

Wibowo Arindrarto | Resume

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Career Profile

- Versatile bioinformatician with years of real-world software development experience and a molecular biology background.
- Well-versed in next-generation sequencing data analysis using high-performance computing clusters.
- Aspires to create computational tools for scientific data analysis.

Education

Utrecht University

Master of Science, Biomedical Science, GPA – 4.0/4.0

Utrecht, The Netherlands

Sep 2010–Oct 2012

- Utrecht Excellence Scholarship recipient.

Atma Jaya Catholic University

Sarjana Sains (B.Sc. equivalent), GPA – 3.8/4.0

Jakarta, Indonesia

Aug 2005–Apr 2009

- Champion, 10th Indonesian Varsities English Debate (2007) in Purwokerto, Indonesia.

Experience

Leiden University Medical Center

Research Analyst (Bioinformatician)

Leiden, The Netherlands

Jan 2013–Present

- Member of the core sequencing analysis support team, mainly involved in analysis of RNA-seq and variant calling data.
- Involved in various programming-related projects, while also working with researchers to analyze their sequencing results.
- Gained experience working with different cluster engines (Open Grid Engine for the local cluster, gLite for the Dutch National Grid).
- Taught courses on RNA-seq analysis (both using the command line and Galaxy), the Python programming language, and the git version control system.

Open Bioinformatics Foundation

Student Developer

remote

Apr 2012–Aug 2012

- Selected for the Google Summer of Code program to work on Biopython, the open source Python bioinformatics library.
- Project was completed successfully and is now included in the main Biopython distribution.

Maastricht University

Student Intern

Maastricht, The Netherlands

Jan 2012–Aug 2012

- Improved methylation array analysis support for <http://arrayanalysis.org>, a publicly-available microarray analysis platform.

Programming Projects

Sentinel

Work-related

Sentinel is a JSON-based database for storing and computing various next-generation sequencing metrics, implemented using the Scalatra framework. Data queries and submissions are all done via a RESTful HTTP API, making it easy for other tools to interact with it. I designed, implemented, tested, and deployed the system.

- *Technologies:* Scala, MongoDB, Ansible
- *Homepage:* <https://github.com/LUMC/sentinel>

NGS Metrics Database

Apr 2015–Present

Gentrap

Work-related

Gentrap is an in-house generic RNA-seq pipeline with pluggable aligners and various abundance estimation methods. The pipeline was initially implemented in GNU Make and then converted to a Scala-based framework. I contributed to the design and implemented the pipeline.

- *Technologies:* Scala, Python, R, GNU Make, Open Grid Engine, GNU Make, various command line tools
- *Homepage:* <http://humgenprojects.lumc.nl/sasc/biopet-docs/pipelines/gentrap/>

RNA-seq Analysis Pipeline

Apr 2013–Present

Colibri

Work-related

Colibri is a Flask web server designed for automation and monitoring of pipeline runs. The system tracks sequencing results deposited to the cluster, starts the pipeline automatically, and monitors the run until it finishes. I designed and implemented the system, which is now maintained by another bioinformatician.

- *Technologies:* Python, MongoDB, GNU Make, Open Grid Engine, various command line tools

Pipeline Automation System

Dec 2013– Jul 2014

Biopython

Personal

Biopython is a collaboration involving various bioinformatician from around the world. I added support for parsing ABI trace files, implemented the SearchIO module, and submitted various bug fixes. SearchIO is a common framework for parsing outputs from sequence search tools such as BLAST, HMMER, and BLAT.

- *Technologies:* Python, SQLite
- *Homepage:* <https://github.com/biopython/biopython/>

Python Bioinformatics Library

Jul 2011–Present

Skills

Programming Languages:

- *Advanced:* Python
- *Intermediate:* Scala, Bash, R
- *Novice:* JavaScript

Database Engines:

- *Intermediate:* MongoDB
- *Novice:* CouchDB, SQLite, MySQL

Build Systems: GNU Make, SBT

Operating Systems: Linux (Ubuntu, Debian, Arch), Windows

Other Tools: git, vim, IntelliJ IDE, various bioinformatics tools

Human Languages: Indonesian (native), English (fluent), Dutch (basic)

Talks

Biopython Project Update. Presented in the 2014 Bioinformatics Open Source Conference in Boston, USA.

RNA-seq Alignment and Quantification. Presented in the 2015 BioSB RNA-seq course in Leiden, The Netherlands.

Publications

Molecular signatures of age-associated chronic degeneration of shoulder muscles. Raz Y, Henseler JF, Kolk A, Tatum Z, Groosjohan NK, Verwey NE, **Arindrarto W**, Kielbasa SM, Nagels J, 't Hoen PAC, Nelissen RGGH, Raz V. 2016. *Oncotarget* 7:8.

KeyGenes, a tool to probe tissue differentiation using a human fetal transcriptional atlas. Roos MS, van Iperen L, Ariyurek Y, Buermans HP, **Arindrarto W**, Devalla HD, Passier R, Mummery CL, Carlotti F, de Koning EJP, van Zwet EW, Goeman JJ, Chuva de Sousa Lopes SM. 2015. *Stem Cell Reports* 4:6.

Uncoupling protein 2 gene polymorphisms are associated with obesity. Oktavianthi S, Trimarsanto H, Febinia CA, Suastika K, Saraswati MR, Dwipayana P, **Arindrarto W**, Sudoyo H, Malik SG. 2012. *Cardiovasc Diabetol* 11:41.

Posters

Genome-wide Allelic Expression Reveals Incomplete Reprogramming in Human Female Germ Cells. Vertesy A, **Arindrarto W**, Roost M, Reinius B, Sandberg R, Mei L, Chuva de Sousa Lopes SM, van Oudenaarden A. Single Cell Genomics Conference in Utrecht, The Netherlands, 2015.

Building Scalable, Maintainable, User-friendly, Robust and Flexible NGS Pipelines. van 't Hof P, **Arindrarto W**, Leung WY, van der Zeeuw S, Bollen S, Laros J, Mei L. BioSB Conference in Lunteren, The Netherlands, 2015.

dbXP: Investigating The Future of Integrative Bioinformatics Research Infrastructure in Europe. Eijssen L, Bouwman J, Dutta A, Nunes N, Radonjic M, Kelder T, Goelela V, Gaj S, Coonen M, Adriaens M, **Arindrarto W**, de Groot P, Jaillard M, van Ommen B, Evelo C. Benelux Bioinformatics Conference in Brussels, Belgium, 2013.

Quantitative Determinations on the Assembly of the Oct4-Sox2-DNA Ternary Complex. Mistri TK, **Arindrarto W**, Ng WP, Sun LL, Robson P, Wohland T. *55th Annual Biophysical Society Meeting* in Baltimore, USA, 2011.

Identification of Neoblast Markers in *Macrostomum lignano*. **Arindrarto W**, De Mulder K, Lansu N, Berezikov E. *4th International Macrostomum Meeting* in Basel, Switzerland, 2010.

Genetic Diversity and Lifestyle-related Disease. Malik SG, Sudoyo H, Trimarsanto H, Oktavianthi S, Saraswati MR, Suastika K, Sulfiанти A, **Arindrarto W**. *12th Symposium on Molecular Diabetology in Asia* in Busan, South Korea, 2010.

UCP2 Gene Polymorphisms are Associated with Type 2 Diabetes Mellitus and Obesity in Balinese. Oktavianthi S, Trimarsanto H, **Arindrarto W**, Saraswati MR, Sudoyo H, Suastika K, Malik SG. *Eijkman Institute and NEHCRI Joint Symposium on Human Genetics and Infection: Towards Better Management of Disease* in Jakarta, Indonesia, 2010.