

Jitao David Zhang

Computational Biologist in Drug Discovery

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Key facts

- Interdisciplinary researcher with more than eight years' experience in drug discovery.
- Supporting 30+ projects per year by algorithm development and data modelling.
- Open-source software developer and open-access author (40+ publications, *h*-index 19).
- Proponent of multiscale modelling of drug mechanism and safety.

Scientific career

- 2011– **Principal Scientist, Computational Biology, F. Hoffmann-La Roche AG, Basel, Switzerland.**
I develop algorithms and software to mine, interpret, model and integrate heterogeneous data, and apply mathematical and computational tools to support preclinical drug discovery projects. I am responsible for target assessment and validation, multiscale modelling of drug mechanism and safety, and MoA characterisation and de-risking of drug candidates. With colleagues I co-develop novel platforms and resources to support drug discovery, for instance the molecular phenotyping platform.
- 2006–2011 **Freelance bioinformatics programmer and biomarker consultant, HUSAR Bioinformatics Group and LIFE Biosystems GmbH, Heidelberg, Germany.**

Teaching, mentoring, and academic commitment

- 2018– Lecture series *Introduction to Applied Mathematics and Informatics In Drug Discovery* (<http://AMIDD.ch>), Department of Mathematics and Informatics, University of Basel
- 2018– Participation in the lecture series *From Novel Targets To Novel Therapeutic Modalities*, MSc Drug Sciences, University of Basel.
- 2016– Supervising master students in bioinformatics and computational biology, and co-supervise PostDocs in collaboration with academic and industrial collaboration partners.
- 2012– Acting as reviewers for *Bioinformatics*, *BMC Syst. Biol.*, *Stat. Biopharm. Res.*, etc.
- 2012– Leading seminar/course series within Roche, on computational topics including *Network Analysis*, *R programming*, *Bioinformatics In Drug Discovery*, etc.

Education

- 2008–2011 **Dr.rer.nat. Bioinformatics, German Cancer Research Center/ Universität Heidelberg.**
Computational and statistical approaches to study gene networks, supervised by Dr. Stefan Wiemann
- 2007–2007 **Marie-Curie Fellow, Huber Group, European Institute of Bioinformatics, Cambridge, UK.**
- 2006–2008 **M.Sc. Bioinformatics, Universität Heidelberg, Germany.**
- 2002–2006 **B.Sc. Biology, hon., Peking University, Beijing, China.**

Selected peer-reviewed publications

Assessment of network module identification across complex diseases. *Nature Methods*, 2019.

Comprehensive evaluation of transcriptome-based cell-type quantification methods for immuno-oncology. *Bioinformatics*, 2019.

A novel orally available small molecule that inhibits hepatitis B virus expression. *Journal of Hepatology*, 2018.

Detect tissue heterogeneity in gene expression data with BioQC. *BMC Genomics*, 2017.

Molecular phenotyping combines molecular information, biological relevance, and patient data to improve productivity of early drug discovery. *Cell Chemical Biology*, 2017.

Genomic analysis of the molecular neuropathology of tuberous sclerosis using a human stem cell model. *Genome Medicine*, 2016.

14-3-3 ζ turns TGF- β 's function from tumor suppressor to metastasis promoter in breast cancer by contextual changes of smad partners from p53 to Gli2. *Cancer Cell*, 2015.

White-to-brown metabolic conversion of human adipocytes by JAK inhibition. *Nature Cell Biology*, 2015.

Highly sensitive amplicon-based transcript quantification by semiconductor sequencing. *BMC Genomics*, 2014.

Data mining reveals a network of early-response genes as a consensus signature of drug-induced *in vitro* and *in vivo* toxicity. *The Pharmacogenomics Journal*, 2013.

Global microRNA level regulation of EGFR-driven cell-cycle protein network in breast cancer. *Molecular Systems Biology*, 2012.

KEGGgraph: a graph approach to KEGG PATHWAY in R and Bioconductor. *Bioinformatics*, 2009.

→ See the full, manually curated list at Google Scholar (<http://goo.gl/CoeJu7>).

Selected open-source software

BioQC	Detecting tissue heterogeneity in high-throughput expression data
RTCA	Open-source analysis software for Roche Real-Time Cell-Analyzer System®
KEGGgraph	Data mining and network analysis of biological pathways as graphs in R and Bioconductor

Computer skills

Programming	R/Bioconductor, C/C++, Java, Python	Database	MySQL, Oracle, PostgreSQL, SQLite
Scripting	Python, Bash, Erlang	Web	HTML, CSS, JavaScript, Flask
OS	Debian Linux, Windows	Others	d3js, OpenCV, ImageMagick, L ^A T _E X

Personal information

Date of Birth	Sept. 28 th , 1983 in Tianjin, China
Marital status	Married, father of two daughters
Hobbies	Family, run & bike, reading, mathematics, programming, music
Languages	English, German, Chinese