Jitao David Zhang

Bioinformatics and Computational Biology

F. Hoffmann-La Roche AG
4070 Basel, Switzerland
☎ *+41-(0)6168-86251*
✉ *jitao_david.zhang@roche.com*

Working experience

2011–   **Computational biologist**, *F. Hoffmann-La Roche AG*, Basel, Switzerland.
My research focuses on analysis, mining, interpretation, and integration of heterogeneous data 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-developed novel platforms and resources such as *Molecular Phenotyping* to support early 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 Medical Chemistry**.

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.
Reerach 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*, 18(1):277, 2017.

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

Genomic analysis of the molecular neuropathology of tuberous sclerosis using a human stem cell model. *Genome Medicine*, 8(1):94, 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*, 27(2):177–192, 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*, 136(5):1013–1023, 2015.

White-to-brown metabolic conversion of human adipocytes by JAK inhibition. *Nature Cell Biology*, 17(1):57–67, 2015.

Highly sensitive amplicon-based transcript quantification by semiconductor sequencing. *BMC Genomics*, 15(1):565, 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*, 14(3):208–216, 2013.

Global microRNA level regulation of EGFR-driven cell-cycle protein network in breast cancer. *Molecular Systems Biology*, 8(1), 2012.

KEGGgraph: a graph approach to kegg pathway in R and Bioconductor. *Bioinformatics*, 25(11):1470–1471, 2009.

→ See full list on Google Scholar at http://goo.gl/ukssrW.

Selected open-source software

BioQC	Detecting tissue heterogeneity in high-throughput expression data
RTCA	Open-source analysis software for the 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	Databank	MySQL, Oracle, PostgreSQL, SQLite
Scripting	Python, Perl, Bash, Erlang	Web	HTML/CSS/JavaScript, Django
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*

Commitment

2016–	Supervising bioinformatics and computational biology master students
2011–	Coaching R programming for basic and advanced levels in Roche
2012–2013	Organize and host the seminar series on *Network Analysis* within Roche
2007–	Member of the professional association *R Foundation*

Personal Information

Date of Birth	Sept. 28, 1983 in Tianjin, China	Nationality	Chinese
Marital status	Married, father of two daughters		
Hobbies	I enjoy every second spent with my family. Otherwise I run and bike almost everyday. When kids sleep I read, learn mathematics, and programm for fun.		
misc.	Holder of *Niederlassungsbewilligung C* of Switzerland		