

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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E-Mails: mauriceling@acm.org, computer.in.science@gmail.com

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 15 years of experience (since 2003) as research and lecturing biologist / bioinformaticist in both academic and industrial settings.
- 68 refereed publications and 1 US patent.
- Collaborated with colleagues across different countries and time-zones.
- Supervised projects from post-primary level, resulting in refereed publications.
- 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

| | |
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| 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

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| 2018- current | Research Assistant Professor , Perdana University (School of Data Sciences). |
| 2017- current | Adjunct Lecturer , Temasek Polytechnic (School of Applied Sciences). |
| 2017- current | Associate Lecturer , Management Development Institute of Singapore (MDIS). |
| 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). I develop course materials, lecture and conduct professional workshops on topics related to bioinformatics (mainly genomics, transcriptomics, and proteomics).
- 2017- current **Associate Lecturer**, Management Development Institute of Singapore (MDIS). I lecture on topics related to 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

- 2018-current **Honorable Editor, MOJ Proteomics & Bioinformatics** (ISSN 2374-6920). MedCrave Publishing Group. I was promoted from Associate Editor to Honorable Editor, after 4 years of associate editorship.
- 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.
- 2015-current **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.
- 2010-current **Chief Editor, iConcept Journal of Computational and Mathematical Biology** (ISSN 2219-1402). iConcept Press Ltd. I was invited by the publisher to chair this journal as chief editor. Currently, I manage the peer-review process.
- 2010-current **Technical Reviewer**, Packt Publishing (IT publishing house). I reviewed 13 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-

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| | 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, in preparation), [14] Python Object Oriented Programming Cookbook (ISBN 978-1-78862-278-3, in preparation). |
| 2014-2018 | Associate Editor, MOJ Proteomics & Bioinformatics (ISSN 2374-6920). MedCrave Publishing Group. I was invited by the editorial office to join the editorial board of this journal. |
| 2008-2017 | Co-Editor-in-Chief and Co-Founder , 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). |
| 2010-2017 | Program Committee Member , Python for High Performance Computing. This workshop is part of International Conference for High Performance Computing, Networking, Storage and Analysis. |
| 2014 | Program Committee Member , 4th International Conference on Electronics, Communications and Networks (CECNet 2014). |
| 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

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| 2000-2008 | Association of Computing Machinery (Student Member) |
| 2008–current | Association of Computing Machinery (Professional Member) |
| 2009–current | Python User Group (Singapore) |

PUBLICATIONS

Refereed Journal Articles:

1. **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.
2. 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.
3. **Ling, MHT.** 2018. *Back-of-the-Envelope Guide (A Tutorial) to 10 Intracellular Landscapes*. *MOJ Proteomics & Bioinformatics* 7(1): 00209.
 4. **Ling, MHT.** 2017. *Towards Portrait [(Auto) Ethnography, Narrative, and Action Research] of Bioinformatics*. *EC Proteomics and Bioinformatics* 2(1): 29-35.
 5. **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.
 6. 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.
 7. 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.
 8. **Ling, MHT.** 2016. *Of (Biological) Models and Simulations*. *MOJ Proteomics & Bioinformatics* 3(4): 00093.
 9. **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.
 10. 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.
 11. 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.
 12. **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.
 13. Keng, BMH, Chan, OYW, **Ling, MHT.** 2014. *Codon Usage Bias is Evolutionarily Conserved*. *Asia Pacific Journal of Life Sciences* 7(3): 233-242.
 14. **Ling, MHT**, Poh, CL. 2014. *A Predictor for Predicting Escherichia coli Transcriptome and the Effects of Gene Perturbations*. *BMC Bioinformatics* 15: 140.
 15. 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.
 16. 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.
 17. Koh, YZ, **Ling, MHT.** 2014. *Catalog of Biological and Biomedical Databases Published in 2013*. *iConcept Journal of Computational and Mathematical Biology* 3: 3.
 18. 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.
 19. 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.
 20. 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.
 21. **Ling, MHT.** 2014. *NotaLogger: Notarization Code Generator and Logging Service*. *The Python Papers* 9: 2.
 22. 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.
 23. Koh, YZ, **Ling, MHT.** 2013. *On the Liveliness of Artificial Life*. *iConcept Journal of Human-Level Intelligence* 3: 1.

24. 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.
25. **Ling, MHT**, Ban, YG, Wen, H, Wang, SM, Ge, X. 2012. *Conserved Expression of Natural Antisense Transcripts in Mammals*. BMC Genomics 14:243.
26. 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.
27. **Ling, MHT**. 2012. *Re-creating the Philosopher's Mind: Artificial Life from Artificial Intelligence*. iConcept Journal of Human-Level Intelligence 2: 1.
28. **Ling, MHT**. 2012. *Ragaraja 1.0: The Genome Interpreter of Digital Organism Simulation Environment (DOSE)*. The Python Papers Source Codes 4: 2.
29. 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.
30. **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.
31. **Ling, MHT**. 2012. *An Artificial Life Simulation Library Based on Genetic Algorithm, 3-Character Genetic Code and Biological Hierarchy*. The Python Papers 7: 5.
32. 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.
33. Dundas, JB, **Ling, MHT**. 2012. *Reference Genes for Measuring mRNA Expression*. Theory in Biosciences 131: 215-223.
34. 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.
35. 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.
36. 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.
37. **Ling, MHT**. 2011. *Bactome II: Analyzing Gene List for Gene Ontology Over-Representation*. The Python Papers Source Codes 3: 3.
38. Tahat, A, **Ling, MHT**. 2011. *Mapping Relational Operations onto Hypergraph Model*. The Python Papers 6(1): 4.
39. 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.
40. 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.
41. **Ling, MHT**. 2010. *Specifying the Behaviour of Python Programs: Language and Basic Examples*. The Python Papers 5(2): 4.
42. 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.
43. 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.
44. **Ling, MHT**. 2010. *COPADS, I: Distances Measures between Two Lists or Sets*. The Python Papers Source Codes 2: 2.
45. 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.
46. 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.

47. 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.
48. 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
49. **Ling, MHT**. 2009. *Ten Z-test Routines from Gopal Kanji's 100 Statistical Tests*. The Python Papers Source Codes 1:5
50. **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
51. **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.
52. **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
53. **Ling, MHT**. 2007. *Firebird Database Backup by Serialized Database Table Dump*. The Python Papers 2 (1): 12-16.
54. **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. Wong, A, **Ling, MHT**. 2018. *Characterization of Transcriptional Activities*. Accepted.
2. Li, BT, Lim, JX, **Ling, MHT**. 2018. *Analyzing Transcriptome-Phenotype Correlations*. Accepted.
3. **Ling, MHT**. 2018. *Survey of Antisense Transcription*. Accepted.
4. Lim, JX, Li, BT, **Ling, MHT**. 2018. *Sequence Composition*. Accepted.
5. **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.
6. **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.
7. **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.
8. 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.
9. 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.
10. **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.
11. **Ling, MHT**, Lefevre, Christophe, Nicholas, Kevin R. 2009. *Biomedical Literature Analysis: Current State and Challenges*. In Internet Policies and Issues, Volume 7. Nova Science Publishers, Inc.
12. **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.

Refereed Conference Papers:

1. **Ling, MHT**, Jean, A, Liao, D, Tew, BBY, Ho, S, Clancy, K. 2011. *Integration of Standardized Cloning Methodologies and Sequence Handling to Support Synthetic Biology Studies*. Third International Workshop on Bio-Design Automation (IWBDa). San Diego, California, USA. 6-7 June 2011.
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. (Eds.), Proceedings of the First Australian Undergraduate Students' Computing Conference. (pp. 40-

Other Publications:

1. **Ling, MHT.** 2017. *Problem-Based Learning (PBL), an Important Paradigm for Bioinformatics Education*. MOJ Proteomics and Bioinformatics 5(4): 00166.
2. **Ling, MHT.** 2017. *AdvanceSyn Studio(TM): A BioCad Tool for Designing and Modeling Microbes in SynBio*. Synthetic Biology and the Bio economy – Accelerating Industrialisation, Commercialisation and Productivity, Singapore. 23-24 January 2017.
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.
6. Castillo, CFG, **Ling, MHT.** 2015. *Improved Implementation of Digital Organism Simulation Environment (DOSE Version 1.0.4)*. Colossus Technologies LLP Technical Report Number 001.
7. **Ling, MHT.** 2014. *Hormonal Regulation of Mouse Lactogenesis: Using Transcriptomics and Literature Analysis*. Scholars' Press. ISBN 978-3-639-66810-0.
8. **Ling, MHT, Poh, CL.** 2013. *Predicting Transcriptome of Escherichia coli using "Marker" Genes*. Proceedings of Synthetic Biology 6.0. Imperial College, London, UK. 9-11 July 2013.
9. **Ling, MHT.** 2012. *Lecturer's Personal Website is a Tool for Improving Lecturer-Students' Rapport*. Journal of Education Research 6(3).
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.
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12. Heng, SSJ, Chan, OYW, Keng, BMH, **Ling, MHT.** 2011. *Identifying Invariant Genes in Escherichia coli*. Proceedings of the 17th Youth Science Conference. Singapore.
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