

# CURRICULUM VITAE: LING HAN TONG MAURICE

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## PERSONAL DATA

NATIONALITY: Singaporean  
Languages (Written): English, Chinese  
Languages (Dialects) Spoken: English, Mandarin, Teochew, Cantonese, Hokkien

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Website: <https://mauriceling.github.io>

## CAREER SUMMARY

- Over 18 years of experience (since 2003) as research and lecturing biologist / bioinformaticist in both academic and industrial settings.
- More than 3,200 hours of lecturing, project supervision, and corporate trainer experience since January 2017.
- 116 refereed publications (including 3 publications from high-school projects, 29 publications from pre-undergraduate projects, and 24 publications from undergraduate projects) and 1 US patent.
- Collaborated with colleagues across different countries and time-zones.
- Co-founded the first synthetic biology company in Singapore.

## ACADEMIC RECORD

2004-2009 **Doctor of Philosophy (Bioinformatics).** The University of Melbourne, Australia  
*Understanding Mouse Lactogenesis by Transcriptomics and Literature Analysis.* Supervisors: Prof KR Nicholas, A/Prof C Lefevre, A/Prof F Lin.  
Degree awarded 24 Dec 2009.

2008-2009 **Certificate in Teaching (Higher Education).** Singapore Polytechnic, Singapore

2005-2007 **Bachelor of Science (Computing).** University of Portsmouth, UK

2003-2004 **Bachelor of Science (Honours, H2A).** The University of Melbourne, Australia  
*Identifying the Roles of Insulin, Prolactin and Glucocorticoid in the Initiation of Murine Lactogenesis.* Supervisor: A/Prof KR Nicholas.

2002-2003 **Bachelor of Science.** The University of Melbourne, Australia

2001-2003 **Advanced Diploma in Computing.** National Computing Centre, United Kingdom  
Project: *InterBase Data Warehouse Builder (IB-DWB) Version 1.0*

## SIGNIFICANT TECHNOLOGY DISCLOSURES

**Ling Han Tong Maurice, Poh Chueh Loo and Lim Yuting Rosary.** *Prediction of Gene Transcription Intensity and Gene Perturbation.*

- United States Provisional Application No. 61/839,046 filed June 26, 2013
- International Patent Application No. PCT/SG2014/000234 filed May 28, 2014.

**Maurice Ling**, Kok Hien Gan, Kevin Clancy, Raymond Tecotzky and Kin Chong Sam.  
*Methods and Systems for In Silico Experimental Design and Performing a Biological Workflow.*

- United States Provisional Application No. 61/578,820
- International Patent Application No. PCT/US2012/071379 filed December 21, 2012
- United States Non-Provisional Application No. 13/724,765 filed December 21, 2012
- United States Application No. 15/259,033 filed September 7, 2016
- United States Patent issued on October 11, 2016; Patent Number 9,465,519

## **AWARDS AND SCHOLARSHIPS**

2010	Science Mentorship Program “Outstanding Mentor Award”, Ministry of Education, Singapore
2005	Melbourne Abroad Traveling Scholarship, The University of Melbourne
2005	Postgraduate Overseas Research Experience Scholarship, The University of Melbourne
2005	F.H. Drummond Travel Award, The University of Melbourne
2005	Melbourne International Fee Remission Scholarship, The University of Melbourne
2004	Science Faculty Scholarship, The University of Melbourne
2004	CRC for Innovative Dairy Products (PhD Scholarship)
2003	CRC for Innovative Dairy Products (Honours Scholarship)

## **RESEARCH AND DEVELOPMENT EXPERIENCES**

2018- current	<b>Research Assistant Professor</b> , Perdana University (School of Data Sciences). I assist the Dean of Data Science to identify research strategies, on top of project supervision and mentoring.
2017- current	<b>Lecturer</b> , Temasek Polytechnic (School of Applied Sciences). I supervise and mentor interns and major project students, which resulted in 11 refereed publications (see Listing 1).
2017- current	<b>Associate Lecturer</b> , Management Development Institute of Singapore (MDIS). I supervise undergraduate students for the honours year projects, mainly in bioinformatics; which resulted in 17 refereed publications (see Listing 2).
2014-current	<b>Co-Founder and Director (Technology)</b> , AdvanceSyn Pte. Ltd. As a biologist turned bioinformaticist, I am responsible for technological developments (both biology and IT tools) of the company.
2010-2017	<b>Honorary Fellow (equivalent to academic rank of Lecturer)</b> , The University of Melbourne (Department of Zoology). I was appointed on basis of continued contributions to the university in terms of outreach programs and research contributions.
2013-2017	<b>Research Fellow</b> , Nanyang Technological University (School of Chemical and Biomedical Engineering). I am part of the synthetic biology group with several responsibilities: <ul style="list-style-type: none"><li>• Developing software tools for modeling and predicting gene expression and protein production</li><li>• Engineering micro-organisms for waste degradation and production of high-valued chemical compounds and peptides</li><li>• Providing advice for experimental procedures on genetic engineering and</li></ul>

- characterization
  - Safety representative for the group
- 2012-2013 **Research Associate**, South Dakota State University (Department of Mathematics and Statistics). I am working on a NIH funded project on antisense transcript, as well as providing bioinformatics support to the university community at large.
- 2010-2012 **Senior Scientist (Bioinformatics)**, Life Technologies. I was in the core team for Vector NTI Express and provided specifications on bioinformatics algorithms, and responsible for drafting the high-level requirements for Vector NTI Designer.
- 2008-2011 **Lecturer**, Singapore Polytechnic (School of Chemical and Life Sciences). I led student/internship projects on experimental evolution. We found that constant chemical stress on *Escherichia coli* leads to rapid adaptation to the stressors, which has significance to antibiotics resistance and food preservation. Using DNA fingerprinting, we had demonstrated that these adaptations are genetic.
- 2004-2009 **Ph.D. Candidate**, The University of Melbourne (Department of Zoology). I developed a system for rapid survey of the literature and used it, together with microarray analysis, to elucidate potentially novel hypotheses for further experimental research.
- 2003-2004 **B.Sc.(Hons) candidate**, The University of Melbourne (Department of Zoology). I proposed a model in which insulin, prolactin and glucocorticoid exert their effects singly and in combination to trigger mouse lactogenesis. Much of the analysis used data from microarray experiments.
- 2003 **Research Experience**, The University of Melbourne (Department of Anatomy and Cell Biology Ocular Development Laboratory), supervised by Dr R de Iongh. I completed expression studies of BMP4 receptors in lens development and assisted in establishing in situ hybridization techniques in the laboratory.
- 2002-2003 **Adv. Dip. Computing candidate**, National Computing Centre, UK. I designed a data warehouse builder based on Borland InterBase 6, which resulted in a paper at the 1st Australian Undergraduate Students' Computing Conference.

## TEACHING AND MENTORING EXPERIENCES

- 2017- current **Lecturer**, Temasek Polytechnic (School of Applied Sciences).
  - Converted from Adjunct Lecturer to Lecturer in March 2020.
  - Supervising and mentoring interns and major project students, which resulted in 11 refereed publications (see Listing 1).
  - Subjects taught:
    - Biological Data Analysis
    - Scripting for Bioinformatics
    - Statistics for Applied Sciences
    - Synthetic Biology
  - Administrative responsibilities:
    - Multidisciplinary major project representative for Diploma in Chemical Engineering and Diploma in Medical Biotechnology
    - Subject leader: Digitalization for Applied Sciences

- Subject leader: Major Project (for Diploma in Medical Biotechnology)
  - Subject leader: Statistics for Applied Sciences
- 2017- current    **Associate Lecturer**, Management Development Institute of Singapore (MDIS). Approved by Committee for Private Education (CPE, Singapore).
  - Supervising honours projects, which resulted in 17 refereed publications (see Listing 2).
  - Lecturing on subjects from Northumbria University (UK):
    - Applied Bioinformatics and Postgenomics (Year 3 BSc(Hons))
    - Genomics (Year 3 BSc(Hons))
    - Introductory Pathological Science (Year 1 BSc (Hons))
    - Investigative Biotechnology (Year 2 BSc(Hons))
    - Practical Skills (Year 1 BSc(Hons))
    - Professional Skills (Year 2 BSc(Hons))
    - Research: Approaches, Methods, and Skills (M Public Health)
    - Research Methods in Applied Sciences (Year 2 BSc(Hons))
    - Scope of Biotechnology (Year 2 BSc(Hons))
  - Lecturing on subjects from Teesside University (UK):
    - Informatics and Technology in Healthcare Management (Year 2 BSc(Hons))
- 2009 – 2020    **Pro Bono Scientific Research Mentor**. I provide research mentorship on a pro bono (voluntary) basis to juniors interested in scientific research, which resulted in more than 20 peer-reviewed publications.
- 2013-2017    **Research Fellow**, Nanyang Technological University (School of Chemical and Biomedical Engineering). I manage and mentor final year project (FYP) students assigned to my research group.
- 2012-2013    **Research Associate**, South Dakota State University (Department of Mathematics and Statistics)
  - Instructor for graduate level statistical methods course; Statistical Methods II; using SAS, Minitab, JMP and R.
  - Judge for East South Dakota Science and Engineering Fair 2012.
- 2008-2011    **Lecturer**, Singapore Polytechnic (School of Chemical and Life Sciences)
  - Diploma in Biotechnology representative, Information Technology in Teaching and Learning Committee
  - Diploma in Biotechnology representative, Alumni and Industry Relations
  - Sharing Session Coordinator
  - Mentored 12 diploma students/interns and 9 specialist diploma students (adult learners).
- 2006-2008    **Resident Adviser and Tutor**, University College, The University of Melbourne, Australia. Provided pastoral care and academic support for undergraduates and postgraduate students. Tutored in “*Academic writing for senior science students*” and “*Introductory Programming in C*” subjects.
- 2004-2005    **Head Demonstrator**, The University of Melbourne (Department of Zoology). I was the lead demonstrator in practical classes in Biology to more than 1100 first year students. Demonstrated in 3<sup>rd</sup> year Development Biology practical classes.

## PROFESSIONAL SERVICES

2022-current	<b>Associate Editor</b> , Computational Genomics [specialty section of Frontiers in Genetics (ISSN 1664-8021), Frontiers in Bioengineering and Biotechnology (ISSN 2296-4185), and Frontiers in Plant Science (ISSN 1664-462X)] and Guest Editor for the research topic of “Current State of Multi-omics Modeling and Simulations”.
2020-current	<b>Honorary Director</b> , Asia Pacific Bioinformatics Network Ltd (UEN 201225997K), which is registered in Singapore as a legal entity to manage the routine operations of Asia Pacific Bioinformatics (APBioNet).
2019-current	<b>Executive Committee Member</b> , Society for Synthetic Biology (Singapore) (SynBioSG).
2019-current	<b>Working Committee Member</b> , MyBioInfoNet. MyBioInfoNet, affiliated with Asia Pacific Bioinformatics Network (APBioNet) is a non-profit entity established in 2018 is dedicated to serve as a networking platform for Malaysians or non-Malaysians, within or outside Malaysia, with interest in growing bioinformatics in the country.
2018-current	<b>Executive Committee Member</b> , Association of Medical and Bio-Informatics, Singapore (AMBIS). Secretary from 2018 to 2020. Treasurer for 2021.
2017-current	<b>Series Editor</b> , Current STEM. Nova Science Publishers, Inc. Current STEM is a broad-spectrum book series for all aspects of STEM (Science, Technology, Engineering, and Mathematics). This includes all philosophical, theoretical and applied aspects of STEM; and STEM-related areas, such as education, industry and economy, ethics and legal aspects.
2010-current	<b>Programme Committee Member.</b> <ul style="list-style-type: none"> <li>▪ Python for High Performance Computing (2010 – 2017), part of International Conference for High Performance Computing, Networking, Storage and Analysis.</li> <li>▪ 4th International Conference on Electronics, Communications and Networks (CECNet 2014) (2014).</li> <li>▪ International Symposium on Bioinformatics 2018 (InSyB 2018) (2018), as Programme Committee Chair.</li> <li>▪ International Conference on Bioinformatics 2019 (InCoB 2019) (2019).</li> </ul>
2008-current	<b>Editorial Committee Member.</b> I was invited to join the editorial committee of the following journals: <ul style="list-style-type: none"> <li>▪ The Python Papers Anthology incorporating The Python Papers (ISSN 1834-3147), The Python Papers Monograph Series (ISSN 1837-7092), and The Python Papers Source Codes (ISSN 1836-621X), as Co-Editor-in-Chief (2008 – 2018).</li> <li>▪ iConcept Journal of Computational and Mathematical Biology (ISSN 2219-1402), iConcept Press Ltd (2010 – 2018).</li> <li>▪ MOJ Proteomics &amp; Bioinformatics (ISSN 2374-6920), MedCrave Publishing Group (2014 – 2018 as Associate Editor, Honorary Editor from 2018).</li> <li>▪ Acta Scientific Microbiology (ISSN 2581-3226), Acta Scientific (from 2018).</li> <li>▪ Acta Scientific Computer Sciences (ISSN , Acta Scientific (from 2018).</li> </ul>
2010-2019	<b>Technical Reviewer</b> , Packt Publishing (IT publishing house). I reviewed 14 books on Python programming – [1] Python Multimedia Beginner’s Guide (ISBN 978-184-951016-5), [2] wxPython 2.8 Application Development

	(ISBN 978-184-951178-0), [3] Python 2.6 Text Processing (ISBN 978-184-951212-1), [4] Python Text Processing with NLTK 3 Cookbook (ISBN 978-178-216785-3), [5] Building Machine Learning Systems with Python (ISBN 978-1-78216-140-0), [6] Python Testing Cookbook (ISBN 978-1-849514-66-8), [7] IPython Interactive Computing and Visualization Cookbook (ISBN 978-178-328481-8), [8] Python for Secret Agents (ISBN 978-178-398042-0), [9] Building Machine Learning Systems with Python, 2nd edition (ISBN 978-1-784392772), [10] Mastering Python for Data Science (ISBN 978-1-78439-015-0), [11] Learning Python Design Patterns, 2nd edition (ISBN 978-1-78588-803-8), [12] Automate it! Recipes to upskill your business (ISBN 978-1-78646-051-6), [13] Python Testing Cookbook, 2nd Edition (ISBN 978-1-78712-252-9), [14] Python Object Oriented Programming Cookbook (ISBN 978-1-78862-278-3), [15] Python GUI Programming Cookbook, Third Edition (ISBN 978-1-83882-754-0, in preparation).
2015-2018	<b>Honorary Auditor</b> , Python User Group (Singapore) (ROS 2060/2009, Singapore). Python User Group acts as a professional entity to promote Python use in education and industry within Singapore. After completion of my terms, in various capacities, in the executive committee; I was elected as Honorary Auditor.
2009-2012	<b>Conference and Publications Co-Chair</b> , PyCon Asia-Pacific I am the co-chair for PyCon Asia-Pacific 2010 to 2012. The community had accepted PyCon Asia-Pacific as one of the 3 major Python conferences worldwide, together with PyCon US and EuroPython.
2009-2015	<b>Committee Member</b> , Python User Group (Singapore) (ROS 2060/2009, Singapore). Python User Group acts as a professional entity to promote Python use in education and industry within Singapore. I serve as Vice-President from 2009 to 2013, and Treasurer from 2013 to 2015. Co-founder of the society and drafted the constitution for submission to Ministry of Home Affairs, Singapore.
2002-2003	<b>Publication Team Member</b> (ISBN 0-646-4275-1-2), Australian Undergraduate Students' Computing Conference 2003.
2001	<b>Operations Manager (Advisory)</b> , Fund Raising Project for Gujarat Earthquake Relief. I was the director of operations and contingency planning on the day of event, managing more than 250 volunteers and coordinating emergency services over 8 operation sectors housing more than 30000 residences.
1996-1999	<b>Deputy S1 (Administration Officer)</b> , Cadet Lieutenant promoted to Senior Cadet Lieutenant, National Cadet Corp, Singapore.

## PROFESSIONAL MEMBERSHIPS

2000-2008	Association of Computing Machinery (Student Member)
2008–current	Association of Computing Machinery (Professional Member)
2009–current	Python User Group (Singapore)
2018–current	Singapore Society for Synthetic Biology
2018–current	Association of Medical and Bio-Informatics, Singapore
2018–current	MyBioInfoNet, Malaysia

## PUBLICATIONS

## Refereed Journal Articles:

1. Chua, MTE, Dumanglas, ABG, **Ling, MHT**. 2022. *Gene Co-Expressions Cannot Predict Protein-Protein Interactions in Escherichia coli*. EC Microbiology 18(3): 102-109.
2. Tan, FL, Kuan, ZJ, Amir-Hamzah, N, Kng, X, Wee, YY, Sor, SX, **Ling, MHT**. 2022. *Significant Differences in Media Components and Predicted Growth Rates of 58 Escherichia coli Genome-scale Models*. Acta Scientific Microbiology 5(2): 56-68.
3. Kuan, ZJ, Amir-Hamzah, N, **Ling, MHT**. 2022. *Kinetic Models with Default Enzyme Kinetics from Genome-scale Models*. Acta Scientific Computer Sciences 4(1): 59-63.
4. **Ling, MHT**. 2021. *ZeroOne: Building and Enhancing Executing Simulation by Incremental Patches*. Acta Scientific Computer Sciences 3(10): 50-52.
5. Sim, KS, **Ling, MHT**. 2021. *Installation and Documentation Evaluation of Recent (01 January 2020 to 15 February 2021) Chatbot Engines from Python Package Index (PyPI)*. Acta Scientific Computer Sciences 3(8): 38-43.
6. Ang, DGY, **Ling, MHT**. 2021. *Sudden and Steep Harsh Environment Results in Over-Compensation in Digital Organisms*. EC Microbiology 17(7): 104-113.
7. Johny, A, Sumedha, PR, **Ling, MHT**. 2021. *Simulation Suggests that One-Off Simple Supplementation from the Wild into Captive Population May Not Increase Captive Genetic Diversity*. EC Veterinary Science 6(7): 107-111.
8. Lim, GZK, Azmi, HH, Dolmatova, M, **Ling, MHT**. 2021. *Significant Differences in Nucleotide and Peptide Features Between Chromosomes Suggesting Sequence Non-Randomness Across Chromosomes*. Acta Scientific Microbiology 4(4): 23-28.
9. Kuan, ZJ, Amir-Hamzah, N, **Ling, MHT**. 2021. *Coffee as a Potential Nutraceutical*. EC Nutrition 16(3): 57-65.
10. Kim, KD, Chua, SCH, **Ling, MHT**. 2021. *Science/Education Portraits VII: Statistical Methods Used in 1081 Papers Published in Year 2020 Across 12 Life Science Journals Under BioMed Central*. Acta Scientific Nutritional Health 5(3): 06-12.
11. Kuan, ZJ, **Ling, MHT**. 2021. *Core Genome of Poales, An Economically Important Order of Monocotyledons*. EC Agriculture 7(2): 24-29.
12. Cho, JL, **Ling, MHT**. 2021. *Adaptation of Whole Cell Kinetic Model Template, UniKin1, to Escherichia coli Whole Cell Kinetic Model, ecoJC20*. EC Microbiology 17(2): 254-260.
13. Chua, SCH, **Ling, MHT**. 2021. *Stop Codon Usage Varies on CDS Length, Nucleotide Compositions, and Peptide Instability in Six Escherichia coli Strains*. EC Clinical and Medical Case Reports 4(2): 39-46.
14. **Ling, MHT**. 2020. *Low Classification Accuracy by Logistic Regression, Support Vector Classifier, and Multi-Layer Perceptron, but Not Decision Tree, on Random Attributes from Hadamard Matrix*. EC Clinical and Medical Case Reports 3(12): 07-10.
15. Teo, YH, **Ling, MHT**. 2020. *A Systematic Review on the Sufficiency of PubMed and Google Scholar for Biosciences*. Acta Scientific Medical Sciences 4(12): 03-08.
16. Wang, VCC, **Ling, MHT**. 2020. *Science/Education Portraits VI: Anecdotes of Life in Singapore During COVID-19 (February 2020 to September 2020)*. EC Clinical and Medical Case Reports 3(11): 98-111.
17. Chew, SSM, Murthy, MV, Kamarudin, NJ, Wang, VCC, Tan, XT, Ramesh, A, Yablochkin, NV, Mathivanan, K, **Ling, MHT**. 2020. *Rapid Genetic Diversity with Variability between Replicated Digital Organism Simulations and its Implications on Cambrian Explosion*. EC Clinical and Medical Case Reports 3(11): 64-68.
18. Liu, TT, **Ling, MHT**. 2020. *BactClass: Simplifying the Use of Machine Learning in Biology and Medicine*. Acta Scientific Medical Sciences 4(11): 43-47.
19. **Ling MHT**. 2020. *AdvanceSyn Toolkit: An Open-Source Suite for Model Development and Analysis in Biological Engineering*. MOJ Proteomics & Bioinformatics 9(4):83-86.
20. Murthy, MV, Balan, D, Kamarudin, NJ, Wang, VCC, Tan, XT, Ramesh, A, Chew, SSM, Yablochkin, NV, Mathivanan, K, **Ling, MHT**. 2020. *UniKin1: A Universal, Non-Species-Specific Whole Cell Kinetic Model*. Acta Scientific Microbiology 3(10): 04-08.
21. Wang, VCC, Kamarudin, NJ, Tan, XT, Ramesh, A, Chew, SSM, Murthy, MV, Yablochkin, NV, Mathivanan, K, **Ling, MHT**. 2020. *A Case Study using Mitochondrial Genomes of the Order Diprotodontia (Australasian Marsupials) Suggests that Single Ortholog is Not Sufficient for Phylogeny*. EC Clinical and Medical Case Reports 3(9): 93-114.
22. Kamarudin, NJ, Wang, VCC, Tan, XT, Ramesh, A, Chew, SSM, Murthy, MV, Yablochkin, NV, Mathivanan, K, **Ling, MHT**. 2020. *A Simulation Study on the Effects of Founding Population Size and Number of Alleles Per Locus on the Observed Population Genetic Profile: Implications to Broodstock Management*. EC Veterinary Science 5(8): 176-180.

23. Tan, XT, Ramesh, A, Wang, VCC W, Kamarudin, NJ, Chew, SSM, Murthy, MV, Yablochkin, NV, Mathivanan, K, **Ling, MHT**. 2020. *Core Pseudomonas Genome From 10 Pseudomonas Species*. MOJ Proteomics & Bioinformatics 9(3): 68–71.
24. Gunalan, K, Wong, CQL, Neo, MPY, **Ling, MHT**. 2020. *One Percent of Escherichia coli O157:H7 Peptides May Contain Putative Beta-Lactamase Activity*. EC Microbiology 16(8): 73-79.
25. Cheong, KC, Hon, RYH, Sander, CJ, Ang, IZL, Foong, JH, **Ling, MHT**. 2020. *A Simulation Study on the Effects of Media Composition on the Growth Rate of Escherichia coli MG1655 using iAF1260 Model*. Acta Scientific Microbiology 3(8): 40-44.
26. Neo, CY, **Ling, MHT**. 2020. *Prevalence and Length of Open Reading Frames Vary Across Randomly Generated Sequences of Different Nucleotide Compositions*. EC Microbiology 16(7): 72-78.
27. Sim, BKY, **Ling, MHT**. 2020. *Possibility of Abiotic Genesis of Biochemistry*. EC Microbiology 16(6): 104-109.
28. Teng, RSY, Kwang, JCY, Chin, ASQ, Sanders, CJ, Ang, IZL, Foong, JH, Cheong, KC, Hon, RYH, **Ling, MHT**. 2020. *Correlation Analysis on Transcriptomes from Published Human Skin Studies Show Variations between Control Samples*. EC Clinical and Medical Case Reports 3(6): 143-146.
29. **Ling, MHT**. 2020. *SeqProperties: A Python Command-Line Tool for Basic Sequence Analysis*. Acta Scientific Microbiology 3(6): 103-106.
30. Usman, S, Chua, JW, Ardhanari-Shanmugam, KD, Thong-Ek C, B, V, Shahrukh, K, Woo, JH, Kwek, BZN, **Ling, MHT**. 2019. *Pseudomonas balearica DSM 6083T promoters can potentially originate from random sequences*. MOJ Proteomics & Bioinformatics 8(2): 66–70.
31. **Ling, MHT**. 2019. *Island: A Simple Forward Simulation Tool for Population Genetics*. Acta Scientific Computer Sciences 1(2): 20-22.
32. **Ling, MHT**. 2019. *Draft Implementation of a Method to Secure Data by File Fragmentation*. Acta Scientific Computer Sciences 1(2): 10-13.
33. Ardhanari-Shanmugam, KD, Shahrukh, K, B, V, Woo, JH, Thong-Ek, C, Usman, S, Kwek, BZN, Chua, JW, **Ling, MHT**. 2019. *De Novo Origination of Bacillus subtilis 168 Promoters from Random Sequences*. Acta Scientific Microbiology 2(11): 07-10.
34. Chang, ED, **Ling, MHT**. 2019. *Explaining Monod in Terms of Escherichia coli Metabolism*. Acta Scientific Microbiology 2(9): 66-71.
35. **Ling, MHT**. 2019. *Science/Education Portraits V: The Scientific Tertiary Education that I had Envisioned*. Acta Scientific Medical Sciences 2(8): 75-79.
36. Kwek, BZN, Ardhanari-Shanmugam, KD, Woo, JH, Usman, S, Chua, JW, B, V, Shahrukh, K, Thong-Ek, C, **Ling, MHT**. 2019. *Random Sequences May Have Putative Beta-Lactamase Properties*. Acta Scientific Medical Sciences 3(7): 113-117.
37. Thong-Ek, C, Usman, S, Woo, JH, Chua, JW, Kwek, BZN, Ardhanari-Shanmugam, KD, B, V, Shahrukh, K, **Ling, MHT**. 2019. *Potential De Novo Origins of Archaeobacterial Glycerol-1-Phosphate Dehydrogenase (GIPDH)*. Acta Scientific Microbiology 2(6): 106-110.
38. Maitra, A, **Ling, MHT**. 2019. *Codon Usage Bias and Peptide Properties of Pseudomonas balearica DSM 6083T*. MOJ Proteomics & Bioinformatics 8(2):27–39.
39. Kim, JH, **Ling, MHT**. 2019. *Proteome Diversities Among 19 Archaeobacterial Species*. Acta Scientific Microbiology 2(5): 20-27.
40. **Ling, MHT**. 2019. *De Novo Putative Protein Domains from Random Peptides*. Acta Scientific Microbiology 2(4): 109-112.
41. **Ling, MHT**. 2019. *Science/Education Portraits IV: Experiences from a Decade as Informal Career Counsellor can be Summarized as Personopreneurship*. Acta Scientific Medical Sciences 3(3): 151-156.
42. Suwinski, P, Ong, CK, **Ling, MH**, Poh, YM, Khan, AM, Ong, HS. 2019. *Advancing Personalized Medicine through the Application of Whole Exome Sequencing and Big Data Analytics*. Frontiers in Genetics 10: 49.
43. Lim, JX, **Ling, MHT**. 2019. *Gene Ontology and KEGG Orthology Mappings for 10 Strains of Pseudomonas stutzeri*. EC Proteomics and Bioinformatics 3(1): 12-18.
44. **Ling, MHT**. 2018. *SEcured REcorder BOx (SEREBO) Based on Blockchain Technology for Immutable Data Management and Notarization*. MOJ Proteomics & Bioinformatics 7(6):169–174.
45. **Ling, MHT**. 2018. *Science/Education Portraits III: Perceived Prevalence of Data Fabrication and/or Falsification in Research*. Advances in Biotechnology and Microbiology 11(5):555824.
46. **Ling, MHT**. 2018. *RANDOMSEQ: Python Command-line Random Sequence Generator*. MOJ



- Proteomics & Bioinformatics 7(4):206–208.
47. **Ling, MHT.** 2018. *Science/Education Portraits II: Pre-Tertiary and Undergraduate Research Mentors Should Consider Publication as Project Endpoint*. MOJ Proteomics & Bioinformatics 7(2):127–129.
  48. Chan, OYW, Keng, BMH, **Ling, MHT.** 2018. *Science/Education Portraits I: Identifying Success Factors of Pre-Tertiary Bioinformatics Research Experience from Students' Perspective*. Advances in Biotechnology and Microbiology 8(2): 555734.
  49. **Ling, MHT.** 2018. *Back-of-the-Envelope Guide (A Tutorial) to 10 Intracellular Landscapes*. MOJ Proteomics & Bioinformatics 7(1): 00209.
  50. **Ling, MHT.** 2017. *Towards Portrait [(Auto) Ethnography, Narrative, and Action Research] of Bioinformatics*. EC Proteomics and Bioinformatics 2(1): 29-35.
  51. **Ling, MHT.** 2017. *A Personal Narrative of 6 Pre-University Research Projects Over 7 Years (2009-2015) Yielding 19 Manuscripts*. MOJ Proteomics & Bioinformatics 6(3): 00193.
  52. Wang, HJ, **Ling, MHT**, Chua, TK, Poh, CL. 2017. *Two Cellular Resource Based Models Linking Growth and Parts Characteristics Aids the Study and Optimization of Synthetic Gene Circuits*. Engineering Biology 1(1): 30-39.
  53. Chay, ZE, Goh, BF, **Ling, MHT.** 2016. *PNet: A Python Library for Petri Net Modeling and Simulation*. Advances in Computer Science: an international journal 5(4): 24-30.
  54. **Ling, MHT.** 2016. *Of (Biological) Models and Simulations*. MOJ Proteomics & Bioinformatics 3(4): 00093.
  55. **Ling, MHT.** 2016. *COPADS IV: Fixed Time-Step ODE Solvers for a System of Equations Implemented as a Set of Python Functions*. Advances in Computer Science: an international journal 5(3): 5-11.
  56. Chew, JS, **Ling, MHT.** 2016. *TAPPS Release 1: Plugin-Extensible Platform for Technical Analysis and Applied Statistics*. Advances in Computer Science: an international journal 5(1): 132-141.
  57. Castillo, CFG, Chay ZE, **Ling, MHT.** 2015. *Resistance Maintained in Digital Organisms Despite Guanine/Cytosine-Based Fitness Cost and Extended De-Selection: Implications to Microbial Antibiotics Resistance*. MOJ Proteomics & Bioinformatics 2(2): 00039.
  58. **Ling, MHT.** 2014. *Applications of Artificial Life and Digital Organisms in the Study of Genetic Evolution*. Advances in Computer Science: an international journal 3(4): 107-112.
  59. Keng, BMH, Chan, OYW, **Ling, MHT.** 2014. *Codon Usage Bias is Evolutionarily Conserved*. Asia Pacific Journal of Life Sciences 7(3): 233-242.
  60. **Ling, MHT**, Poh, CL. 2014. *A Predictor for Predicting Escherichia coli Transcriptome and the Effects of Gene Perturbations*. BMC Bioinformatics 15: 140.
  61. Castillo, CFG, **Ling, MHT.** 2014. *Resistant Traits in Digital Organisms Do Not Revert Preselection Status despite Extended Deselection: Implications to Microbial Antibiotics Resistance*. BioMed Research International 2014, Article ID 648389.
  62. Chan, OYW, Keng, BMH, **Ling, MHT.** 2014. *Bactome III: OLlgonucleotide Variable Expression Ranker (OLIVER) 1.0, Tool for Identifying Suitable Reference (Invariant) Genes from Large Microarray Datasets*. The Python Papers Source Codes 6: 2.
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4. **Ling, MHT**. 2019. *Survey of Antisense Transcription*. In Guenther, R. and Steel, D. (eds.), Encyclopedia of Bioinformatics and Computational Biology, Volume 3, pages 842-846. Elsevier. ISBN 978-0-12811-414-8.
5. Lim, JX, Li, BT, **Ling, MHT**. 2019. *Sequence Composition*. In Guenther, R. and Steel, D. (eds.), Encyclopedia of Bioinformatics and Computational Biology, Volume 3, pages 323-326. Elsevier. ISBN 978-0-12811-414-8.
6. **Ling, MHT**. 2018. *COPADS VI: Fixed Time-Step ODE Solvers with Mixed ODE and non-ODE Function, and Script Generator*. In Current STEM, Volume 1, pp. 173-212. Nova Science Publishers, Inc. ISBN 978-1-53613-416-2.
7. **Ling, MHT**. 2018. *COPADS V: Lindenmayer System with Stochastic and Function-Based Rules*. In Current STEM, Volume 1, pp. 143-172. Nova Science Publishers, Inc. ISBN 978-1-53613-416-2.
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11. **Ling, MHT**, Lefevre, Christophe, Nicholas, KR. 2010. *Mining Protein-Protein Interactions from Published Abstracts with MontyLingua*. In Sequence and Genome Analysis: Methods and Applications. iConcept Press Pty Ltd.

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13. **Ling, MHT**, Lefevre, C, Nicholas, KR, Lin, F. 2007. *Re-construction of Protein-Protein Interaction Pathways by Mining Subject-Verb-Objects Intermediates*. In Proceedings of the Second IAPR Workshop on Pattern Recognition in Bioinformatics (PRIB 2007). Lecture Notes in Bioinformatics 4774. (pp. 286-299) Springer-Verlag.

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2. **Ling, MHT** and So, CW. 2003. *Architecture of an Open-Sourced, Extensible Data Warehouse Builder: InterBase 6 Data Warehouse Builder (IB-DWB)*. In Rubinstein, B. I. P., Chan, N. & Kshetrapalapuram, K. K. (Eds.), Proceedings of the First Australian Undergraduate Students' Computing Conference. (pp. 40-45).

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3. **Ling, MHT**. 2016. *The Bioinformaticist's/Computational Biologist's Laboratory*. MOJ Proteomics and Bioinformatics 3(1): 00075.
4. **Ling, MHT**. 2016. *Using Artificial Life Simulation to Gain Insights into Contradictory Field Evidence*. PyCon SG 2016, Singapore.
5. **Ling, MHT**, Fane, AG, Poh, CL. 2016. *Right Enzyme Concentration is Needed to Reduce Initial Biofilm Formation*. Biosystems Design 2.0, Singapore.
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7. **Ling, MHT**. 2014. *Hormonal Regulation of Mouse Lactogenesis: Using Transcriptomics and Literature Analysis*. Scholars' Press. ISBN 978-3-639-66810-0.
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10. **Ling, MHT**, Chen, YJ, Stanton, B, Rhodius, V, Temme, K, Jean, A, Voigt, C, Peterson, T, Clancy, K. 2011. *Development of Characterized Parts Libraries for Control of Expression*. Global Knowledge Day 2011. Life Technologies.
11. Angelica, R, Liao, D, Chen, YM, Jean, A, **Ling, MHT**, Abdul Kahar, A, Palaniappan, K, Kee, MS, Ho, S, Tew, BY, Sam, KC, Gan, KH, Loh, LS, Cheng, S, Peterson, T, Clancy, K. 2011. *Development of a Desktop Application Framework for Vector NTI Express and Future Synthetic Biology Software*. Global Knowledge Day 2011. Life Technologies.
12. Heng, SSJ, Chan, OYW, Keng, BMH, **Ling, MHT**. 2011. *Identifying Invariant Genes in Escherichia coli*. Proceedings of the 17th Youth Science Conference. Singapore.
13. Lim, JZR, Goh, DJW, How, JA, **Ling, MHT**. 2011. *Gradually Evolving Escherichia coli to Grow in 10% NaCl in 6 Months*. Singapore Society of Biochemistry and Molecular Biology Young Scientists' Symposium 2011. Singapore Science Centre, 11th March 2010.
14. Aw, ZQ, Low, SXZ, Loo, BZL, **Ling, MHT**. 2011. *Ecological Specialisation of Escherichia coli within 1000 Generations*. Singapore Society of Biochemistry and Molecular Biology Young Scientists' Symposium 2011. Singapore Science Centre, 11th March 2010.
15. Kuo, CJ, **Ling, MHT**, Hsu, CN. 2010. *Gene Normalization as a Problem of Information Retrieval*. Proceedings of BioCreative III Workshop. Bethesda, Maryland, USA. 13-15 September 2010.
16. Kuo, CJ, Hsu, CN, **Ling, MHT**. 2010. *Advanced Gene Mention Tagging System for CALBC Challenge*. In

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17. Chu, QH, Lin, YJ, Ang, EJG, **Ling, MHT**. 2010. *Identification of Transcriptional Invariant Genes in Mouse Endocrine Glands from Microarray Data*. Proceedings of the 16th Youth Science Conference. Singapore.
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  19. Kuo, CJ, **Ling, MHT**, Hsu, CN. 2009. *Applying Lazy Local Learning in BCII.5 Article Categorization Task*. BioCreative II.5 Workshop Special Session on Digital Annotations. Centro Nacional de Investigaciones Oncologicas, Spain. 7-9 October 2009.
  20. Lim, MH, Quek, SG, Teoh, EJM, **Ling, MHT**, Chan, CY. 2009. *Protein Profiles of Bacteria under Short Term and Long Term Exposure to Environmental Stress*. Young Scientists' Symposium. Singapore Science Centre. 6<sup>th</sup> March 2009.
  21. Chia, CY, Lim, CWX, Leong, WT, **Ling, MHT**. 2009. *Identification of Transcriptionally Invariant Genes in Mouse Liver from Microarray Data*. Proceedings of the 15<sup>th</sup> Youth Science Conference. Singapore.
  22. Ng, JPH, Ong, YC, **Ling, MHT**, Xu, WJ. 2009. *Properties of Histatin 5*. Proceedings of the 15<sup>th</sup> Youth Science Conference. Singapore.
  23. **Ling, MHT**, Lefevre, C, and Nicholas, KR. 2006. *A Pipeline for Analysis of Published Abstracts for Information on Protein-Protein Inter-Relations*. Proceedings of the Fourth Asia-Pacific Bioinformatics Conference.
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### **Listing 1: Publications from Temasek Polytechnic**

1. Sim and Ling. 2021. *Installation and Documentation Evaluation of Recent (01 January 2020 to 15 February 2021) Chatbot Engines from Python Package Index (PyPI)*. Acta Scientific Computer Sciences 3(8): 38-43.
2. Kuan, et al. 2021. *Coffee as a Potential Nutraceutical*. EC Nutrition 16(3): 57-65.
3. Kim, et al. 2021. *Science/Education Portraits VII: Statistical Methods Used in 1081 Papers Published in Year 2020 Across 12 Life Science Journals Under BioMed Central*. Acta Scientific Nutritional Health 5(3): 06-12.
4. Cho and Ling. 2021. *Adaptation of Whole Cell Kinetic Model Template, UniKin1, to Escherichia coli Whole Cell Kinetic Model, ecoJC20*. EC Microbiology 17(2): 254-260.
5. Chua and Ling. 2021. *Stop Codon Usage Varies on CDS Length, Nucleotide Compositions, and Peptide Instability in Six Escherichia coli Strains*. EC Clinical and Medical Case Reports 4(2): 39-46.
6. Kuan and Ling. 2021. *Core Genome of Poales, An Economically Important Order of Monocotyledons*. EC Agriculture 7(2): 24-29.
7. Teo and Ling. 2020. *A Systematic Review on the Sufficiency of PubMed and Google Scholar for Biosciences*. Acta Scientific Medical Sciences 4(12): 03-08.
8. Cheong, et al. 2020. *A Simulation Study on the Effects of Media Composition on the Growth Rate of Escherichia coli MG1655 using iAF1260 Model*. Acta Scientific Microbiology 3(8): 40-44.
9. Neo and Ling, MHT. 2020. *Prevalence and Length of Open Reading Frames Vary Across Randomly Generated Sequences of Different Nucleotide Compositions*. EC Microbiology 16(7): 72-78.
10. Teng, et al. 2020. *Correlation Analysis on Transcriptomes from Published Human Skin Studies Show Variations between Control Samples*. EC Clinical and Medical Case Reports 3(6): 143-146.
11. Chang and Ling. 2019. *Explaining Monod in Terms of Escherichia coli Metabolism*. Acta Scientific Microbiology 2(9): 66-71.

### **Listing 2: Publications from Honours Projects via MDIS**

1. Ang, and Ling. 2021. *Sudden and Steep Harsh Environment Results in Over-Compensation in Digital Organisms*. EC Microbiology 17(7): 104-113.
2. Johnny, et al. 2021. *Simulation Suggests that One-Off Simple Supplementation from the Wild into Captive Population May Not Increase Captive Genetic Diversity*. EC Veterinary Science 6(7): 107-111.
3. Lim, et al. 2021. *Significant Differences in Nucleotide and Peptide Features Between Chromosomes Suggesting Sequence Non-Randomness Across Chromosomes*. Acta Scientific Microbiology 4(4): 23-28.

4. Kim, et al. 2021. *Science/Education Portraits VII: Statistical Methods Used in 1081 Papers Published in Year 2020 Across 12 Life Science Journals Under BioMed Central*. Acta Scientific Nutritional Health 5(3): 06-12.
5. Cho, and Ling. 2021. *Adaptation of Whole Cell Kinetic Model Template, UniKin1, to Escherichia coli Whole Cell Kinetic Model, ecoJC20*. EC Microbiology 17(2): 254-260.
6. Chew, et al. 2020. *Rapid Genetic Diversity with Variability between Replicated Digital Organism Simulations and its Implications on Cambrian Explosion*. EC Clinical and Medical Case Reports 3(11): 64-68.
7. Murthy, et al. 2020. *UniKin1: A Universal, Non-Species-Specific Whole Cell Kinetic Model*. Acta Scientific Microbiology 3(10): 04-08.
8. Wang, et al. 2020. *A Case Study using Mitochondrial Genomes of the Order Diprotodontia (Australasian Marsupials) Suggests that Single Ortholog is Not Sufficient for Phylogeny*. EC Clinical and Medical Case Reports 3(9): 93-114.
9. Kamarudin, et al. 2020. *A Simulation Study on the Effects of Founding Population Size and Number of Alleles Per Locus on the Observed Population Genetic Profile: Implications to Broodstock Management*. EC Veterinary Science 5(8): 176-180.
10. Tan, et al. 2020. *Core Pseudomonas Genome From 10 Pseudomonas Species*. MOJ Proteomics & Bioinformatics 9(3): 68-71.
11. Gunalan, et al. 2020. *One Percent of Escherichia coli O157:H7 Peptides May Contain Putative Beta-Lactamase Activity*. EC Microbiology 16(8): 73-79.
12. Usman, et al. 2019. *Pseudomonas balearica DSM 6083T promoters can potentially originate from random sequences*. MOJ Proteomics & Bioinformatics 8(2): 66-70.
13. Ardhanari-Shanmugam, et al. 2019. *De Novo Origination of Bacillus subtilis 168 Promoters from Random Sequences*. Acta Scientific Microbiology 2(11): 07-10.
14. Kwek, et al. 2019. *Random Sequences May Have Putative Beta-Lactamase Properties*. Acta Scientific Medical Sciences 3(7): 113-117.
15. Thong-Ek, et al. 2019. *Potential De Novo Origins of Archaeobacterial Glycerol-1-Phosphate Dehydrogenase (GIPDH)*. Acta Scientific Microbiology 2(6): 106-110.
16. Maitra, and Ling. 2019. *Codon Usage Bias and Peptide Properties of Pseudomonas balearica DSM 6083T*. MOJ Proteomics & Bioinformatics 8(2):27-39.
17. Kim, and Ling. 2019. *Proteome Diversities Among 19 Archaeobacterial Species*. Acta Scientific Microbiology 2(5): 20-27.

### **Listing 3: Advised Undergraduate and Postgraduates**

#### ***Postgraduates***

1. **Argho MAITRA** (2020 – present): MSc at School of Data Sciences, Perdana University, Malaysia.
2. **Jack Jian Ming LEE** (2018 – 2021): MSc at School of Data Sciences, Perdana University, Malaysia. Thesis: Meta-ome for Homology Search.

#### ***Undergraduates***

1. **Katheresan Selvam Sooriya KANNAN** (2021-2022): BSc(Hons) at Northumbria University (UK); via MDIS, Singapore.
2. **Tanmay PATIL** (2021-2022): BSc(Hons) at Northumbria University (UK); via MDIS, Singapore.
3. **Rohit VIJ** (2021-2022): BSc(Hons) at Northumbria University (UK); via MDIS, Singapore.
4. **Behnjemyn Jeng Kit LOH** (2021-2022): BSc(Hons) at Northumbria University (UK); via MDIS, Singapore.
5. **Eugene Wei Jun THIA** (2020-2021): BSc(Hons) at Northumbria University (UK); via MDIS, Singapore. Thesis: Equal Proportion of Source Population to Admixed Population May Not Result in Stable Population Genetic Structure.
6. **Alan JOHNNY** (2020-2021): BSc(Hons) at Northumbria University (UK); via MDIS, Singapore. Thesis: Simulation Suggests that One-Off Simple Supplementation from the Wild into Captive Population May Not Increase Captive Genetic Diversity.
7. **Pasumarthi SUMEDHA** (2020-2021): BSc(Hons) at Northumbria University (UK); via MDIS, Singapore. Thesis: Supplementation from the Wild as a Means to Mitigate Domestic Inbreeding.
8. **Garg Shubhangi VIBHOR** (2020-2021): BSc(Hons) at Northumbria University (UK); via MDIS, Singapore. Thesis: Effect of Bottlenecking on the Population Genetic Structure of an Isolated Population.
9. **Dennis Gee Yao ANG** (2020-2021): BSc(Hons) at Northumbria University (UK); via MDIS, Singapore. Thesis: Niche Adaptation as a Driver of Evolution: How does adaptation to environment drive evolution?

10. **Aarthi RAVICHANDRAN** (2020-2021): BSc(Hons) at Northumbria University (UK); via MDIS, Singapore. Thesis: The Effects of Coding Density on Organism Fitness.
11. **Leejun CHO** (2020-2021): BSc(Hons) at Northumbria University (UK); via MDIS, Singapore. Thesis: Adaptation of Whole Cell Kinetic Model Template, UniKin1, to *Escherichia coli* Whole Cell Kinetic Model, ecoJC20.
12. **Mariia DOLMATOVA** (2020-2021): BSc(Hons) at Northumbria University (UK); via MDIS, Singapore. Thesis: Chromosomal Organization of *Plasmodium falciparum*.
13. **Phebe Hwee Boon LOH** (2020-2021): BSc(Hons) at Northumbria University (UK); via MDIS, Singapore. Thesis: Core and Pan-Genome of *Saccharolobus solfaraticus*.
14. **Zhe En PHUA** (2020-2021): BSc(Hons) at Northumbria University (UK); via MDIS, Singapore. Thesis: A Simulation Study on the Effects of Contamination on the Wild Population with Those in Captivity.
15. **Hykal Hassan AZMI** (2020-2021): BSc(Hons) at Northumbria University (UK); via MDIS, Singapore. Thesis: Logic of Chromosomal Organization in *Prunus dulcis* – Are Genes Organized into Chromosomes Randomly or Is There a Logical Aspect?
16. **Gabriel Zhen Kang LIM** (2020-2021): BSc(Hons) at Northumbria University (UK); via MDIS, Singapore. Thesis: Investigation of Non-Uniform Organization by Comparing Differences in Nucleotide and Peptide Properties Between Chromosomes *Sacrophilus harisii*.
17. **Si Min Shermaine CHEW** (2019-2020): BSc(Hons) at Northumbria University (UK); via MDIS, Singapore. Thesis: Rapid Genetic Diversity with Variability between Replicated Digital Organism Simulations and its Implications on Cambrian Explosion.
18. **Nikita YABLOCHKIN** (2019-2020): BSc(Hons) at Northumbria University (UK); via MDIS, Singapore. Thesis: Evolvability of Protein Domain Sequences.
19. **Xue Ting TAN** (2019-2020): BSc(Hons) at Northumbria University (UK); via MDIS, Singapore. Thesis: Core Pseudomonas Genome From 10 *Pseudomonas* Species.
20. **Avettra RAMESH** (2019-2020): BSc(Hons) at Northumbria University (UK); via MDIS, Singapore. Thesis: Biological Evolution – A Perspective on the Increase of Fitness Score Based on Genetic Variations.
21. **Nur Jannah KAMARUDIN** (2019-2020): BSc(Hons) at Northumbria University (UK); via MDIS, Singapore. Thesis: A Simulation Study on the Effects of Founding Population Size and Number of Alleles Per Locus on the Observed Population Genetic Profile.
22. **Chieh Victor WANG** (2019-2020): BSc(Hons) at Northumbria University (UK); via MDIS, Singapore. Thesis: A Case Study Using Comparative Phylogeny on Mitochondrial Genomes of Twenty-Four Organisms in the *Diprotodontia* Order (Australian Marsupials) Suggests That Single Ortholog Is Not Sufficient for Phylogeny.
23. **Vinayaka Murthy MADHURYA** (2019-2020): BSc(Hons) at Northumbria University (UK); via MDIS, Singapore. Thesis: Metabolic Flux Alteration Due to Varying Enzyme Parameters in a Universal Glycolysis Model.
24. **Celine Wong** (2019): BSc(Hons) at Northumbria University (UK); via MDIS, Singapore. Thesis Probability of Beta-Lactamase Activity in *Lactobacillus*.
25. **Krishneswari Gunasekaran** (2019): BSc(Hons) at Northumbria University (UK); via MDIS, Singapore. Thesis: One Percent of *Escherichia coli* O157:H7 Peptides May Contain Putative Beta-Lactamase Activity.
26. **Marilyn Neo** (2019): BSc(Hons) at Northumbria University (UK); via MDIS, Singapore. Thesis: Evolution of Apicoblast.
27. **Junhong WOO** (2018-2019): BSc(Hons) at Northumbria University (UK); via MDIS, Singapore. Thesis: De Novo Origins of Origin of Replications.
28. **Sharlene USMAN** (2018 - 2019): BSc(Hons) at Northumbria University (UK); via MDIS, Singapore. Thesis: De Novo Origins of *Pseudomonas balearica* Promoters.
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42. **Min Yi KOH** (2018): BSc(Hons) at Northumbria University (UK); via MDIS, Singapore. Thesis: GC variation and Codon Usage Bias in *Corynebacterium striatum*.
43. **Argho MAITRA** (2018): BSc(Hons) at Northumbria University (UK); via MDIS, Singapore. Thesis: Demystifying the Mechanism Underlying Codon Usage Bias in the *Pseudomonas balearica* DSM 6083<sup>T</sup> Genome.
44. **Wei Jie CHEAH** (2018): BSc(Hons) at Northumbria University (UK); via MDIS, Singapore. Thesis: GC-content affects amino-acid usage and peptide physical properties to varying degrees in *Anopheles gambiae*.
45. **Fong Guan LAI** (2018): BSc(Hons) at Northumbria University (UK); via MDIS, Singapore. Thesis: From Gene to Peptide: The Secret within Honeybee.