

DANANG CRYSNANTO

Interested in the **bioinformatics** of the large-scale whole-genome sequencing data. Current work **first to propose** the transition from linear to more representative, **graph-based reference genome** for unbiased sequence variant analysis.

EDUCATION

Current
|
2018

PhD Candidate in Computational Animal Genomics

Zurich Switzerland

📍 Swiss Federal Institute of Technology (ETH Zurich)

- **Research project:** Graph-based genomic analysis
- **Skills learned:** Graph analytics, Bioinformatics pipeline management

2017
|
2016

Msc in Quantitative Genetics and Genome Analysis

Edinburgh United Kingdom

📍 The University of Edinburgh

- **Thesis:** Widespread gene duplication in *Drosophila* RNAi pathways
- **Skills learned:** Phylogenetic analysis, Bayesian statistics
- The best master thesis with **distinction** (average marks > 85)

SELECTED PUBLICATIONS

2019

Accurate sequence variant genotyping in cattle using variation-aware genome graphs

Genetic Selection Evolution

- Published within the first year of PhD
- First work of using graphs for sequence variant discovery in livestock

2019

Widespread gene duplication and adaptive evolution in the RNA-interference pathways of the *Drosophila obscura* group

BMC Evolutionary Biology

- Published from Master's work
- Identified massive gene amplifications from analysis >30 *Drosophila* genome

SELECTED AWARDS

2018

Sir Kenneth Mather Memorial Prize

📍 The Genetics Society

- Rewards a BSc, MSc or PhD student of any UK University or Research Institution who has shown outstanding performance in the area of population genomics or quantitative genetics.

2017

The Douglas Falconer Prize

📍 The University of Edinburgh

- Awarded as the best Master's thesis in the area of Quantitative Genetics and Genome Analysis

2010

Bronze Medalist 21st International Biology Olympiad (IBO)

Changwon South Korea

📍 International Biology Olympiad

- International biology competition for high school students from 60 countries, who are winners of their respective National Biology Olympiad.



CONTACT

✉ danangcrysnanto@gmail.com

✉ danang.crysnanto@usys.ethz.ch

🐦 [crdanang](https://twitter.com/crdanang)

🌐 github.com/danangcrysnanto

🔗 danangcrysnanto.github.io

📞 +41 766 218 242

SKILLS

📊 R

📊 Tidyverse

🐍 Python

🔑 Git

🐳 Docker

>_ Bash

🖨 HPC (IBM LSF)




Highly experienced in designing and maintaining bioinformatic pipeline for large scale whole genome sequencing data

Created with the R package
[pagedown](https://github.com/jgm/pagedown).

Source code available at
github.com/danangcrysnanto/cv.
Last updated on 2019-11-20.



SELECTED CONFERENCE AND TALKS

- 2020 • **Plant and Animal Genome (PAG) Conference**
San Diego USA
· Talk title: Mapping sequencing read to bovine genome graph
- 2019 • **Computational PANgenomics**
Oeiras Portugal  Gulbekian Training Program in Bioinformatics
· Training with mini-hackaton on graph genomics
- 2018 • **Genome Informatics and Livestock Genomics Conference**
Cambridge United Kingdom  Wellcome Genome Cambridge
· Talk title: Assessment of the graph-based genotyping with bovine short-read data
- 2018 • **Population Genetics Group Conference**
Oxford United Kingdom  The Genetics Society
· Talk title: Widespread gene duplication in *Drosophila* immune pathways (Invited talk)



SELECTED TRAINING

- 2019 • **Nextflow for reproducible genomics**
Tubingen Germany  Quantitative Biology Center (QBIC)
· Workshop on implementation of reproducible genomics
- 2019 • **R packages**
Swiss Institute of Bioinformatics  University of Zurich
· Training on creating R packages using *devtools*
- 2019 • **Basic Tensorflow**
Lausanne Switzerland  Google Zurich
· Training on basic machine learning in Swiss Applied Machine Learning Days
- 2018 • **Docker for reproducible computational research**
Swiss Institute of Bioinformatics  University of Bern
· Training on reproducibility genomic analysis using Docker
- 2018 • **Bioinformatics of Long-Range Sequencing**
Swiss Institute of Bioinformatics  University of Zurich
· Training on long-read (*Pacbio* and *Nanopore*) data analysis
- 2017 • **Python for Life Science**
Edinburgh United Kingdom  Edinburgh Genomics
· Using Python data science stack (e.g., Pandas, Jupyter) for genomics data analysis
- 2017 • **High performance computing for genomics application**
Scientific IT Services  ETH Zurich
· Training on best practice of using ETH big data cluster for genomic analysis
- 2017 • **GATK Best Practice for Genomic Data Analysis**
Broad Institute  Harvard MA USA
· Training on the best practice variant discovery with Genomic analysis toolkit (GATK)