

# 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 and 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.
- 2017– Leading the course series *Bioinformatics In Drug Discovery* within Roche.
- 2016– Supervising master students in computational biology, and co-supervise PostDocs, in collaboration with academic and industrial collaboration partners.
- 2012– Organizing and hosting the seminar series on *Network Analysis* and *R programming* within Roche.
- 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.

14-3-3 $\zeta$  turns TGF- $\beta$ '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 <sup>A</sup> T <sub>E</sub> 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                             |

## Personal Information

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