate Professor, Computer Science, and Biochemistry and Molecular Biology
10. Dr. Edward Susko, Professor, Mathematics and Statistics

2.1.2 List administrative and technical staff involved in the C/I (*include name, role*)

1. Katherine Dunn, Research Associate – Bielawski lab
2. Wanda Danilchuk, CGEB Administrator – Doolittle / Roger lab
3. Jacquie De Mestral, Lab Manager – Roger lab
4. Marlena Dlutek, Lab Manager – Archibald lab
5. Naoko Tanifuji, Lab Technician – Archibald lab
6. Danielle Wentzell, Lab Technician – Slamovits lab
7. Katherine Rutherford, Lab Technician – Beiko lab
8. Alexander Keddy, Lab Technician – Beiko lab

2.1.3 Optional – list other research personnel in other categories not covered in 2.1.1 and 2.1.2 but included in Summary Table; note that students will be listed in 2.5

There were 20 Postdoctoral Fellows in CGEB labs during the reporting period.

Name	Department	Supervisors
Brown, Matt (completed)	Biochemistry & Mol. Biol.	A.J. Roger
Eme, Laura (ongoing)	Biochemistry & Mol. Biol.	A.J. Roger
Gentekaki, Eleni (ongoing)	Biochemistry & Mol. Biol.	A.J. Roger
Kolisko, Martin (completed)	Biochemistry & Mol. Biol.	A.J. Roger
Gawryluk, Ryan (completed)	Biochemistry & Mol. Biol.	A.J. Roger
Wang, Huaichun (ongoing)	Mathematics & Statistics	E. Susko / A. Roger
Curtis, Bruce (ongoing)	Biochemistry & Mol. Biol.	J. Archibald / A. Roger C. Slamovits
Gruber, Ansgar (completed)	Biochemistry & Mol. Biol.	J. Archibald
Hopkins, Julia (completed)	Biochemistry & Mol. Biol.	J. Archibald
Hua, Jimeng (completed)	Biochemistry & Mol. Biol.	J. Archibald
Maruyama, Shinichiro (completed)	Biochemistry & Mol. Biol.	J. Archibald
Nakayama, Takuro (completed)	Biochemistry & Mol. Biol.	J. Archibald
Tanifuji, Goro (completed)	Biochemistry & Mol. Biol.	J. Archibald
Boon, Eva (ongoing)	Biology	J. Bielawski
Shafiei, Mahdi (completed)	Biology	J. Bielawski
Langille, Morgan (ongoing)	Computer Science	R. Beiko
Meehan, Conor (ongoing)	Computer Science	R. Beiko / J. Bielawski
Breglia, Susana (ongoing)	Biochemistry & Mol. Biol.	C. Slamovits
Gile, Gillian (ongoing)	Biochemistry & Mol. Biol.	C. Slamovits
Malik, Shehre-Banoo (completed)	Biochemistry & Mol. Biol.	C. Slamovits

Visiting (International) Students and Researchers:

1. Vojta David, Master's student, University of South Bohemia, Czech Republic (Archibald lab; July 17-Sept. 17, 2013)
2. Tomas Panek, PhD student, Charles University, Czech Republic (Roger lab; June 26-Oct. 1, 2013)
3. Sebastien Najle, Visiting Scientist, Instituto de Biologia Molecular y Celular de Rosario, Argentina (Slamovits lab; April 1 – July 30, 2013)
4. Eliska Ptackova, PhD student, Charles University, Czech Republic (Roger lab; Oct. 1 – Nov. 30, 2012)
5. Guifre Torruella, PhD student, Institut de Biologia Evolutiva, Spain (Roger lab; Sept. 1 – Dec. 7, 2012)
6. Dr. Ryoma Kamikawa, Assistant Professor, University of Tsukuba, Japan (Roger lab; July 1-26, 2012)
7. Dr. Wonje Lee, Professor, Kyungnam University, Korea (Simpson lab; Feb. 2012-Feb. 2013)

CGEB 'Associate' Members:

1. Dr. Julie LaRoche, Professor of Biology (Marine Geochemistry), and Tier I Canada Research Chair
2. Dr. Sean Myles, Assistant Professor, Faculty of Agriculture, and Tier I Canada Research Chair
3. Dr. Hong Gu, Associate Professor, Mathematics and Statistics
4. Dr. Christopher Field, Professor Emeritus, Mathematics and Statistics
5. Dr. Robert Lee, Adjunct Professor, Biology

2.2 PUBLICATIONS ASSOCIATED WITH C/I (July 1, 2012 - June 30, 2013)

Summary of Publications: total 74

Publication Type	Number
Peer-reviewed journals	64
Book chapters	10

2.2.1 List of Publications (include only those publications in print in the reporting period)

[Note: CGEB members and trainees are in bold]

I. Peer-Reviewed Journal Publications (64)

Adl, S.M., **Simpson, A.G.B.**, Lane, C.E., Lukes, J., Bass, D., Bowser, S.S., **Brown, M.W.**, Burki, F., Dunthorn, M., Hampl, V., **Heiss, A.**, Hoppenrath, M., Lara, E., Legall, L., Lynn, D.H., McManus, H., Mitchell, E.A.D., Mozley-Stanridge, S.E., Parfrey, L.W., Pawlowski, J., Rueckert, S., Shadwick, L.L., Schoch, C., Smirnov, A. and Spiegel, F.W. (2012) The revised classification of eukaryotes. *J. Eukaryot. Microbiol.*, 59: 429-493.

Bay, R.A. and **Bielawski, J.P.** (2013) Inference of functional divergence among proteins when the evolutionary process is non-stationary. *J. Mol. Evol.* 76: 205-215.

Bielawski, J.P. (2013) Detecting the signatures of adaptive evolution in protein-coding genes. *Curr. Protoc. Mol. Biol.* Jan; Chapter 19: Unit 19.1.

Boon, E., Meehan, C.J., Whidden, C., Wong, D.H., Langille, M.G. and Beiko, R.G. (2013). Interactions in the microbiome: communities of organisms and communities of genes. *FEMS Microbiol. Rev.* [epub ahead of print, doi: 10.1111/1574-6976.12035].

Breglia, S.A., Yubuki, N. and Leander, B.S. (2013) Ultrastructure and molecular phylogenetic position of *Heteronema scaphurum*: a eukaryovorous euglenid with a cytoproct. *J. Eukaryot. Microbiol.* 60: 107-120.

Brown, M.W., Kolisko, M., Silberman, J.D. and Roger, A.J. (2012) Aggregative multicellularity evolved independently in the eukaryotic supergroup Rhizaria. *Curr. Biol.* 22: 1123-1127.

Burger, G., **Gray, M.W.**, Forget, L. and Lang, B.F. (2013) Strikingly bacteria-like and gene-rich mitochondrial genomes throughout jakobid protists. *Genome Biol. Evol.* 5: 418-438.

Curtis BA, Tanifuji G, Burki F, **Gruber A**, Irimia M, **Maruyama S**, Arias MC, Ball SG, **Gile GH**, Hirakawa Y, **Hopkins JF**, Kuo A, Rensing SA, Schmutz J, Symeonidi A, Elias M, Eveleigh RJ, Herman EK, Klute MJ, **Nakayama T**, Oborník M, Reyes-Prieto A, Armbrust EV, Aves SJ, **Beiko RG**, Coutinho P, Dacks JB, Durnford DG, Fast NM, Green BR, Grisdale CJ, Hempel F, Henrissat B, Höppner MP, Ishida K, **Kim E**, Kořený L, Kroth PG, Liu Y, **Malik SB**, Maier UG, McRose D, Mock T, Neilson JA, Onodera NT, Poole AM, Pritham EJ, Richards TA, Rocop G, Roy SW, Sarai C, Schaack S, Shirato S, **Slamovits CH**, Spencer DF, Suzuki S, Worden AZ, Zauner S, Barry K, Bell C, Bharti AK, Crow JA, Grimwood J, Kramer R, Lindquist E, Lucas S, Salamov A, McFadden GI, Lane CE, Keeling PJ, **Gray MW**, Grigoriev IV and **Archibald JM** (2012) Algal genomes reveal evolutionary mosaicism and the fate of nucleomorphs. *Nature* 492: 59-65.

Doolittle, W.F. (2013) Natural selection through survival alone, and the possibility of Gaia. *Biology and Philosophy* (published online; 9 June).

Doolittle, W.F. (2013) Is junk DNA bunk? A critique of ENCODE. *Proc. Natl. Acad. Sci. USA* 110: 5294-5300.

Doolittle, W.F., Fraser, P., Gerstein, M.B., Graveley, B.R., Henikoff, S., Huttenhower, C., Oshlack, A., Ponting, C.P., Rinn, J.L., Schatz, M.C., Ule, J., Weigel, D. and Weinstock, G.M. (2013) Sixty years of genome biology. *Genome Biol.* 14: 113.

Doolittle, W.F. (2013) Carl R. Woese (1928-2012). *Current Biol.* 23: R183-185.

Doolittle, W.F. (2012) Population genomics: how bacterial species form and why they don't exist. *Current Biol.* 22: R451-453.

Doolittle, W.F. (2012) Microbial neopleomorphism. *Biology and Philosophy* 28: 351-378.

Dunn, K.A., Jiang, W., **Field, C.** and **Bielawski, J.P.** (2013) Improving evolutionary models for mitochondrial protein data with site-class specific amino acid exchangeability matrices. *PLoS One* 8: e55816.

Feehan, C.J., **Johnson-Mackinnon, J.**, Scheibling, R.E., Lauzon-Guay, J.-S. and **Simpson, A.G.B.** (2013) Validating the identity of *Paramoeba invadens*, the causative agent of recurrent mass mortality of sea urchins in Nova Scotia. *Diseases of Aquatic Organisms* 103: 209-227.

Gaston, D. and **Roger, A.J.** (2013) Functional divergence and convergent evolution in the plastid-targeted glyceraldehyde-3-phosphate dehydrogenases of diverse eukaryotic algae. *PLoS ONE* 8: e70396.

Gawryluk, R.M., Chisholm, K.A., Pinto, D.M. and **Gray, M.W.** (2012) Composition of the mitochondrial electron transport chain in *Acanthamoeba castellanii*: structural and evolutionary insights. *Biochim. Biophys. Acta.* 1817: 2027-2037.

Gile, G.H., Carpenter, K.J., James, E.R., Scheffrahn, R.H. and Keeling, P.J. (2013) Morphology and molecular phylogeny of *Staurojoenina mulleri* sp. nov. (Trichonymphida, Parabasalia) from the hindgut of the kalotermitid *Neotermes jouteli*. *J. Eukaryot. Microbiol.* 60:203-213.

Gile, G.H. and **Slamovits, C.H.** (2012) Phylogenetic position of *Lophomonas striata* Butschli (Parabasalia) from the hindgut of the cockroach *Periplaneta americana*. *Protist* 163: 274-283.

Gray, M.W. (2012) Mitochondrial evolution. *Cold Spring Harb Perspect Biol.* 4: a011403.

Gray, M.W. (2012) Evolutionary origin of RNA editing. *Biochemistry* 51: 5235-5242.

Harding, T., **Brown, M.W.**, Plotnikov, A., Selivanova, E., Park, J.S., Gunderson, J.H., Baumgartner, M., Silberman, J.D., **Roger, A.J.** and **Simpson, A.G.B.** (2013) Amoeba stages in the deepest branching heteroloboseans, including *Pharyngomonas*: Evolutionary and systematic implications. *Protist* 164: 272-286.

Heiss, A.A., Walker, G. and **Simpson, A.G.B.** (2013) The microtubular cytoskeleton of the apusomonad *Thecamonas*, a sister lineage to the opisthokonts. *Protist* 164: 598–621.

Hopkins, J.F., Spencer, D.F., Laboissiere, S., Neilson, J.A., **Eveleigh, R.J.**, Durnford, D.G., **Gray, M.W.** and **Archibald, J.M.** (2012) Proteomics reveals plastid- and periplastid-targeted proteins in the chlorarachniophyte alga *Bigeloviella natans*. *Genome Biol. Evol.* 4: 1391-1406.

Hug, L.A., **Beiko, R.G.**, Rowe, A.R., Richardson, R.E. and Edwards, E.A. (2012) Comparative metagenomics of three Dehalococcoides-containing enrichment cultures: the role of the non-dechlorinating community. *BMC Genomics* 13: 327.

Jiang, X., **Langille, M.G.I.**, Neches, R.Y., Elliot, M., Levin, S.A., Eisen, J.A., Weitz, J.S., Dushoff, J. (2012) Functional biogeography of ocean microbes revealed through non-negative matrix factorization. *PLoS ONE* 7: e43866.

Kamikawa, R., **Brown, M.W.**, Nishimura, Y., Sako, Y., **Heiss, A.A.**, Yubuki, N., **Gawryluk, R.**, **Simpson, A.G.B.**, **Roger, A.J.**, Hashimoto, T. and Inagaki, Y. (2013) Parallel re-modeling of EF-1a function: divergent EF-1 a genes co-occur with EFL genes in diverse distantly related eukaryotes. *BMC Evol. Biol.* 13: 131.

Kim, E. and **Archibald, J.M.** (2013) Ultrastructure and molecular phylogeny of the cryptomonad *Goniomonas Avonlea* sp. nov. *Protist* 164: 160-182.

Lepetit, B., Sturm, S., Rogato, A., **Gruber, A.**, Sachse, M., Falciatore, A., Kroth, P.G., Lavaud, J. (2013) High light acclimation in the secondary plastids containing diatom *Phaeodactylum tricorutum* is triggered by the redox state of the plastoquinone pool. *Plant Physiol.* 161: 853–865.

Li, L., Nelson, C.J., Carrie, C., **Gawryluk, R.M.**, Solheim, C., **Gray, M.W.**, Whelan, J. and Millar, A.H. (2013) Subcomplexes of ancestral respiratory complex I subunits rapidly turn over in *in vivo* as productive assembly intermediates in Arabidopsis. *J. Biol. Chem.* 288: 5707-5717.

Liberles, D., Teichmann, S., Bahar, I., Bastolla, U., Bloom, J., Bornberg-Bauer, E., Colwell, L., de Koning, J., Dokholyan, N., Echave, J., Elofsson, A., Gerloff, D., Goldstein, R., Grahnen, J., Holder, M., Lakner, C., Lartillot, N., Lovell, S., Naylor, G., Perica, T., Pollock, D., Pupko, T., Regan, L., **Roger, A.**, Rubinstein, N., Shakhnovich, E., Sjölander, K., Sunyaev, S., Teufel, A., Thorne, J., Thornton, J., Weinreich, D. and Whelan, S. (2012) The interface of protein structure, protein biophysics, and molecular evolution. *Protein Sci.* 21: 769-785.

Lommer, M., Specht, M., Roy, A.S., Kraemer, L., Andreson, R., Gutowska, M.A., Wolf, J., Bergner, S.V., Schilhabel, M.B., Klostermeier, U.C., **Beiko, R.G.**, Rosenstiel, P., Hippler, M. and Laroche, J. (2012) Genome and low-iron response of an oceanic diatom adapted to chronic iron limitation. *Genome Biol.* 13: R66.

Lynch, E.A., **Langille, M.G.I.**, Darling, A., Wilbanks, E.G., Haltiner, C., Shao, K.S.Y., Starr, M.O., Teiling, C., Harkins, T.T., Edwards, R.A., Eisen, J.A. and Facciotti, M.T. (2012) Sequencing of seven haloarchaeal genomes reveals patterns of genomic flux. *PLoS ONE* 7: e41389.

MacDonald, N.J., **Parks, D.H.** and **Beiko, R.G.** (2012) Rapid identification of high-confidence taxonomic assignments for metagenomic data. *Nucleic Acids Res.* 40: e111.

Maruyama, S., **Eveleigh, R.J.** and **Archibald, J.M.** (2013) Treetrimmer: a method for phylogenetic dataset size reduction. *BMC Res. Notes* 6: 145.

Meehan, C.J. and **Beiko, R.G.** (2012) Lateral gene transfer of an ABC transporter complex between major constituents of the human gut microbiome. *BMC Microbiol.* 12: 248.

Moore, C.E., **Curtis, B.**, Mills, T., **Tanifuji, G.** and **Archibald, J.M.** (2012) Nucleomorph genome sequence of the cryptophyte alga *Chroomonas mesostigmatica* CCMP1168 reveals lineage-specific gene loss and genome complexity. *Genome Biol. Evol.* 4: 1162-1175.

Nakayama, T. and **Archibald, J.M.** 2012. Evolving a photosynthetic organelle. *BMC Biol.* 10: 35 (invited review article).

Nakayama, T., Ishida, K. and **Archibald, J.M.** (2012) Broad distribution of TPI-GAPDH fusion proteins among eukaryotes: evidence for glycolytic reactions in the mitochondrion? *PLoS One* 7: e52340.

O'Malley, M.A., **Simpson, A.G.B.** and **Roger, A.J.** (2013) The other eukaryotes in light of evolutionary protistology. *Biol. Philos.* 28: 299-330.

Onodera, N.T., Ryu, J., Durbic, T., Nislow, C., **Archibald, J.M.** and Rohde, J.R. (2012) Genome sequence of *Shigella flexneri* serotype 5a strain M90T Sm. *J. Bacteriol.* 194: 3022.

Park, J.S., DeJonckheere, J.F. and **Simpson, A.G.B.** (2012) Characterization of *Selenaion koniopes* n. gen., n. sp., an amoeba that represents a new major lineage within Heterolobosea, isolated from the Wieliczka salt mine. *J. Euk. Microbiol.* 59: 601-613.

Parks, D.H. and **Beiko, R.G.** (2013) Measures of phylogenetic differentiation provide robust and complementary insight into microbial communities. *ISME J.* 7: 173-183.

Parks, D.H. and **Beiko, R.G.** (2012) Measuring community similarity with phylogenetic networks. *Mol. Biol. Evol.* 29: 3947-3958.

Parks, D.H., Mankowski, T., Zangooui, S., **Porter, M.S.**, Armanini, D.G., Baird, D.J., **Langille, M.G.** and **Beiko, R.G.** (2013) GenGIS 2: Geospatial analysis of traditional and genetic biodiversity, with new gradient algorithms and an extensible plugin framework. *PLoS One* 8: e69885.

Pawlowski J., Audic S., Adl S., Bass D., Belbahri L., Berney C., Bowser SS, Cepicka I., Decelle J., Dunthorn M., Fiore-Donno AM, **Gile GH**, Holzmann M., Jahn R., Jirků M., Keeling PJ, Kostka M., Kudryavtsev A., Lara E., Lukeš J., Mann DG, Mitchell EA, Nitsche F., Romeralo M., Saunders GW, **Simpson AG**, Smirnov AV, Spouge JL, Stern RF, Stoeck T, Zimmermann, J., Schindel, D. and de Vargas, C. (2012) CBOL protist working group: Barcoding eukaryotic richness beyond the animal, plant and fungal kingdoms. *PLoS Biology* 10: e1001419.

Porter, M.S. and **Beiko, R.G.** (2013) SPANNER: Taxonomic assignment of sequences using pyramid matching of similarity profiles. *Bioinformatics* 29: 1858-1864.

Rao, B.S., Mohammad, F., **Gray, M.W.** and Jackman, J.E. (2013) Absence of a universal element for tRNA^{His} identity in *Acanthamoeba castellanii*. *Nucleic Acids Res.* 41: 1885-1894.

Sharpton, T.J., Jospin, G., Wu, D., **Langille, M.G.I.**, Pollard, K.S. and Eisen, J.A. (2012) Sifting through genomes with iterative-sequence clustering produces a large, phylogenetically diverse protein-family resource. *BMC Bioinformatics* 13: 624.

Smith, D.R., Hua, J., **Archibald, J.M.** and **Lee, R.W.** (2013) Palindromic genes in the linear mitochondrial genome of the nonphotosynthetic green alga *polytomella magna*. *Genome Biol. Evol.* 5: 1661-1667.

Smith, S.E., Showers-Corneli, P., Dardenne, C.N., Harpending, H.H., Martin, D.P., **Beiko, R.G.** (2012) Comparative genomic and phylogenetic approaches to characterize the role of genetic recombination in mycobacterial evolution. *PLoS One* 7: e50070.

Sturm, S., Engelken, J., **Gruber, A.**, Vugrinec, S., Kroth, P.G., Adamska, I. and Lavaud, J. (2013) A novel type of light-harvesting antenna protein of red algal origin in algae with secondary plastids. *BMC Evol. Biol.* 13: 159.

Susko, E. (2013). Likelihood ratio tests with boundary constraints using data-dependent degrees of freedom. *Biometrika* - advance access doi: 10.1093/biomet/ast032.

Susko, E. and Roger, A.J. (2013) Problems with estimation of ancestral frequencies under stationary models. *Syst. Biol.* 62: 330-338.

Susko, E. and Roger A.J. (2012) The probability of correctly resolving a split as an experimental design criterion in phylogenetics. *Syst. Biol.* 61: 811-821.

Tsaousis, A.D., Ollagnier de Choudens, S., **Gentekaki, E.**, Long, S., **Gaston, D.**, Stechmann, A., Vinella D., Py, B., Fontecave, M., Barras, F., Lukeš, J. and **Roger A.J.** (2012) Evolution of Fe/S cluster biogenesis in the anaerobic parasite *Blastocystis*. *Proc. Natl. Acad. Sci. USA* 109: 10426-10431.

Wang, H.-C., Susko, E. and Roger, A.J. (2013) The site-wise log-likelihood score is a good predictor of genes under positive selection. *J. Mol. Evol.* 76: 280-294.

Whidden, C., Beiko, R.G., and Zeh, N. (2013) Fixed-parameter and approximation algorithms for maximum agreement forests. *SIAM Journal on Computation* 42: 1431-1466.

Yubuki, N., **Simpson, A.G.B.** and Leander, B.S. (2013) Comprehensive ultrastructure of *Kipferlia bialata* provides evidence for character evolution within the Fornicata (Excavata). *Protist*, **164**: 423-439.

Yubuki, N., **Simpson, A.G.B.** and Leander, B.S. (2013) Reconstruction of the feeding apparatus in *Postgaardi mariagerensis* provides evidence for character evolution within the Symbiontida (Euglenozoa). *Eur. J. Protistology*, 49: 32-39.

Zhang, Q., **Simpson, A.G.B.** and Song, W. (2012) Insights into the phylogeny of systematically controversial haptorian ciliates (Ciliophora, Litostomatea) based on multigene analyses. *Proc. Royal Society, Series B*, 279: 2625-2635.

Zhaxybayeva, O., Swithers, K.S., Foght, J., Green, A., Bruce, D., Detter, C., Tapia, R., Han, S., Teshima, H., Han, J., Woyke, T., Pitluck, S., Nolan, M., Ivanova, N., Pati, A., Land, M.L., Dlutek, M., **Doolittle, W.F.**, Noll, K.M. and Nesbø, C.L. (2012) Genome sequence of the mesophilic Thermotogales bacterium *Mesotoga prima* MesG1.Ag.4.2 reveals the largest Thermotogales genome to-date. *Genome Biol. Evol.* 4: 700-708.

Zou, L., Susko, E., Field, C. and Roger, A.J. (2012) Fitting nonstationary general-time-reversible models to obtain edge-lengths and frequencies for the Barry-Hartigan Model. *Syst. Biol.* 61: 927-40.

II. Book Chapters (10)

Archibald, J.M. (2012.) The evolution of algae by secondary and tertiary endosymbiosis. In: *Advances in Botanical Research*, G. Piganeau (Ed.), pp. 87-118, Elsevier Press.

Archibald, J.M. (2012) Plastid origins. In: *Organelle Genetics: evolution of organelle genomes and gene expression*, C. Bullerwell (Ed.), pp. 19-38, Springer-Verlag.

Brown, M.W. and Silberman, JD. (2013) The non-dictyostelid sorocarpic amoebae. In: *Dictyostelia - Evolutionary Patterns and Processes in a Social Amoeba*, Baldauf, Romeralo & Escalante (Eds.), Springer, Heidelberg, Germany.

Doolittle, W.F. and Zhaxybayeva, O. (2013) What is a prokaryote? In: *The Prokaryotes – Vol. 1: Prokaryotic Biology and Symbiotic Associations*, edited by E. Rosenberg *et al.*, pp. 41-58, Springer-Verlag.

Gray, M.W. (2013) RNA Editing: Evolutionary Implications. *ELS. Citable Reviews in the Life Sciences*, John Wiley & Sons; online June 2013, DOI:10.1002/9780470015902.a0003069.pub3.

Gray, M.W. and **Archibald, J.M.** (2012) Origins of mitochondria and plastids. In: *Advances in Photosynthesis and Respiration (Genomics of Chloroplasts and Mitochondria)*, R. Bock & V. Knoop (Eds.), pp. 1-30, Springer.

Maruyama, S. and **Archibald, J.M.** (2012) Endosymbiosis, gene transfer, and algal cell evolution. In: *Advances in Algal Cell Biology*, K. Heimann & C. Katsaros (Eds.), pp. 21-41, Walter de Gruyter.

Slamovits, C.H. (2013) Extreme genome reduction in microbial parasites. In: *Comparative Genomics in Neglected Human Parasites*, M.C. López-Camarillo & L.A. Marchat (Eds.), Nova Publishers.

Tsaousis, A.D., Leger, M.L., Stairs, C.W. and **Roger, A.J.** (2012) The biochemical adaptations of mitochondrion-related organelles of parasitic and free-living microbial eukaryotes to low oxygen environments. In *Anoxia, Vol. 21: Cellular Origin, Life in Extreme Habitats and Astrobiology*, pp. 51-81, A.V. Altenbach, J.M. Bernhard & J. Seckbach (Eds.), Springer.

Roger, A.J., Kolisko, M. and **Simpson, A.G.B.** (2012) Phylogenomic analysis. In: *Evolution of Virulence in Eukaryotic Microbes*, L.D. Sibley, B.J. Howlett & J. Heitman (Eds.), pp. 44-69, Wiley-Blackwell.

2.3 PARTICIPATION IN RELEVANT EVENTS FOR RESEARCH DISSEMINATION (including conferences, workshops, symposia, etc.)

What is the number of C/I personnel who participated in <u>international</u> events? - here we've counted those outside Canada.	Professors & Number of Events (<i>i.e. professors who presented at the events</i>)	Students & Number of Events (<i>i.e. students who attended the events</i>)
	Professors: 9 # of events: 28	Students/PDFs: 21 # of events: 12
What is the number of C/I personnel who participated in <u>domestic</u> events? - here we've counted those locally and within Canada.	Professors & Number of Events (<i>i.e. professors who presented at the events</i>)	Students & Number of Events (<i>i.e. students who attended the events</i>)
	Professors: 9 # of events: 16	Students/PDFs: 19 # of events: 13

2.4 COURSES TAUGHT BY MEMBERS OF THE C/I WITH SIGNIFICANT CONTENT RELATED TO THE C/I MISSION STATEMENT

- Please indicate if courses are graduate or undergraduate
- Provide Course Name and Number, Instructor, Course Enrolment (*if known*)

BIOC 4010: Bioinformatics (20 undergraduates); Instructor: Andrew Roger

BIOC 5010: Bioinformatics (4 graduate students); Instructor: Andrew Roger

BIOC 5910: Special Topics (1 graduate student); Instructor: Andrew Roger

BIOC 4010/5010: Bioinformatics (50% of class/labs, 24 graduate & undergraduates); Instructor: Morgan Langille

BIOL 5705: Graduate Modules Course (4 graduate students); Instructor: Morgan Langille

INFX 1615: Concepts of Computing (~ 100 undergraduates); Instructor: Christian Blouin

STAT 5067: Advanced Statistical Theory II (3 graduate students); Instructor: Ed Susko

STAT 4370/5370: Stochastic Processes (4 graduates, 1 undergraduate); Instructor: Ed Susko

STAT 4066/5066: Advanced Statistical Theory (3 graduates, 1 undergraduate); Instructor: Ed Susko

BIOC 3400: Nucleic Acids (~ 80 undergraduates); Instructor: Claudio Slamovits

BIOL 1010.03: Principles of Biology I (33% evolution unit; ~900 undergraduates);

Instructor: Alastair Simpson

BIOL 2004.03: Diversity of Life II (50% 'microbial diversity' section; ~ 250 undergraduates);

Instructor: Alastair Simpson

BIOL 3102.03: Microbial eukaryotes: diversity and evolution (28 undergraduates);

Instructor: Alastair Simpson

BIOL 2030: Genetics and Molecular Biology (200 undergraduates); Instructor: Joe Bielawski

BIOL 3046: Molecular Evolution (47 undergraduates, 1 graduate student); Instructor: Joe Bielawski

BIOL 5705: Biology Graduate Module (16 graduate students); Instructor: Joe Bielawski

BIOL 5706: Biology Graduate Module (Winter term 1 student, full year 1 student);

Instructor: Joe Bielawski

STAT 1060: Introductory Statistics (Fall term, 436 undergraduates; Winter term, 677 undergraduates); Instructor: Joe Bielawski

SCIE 1500: 1 lecture on Bioinformatics for DISP; Instructor: Joe Bielawski

2.5 STUDENT RESEARCH ACTIVITIES RELATED TO THE C/I MISSION

Student Name / Degree + Status / Supervisor / Thesis Title (if applicable)

Courtney Stairs; PhD student (in progress); A.J. Roger

Michelle Leger; PhD student (in progress); A.J. Roger

Susan Sharpe; PhD student (in progress); A.J. Roger

Tommy Harding; PhD student (in progress); co-supervised by A.J. Roger & A. Simpson

Javier Alfaro; Masters student (completed Sept. 2012); A.J. Roger; "*Protein sequence evolution through structurally constrained phylogenetic models*"

Cornelis Mutsaers; Honours student (completed April 2013); A.J. Roger

Bruce Curtis; PhD student (completed Oct. 2012); J. Archibald; "*Endosymbiotic gene transfer in the nucleomorph containing organisms B. natans and G. theta*"

Christa Moore; PhD student (completed June 2013); J. Archibald; "*Comparative genomics of endosymbiotically-derived organelles in cryptophyte algae*"

Sergio Hleap Lozano; PhD student (in progress); C. Blouin

Amin Khalafvand; Master's student (in progress); C. Blouin
 Alex Safatli; Master's student (in progress); C. Blouin
 Wilson Chan; Honours student (completed 2013); C. Blouin
 Kyle Nguyenpi; summer student (completed 2013); C. Blouin
 Robyn Buchwald; Honours student (in progress); A. Simpson
 Jessica Johnson-Mackinnon; Honours student (completed April 2013); A. Simpson
 Kai Miller; Honours student (completed 2013); A. Simpson
 Aaron Heiss, PhD (completed August 2012); A. Simpson; "*Studies on morphology and evolution of 'orphan' eukaryotes*"
 Renny Lee, PhD student (in progress); C. Slamovits
 Mandy McConnell; Honours student (completed April 2013); C. Slamovits
 Donovan Parks, PhD student (completed July 2012); R. Beiko; "*Georeferenced trees and the phylogenetic similarity of biological communities*"
 Christopher Whidden, PhD student (completed July 2013); R. Beiko; "*Efficient computation and application of maximum agreement forests*"
 Dennis Wong, PhD student (in progress); R. Beiko
 Mike Porter; Masters student (completed 2012); R. Beiko; "*Sequence classification and analysis of metabolic networks*"
 Alexander Keddy; undergraduate student (completed 2012); R. Beiko; "*Machine learning classification of mouse frailty genotypes*"
 Brett O'Donnell; undergraduate student (completed 2012); R. Beiko; "*Optimal geographic gradients from many trees*"
 Jose Luis Navarrete; undergraduate student (completed 2012); R. Beiko (co-supervisor); "*Supertrees based on the subtree prune-and-regraft distance*"
 Wei Chen; Masters student (in progress); co-supervised by J. Bielawski & H. Gu
 Jasmin Astle; Honours student (completed 2013); J. Bielawski
 Shelley MacDonald; NSERC-USRA student (completed 2012; now Honours); J. Bielawski
 Sophia Halassy; Master's/PhD student (entered Medical School 2013); J. Bielawski
 Joseph Mingrone; PhD student (in progress); co-supervised by E. Susko & J. Bielawski

(51) PRESENTATIONS by CGEB Trainees [i.e. those listed in Section 2.5 (students) & 2.1.3 (postdocs)]. Presenter and other trainees' names are underlined.

Boon, E. 2013. How many genomes can you fit in a fungus. Biology Department - Friday Informal Seminar Hour, January 18, Dalhousie University. Invited talk.

Boon, E. 2012. Celebrating diversity: genetically differentiated nuclei in arbuscular mycorrhizal fungi. CGEB Joint Lab Seminar, Nov. 1, Dalhousie University. Invited talk.

Breglia, S., Yubuki, N., Leander, B. and Slamovits, C. 2012. Symbiosis between a euglenid and verrucomicrobial bacteria with extrusive structures. Extrusomes in the making? Protist 2012, July 31, Oslo, Norway. Poster.

Brown, M.W., Sharpe, S.C., Silberman, J.D., Simpson, A.G.B., Heiss, A.A. and Roger, A.J. 2012. Finding homes for outcast protistan lineages through phylogenomics; the case of the breviate. Protist 2012, Aug. 3, Oslo, Norway. Invited talk.

Chan, W. 2012. Testing for modularity in protein from molecular dynamics stimulation. Biochemistry Department - Honours Student Seminar, November 15, Dalhousie University.

Eme, L., Gentekaki, E., Curtis, B., Archibald, J.A. and Roger A.J. 2013. Phylogenomic analysis of *Blastocystis* sp. subtype 1 reveals an important role for lateral gene transfer in adaptation to parasitism of the human gut. SMBE Satellite Eukaryotic-omics, April, Davis, CA. Invited talk.

Eme, L. and Roger, A.J. 2012. Pinpointing the root of extant eukaryotic diversity. Protist 2012, July 31, Oslo, Norway. Invited talk.

Gawryluk, R. 2012. A combined proteomic and bioinformatics investigation of the *Acanthamoeba castellanii* mitochondrial proteome. Gordon Research Conference, July 29-Aug. 3, Smithfield, R.I. Poster presentation.

Gentekaki, E. 2013. Comparative genomics of two *Blastocystis* subtypes reveals extensive variability in genome size, content and pathogenic potential. CIFAR – IMB Program Annual Meeting, May 14-17, Whistler, BC. Invited talk.

Gentekaki, E., Eme, L., Curtis, B., Tsaousis, A., Archibald, J. and Roger, A.J. 2012. *Blastocystis* sp. Nand II strain: an evolutionary mosaic or a deeply divergent organism? Protist 2012, Aug. 2, Oslo, Norway. Invited talk.

Harding, T., Simpson, A.G.B. and Roger, A.J. 2013. Molecular signatures of halophilic lifestyle of the heterotrophic protist *Halocafeteria seosinensis*. Halophiles 2013, Storrs, USA, June 2013 (poster).

Harding, T., Simpson, A.G.B. and Roger, A.J. 2013. Molecular signatures of halophilic lifestyle of the heterotrophic protist *Halocafeteria seosinensis*. CIFAR - Integrated Microbial Biodiversity Program Meeting, Whistler, May 2013 (poster).

Heiss, A. 2012. Understanding the evolution of eukaryotic cells, using supercomputers, electron microscopes, and play-doh. Biology Department Seminar, September 28, Dalhousie University. Seminar.

Heiss, A.A., Walker, G. and Simpson, A.G.B. 2012. The cytoskeleton of *Breviata*, and the nature of the ancestral eukaryote flagellar apparatus. Protist 2012, Aug. 3, Oslo, Norway. Invited talk.

Hleap, J.S., Nguyen, K.N., Safatli, A. and Blouin, C. 2013. Reference matters: an efficient and scalable algorithm for large multiple structure alignment. International Conference on Bioinformatics and Computational Biology (BICoB), March 4-6, Honolulu, USA. Talk.

Hleap, J.S. and Blouin, C. 2012. The evolutionary modules round rays, foxes and the tim-barrel of α -amylase: modularity as evolutionary integration. 1st Joint Congress on Evolutionary Biology, July, Ottawa. Poster.

Hleap, J.S. and C. Blouin. 2012. Robust inference of structural modules in sets of homologous proteins. iEvoBio 2012, July 11, Ottawa. Talk.

Kamikawa, R., Nishimura, Y., Yabuki, A., Kolisko, M., Simpson, A.G.B., Roger, A.J., Ishida, K.-I., Hashimoto, T. and Inagaki, Y. 2012. The phylogenetic position and mitochondrial genome sequence of the enigmatic discobid *T. globosa*. Protist 2012, Aug. 2, Oslo, Norway. Invited talk.

Kim, E. 2012. Origin of photosynthetic eukaryotes: inferring traits of pre-green ancestors. Protist 2012, July 31, Oslo, Norway. Invited talk.

Klimes, V., Vlcek, C., Elias, M., Fousek, J., Paces, J., Gray, M.W., Leger, M.M., Roger, A.J. and Lang, B.F. (2012). Assembling and annotating the nuclear genome of the jakobid flagellate *Andalucia godoyi*. Protist 2012, July 29-August 3, Oslo, Norway. Poster.

Kolisko, M., Kamikawa, R., Takishita, K., Cepicka, I., Zhang, Q., Hashimoto, T., Akinori, Y., Inagaki, Y., Roger, A.J. and Simpson, A.G.B. 2012. Evolutionary analysis of mitochondrial ancestry of diplomonads: Phylogenomics of mitochondrial-related organelles in Carpediemonas-like organisms. Protist 2012, Aug. 2, Oslo, Norway. Invited talk.

Langille, M. 2013. Discovering human microbial interactions using next-gen bioinformatics. Department of Pharmacology – Faculty Interview Lecture, June 17, Dalhousie University. Invited lecture.

Langille, M. 2013. Predictive functional profiling of microbial communities using 16S marker gene sequences. CAU Kiel Joint Workshop, April 19, 2013, Dalhousie University. Invited talk.

Langille, M. 2013. Git and GitHub. Faculty of Computer Science Free School, March 21, Dalhousie University. Invited talk.

Langille, M. 2012. Inferring microbial community function from taxonomic composition. Microbial Genomics 2012, Sept. 19, Lake Arrowhead, CA. Invited talk.

Langille, M. 2012. Leveraging ancestral state reconstruction to infer community function from a single marker gene. iEvoBio 2012, July 11, Ottawa. Invited talk.

Lax, G. and Simpson, A. 2012. Combining molecular data with classical morphology for uncultured phagotrophic euglenids. Protist 2012, August 1, Oslo, Norway. Invited talk.

Lee, R. 2012. Ivy: Interactive, visual programming for phylogenetics. iEvoBio 2012, July 10, Ottawa, Canada. Talk.

Leger, M.M., Hug, L.A. and Roger, A.J. 2012. Adaptations to anaerobiosis in the hydrogenosome of *Andalucia incarcerata*. Protist 2012, Aug. 2, Oslo, Norway. Invited talk.

McConnell, M. 2013. Characterization of spliceosomal introns in dinoflagellate protists. Biochemistry Department - Honours Student Seminar, March 21, Dalhousie University.

Meehan, C.J. 2013. Workshop on Molecular Evolution, Cesky Krumlov, Czech Republic. Head TA and 2 course lectures taught to 70 students, Jan. 21-Feb. 1. Invited course lectures.

Meehan, C.J. 2012. Microbes: what, where and how? Kiel University-Dalhousie University joint workshop, Sept. 13-14, Kiel, Germany. Invited talk.

Meehan, C.J. 2012. Workshop on Molecular Evolution, MBL, Woods Hole, MA. Head TA and 2 course lectures taught to 60 students, July 2012. Invited course lectures.

Mutsaers, C. 2013. Evolution of iron sulphur cluster biogenesis in *Pygsuia biforma*. Biochemistry Department - Honours Student Seminar, March 20, Dalhousie University.

Naijle, S. 2013. Evolutionary history of sterols metabolism in microbial eukaryotes. CIFAR – IMB Program Annual Meeting, May 14-17, Whistler, BC. Invited talk.

Najle, S. 2013. Gene discovery and characterization of sterol metabolism enzymes in *Tetrahymena thermophile*. Biochemistry Departmental Seminar, May 9, Dalhousie University. Invited seminar.

Nakayama, T., Ishida, K.-I. and Archibald, J.M. 2012. Broad distribution of TI-GAPDH fusion proteins among eukaryotes: evidence for glycolysis in the mitochondrion? Protist 2012, Aug. 2, Oslo, Norway. Invited talk.

Parks, D. et al. 2012. Geospatial analysis of genetic and genomic datasets, with new gradient algorithms and an extensible framework. iEvoBio 2012, July 10, Ottawa. Talk.

Parks, D. et al. 2012. Gengis: a geospatial information system for genomic data. iEvoBio 2012, July 11, Ottawa. Talk.

Sharpe, S. 2013. Graduate Student Symposium – Recent Papers for Nature & Science, March 7, Dalhousie University. Talk.

Stairs, C. 2012. Metabolic novelty in the mitochondrion-related organelles of *Beckmonas plexus*: a pathway disappearing act. Recipient of the 2012 Doug Hogue Award in Biochemistry & Molecular Biology, October 18, Dalhousie University. Invited seminar.

Sturm, S., Engelken, J., Gruber, A., Vugrinec, S., Adamska, I., Kroth, P.G. and Lavaud, J. 2012. LHC-like superfamily proteins in diatoms. 22nd International Diatom Symposium, August 28, Ghent. Invited talk.

Tanifuji, G. and Archibald, J. M. 2012. Genomics-enabled insight into the periplastidial compartments of cryptophyte and chlorarachniophyte algae. Protist 2012, August 2, Oslo, Norway. Invited talk.

Tanifuji, G., Onodera, NT, Moore, CE, Hopkins J. and Archibald, JM. 2012. Comparative analysis of nuclear and nucleomorph gene expression in cryptomonad and chlorarachniophyte algae. Protist 2012, 29 July – 3 Aug, Oslo, Norway. Poster.

Tanifuji, G. 2013. Genome and transcriptome analysis of the kinetoplastid endosymbiont of *Neoparamoeba pemaquidensis* (Amoebozoa). CIFAR-IMB Program Meeting, 14-17 May, Whistler, Canada. Invited talk.

Tsaousis, A.D., Gentekaki, E., Nyvltova, Stevens, G.C., Hrdy, I., Roger, A.J. and Tachezy, J. 2012. The anaerobic adaptations of Blastocystis mitochondrion-related organelles and the evolution of mitochondria. Protist 2012, Aug. 2, Oslo, Norway. Invited talk.

Tsaousis, A.D., Gentekaki, E., Gaston, D. and Roger, A.J. 2012. Adaptations of the cytosolic iron/sulfur cluster assembly machinery in microbial eukaryotes. Protist 2012, Aug. 1, Oslo, Norway. Poster.

Whidden, C. 2013. Inferring highways of gene sharing in prokaryotes via agreement forest based models. SMBE 2013, July 7-11, Chicago, USA. Talk.

Whidden, C. 2013. Fixed-parameter algorithms for maximum agreement forests. The 17th Annual New Zealand Phylogenomics Meeting (DOOM 13), February 3-8, Mount Ruapehu, New Zealand. Talk.

Whidden, C. 2012. Observations from a 244-taxa bacterial supertree constructed to minimize lateral genetic transfer. Dalhousie Computer Science in-house conference (DCSI 2012), September 21-22, Halifax, Canada. Awarded Best Oral Presentation.

Whidden, C. 2012. Observations from a 244-taxa bacterial supertree constructed to minimize lateral genetic transfer. iEvoBio 2012, July 11, Ottawa. Talk (received a conference award for this presentation).

Wong, D. and Beiko, R. 2012. Finding lateral gene transfer in microbial communities using metagenomic data. iEvoBio 2012, July 11, Ottawa. Talk.

2.6 MEDIA ENGAGEMENT

a) Broadcast Interview

Andrew Roger: Radio interview on *CBC Radio – Information Morning* following nomination to Fellowship in the Royal Society of Canada, November 14, 2012.

b) Text Interview

Andrew Roger: *The Globe and Mail* - Dalhousie feature article (“Jolly Good Fellows”) on nomination to Fellowship in the Royal Society of Canada, November 19, 2012.

2.7 OUTREACH STRATEGY

- Provide information on events organized by C/I to meet the outreach strategy related to mission.
- see **Section 1.2 (A. Current Year's Activities)** for CGEB-sponsored guest speakers
- see **Section 1.2 (B. Sponsorship of Meeting Symposia)**

2.8 TECHNOLOGY DEVELOPMENT, PATENT OR COMMERCIALIZATION

- see **Section 2.9** (below)

2.9 OTHER ACTIVITIES RELATED TO KNOWLEDGE EXCHANGE

(New) CGEB Developed Software (2012-2013)

Program Name: *ExpressBetaDiversity*, version 1.0

Author: Donovan Parks *et al.* (Beiko lab)

Description: software to compute phylogenetic beta-diversity measures from DNA sample data

<http://kiwi.cs.dal.ca/Software/ExpressBetaDiversity>

Program Name: *NetworkDiversity*, version 1.0

Author: Donovan Parks *et al.* (Beiko lab)

Description: software to compute beta-diversity over phylogenetic networks

<http://kiwi.cs.dal.ca/Software/NetworkDiversity>

Program Name: *rSPR*, version 1.2.0

Author: Chris Whidden *et al.* (Beiko lab)

Description: software for computing the rooted SPR distance, a measure of lateral genetic transfer, for two phylogenetic trees

<http://kiwi.cs.dal.ca/Software/RSPR>

Program Name: *SPR Supertrees*, version 1.2.0

Author: Chris Whidden *et al.* (Beiko lab)

Description: software for computing supertrees with minimal SRP distances from a collection of gene trees

<http://kiwi.cs.dal.ca/Software/SPRSupertrees>

Program Name: *PICRUSt*, version 1.0.0

Author: Morgan Langille (Beiko lab)

Description: bioinformatics software package designed to predict metagenome functional content from marker gene surveys and full genomes

<http://picrust.github.io/>

Program Name: *IslandViewer 2*

Author: Morgan Langille (Beiko lab)

Description: a computational tool that integrates three different genomic island prediction methods: IslandPick, IslandPath-DIMOB, and SIGI-HMM

<http://www.pathogenomics.sfu.ca/islandviewer/query.php>

Program name: *NSGTR-BH*

Author: Liwen Zou (Susko lab)

Description: the program allows one to fit the NSGTR-BH substitution models

<http://www.mathstat.dal.ca/~tsusko>

Program Name: *QmmRAxML, version 2.0*

Author: Huaichun Wang (Susko lab)

Description: software to fit class-frequency mixture models

<http://www.mathstat.dal.ca/~hcwang/QmmRAxML/>

Program name: *pr4design, pr4addbranch, pr4deltaxa and pr4list*

Author: Ed Susko

Description: software to determine the probability of correctly resolving a split for a given tree, substitution process and sequence length

<http://www.mathstat.dal.ca/~tsusko>

Update on *Proteus* (developed in 2011)

Author: Joe Bielawski

Description: This computer program for probability models of gene sequence evolution was continually developed throughout the current year. Last year we reported the program having around 40,000 lines of code. This year we have greatly expanded the models within the program, as well as its capacity to do Bayesian analyses. The program now has 61,245 lines of code.

SECTION 3 – FINANCIAL INFORMATION (April 1 – March 31)

3.1 DOES THE C/I HAVE A SEPARATE OVERALL OPERATING AND ADMINISTRATIVE BUDGET? Yes.

Name of Funding Sources:

- I. Tula Foundation
- II. Dalhousie University (Faculties of Medicine, Science, Computer Science, and VP-Academic & Provost)

Annual Operating/Administration Funds in Reporting Year:

I. TULA FOUNDATION

A. *Administration/Seminar Series/Student Travel* (\$50,000 per annum): this covers \$25,000 toward the Administrator’s salary, \$15,000 for seminar series speakers, and \$10,000 for trainees travel to meetings. This support commenced in July 2007, with an 8-year commitment from Tula (i.e. 2007-2015). Aggregate over 8 years: \$400,000

B. *Research Traineeships (for Postdocs & PhD students)*: these are 5-year ‘slots’ awarded to CGEB faculty for their trainee stipends, plus research expense allowance. Listed below are current slots that are still active (5 others have completed their 5-year installments):

- Archibald lab: \$64,000/year (April 2011 – 2016)
- Blouin lab: \$27,500/year (May 2008 – 2013); 2nd slot \$27,500 (Sept. 2010 – 2015)
- Beiko lab: \$27,500/year (May 2008 – 2013); 2nd slot \$27,500 (May 2010 – 2015)
- Doolittle: installments completed; residual funds supporting a PDF salary until 03/2014
- Susko lab: \$49,000/year (Sept. 2008 – 2013)
- Simpson lab: \$64,000/year (Nov. 2008 – 2013)
- Slamovits lab: \$64,000/year (Dec. 2011 – 2016)

II. DALHOUSIE UNIVERSITY

The Faculties of Medicine, Science, and Computer Science, and the Office of the VP-Academic & Provost collectively committed funding for Years 1-7 (i.e. 2008-2015) to at least match the \$25,000/year committed by the Tula Foundation for CGEB administration.

CGEB - Financial Commitments from Dalhousie:

	Faculty of Medicine	VP, Academic & Provost	Faculty of Science	Faculty of Comp. Science	TOTAL
Year 1: 2008-2009	\$15,000	\$10,000	N/A	N/A	\$25,000
Year 2: 2009-2010	\$15,000	\$10,000	\$1,000	\$1,000	\$27,000
Year 3: 2010-2011	\$10,000	\$10,000	\$6,000	\$3,000	\$29,000
Year 4: 2011-2012	\$10,000	\$10,000	\$7,000	\$4,000	\$31,000
Year 5: 2012-2013	\$10,000	\$10,000	\$8,000	\$5,000	\$33,000
Year 6: 2013-2014	\$10,000	\$10,000	\$8,000	\$5,000	\$33,000
Year 7: 2014-2015	\$10,000	\$10,000	\$8,000	\$5,000	\$33,000

III. OTHER – CGEB NEW OPPORTUNITIES FUND

Another source of funds available to finance CGEB activities is our *New Opportunities Fund*. This is a ‘special purpose account’ (68292) that was originally opened to receive transfers of revenue that was previously generated by CGEB members’ activities (i.e. scientific meetings). The current balance in this account is \$39,697.

The purpose of this fund is to provide additional partial funding or ‘seed’ monies for CGEB activities, the costs of which either exceed existing allocated funds (e.g. the Trainee Travel to Meeting fund, the Seminar Series fund) or one-time events/activities/opportunities that fall under the CGEB mandate. Through this fund CGEB co-sponsored the *CIFAR-IMB Workshop on Eukaryotic Genome Annotation* at Dalhousie in 2010 with the Canadian Institute for Advanced Research (CIFAR). To date these funds have also been used for costs associated with recruitment of potential trainees to CGEB labs (e.g. interview travel and accommodation costs), as well as the initial CGEB website design.

3.2 WHAT RESEARCH GRANTS/AWARDS DIRECTLY RELATED TO THE MISSION STATEMENT WERE AWARDED TO THE ACADEMIC AND RESEARCH POPULATION WITHIN THE C/I NOT LISTED ABOVE?

3.2.1 Current External Research Grants and other Funding

Collectively CGEB faculty members received [**\$1,986,580**] from external research grants and other funding during this reporting period. Grants involving more than one CGEB faculty were only counted once (i.e. for the primary P.I.) to obtain the above total.

John Archibald

- 2011-2016 **Canadian Institutes of Health Research – Operating Grant:** *Endosymbiosis, parasitism, and genome evolution*: \$115,000/year
- 2009-2014 **NSERC Discovery Grant** – *Genome and proteome evolution in nucleomorph-containing algae*: \$34,000/year
- 2011-2016 **Tula Foundation - CGEB Postdoctoral Research Fellowship** (funding for postdoctoral fellowship plus research allowance): \$64,000/year
- 2012-2017 **Canadian Institute for Advanced Research, Program in Integrated Microbial Biodiversity**—research allowance for program fellows: \$24,000/year

Robert Beiko

- 2013-2015 **Genome Canada:** *A federated bioinformatics platform for public health microbial genomics*: \$500,000/year (not counted in above total)
(co-applicant with Fiona S.L. Brinkman, P.I.)
- 2013-2014 **Nova Scotia Health Research Foundation – Scotia Support Grant:** *Frailty and the Microbiome*: \$25,000/year
- 2013-2014 **Nova Scotia Health Research Foundation – Discovery/Innovative Grant:** *A pilot project to assess the gut microbes of patients in an assisted care facility*: \$15,000/year
- 2013-2014 **NRC-IRAP:** *Comparative genomics to identify genes and pathways controlling reproductive longevity of mammals*: \$102,000/year

- 2013-2014 **Nova Scotia Health Research Foundation – Discovery/Innovative Grant:** *The role of the complement system in post-colitis colonization and recovery from injury:* \$15,000/year (co-applicant with A. Stadnyk *et al.*)
- 2011-2014 **Genome Canada, Large-Scale Applied Research Project:** *Biomonitoring 2.0: A high-throughput genomics approach for comprehensive biological assessment of environmental change* (co-applicant with P.I. - M. Hajibabaei, Guelph): ~\$1 million/year (not counted in above total)
- 2010-2013 **Canadian Institutes of Health Research - Emerging Team Grant: Canadian Microbiome Initiative:** *Modeling and mapping microbial diversity and function with marker genes, genomes and metagenomes:* \$223,000/year (with co-PIs: W.F. Doolittle, J. Bielawski & M. Ereshefsky – only counted for Doolittle for above total)
- 2010-2013 **Genome Canada – Applied Genomics Research:** *BEEM: Bioproducts and enzymes from environmental metagenomes* (co-applicant with E. Edwards, P.I.): \$1,250,00/year (not counted in above total)
- 2008-2013 **Tula Foundation** – funding for PhD student traineeship plus research allowance: \$27,500/year
- 2010-2015 **Tula Foundation** – funding for PhD student traineeship plus research allowance: \$27,500/year
- 2012-2016 **NSERC - Discovery Grant:** *Untangling the complex geographic and evolutionary patterns of microbes:* \$33,000/year
- 2012-2017 **Canada Research Chairs (CIHR) – Canada Research Chair (Tier II) in Bioinformatics:** \$100,000/year
- 2012-2013 **NSERC – Engage:** *Machine-learning classification of genomic polymorphism data relating to fertility and reproductive longevity:* \$25,000/year

Joseph Bielawski

- 2011-2012 **ACEnet/Sun Microsystems Research Fellowship:** \$20,000
- 2010-2013 **Canadian Institutes of Health Research – Emerging Team Grant: Canadian Microbiome Initiative:** *Modeling and mapping microbial diversity and function with marker genes, genomes and metagenomes:* \$223,000/year (with co-PIs: W.F. Doolittle, R. Beiko, & M. Ereshefsky – only counted for Doolittle for above total)
- 2009-2013 **NSERC – Discovery Grant:** *Evolutionary analysis of protein diversification: model improvement, assessment and application to real data:* \$36,250/year
- 2007-2012 **Tula Foundation – CGEB Postdoctoral Research Fellowship** (funding for postdoctoral fellowship plus research allowance): \$49,000/year

Christian Blouin

- 2010-2015 **NSERC – Individual Discovery Grant:** *Exploring the landscape of phylogenies:* \$24,000/year
- 2009-2014 **CFI (Infrastructure Operating Funds):** *A high performance computational platform for bioinformatics:* \$12,000/year
- 2010-2015 **Tula Foundation** – CGEB funding for PhD student traineeships plus research allowance: \$27,500/year
- 2008-2013 **Tula Foundation** – CGEB funding for PhD student traineeship plus research allowance: \$27,500/year

W. Ford Doolittle

2010-2013 **Canadian Institutes of Health Research - Emerging Team Grant: Canadian Microbiome Initiative: *Modeling and mapping microbial diversity and function with marker genes, genomes and metagenomes***: \$223,000/year
(P.I. – W.F. Doolittle, with co-PIs: J. Bielawski, R. Beiko)

Andrew Roger

2011-2016 **NSERC Discovery Grant – *Phylogenomic approaches to ancient relationships amongst eukaryotes***: 54,000/year
2011-2014 **NSERC Discovery Grant – Accelerator Supplement**: \$40,000/year
2010-2017 **Canada Research Chairs – Tier I (CIHR) in Comparative Genomics and Evolutionary Bioinformatics**: \$200,000/year (includes 7-yr. salary award, 20% of which is research allowance)
2008-2013 **Canadian Institutes of Health Research, Operating Grant – *Major transitions in eukaryotic cell evolution***: \$719,381 over 5 years
2012-2017 **Canadian Institute for Advanced Research - Program in Integrated Microbial Biodiversity**— research allowance for program fellows: \$24,000/year
2007-2015 **Tula Foundation, Centre for Comparative Genomics & Evolutionary Bioinformatics (CGEB) - administration, seminar series and student travel funds**: \$50,000/year
2007-2012 **Tula Foundation - CGEB Postdoctoral Research Fellowship** (funding for postdoctoral fellowship plus research allowance): \$64,000/year

Alastair Simpson

2009-2014 **NSERC – Individual Discovery Grant: *Microbial eukaryote diversity and evolution in extraordinary environments***: \$34,000/year
2008-2013 **Tula Foundation - CGEB Postdoctoral Research Fellowship** (funding for postdoctoral fellowship plus research allowance): \$64,000/year
2008-2013 **CIHR Operating Grant** (co-applicant with A.J. Roger, P.I.: \$143,876/year – *not counted in above total*)
2012-2017 **Canadian Institute for Advanced Research - Program in Integrated Microbial Biodiversity** - research allowance for program fellows: \$24,000/year

Claudio Slamovits

2013 **NSERC Engage** (in partnership with N.S. Aquaculture Association): Developing diagnostic molecular tools for MSX parasitic disease affecting the oyster industry in Nova Scotia: \$25,000
2012-2013 **Nova Scotia Health Research Foundation – Development/Innovative Grant**: \$15,000
2012-2017 **CFI-NSRIT – Leaders Operating Fund**: \$5,000/year (for infrastructure maintenance)
2011-2016 **Tula Foundation – CGEB Postdoctoral Research Fellowship** (funding for postdoctoral fellowship plus research allowance): \$64,000/year
2013 **NSERC EQPEQ – Research Tools and Instruments - Category 1**: \$147,455
(PI – C. Slamovits, with co-investigators: A.J. Roger, J.M. Archibald, A. Simpson)
2010-2015 **NSERC Discovery Grant: *Genomes of alveolate protists: structure, function and evolution***: \$33,000/year

2012-2017 **Canadian Institute for Advanced Research - Program in Integrated Microbial Biodiversity**— research allowance for program members: \$24,000/year

Ed Susko

2008-2013 **NSERC – Discovery Grant: *Statistical evolutionary bioinformatics***: \$21,000/year

2008-2013 **Tula Foundation – CGEB Postdoctoral Research Fellowship** (funding for postdoctoral fellowship plus research allowance): \$49,000/year

3.2.2 Honours, Awards and Distinctions Received by CGEB Members

We've listed new awards received 2012-2013, as well as ongoing salaried fellowships and scholarships, and lifetime fellowships and honorary memberships.

John Archibald

- Seymour H. Hutner Young Investigator Prize, International Society of Protistologists (2013)
- New Investigator Award, Canadian Institutes of Health Research (5-yr. salary) (2008-2013)
- Fellow, Canadian Institute for Advanced Research - Integrated Microbial Biodiversity Program (2012-2017); previously Scholar (2009-2012)

Robert Beiko

- Canada Research Chair (Tier II) in Bioinformatics (2006 – present; renewed in 2011)

Christian Blouin

- Dean's Award for Excellence in Teaching, Faculty of Computer Science (2012)

W. Ford Doolittle

- Elected Member, The Norwegian Academy (2009-present)
- Institute Fellow, Canadian Institute for Advanced Research (2008-present)
- Member, U.S. National Academy of Sciences (2002-present)
- Fellow, American Academy of Microbiology (1999-present)
- Fellow, Royal Society of Canada (1991-present)
- Fellow, American Association for the Advancement of Science (1985-present)

Michael Gray

- Fellow, American Academy of Microbiology (2012-present)
- Fellow, Royal Society of Canada (1996-present)

Andrew Roger

- President, International Society of Evolutionary Protistology (2012-2014)
- Elected Fellow, Royal Society of Canada (2012)
- Fellow, Canadian Institute for Advanced Research - Integrated Microbial Biodiversity Program (2012-2017; previously 2007-2012)
- Canada Research Chair (Tier I) in Comparative Genomics and Evolutionary Bioinformatics (2010-2017)

Alastair Simpson

- Seymour H. Hutner Young Investigator Prize, International Society of Protistologists (2012)
- Fellow, Canadian Institute for Advanced Research - Integrated Microbial Biodiversity Program (2012-2017); previously Scholar (2009-2012)

Claudio Slamovits

- Scholar, Canadian Institute for Advanced Research - Integrated Microbial Biodiversity Program (2012-2017; previously 2009-2012)