Jitao David Zhang

Bioinformatics and Computational Biology

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Profession

2011– **Principal Scientist, Computational Biology**, *F. Hoffmann-La Roche AG*, Basel, Switzerland.
As a research scientist, my work focuses on mining, analysis, interpretation and integration of heterogeneous data using mathematical and bioinformatics tools to support preclinical drug discovery projects. I am responsible for target assessment and validation, stem-cell and animal-model based disease modelling, and MoA characterisation and de-risking of drug candidates. With colleagues I co-develop novel platforms and resources, *e.g.* molecular phenotyping.

2010–2011 **Bioinformatics biomarker consultant**, *LIFE Biosystems GmbH*, Heidelberg, Germany.

2006–2008 **Scientific programmer**, *HUSAR Bioinformatics Group*, Heidelberg, Germany.

Teaching, mentoring, and academic commitment

2018– *Planned* Organizing and teaching the lecture series *Introduction to Applied Mathematics and Informatics In Drug Discovery* at the University Basel.

2018– Teaching in the lecture series *From Novel Targets To Novel Therapeutic Modalities* led by Dr. Adrian Roth at the University of Basel.

2016– Supervising master students in 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 diverse topics including *Network Analysis*, *R programming*, *Bioinformatics In Drug Discovery*, *etc.*

2007– Member of the professional association *R Foundation*.

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

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. **Featured**

as the journal cover story and accompanied with *News and Views* by J. Moffat.

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

14-3-3ζ 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.

Combined DNA methylation and gene expression profiling in gastrointestinal stromal tumors reveals hypomethylation of SPP1 as an independent prognostic factor. *International Journal of Cancer*, 2015.

White-to-brown metabolic conversion of human adipocytes by JAK inhibition. *Nature Cell Biology*, 2015. **Featured on the journal cover and covered by presses**.

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. **Accompanied with *News and Views* by M. Malumbres**.

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

→ See the full list at Google Scholar.

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, Solaris, Windows	Others	d3js, OpenCV, ImageMagick, LaTeX

Languages

English	Business fluent	*6-month stay in Cambridge, UK with fellowship*
German	Business fluent	*Since 2006 residing in Germany/Switzerland*
Chinesisch	Native	*Mandarin speaking*

Personal Information

Date of Birth	Sept. 28th, 1983 in Tianjin, China
Marital status	Married, father of two daughters
Hobbies	Family, run & bike, reading, mathematics, programming, music
Nationality	Chinese, holder of *Niederlassungsbewilligung C* of Switzerland