

CURRICULUM VITAE: LING HAN TONG MAURICE

PERSONAL DATA

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

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ONLINE PROFILES: LinkedIn: <http://www.linkedin.com/in/mauriceling>
Personal Website: <http://maurice.vodien.com>
Professional Portfolio: <http://maurice.vodien.com/portfolio>

CAREER SUMMARY

- Over 16 years of experience (since 2003) as research and lecturing biologist / bioinformaticist in both academic and industrial settings.
- More than 1,500 hours of lecturing, project supervision, and corporate trainer experience since January 2017.
- 80 refereed publications (3 publications from high-school projects, 17 publications from pre-undergraduate projects, and 9 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	Research Assistant Professor , 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	Associate Lecturer , Management Development Institute of Singapore (MDIS). I supervise 19 undergraduate students for the honours year projects to date, mainly in bioinformatics.
2014-current	Co-Founder and Principal Partner , Colossus Technologies LLP. I chair the executive committee and am responsible for the strategic directions of the research and technological developments within the partnership.
2014-current	Co-Founder and Director (Technology) , AdvanceSyn Pte. Ltd. As a biologist turned bioinformaticist, I am responsible for technological developments (both biology and IT tools) of the company.
2010-2017	Honorary Fellow (equivalent to academic rank of Lecturer) , 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	Research Fellow , 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"> • Developing software tools for modeling and predicting gene expression and protein production • Engineering micro-organisms for waste degradation and production of high-valued chemical compounds and peptides • Providing advice for experimental procedures on genetic engineering and

- 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 Jongh. 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 **Adjunct Lecturer**, Temasek Polytechnic (School of Applied Sciences).
 - Develop course materials, lecture and conduct professional workshops on topics related to bioinformatics (mainly genomics, transcriptomics, and proteomics) and statistics.
 - Supervising and mentoring total of 3 interns and major project students.
- 2017- current **Associate Lecturer**, Management Development Institute of Singapore (MDIS). I lecture on topics related to practical skills, bioinformatics, statistics and research methods; as well as supervising honours projects. Approved by Committee for Private Education (CPE, Singapore) and registered as
 - Staff at Partner Institute, Northumbria University (UK)
- 2009 – current **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 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 3rd year Development Biology practical classes.

PROFESSIONAL SERVICES

- 2019-current **Working Committee Member**, 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 **Secretary**, Association of Medical and Bio-Informatics, Singapore (AMBIS).
- 2017-current **Series Editor**, 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 **Technical Reviewer**, 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).
2010-current	Programme Committee Member. <ul style="list-style-type: none"> ▪ Python for High Performance Computing (2010 – 2017), part of International Conference for High Performance Computing, Networking, Storage and Analysis. ▪ 4th International Conference on Electronics, Communications and Networks (CECNet 2014) (2014). ▪ International Symposium on Bioinformatics 2018 (InSyB 2018) (2018), as Programme Committee Chair. ▪ International Conference on Bioinformatics 2019 (InCoB 2019) (2019).
2008-current	Editorial Committee Member. I was invited to join the editorial committee of the following journals: <ul style="list-style-type: none"> ▪ 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). ▪ iConcept Journal of Computational and Mathematical Biology (ISSN 2219-1402), iConcept Press Ltd (2010 – 2018). ▪ MOJ Proteomics & Bioinformatics (ISSN 2374-6920), MedCrave Publishing Group (2014 – 2018 as Associate Editor, Honorary Editor from 2018). ▪ Acta Scientific Microbiology. Acta Scientific (from 2018). ▪ Acta Scientific Computer Sciences, Acta Scientific (from 2018).
2015-2018	Honorary Auditor, 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	Conference and Publications Co-Chair, 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	Committee Member, 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	Publication Team Member (ISBN 0-646-4275-1-2), Australian Undergraduate Students' Computing Conference 2003.
2001	Operations Manager (Advisory), 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 **Deputy S1 (Administration Officer)**, 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. 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.
2. 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 (G1PDH). *Acta Scientific Microbiology* 2(6): 106-110.
3. Maitra, A, **Ling, MHT**. 2019. Codon Usage Bias and Peptide Properties of *Pseudomonas balearica* DSM 6083T. *MOJ Proteomics & Bioinformatics* 8(2):27–39.
4. Kim, JH, **Ling, MHT**. 2019. Proteome Diversities Among 19 Archaeobacterial Species. *Acta Scientific Microbiology* 2(5): 20-27.
5. **Ling, MHT**. 2019. *De Novo Putative Protein Domains from Random Peptides*. *Acta Scientific Microbiology* 2(4): 109-112.
6. **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.
7. 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.
8. **Ling, MHT**. 2018. *SEcured REcorder BOx (SEREBO) Based on Blockchain Technology for Immutable Data Management and Notarization*. *MOJ Proteomics & Bioinformatics* 7(6):169–174.
9. **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.
10. Lim, JX, **Ling, MHT**. 2018. *Gene Ontology and KEGG Orthology Mappings for 10 Strains of Pseudomonas stutzeri*. To appear in *EC Proteomics and Bioinformatics*.
11. **Ling, MHT**. 2018. *RANDOMSEQ: Python Command–line Random Sequence Generator*. *MOJ Proteomics & Bioinformatics* 7(4):206–208.
12. **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.
13. 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.
14. **Ling, MHT**. 2018. *Back-of-the-Envelope Guide (A Tutorial) to 10 Intracellular Landscapes*. *MOJ Proteomics & Bioinformatics* 7(1): 00209.
15. **Ling, MHT**. 2017. *Towards Portrait [(Auto) Ethnography, Narrative, and Action Research] of Bioinformatics*. *EC Proteomics and Bioinformatics* 2(1): 29-35.
16. **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.

17. 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.
18. 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.
19. **Ling, MHT**. 2016. *Of (Biological) Models and Simulations*. MOJ Proteomics & Bioinformatics 3(4): 00093.
20. **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.
21. 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.
22. 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.
23. **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.
24. Keng, BMH, Chan, OYW, **Ling, MHT**. 2014. *Codon Usage Bias is Evolutionarily Conserved*. Asia Pacific Journal of Life Sciences 7(3): 233-242.
25. **Ling, MHT**, Poh, CL. 2014. *A Predictor for Predicting Escherichia coli Transcriptome and the Effects of Gene Perturbations*. BMC Bioinformatics 15: 140.
26. 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.
27. Chan, OYW, Keng, BMH, **Ling, MHT**. 2014. *Bactome III: OLigonucleotide Variable Expression Ranker (OLIVER) 1.0, Tool for Identifying Suitable Reference (Invariant) Genes from Large Microarray Datasets*. The Python Papers Source Codes 6: 2.
28. Koh, YZ, **Ling, MHT**. 2014. *Catalog of Biological and Biomedical Databases Published in 2013*. iConcept Journal of Computational and Mathematical Biology 3: 3.
29. Loo, BZL, Low, SXZ, Aw, ZQ, Lee, KC, Oon, JSH, Lee, CH, **Ling, MHT**. 2014. *Escherichia coli ATCC 8739 Adapts Specifically to Sodium Chloride, Monosodium Glutamate, and Benzoic Acid after Prolonged Stress*. Asia Pacific Journal of Life Sciences 7(3): 243-258.
30. Castillo, CFG, **Ling, MHT**. 2014. *Digital Organism Simulation Environment (DOSE): A Library for Ecologically-Based In Silico Experimental Evolution*. Advances in Computer Science: an international journal 3(1): 44-50.
31. Chan, OYW, Keng, BMH, **Ling, MHT**. 2014. *Correlation and Variation Based Method for Reference Genes Identification from Large Datasets*. Electronic Physician 6(1): 719-727.
32. **Ling, MHT**. 2014. *NotaLogger: Notarization Code Generator and Logging Service*. The Python Papers 9: 2.
33. Chen, KFQ, **Ling, MHT**. 2013. *COPADS III (Compendium of Distributions II): Cauchy, Cosine, Exponential, Hypergeometric, Logarithmic, Semicircular, Triangular, and Weibull*. The Python Papers Source Codes 5: 2.
34. Koh, YZ, **Ling, MHT**. 2013. *On the Liveliness of Artificial Life*. iConcept Journal of Human-Level Intelligence 3: 1.
35. Keng, BMH, Chan, OYW, Heng, SSJ, **Ling, MHT**. 2013. *Transcriptome Analysis of *Spermophilus lateralis* and *Spermophilus tridecemlineatus* Liver Does Not Suggest the Presence of *Spermophilus*-liver-specific Reference Genes*. ISRN Bioinformatics 2013, Article ID 361321.
36. **Ling, MHT**, Ban, YG, Wen, H, Wang, SM, Ge, X. 2012. *Conserved Expression of Natural Antisense Transcripts in Mammals*. BMC Genomics 14:243.
37. Low, SXZ, Aw, ZQ, Loo, BZL, Lee, KC, Oon, JSH, Lee, CH, **Ling, MHT**. 2012. *Viability of Escherichia coli ATCC 8739 in Nutrient Broth, Luria-Bertani Broth and Brain Heart Infusion over 11 Weeks*. Electronic Physician 5:576-581.
38. **Ling, MHT**. 2012. *Re-creating the Philosopher's Mind: Artificial Life from Artificial Intelligence*. iConcept Journal of Human-Level Intelligence 2: 1.

39. **Ling, MHT.** 2012. *Ragaraja 1.0: The Genome Interpreter of Digital Organism Simulation Environment (DOSE)*. The Python Papers Source Codes 4: 2.
40. How, JA, Lim, JZR, Goh, DJW, NG, WC, Oon, JSH, Lee, KC, Lee, CH, **Ling, MHT.** 2013. *Adaptation of Escherichia coli ATCC 8739 to 11% NaCl*. Dataset Papers in Biology 2013, Article ID 219095.
41. **Ling, MHT,** Rabara, RC, Tripathi, P, Rushton, PJ, Ge, X. 2013. *Extending MapMan Ontology to Tobacco for Visualization of Gene Expression*. Dataset Papers in Biology 2013, Article ID 706465.
42. **Ling, MHT.** 2012. *An Artificial Life Simulation Library Based on Genetic Algorithm, 3-Character Genetic Code and Biological Hierarchy*. The Python Papers 7: 5.
43. Goh, DJW, How, JA, Lim, JZR, NG, WC, Oon, JSH, Lee, KC, Lee, CH, **Ling, MHT.** 2012. *Gradual and Step-wise Halophilization Enables Escherichia coli ATCC 8739 to Adapt to 10% NaCl*. Electronic Physician 4(3): 527-535.
44. Dundas, JB, **Ling, MHT.** 2012. *Reference Genes for Measuring mRNA Expression*. Theory in Biosciences 131: 215-223.
45. Lee, CH, Oon, JSH, Lee, KC, Lee, CH, **Ling, MHT.** 2012. *Escherichia coli ATCC 8739 Adapts to the Presence of Sodium Chloride, Monosodium Glutamate, and Benzoic Acid after Extended Culture*. ISRN Microbiology 2012, Article ID 965356.
46. Too, IHK, **Ling, MHT.** 2012. *Signal Peptidase Complex Subunit 1 (SPCS1) and Hydroxyacyl-CoA Dehydrogenase Beta Subunit (HADHB) are Suitable Reference Genes in Human Lungs*. ISRN Bioinformatics 2012, Article ID 790452.
47. Heng, SSJ, Chan, OYW, Keng, BMH, **Ling, MHT.** 2011. *Glucan biosynthesis protein G (mdoG) is a Suitable Reference Gene in Escherichia coli K-12*. ISRN Microbiology 2011, Article ID 469053.
48. **Ling, MHT.** 2011. *Bactome II: Analyzing Gene List for Gene Ontology Over-Representation*. The Python Papers Source Codes 3: 3.
49. Tahat, A, **Ling, MHT.** 2011. *Mapping Relational Operations onto Hypergraph Model*. The Python Papers 6(1): 4.
50. Kuo, CJ, **Ling, MHT,** Hsu, CN. 2011. *Soft Tagging of Overlapping High Confidence Gene Mention Variants for Cross-Species Full-Text Gene Normalization*. BMC Bioinformatics 12(Suppl 8):S6.
51. Lim, JZR, Aw, ZQ, Goh, DJW, How, JA, Low, SXZ, Loo, BZL, **Ling, MHT.** 2010. *A Genetic Algorithm Framework Grounded in Biology*. The Python Papers Source Codes 2: 6.
52. **Ling, MHT.** 2010. *Specifying the Behaviour of Python Programs: Language and Basic Examples*. The Python Papers 5(2): 4
53. Chay, ZE, **Ling, MHT.** 2010. *COPADS, II: Chi-Square test, F-Test and t-Test Routines from Gopal Kanji's 100 Statistical Tests*. The Python Papers Source Codes 2:3.
54. Chay, ZE, Lee, CH, Lee, KC, Oon, JSH, **Ling, MHT.** 2010. *Russel and Rao Coefficient is a Suitable Substitute for Dice Coefficient in Studying Restriction Mapped Genetic Distances of Escherichia coli*. iConcept Journal of Computational and Mathematical Biology 1:1.
55. **Ling, MHT.** 2010. *COPADS, I: Distances Measures between Two Lists or Sets*. The Python Papers Source Codes 2: 2.
56. Ng, YY and **Ling, MHT.** 2010. *Electronic Laboratory Notebook on Web2Py Framework*. In: Peer-Reviewed Articles from PyCon Asia-Pacific 2010. The Python Papers 5(3): 7.
57. Lee, CH, Lee, KC, Oon, JSH, **Ling, MHT.** 2010. *Bactome, I: Python in DNA Fingerprinting*. In: Peer-Reviewed Articles from PyCon Asia-Pacific 2010. The Python Papers 5(3): 6.
58. Chia, CY, Lim, CWX, Leong, WT, **Ling, MHT.** 2010. *High Expression Stability of Microtubule Affinity Regulating Kinase 3 (MARK3) Makes It a Reliable Reference Gene*. IUBMB Life 62(3): 200-203.
59. Kuo, CJ, **Ling, MHT,** Lin, KT, Hsu, CN. 2009. *BIOADI: A Machine Learning Approach to Identify Abbreviations and Definitions in Biological Literature*. BMC Bioinformatics 10(Suppl 15):S7
60. **Ling, MHT.** 2009. *Ten Z-test Routines from Gopal Kanji's 100 Statistical Tests*. The Python Papers Source Codes 1:5
61. **Ling, MHT.** 2009. *Compendium of Distributions, I: Beta, Binomial, Chi-Square, F, Gamma, Geometric, Poisson, Student's t, and Uniform*. The Python Papers Source Codes 1:4
62. **Ling, MHT,** Lefevre, C, Nicholas, KR. 2008. *Filtering Microarray Correlations by Statistical Literature Analysis Yields Potential Hypotheses for Lactation Research*. The Python Papers 3(3): 4.

63. **Ling, MHT**, Lefevre, C, Nicholas, KR. 2008. *Parts-of-Speech Tagger Errors Do Not Necessarily Degrade Accuracy in Extracting Information from Biomedical Text*. The Python Papers 3 (1): 65-80
64. **Ling, MHT**. 2007. *Firebird Database Backup by Serialized Database Table Dump*. The Python Papers 2 (1): 12-16.
65. **Ling, MHT**. 2006. *An Anthological Review of Research Utilizing MontyLingua, a Python-Based End-to-End Text Processor*. The Python Papers 1 (1): 5-12.

Refereed Book Chapters:

1. **Ling, MHT**. 2019. SEcured REcorder BOx (SEREBO) Version 1.0. To appear in Current STEM, Volume 1. Nova Science Publishers, Inc.
2. Wong, A, **Ling, MHT**. 2019. *Characterization of Transcriptional Activities*. In Guenther, R. and Steel, D. (eds.), Encyclopedia of Bioinformatics and Computational Biology, Volume 3, pages 830-841. ISBN 978-0-12811-414-8.
3. Li, BT, Lim, JX, **Ling, MHT**. 2019. *Analyzing Transcriptome-Phenotype Correlations*. In Guenther, R. and Steel, D. (eds.), Encyclopedia of Bioinformatics and Computational Biology, Volume 3, pages 819-824. ISBN 978-0-12811-414-8.
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. 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. 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.
8. **Ling, MHT**. 2018. *A Cryptography Method Inspired by Jigsaw Puzzles*. In Current STEM, Volume 1, pp. 129-142. Nova Science Publishers, Inc. ISBN 978-1-53613-416-2.
9. Castillo, CFG, **Ling, MHT**. 2018. *Digital Organism Simulation Environment (DOSE) Version 1.0.4*. In Current STEM, Volume 1, pp. 1-106. Nova Science Publishers, Inc. ISBN 978-1-53613-416-2.
10. Too, IHK, Heng, SSJ, Chan, OYW, Keng, BMH, Chia, CY, Lim, CWX, Leong, WT, Chu, QH, Ang, EJG, Lin, YJ, **Ling, MHT**. 2014. Identification of Reference Genes by Meta-Microarray Analyses. In Microarrays: Principles, Applications and Technologies. Nova Science Publishers, Inc.
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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