

# Adrianto Wirawan

348 Clementi Avenue 5, #05-50

Singapore 120348

☎ (+65) 9459 8176

✉ [adrianto@gmail.com](mailto:adrianto@gmail.com)

🌐 [www.adriantowirawan.com](http://www.adriantowirawan.com)



## *Curriculum Vitae*

---

### SUMMARY

Proven scientist cum engineer with more than 12 years experience in the development of bioinformatics algorithms, tools and pipelines as well as analysis of Next Generation Sequencing (NGS) data. Most recently played a key leadership role in developing a platform for storage, retrieval and analysis of NGS and high quality clinical data. Holds a PhD from Nanyang Technological University with the thesis titled Heterogeneous Multi-Core Systems in Bioinformatics.

- Expertise in analysis and interpretation of NGS data
- Development of storage, infrastructure and analytics solutions for NGS related big data
- Demonstrated ability to innovate and collaborate across multidisciplinary and multicultural teams
- Experience working in fast-paced start-up environment
- Results and delivery driven approach
- Hybrid bioinformatics scientist and software engineering skillset
- Extensive high performance and cloud computing experience
- Multi-lingual proficiency and strong global communication skillset
- Proven effective and efficient organizational and leadership skills
- Demonstrated ability to learn new skills

---

### EMPLOYMENT HISTORY

**HUMAN LONGEVITY SINGAPORE PTE, SINGAPORE**  
**Senior Bioinformatics Scientist Engineer**

**MAY 2015-PRESENT**

#### *Key Responsibilities*

- Key leadership role in development of Human Longevity Inc. (HLI) Knowledgebase™, winner of Bio-IT Best Practices Award 2016.
- Communication bridge translating bioinformatics analyses into production ready software.
- Development of novel algorithms for the integration and analysis of various omics data.
- Carried out association analyses with genomic (30K+ whole genome sequences, 600M+ variants), microbiomic, metabolomic, and phenotypic information.
- Guided the organization through the selection of innovative computing technologies.
- Utilized Amazon Web Services (AWS) infrastructures.
- Followed Agile development methodologies. (Scrum, Kanban)

### ***Key Achievements***

- ❖ 2016 BioIT World Best Practice Award for HLI Knowledgebase™.
- ❖ Launch of HLI Knowledgebase beta version to Pharma clients and Physicians.
- ❖ Development of genome browser for HLI's internal use.
- ❖ Development of analysis service and novel visualizations for genomic and metabolomic pathways.
- ❖ Development of novel visualizations for microbiomic phylogenetic tree triggered by AWS Lambda.
- ❖ Development of the Genome Wallmap, a software to produce personalized posters with the graphical representation of an individual's whole genome.
- ❖ Company-wide adoption of the Genome Wallmap for all HLI and Health Nucleus clients.
- ❖ Continuous development and deployment of a pipeline that manages genome annotation sources.

**JOHANNES GUTENBERG UNIVERSITÄT MAINZ, GERMANY**  
**INSTITUTE OF COMPUTER SCIENCE**  
**Postdoctoral Research Fellow**

**APR 2012-MAY 2015**

### ***Key Responsibilities***

- Led development of cutting-edge bioinformatics algorithms and tools using High Performance Computing for Next Generation Sequencing (NGS) data.
- Key role in several important external collaborations (Institute of Molecular Biology Mainz, ).
- Teaching Assistant and Tutor for Parallel Algorithms and Architecture, Theoretische Grundlagen der Informatik I / Berechenbarkeit und Komplexität (Theoretical Computer Science) and Technische Informatik (Technical Computer Science). Class size is up to 210 students.
- Instructor for Parallel Programming with CUDA Practicals. Class size of 10 students.

### ***Key Achievements***

- ❖ Developed a ChIP-Seq analysis pipeline for peak detection with respect to repetitive DNA regions.
- ❖ Developed HECTOR, a parallel error corrector for 454 NGS data.
- ❖ Developed CUDASW++, one of the most popular parallel Smith Waterman protein database search algorithm for GPGPUs using CUDA.

**NATIONAL UNIVERSITY OF SINGAPORE, SINGAPORE**  
**YONG LOO LIN SCHOOL OF MEDICINE**  
**Postdoctoral Research Fellow**

**NOV 2009-MAR 2012**

### ***Key Responsibilities***

- Led identification of genetic mutations and phenotypic changes associated with the development of in vitro and in vivo polymyxin resistance in paired clinical *Acinetobacter baumannii* isolates.
- Key role in several important external collaborations (Genome Institute of Singapore, Singapore General Hospital, Singapore Eye Research Institute).

### ***Key Achievements***

- ❖ Developed a pipeline used by Genome Institute of Singapore (GIS) for sequence assembly, single-nucleotide polymorphism (SNP) calling and gene annotation.
- ❖ Developed a variable tandem repeat finder and visualization tool in collaboration with biologists for National University of Singapore and Singapore General Hospital.
- ❖ Genomic analysis and development of a new multilocus variable-number tandem-repeat analysis scheme for molecular epidemiological typing of *Acinetobacter baumannii*.
- ❖ Developed a machine learning algorithm to select features for computer-aided Angle Closure Glaucoma mechanism detection from images of patients' eyes.

**PHD, NANYANG TECHNOLOGICAL UNIVERSITY**

**JUL 2005-OCT 2010**

*See Qualifications/Education below for details.*

**Key Achievements**

- ❖ Developed fast parallel Smith Waterman and BLAST protein database search algorithms on the PlayStation 3.
- ❖ Developed a multi-threaded vectorized distance matrix computation on the Cell Broadband Engine and x86/SSE2 architectures.

**NANYANG TECHNOLOGICAL UNIVERSITY  
SCHOOL OF COMPUTER ENGINEERING  
Research Assistant**

**JUL 2005-NOV 2009**

**Responsibilities**

- Co-Supervisor of Final Year Undergraduate Students' and Masters' Projects.
- Laboratory Supervisor and Instructor for Introduction to Programming. Class size of 40 students.

**QUALIFICATIONS/EDUCATION**

**Doctor of Philosophy (Ph.D.)  
School of Computer Engineering, Nanyang Technological University**

**JUL 2005-NOV 2010**

*Supervisor:* A/Professor Kwoh Chee Keong  
*Thesis:* Heterogeneous Multi-Core Systems in Bioinformatics  
*GPA:* 4.6/5.0

**Bachelor of Engineering (Hons)  
School of Computer Engineering, Nanyang Technological University**

**JUL 2001-JUN 2005**

Second class (Upper) Hons

**SELECTED SKILLS**

- Programming languages: C, C++, C#, Python, JavaScript, Scala, R, Matlab, SQL
- Frameworks: .NET, ASP.NET MVC, Web API, Entity Framework, Node.js, AngularJS, ReactJS, Redux
- Data Visualization: D3.js, Cytoscape
- Applications: Docker, Spark, Elasticsearch, Samtools, Bcftools, GATK, WEKA, JetBrains Suite, MS Visual Studio, Eclipse, LaTeX
- Platforms: Amazon Web Services (AWS), Windows/Windows Server, Linux, MacOS
- Agile methodology: Scrum, Kanban

**SELECTED PUBLICATIONS**

- A. Wirawan, R. S. Harris, Y. Liu, B. Schmidt and J. Schröder: *HECTOR: A parallel multistage homopolymer spectrum based error corrector for 454 sequencing data*, **BMC Bioinformatics**, 15:131, 2014.

- Y. Liu, A. Wirawan and B. Schmidt: *CUDASW++ 3.0: accelerating Smith-Waterman protein database search by coupling CPU and GPU SIMD instructions*, **BMC Bioinformatics**, 14(117), 2013.
- A. Wirawan, C. K. Kwoh, P. T. K. Chew, M. C. D. Aquino, S. C. Loon, J. See, C. Zheng, W. Lin: *Feature Selection for Computer-Aided Angle Closure Glaucoma Mechanism Detection*, **J. Med. Imaging Health Inf.** Vol 2, No. 4, pp. 438-444, 2012
- K.G. Lim, C.K. Kwoh, L.Y. Hsu, A. Wirawan: *Review of Tandem Repeat Search Tools: A Systematic Approach to Evaluating Algorithmic Performance*, **Briefings in Bioinformatics** (2013) 14 (1): 67-81.
- A. Wirawan, C.K. Kwoh, B. Schmidt: *Multi Threaded Vectorized Distance Matrix Computation on the Cell/BE and x86/SSE2 Architectures*, **Bioinformatics**, Vol. 26, No. 10, pp. 1368-1369, 2010
- A. Wirawan, C.K. Kwoh, L.Y. Hsu, T.H. Koh: *INVERTER: INtegrated Variable number Tandem rEpeat finder*, **Communications in Computer and Information Science**, Volume 115, Part 4, pp. 151-164, Springer, 2010. DOI: 10.1007/978-3-642-16750-8\_14.
- A. Wirawan, B. Schmidt, H. Zhang, C.K. Kwoh: *High Performance Protein Sequence Database Scanning on the Cell B.E. Processor*, **Scientific Programming**, Vol. 17, No. 1-2, pp. 97-111, 2009.
- A. Wirawan, C.K. Kwoh, T.H. Nim, B. Schmidt: "CBESW: Sequence Alignment on the Playstation 3", **BMC Bioinformatics**, Vol. 9:377, 2008.
- A. Wirawan, B. Schmidt, C.K. Kwoh: *Pairwise Distance Matrix Computation for Multiple Sequence Alignment on the Cell Broadband Engine*, **Lecture Notes in Computer Science**, Vol. 5544, pp. 954-963, Springer, 2009. DOI: 10.1007/978-3-540-68111-3\_132.
- A. Wirawan, B. Schmidt, C.K. Kwoh: *Parallel DNA Sequence Alignment on the Cell Broadband Engine*, **Lecture Notes in Computer Science**, Vol. 4967, pp. 1249-1256, Springer, 2008. DOI: 10.1007/978-3-642-01970-8\_96.
- A. Wirawan, B. Schmidt: *Parallel Discovery of Transcription Factor Binding Sites*, **IEEE Asia Pacific Conference on Circuits and Systems (APCCAS 2006)**, Singapore, IEEE Press, 2006

## **HONORS AND AWARDS**

- Amazon Web Services (AWS) Certified Developer, 2015
- RSS Scholarship Award for Ph.D, Singapore, July 2005 – 2010
- ASEAN Scholarship Award for B. Eng, Singapore, July 2001 – June 2005
- NTU Cultural Activities Club Merit Cultural Award, Singapore, 2003

## **PERSONAL INFORMATION**

- Indonesian Citizen, Singapore Permanent Resident (PR).
- Open to relocation.
- Male, married, 33 years old.
- Proficiency in English, Malay and Bahasa Indonesia; Intermediate German (B1) and Introductory Chinese.
- Hobbies: Football, Basketball, Travelling, Music.

## **REFERENCES**

Available upon request