**Matthew S. Fullmer, PhD**

30 Caithness Place, Farm Cove, Auckland, New Zealand | +1 (508) 463-6914

m.fullmer@auckland.ac.nz

Google Scholar: http://tinyurl.com/ScholarMSF

OrcID: http://orcid.org/0000-0002-7391-9048

Current Position

**Lecturer**

School of Biological Sciences, University of Auckland – Auckland, NZ 2023 – Present

Previous Academic Positions

**Research Fellow**, Takeuchi Lab

School of Biological Sciences, University of Auckland – Auckland, NZ

PI: Nobuto Takeuchi 2021 – 2022

**Research Fellow**, Bioinformatics Institute

School of Biological Sciences, University of Auckland – Auckland, NZ

Mentor: Anthony M. Poole 2018 - 2020

EDUCATION

**Postgraduate Certificate in Higher Education** 2023

University of Auckland – Auckland, New Zealand

PhD in Molecular & Cell Biology department, Microbiology program 2011 - 2018

University of Connecticut – Storrs, Storrs, CT

Advisor: J. Peter Gogarten

Thesis Title: Phylogeny, Taxonomy, and the Concept of Lineage in

the Presence of Horizontal Gene Transfer

B.S. Honors in Biology

University of Massachusetts – Amherst, Amherst, MA

Academic Labs: M.A. Riley (02/2006 – 05/2007) & B.B Normark (09/2006-11/2006) 2004 - 2007

Honors Thesis: Characterization of *ampC* *Beta*-Lactamases in Australian Isolates of *Hafnia alvei* and *Escherichia coli*

1st Author Peer-reviewed PUBLICATIONS

**Fullmer, M. S.**\*, Ouellette, M.\*, Louyakis, A.S.\*, Papke, R.T., and Gogarten, J. P. (2019). **The Patchy Distribution of Restriction-Modification System Genes and the Conservation of Orphan Methyltransferases in Halobacteria.** *Genes.* 10, 233. doi: ﻿10.3390/genes10030233 2019

\***Contributed equally**

**Fullmer, M. S.**, Soucy, S. M., and Gogarten, J. P. (2015). **The pan-genome as a shared genomic resource: mutual cheating, cooperation and the black queen hypothesis.** *Front. Microbiol.*, 728. doi:10.3389/fmicb.2015.00728. 2015

Colston, S. M**.**\***, Fullmer, M. S.**\*, Beka, L., Lamy, B., Gogarten, J. P., and Graf, J. (2014). **Bioinformatic Genome Comparisons for Taxonomic and Phylogenetic Assignments Using *Aeromonas* as a Test Case**. *mBio* 5, e02136–14. doi:10.1128/mBio.02136-14.

\***Contributed equally** 2014

**Fullmer, M. S.**, Soucy, S. M., Swithers, K. S., Makkay, A. M., Wheeler, R., Ventosa, A., Gogarten, J. P., and Papke, R. T. (2014). **Population and genomic analysis of the genus *Halorubrum*.** *Front. Microbiol.* 5, 140. doi:10.3389/fmicb.2014.00140. 2014

1st Author Pre-Prints (Non-peer reviewed)

**Fullmer, M. S.**, Puente-Lelievre, C., and Matzke, N. (2025). **Adding 3Di characters to amino acid datasets can improve resolution, but the effect is weaker in shorter and alpha-helical proteins such as histones. ﻿***bioRxiv* 2025.06.30.662300doi: 10.1101/2025.06.30.662300. 2025

**Fullmer, M. S.**, van Dijk, B., and Takeuchi, N. (2024). **Interaction range of common goods shapes Black Queen dynamics beyond the cheater-cooperator narrative. ﻿***bioRxiv* 2024.07.16.603646doi: 10.1101/2024.07.16.603646. 2024

Gosselin S.\*, **Fullmer M.S.**\*, Feng Y., Gogarten J.P. **Expanding the utility of sequence comparisons using data from whole genomes.** *bioRxiv 2020; 2020.01.15.908137.*

\***Contributed equally** 2020

Other Peer-reviewed PUBLICATIONS

Takeuchi N., **Fullmer, M. S.**\*, Maddock D.\*, Poole AM (2024). **The constructive black queen hypothesis: new functions can evolve under conditions favouring gene loss.** *ISMEJ.* 10, 233. doi: ﻿ 10.1093/ismejo/wrae011 2024

\***Contributed equally**

Gosselin, S., **Fullmer, M. S.**, Feng, Y., and Gogarten, J. P. (2022). **Improving Phylogenies Based on Average Nucleotide Identity, Incorporating Saturation Correction and Nonparametric Bootstrap Support.** *Syst. Biol.* 71, 396–409. doi:10.1093/sysbio/syab060. 2022

Kloub, L., Gosselin, S., **Fullmer, M.S.**, Graf, J., Gogarten, J.P., Bansal, M.S. (2021). **Systematic Detection of Large-Scale Multi-Gene Horizontal Transfer in Prokaryotes.** *Mol. Biol. Evol.* 38, 2639–2659. doi:10.1093/molbev/msab043. 2021

Beka, L., **Fullmer, M.S.**, Colston, S.M., Nelson, M.C., Talagrand-Reboul, E., Walker, P., Ford, B., Whitaker, IS, Lamy, B., Gogarten, J. P. and Graf, J. (2018**). *Leisingera* sp. JC1, a Low-Level Antimicrobials in the Medicinal Leech Select for Resistant Pathogens That Spread to Patients.** *mBio.* 9 (4). ﻿10.1128/mBio.01328-18 2018

Gromek, S.M, Suria, A.M., **Fullmer, M. S.**, Garcia, J.L., Gogarten, J. P. and Nyholm, S.V. (2016**)**. ***Leisingera* sp. JC1, a Bacterial Isolate from Hawaiian Bobtail Squid Eggs, Produces Indigoidine and Differentially Inhibits Vibrios.** *Front. Microbiol.* 7. 10.3389/fmicb.2016.01342. 2016

Collins, A.J., **Fullmer, M. S.**, Gogarten, J. P. and Nyholm, S.V. (2015). **Comparative genomics of *Roseobacter* clade bacteria isolated from the accessory nidamental gland of *Euprymna scolopes*.** *Front. Microbiol.* 6. doi:10.3389/fmicb.2015.00123. 2015

Soucy, S. M., **Fullmer, M. S.**, Papke, R. T., and Gogarten, J. P. (2014). **Inteins as indicators of gene flow in the Halobacteria**. *Front. Microbiol.* 5, 299. doi:10.3389/fmicb.2014.00299. 2014

Ram Mohan, N., **Fullmer, M. S.**, Makkay, A. M., Wheeler, R. W., Ventosa, A., Naor, A., Gogarten, J. P., and Papke, R. T. (2014). **Evidence from phylogenetic and genome fingerprinting analyses suggests rapidly changing variation in *Halorubrum* and *Haloarcula* populations.** *Front. Microbiol.* 5, 143. doi:10.3389/fmicb.2014.00143. 2014

Book Chapters

**Fullmer, M.S.**, Gogarten, J.P. andPapke, R.T. **Horizontal gene transfer in Halobacteria**, in *Genetics and Genomics of Halophiles* (Papke, R.T. and Oren, A., eds.) Horizon Scientific Press, Norwich, UK 2014

Pre-Prints (Non-peer reviewed)

Puente-Lelievre C, Malik AJ, Douglas J, Ascher D, Baker M, Allison J, Poole AM, Lundin D, **Fullmer M**, Bouckert R, Kim H, Steinegger M, and Matzke,N **Tertiary-interaction characters enable fast, model-based structural phylogenetics beyond the twilight zone.** *bioRxiv 2023; 2023.12.12.571181.* 2023

Grants and Fellowships as PI

**Royal Society Marsden Fund – Fast Start** 2022

Is the mutualistic cheating of the strong black queen hypothesis robust to disturbances?

PI: **Matthew S. Fullmer** Value: **$360,000 NZD** Dates 2023 - 2025

OTher grants and Fellowships as Named AI

**University of Auckland – Faculty Research Development Fund** 2019

Constructing a population genetics theory of bacterial genome evolution

PI: Nobuto Takeuchi Value: $168,000 NZD Dates 2019 - 2020

OTher grants AS PI That reached Finalist stage (Un-Funded)

**Google Research Fund** 2025

Bringing AI to agent-based modelling in microbial ecology

PI: **Matthew S. Fullmer**

**Human Frontier Science Program (HFSP) – Early Career** 2024

The impact of RNA phages on natural ecosystems

PI: Nela Nikolic

Co-PI: **Matthew S. Fullmer**

Co-PI: Fatima Hussain

**Royal Society Marsden Fund – Fast Start** 2021

Does mutualistic cooperation evolve through cheating?

PI: **Matthew S. Fullmer**

**Royal Society Marsden Fund – Fast Start** 2020

Does mutualistic cooperation evolve through cheating?

PI: **Matthew S. Fullmer**

TEACHING EXPERIENCE

Invited Lecturer – Phylogenetics, University of Auckland Early 2025

1/2 of course, 16 enrolled, *post-grad course*

Invited Lecturer – Modelling Biological Processes, University of Auckland Late 2024

~1/9th of course, 28 enrolled, *post-grad course*

Invited Lecturer – Evolution of Genes, Populations, and Species, University of Auckland Late 2024

~1/4 of course, 38 enrolled

Invited Lecturer – Phylogenetics, University of Auckland Early 2024

1/2 of course, 19 enrolled, *post-grad course*

Invited Lecturer – Evolution of Genes, Populations, and Species, University of Auckland Late 2023

~1/4 of course, 17 enrolled

Invited Lecturer – Phylogenetics, University of Auckland Early 2023

1/2 of course, 17 enrolled, *post-grad course*

Invited Lecturer – Microbial Genomics & Metabolism, University of Auckland Early 2020

4 seminars (1/3rd of course), 16 enrolled, *post-grad course*

Invited Lecturer – Evolution and the Origins of Life, University of Auckland Late 2019

Phylogenetics section, 3 lectures, 120 enrolled, 2nd year course

Invited Lecturer – Microbial Genomics & Metabolism, University of Auckland Early 2019

2 seminars, 14 enrolled, *post-grad course*

Invited Lecturer – Evolution and the Origins of Life, University of Auckland Late 2018

Phylogenetics section, 3 lectures, 129 enrolled, 2nd year course

Teaching Assistant – Introduction to Molecular Evolution and Bioinformatics, UConn Late 2017

Included 2 lab sections (~15 students, each). Administered majority of grading.

Teaching Assistant – Fundamentals of Microbiology lab sections, UConn Late 2015

Ran 3 lab sections (~20 students, each). Administered half of all grading.

Teaching Assistant – Introduction to Biology lab sections, UConn Early 2013

Ran 3 lab sections (~40 students, each). Administered half of all grading.

Teaching Assistant – Fundamentals of Microbiology lab sections, UConn Late 2011 – Early 2012

Ran 3 lab sections (~20 students, each). Administered half of all grading.

Mentoring

**University of Auckland:**

Advisor to **Masters** student Feng-Min Cheng (Jul 2024 – Present)

Co-advisor to **PhD** student Masafumi Obara (Jun 2024 – Present)

Advisor to **Masters** student Zhongyu Liu (Jul 2023 – Jun 2025)

Co-advisor to ***Masters*** student Vijayraj Singh w/major advisor Dr. Nobuto Takeuchi (Sep 2022 – Jul 2024)

Co-advisor to ***Masters*** student Daniel Harrison w/major advisor Dr. Nobuto Takeuchi (Jan 2021 – Nov 2022)

**University of Connecticut**:

Had responsibility for **four undergraduate students** in the Gogarten lab, UConn (Jan 2014 – May 2014, Sept 2014 – Spring 2018, Jan 2016 – Spring 2017, and Sept 2016 – Spring 2018)

UConn Mentor Connection (high school students interning for a month over summer break):

UConn Mentor Connection 2015 (July 2015)

UConn Mentor Connection 2014 (July 2014)

UConn Mentor Connection 2012 (July 2012)

**Notable Mentoring Outcomes:**

**University of Auckland:**

**Zhongyu Liu** received a Honours, 2nd Class, 2nd division

**Vijayraj Singh** received a **grade of ‘A+’** on his Masters dissertation

**Daniel Harrison** received a **grade of ‘A’** on his Masters dissertation

See **Posters** above (FAOBMB, 2021; NZMS 2022)

**University of Connecticut**:

**Sean Gosselin** was accepted to the UConn research Masters program and began classes in Fall 2017.

Sean applied to the UConn MCB Ph.D. program and was accepted, beginning his studies in Spring 2018.

See **Other Peer Reviewed Publications** above (Gosselin et al., 2022) and **Pre-Prints (Non-Peer Reviewed)** above (Gosselin & Fullmer et al., 2020)

See **Posters** above (PVMS 2017 - **best poster award winner**, UConn Frontiers 2017, UConn All Biology 2017, Astrobiology Grad 2017, CT branch ASM 2017, 15th Annual Microbial Sciences Symposium 2018)

**Talks** given by Sean during period of mentorship:

Undergraduate All Biology Research Symposium (April 2017) - *A Fast and Easy Methodology for Constructing Phylogenies From ANI Data*

\***Excellence in Applied Genetics and Technology Award**

Undergraduate Research Symposium in Molecular and Cell Biology (April 2017) -*An ANI-Derived Distance Approach for Delimitating Species and Constructing Phylogenies*

Department of Molecular and Cell Biology Graduate Seminar (Feb 2017) - *ANI as a Distance Based Approach to Understanding Phylogeny and Taxonomy*

**Ryan Englander** was accepted to the MD/PhD program at the UConn Health Center beginning May of 2018

See Posters above (NEMPET 2015, PVMS 2017)

**Jeffery O’Brien** was accepted to U. of Pittsburgh’s medical school in but returned to the lab for a 1-year research masters before graduating after spring 2017.

Conference Talks

**Modelling Black Queen Hypotheses: Non-Producers and Mutualistic Communities Exclude Each Other by Frequency Dependent Selection**

Talk presented at NZ Microbiological Society Annual Conference

*Auckland, NZ on November 22, 2023* 2023

**Some limitations of rigid structure comparisons**

Talk presented at Australasian Structural Phylogenetics Meeting 2023

*Auckland, NZ on October 25, 2023* 2023

**Non-producers stall division of labour in microbial ecosystems driven by black queen dynamics**

Talk presented at NZ Microbiological Society Annual Conference

*Wellington, NZ on November 24, 2022* 2022

**Illuminating the twilight zone with phylogenetic analysis of protein structures**

Talk presented at Origins of Coding: DNA, RNA and Proteins

*Auckland, NZ on February 29, 2019* 2019

**Illuminating the twilight zone with phylogenetic analysis of protein structures**

Talk presented at NZ Phylogenomics 2018 DECO 2019 Conference

*Napier, NZ on February 10-14, 2019* 2019

**From a Farm to Your Blood: Resistant Bacterial Infections Transmitted via the Medicinal Leech**

Talk presented at North Eastern Microbiologists: Physiology, Ecology and Taxonomy in

*Blue Mountain Lake, NY on June 26-28, 2015* 2015

**The Pan-Genome as a Shared Genomic Resource: Mutual Cheating, Cooperation and the Black Queen Hypothesis**

*Talk presented at 4th Annual CT Symbiosis Conference in Storrs, CT on 11 May, 2015* 2015

**When Genomics Meets Taxonomy: Phylogenetics & niche-specialization in *Aeromonas***

*Talk presented at 3rd Annual CT Symbiosis Conference in New Haven, CT on 25 April, 2014* 2014

Departmental Talks

**Non-producers stall division of labour in microbial ecosystems driven by black queen dynamics** 2022

Talk presented at Uni of Auckland EEB Seminar in Auckland, NZ on 01 Nov, 2022

**Non-producers stall division of labour in microbial ecosystems driven by black queen dynamics** 2022

Talk presented at Uni of Auckland Microbiolgy Seminar in Auckland, NZ on 12 October, 2022

**Where one ends, another begins: evaluating hypotheses of microbial evolution** 2022

Talk presented at Uni of Auckland CMP Seminar in Auckland, NZ on 27 April, 2022

**Transitive Treasures From Transferred Genetic Elements?** 2017

Talk presented at UConn MCB Departmental Graduate Seminar in Storrs, CT on 27 October, 2017

**What can neighbors tell us about *Aeromonas*?** 2016

Talk presented at UConn MCB Departmental Graduate Seminar in Storrs, CT on 02 December, 2016

**Exploring *Aeromonas*: Phylogenetics and Niche-adaptivity** 2014

Talk presented at UConn MCB Departmental Graduate Seminar in Storrs, CT on 05 December, 2014

**When Genomics Meets Taxonomy: Phylogenetics in *Aeromonas*** 2014

Talk presented at UConn MCB Departmental Graduate Seminar in Storrs, CT on 28 February, 2014

Poster Presentations

Daniel Harrison, **Mathew S. Fullmer**, Nobuto Takeuchi. **Why are there no pathogenic**2022**archaea?**

*Poster presented at NZ Microbiology Society conference, on 21-24 November, 2022*

**Matthew S. Fullmer**, Nobuto Takeuchi. **Mutualisms out of public goods? Testing the**2021**strong Black Queen hypothesis**

*Poster presented at FAOBMB, virtual conference, on 22 November, 2021*

Daniel Harrison, **Mathew S. Fullmer**, Nobuto Takeuchi. **Why are there no pathogenic**2021**archaea? Genomic analyses of pathogenic potentials of archaea**

*Poster presented at FAOBMB, virtual conference, on 22 November, 2021*

**Matthew S. Fullmer**, Ashar J. Malik, Jane R. Allison, Anthony M. Poole. ***Illuminating the*** 2018 ***Twilight Zone with Phylogenetic Analysis of Protein Structures***

Poster presented at NZ Microbial / Biochemistry and Molecular Biology Societies Conference,

*Dunedin, NZ on 26-29 November, 2018*

**Matthew S. Fullmer**, Ashar J. Malik, Jane R. Allison, Anthony M. Poole. ***Illuminating the*** 2018 ***Twilight Zone with Phylogenetic Analysis of Protein Structures***

Poster presented at Te Ao Marama Conference, at the Royal New Zealand Yacht Squadron

*Auckland, NZ on 24-25 October, 2018*

Sean P. Gosselin, **Mathew S. Fullmer**, J. Peter Gogarten. ***A Distance-Based ANI*** 2018  ***Approach for Constructing Phylogenetic Trees and Species Delimitation***

Poster presented at 15th Annual Microbial Sciences Symposium,

*Harvard, MA on 14 April, 2018*

Sean P. Gosselin, **Mathew S. Fullmer**, J. Peter Gogarten. **A Distance-Based ANI Approach** 2017 **for Constructing Phylogenetic Trees and Species Delimitation**

Poster presented at CT Valley Branch of the American Society for Microbiology,

*Storrs, CT on 13 October, 2017*

Sean P. Gosselin, **Mathew S. Fullmer**, J. Peter Gogarten. **A Distance-Based ANI Approach** 2017 **for Constructing Phylogenetic Trees and Species Delimitation**

Poster presented at CT Valley Branch of the American Society for Microbiology,

*Storrs, CT on 13 October, 2017*

**Matthew S. Fullmer**, Matthew Ouellette, R. Thane Papke, and Johann Peter Gogarten. 2017 **Methylation and CRISPRs as possible drivers of incipient speciation in archaeal populations**

Poster presented at Gordon Research Conference - Archaea,

*Waterville Valley, NH on July 23-28, 2017*

Sean P. Gosselin, **Mathew S. Fullmer**, J. Peter Gogarten. ***A Distance-Based ANI Approach*** 2017 ***for Constructing Phylogenetic Trees and Species Delimitation***

Poster presented at Astrobiology Graduate Conference,

*Charlottesville, VA, June, 2017*

Sean Gosselin, **Matthew S. Fullmer**, and Johann Peter Gogarten. **Approach for** 2017 **Constructing Phylogenetic Trees and Species Delimitation**

Poster presented at UConn All Biology Research Symposium,

*Storrs, CT on April 28, 2017*

Sean Gosselin, **Matthew S. Fullmer**, and Johann Peter Gogarten. **A Distance-Based ANI** 2017 **Approach for Constructing Phylogenetic Trees and Species Delimitation**

Poster presented at 20th Annual Frontiers in Undergraduate Research Poster Exhibition,

*Storrs, CT on April 7-8, 2017*

Sean Gosselin, **Matthew S. Fullmer**, and Johann Peter Gogarten. **ANI as a Tool to** 2017 **Understand Phylogenetic Relationships**

Poster presented at Pioneer Valley Microbiology Symposium at UMass Amherst,

*Amherst, MA on January 14, 2017*

**Received PVMS Best Poster Award**

**Matthew S. Fullmer**, Matthew Ouellette, R. Thane Papke, and Johann Peter Gogarten. 2017 **Distribution of Restriction Modification Systems in natural populations of *Halorubrum***

Poster presented at Pioneer Valley Microbiology Symposium at UMass Amherst,

*Amherst, MA on January 14, 2017*

Ryan Englander, **Matthew S. Fullmer**, and Johann Peter Gogarten. **How Cheating Leads** 2017 **to Interdependence: The Black Queen Hypothesis Tested in *Aeromonas***

Poster presented at Pioneer Valley Microbiology Symposium at UMass Amherst,

*Amherst, MA on January 14, 2017*

Ryan Englander, **Matthew S. Fullmer**, and Johann Peter Gogarten. **Searching for Niche-** 2015 **Adaptive Genes in *Aeromonas***

Poster presented at North Eastern Microbiologists: Physiology, Ecology and Taxonomy in

*Blue Mountain Lake, NY on June 26-28, 2015*

Andrew J. Collins, **Matthew S. Fullmer**, Spencer V. Nyholm. **Genome analysis of** 2014 **Roseobacter-clade bacteria isolated from the Accessory Nidamental Gland of *Euprymna scalopes***

Poster presented at American Society of Microbiologists General Meeting in Boston, MA

*on 18-20 May 2014*

Soucy SM, **Fullmer MS**, Gogarten JP. **Inteins to Illuminate Threads in the Web of Life** 2014

Poster presented at Society for Molecular Biology and Evolution satellite meeting on Reticulated

*Microbial Evolution in Kiel, Germany on 27-30 April 2014*

Lidia Beka, **Matthew Fullmer**, Sophie Colston, Michael C. Nelson, Bradley Ford, Paul 2014 Walker, Brigitte Lamy, J. Peter Gogarten, Joerg Graf. **An Analysis of Antibiotic Resistance in the *Aeromonas* population of the Medicinal Leech**

Poster presented at 11th International Symposium on Aeromonas and Plesiomonas in

Montpellier, France on 25-27 June 2014

**Received Biovac best poster award.**

Poster presented at 3rd Annual Connecticut Symbiosis Conference in New Haven, CT on

25 April 2014

Poster presented at American Society of Microbiologists General Meeting in Boston, MA

on 18-20 May 2014

Lidia Beka, **Matthew S. Fullmer**, Michael C. Nelson, J Peter Gogarten and Joerg Graf2013-2014 **Characterizing A Broad Range of Antibiotic Resistance in Symbionts of the Medicinal Leech**

Poster presented at UConn MCB-PNB departmental retreat in Bolton CT on 07 September, 2013

Presented at CT Valley Branch of the American Society for Microbiology meeting in Storrs CT on

*October 25-26, 2013*

Sophie M. Colston, Matthew S. Fullmer, J. Peter Gogarten and Joerg Graf **Investigating** 2013 **the Broad Host Range of *Aeromonas veronii* Using Comparative Genomic and Mutational Analyses**

Presented at CT Valley Branch of the American Society for Microbiology meeting in Storrs CT on

*October 25-26, 2013*

**Fullmer, Matthew S**.; Soucy, Shannon M.; Makkay, Andrea; Wheeler, Ryan; Swithers, 2013 Kristen S.; Gogarten, J. Peter; and Papke, R. Thane. **Population genomics analysis of *Halorubrum* isolates from Aran-Bidgol, Iran**

Poster presented at UConn MCB-PNB departmental retreat in Bolton CT on 07 September 2013

**Received Best Poster Award**

Poster presented at CT Valley Branch of the American Society for Microbiology meeting in

Storrs CT on October 25-26, 2013

**Received 3rd Place Best Poster Award.**

**Fullmer**, **Matthew S.**; Ram Mohan, Nikhil M.; Makkay, Andrea;Wheeler, Ryan; Soucy, 2013 Shannon M.; Swithers, Kristen S.; Gogarten, J. Peter; and Papke, R. Thane. **Population genomics analysis of *Halorubrum* isolates from Aran-Bidgol, Iran**

Poster presented at Halophiles Conference in Storrs CT on Jun 23-27, 2013.

**Received Award for Outstanding Research presented in Poster Format**

Poster presented at North Eastern Microbiologists: Physiology, Ecology and Taxonomy in

Blue Mountain Lake, NY on June 21-23, 2013

Computer Skills

Command line and scripting:

Linux/Unix Command Line – Intermediate+ proficiency.

Perl scripting – Intermediate+ proficiency.

R – Basic to intermediate proficiency; variety of packages, primarily in phylogenetics and graphics areas.

Python – Basic to lower intermediate proficiency.

Phylogenetics programs:

Various – some of the most used examples include: RAxML, MrBayes, IQ-TREE, R’s Ape and Phangorn libraries.

Protein modelling and simulation:

GROMACS – Basic to lower intermediate knowledge and proficiency.

MODELLER – Elementary knowledge and proficiency.

Agent-based modelling:

Javascript – Cacatoo modeling module. Basic knowledge and proficiency.

NetLogo – Basic knowledge and proficiency.

GUIs for writing or presentation of data:

Word, Excel & PowerPoint – Intermediate+ proficiency.

Adobe Illustrator – Intermediate proficiency.

RELATED Work EXPERIENCE

IQuum, Inc., Marlborough MA

Manufacturing Technician March 2010 – July 2011

Oversee filling personnel and operations of robotic liquid autofillers. Calibration and maintenance of autofillers. Validation of new equipment and procedures. Implement assay transfer from bench scale production to automated filling. cGMP prep. of reagents. Implement cGMP practices in novel manufacturing processes. Assist in development of Quality Systems Documentation Systems. Develop and refine system documentation of manufacturing Standard Operating Procedures (SOP). Development of End-User documentation for *in vitro* diagnostic device. Compose and review documentation as part of FDA 501k submission.

Abbott Bioresearch Center via Manpower Professional, Worcester, MA

Biologist (Cell Culture/Fermentation) November 2009 – January 2010

Follow SOPs & cGMPs as part of culturing Cho-cells. Observe FDA standards for cleanspace manufacturing.

Siemens Healthcare, East Walpole, MA

Reagent Manufacturing Technician November 2007 – October 2009

Follow SOP & cGMPs in manufacturing of *in vitro* diagnostic reagents. Worked in FDA & ISO certified cleanspace. Compose material non-conformance reports. Update & revise quality system documentation.

LANGUAGES

English – Native language.

Spanish – Taken through university intermediate level. Can read & write at rudimentary level.

Italian – Taken through university intermediate level. Can read & write at rudimentary level.

MEMBERSHIPS

Genetics Society Australasia (GSA)

New Zealand Microbiological Society (NZMS)

Society for Molecular Biology and Evolution (SMBE)

American Society of Microbiologists (ASM)