

Jitao David Zhang

Bioinformatics and Computational Biology

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Profession

- 2011– **Principal Scientist, Computational Biology**, F. Hoffmann-La Roche AG, Basel, Switzerland.
My research focuses on analysis, mining, interpretation, and integration of heterogeneous data using bioinformatics and statistical tools to support early drug discovery. My work contributes to target assessment and validation, stem-cell and animal-model based disease modelling, and mode-of-action characterisation and de-risking of drug candidates. With colleagues I co-develop novel platforms and resources such as *molecular phenotyping* to support translational drug discovery.
- 2010–2011 **Bioinformatics consultant**, LIFE Biosystems GmbH, Heidelberg, Germany.
Identified plasma microRNAs as signatures for bladder cancer.
- 2006–2008 **Scientific programmer**, HUSAR Bioinformatics Group, Heidelberg, Germany.
Bioinformatic programming in Perl, C, and C++ for web service and sequence analysis tools.

Education

- 2016–2017 **Online training in medicinal chemistry and deep-neural networks.**
- 2008–2011 **Dr.rer.nat. Bioinformatics and Biostatistics**, German Cancer Research Center (DKFZ) and Universität Heidelberg, Germany.
Thesis: “Computational and statistical approaches to profile cancer-related gene regulatory network with integrated high-throughput data”, supervised by PD Dr. Stefan Wiemann.
- 2007–2007 **Marie-Curie Fellow**, European Institute of Bioinformatics, Cambridge, UK.
Research stay in Dr. Wolfgang Huber’s lab to study yeast genetics.
- 2006–2008 **M.Sc. Bioinformatics**, Universität Heidelberg, Germany.
Thesis: “Data analysis of a genome-wide RNAi screen to identify modulators of human p38 MAP kinase”, supervised by PD Dr. Stefan Wiemann.
- 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.

14-3-3 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.

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, L ^A T _E X

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

Commitment

2017–	Leading the course series <i>Bioinformatics In Drug Discovery</i> within Roche
2016–	Supervising master students in computational biology, and co-supervise PostDocs
2012–	Organize and host the seminar series on <i>Network Analysis</i> and <i>R programming</i> within Roche
2007–	Member of the professional association <i>R Foundation</i>

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
Nationality	Chinese, holder of <i>Niederlassungsbewilligung C</i> of Switzerland