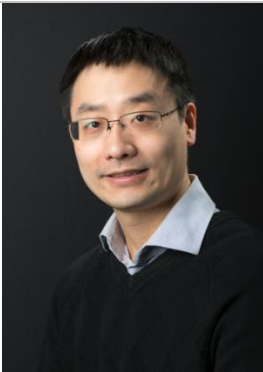


Basic information

Personal data and contact information

Name:	Jing Tang	
Date and place of birth:	September 20, 1980, Hubei, China	
Nationality:	Finnish	
Present employer:	Institute for Molecular Medicine Finland (FIMM), University of Helsinki, Finland	
Position title:	Assistant Professor in statistics (Tenure track) Group leader, Academy Research Fellow PI at the Faculty of Medicine, University of Helsinki	
Work address:	Tukholmankatu 8, Biomedicum Helsinki 2U, FI-00014, Helsinki, Finland	
E-mail:	jing.tang@helsinki.fi	
Telephone:	+358458689708	
ResearcherID:	H-4084-2012	
ORCID:	0000-0001-7480-7710	
Website:	https://scholar.google.com/citations?user=6sNdZq8AAAAJ&hl=en	
Group website:	https://www.helsinki.fi/en/researchgroups/network-pharmacology-for-precision-medicine https://www.fimm.fi/en/research/groups/tang	

Docentship

29/01/2016 Docent in Biometry, Department of Mathematics and Statistics, University of Helsinki, Finland

Degrees

18/06/2009 Ph.D. (Statistics, Department of Mathematics and Statistics, University of Helsinki, Finland)

Thesis: Bayesian statistical analysis of bacterial diversity

17/08/2004 M.Sc.Eng. (Complex Adaptive Systems, Department of Physics and Engineering Physics, Chalmers University of Technology, Sweden)

Thesis: Approximating selective sweeps using the lambda coalescent

28/06/2000 B.S.Eng. (Industrial Automation, Department of Energy Engineering, Wuhan University, China)

Previous employment

01/2012- Senior researcher

06/2017 Institute for Molecular Medicine Finland, University of Helsinki

05/2008- 12/2011	Research scientist Quantitative Biology and Bioinformatics Group VTT Technical Research Centre of Finland, Finland
09/2004- 04/2008	PhD student Division of Biometry and Bioinformatics Department of Mathematics and Statistics, University of Helsinki, Finland

Research activities

Current research grants as PI

2018-2023	Academy Research Fellow, Academy of Finland
2017-2022	ERC Starting grant
2017-2022	FIMM basic funding
2017-2020	HiLIFE Fellow grant
2018-2020	Helsinki Challenge Award funding

Previous research grants

2014-2016	Co-PI (with Prof. Tero Aittokallio and Dr. Krister Wennerberg) Cancer society of Finland - Individualized drug target combinations: prediction, testing and translation, 80,000 EUR
2013	Biocentrum Helsinki Foundation - Connecting Scientists: Networking and Grant Opportunity, 5,000 EUR
2009	China Scholarship Council - Chinese Government Award for Outstanding Self-financed Students Abroad, 5,000 EUR
2008	Chancellor's Travel Grant, University of Helsinki, 2,000 EUR

Research awards

11/2017	Team leader of the winning team iCombine in Helsinki Challenge
05/2017	Member of the winning team in the Idea DREAM Challenge.
10/2014	Member of the winning team in the NCI-Dream8.5 challenge on prediction of Rheumatoid Arthritis responders using genotype data.
12/2014	Member of the winning team in the NCI-Dream9 challenge, the BROAD-DREAM gene essentiality prediction challenge.

Publications

- ü 38 articles in refereed international journals
- ü 16 of which are with first or correspondence authorship
- ü Total citations: 2087 (Google scholar)
- ü H-index: 19 (Google scholar)
- ü Total impact factors: 280

Referee for 23 international journals

Guest editor for PLOS Computational Biology 2017

Coordination of research projects

- | | |
|-----------|---|
| 2014-2017 | Project coordinator
CONTROL (Synthetic controllability of biological networks through understanding and engineering control elements), Academy of Finland, Synthetic Biology Programme |
| 2011-2014 | Project manager
DEXLIFE (Mechanisms of prevention of type 2 diabetes by lifestyle intervention in subjects with pre-diabetes or at high risk for progression), European Commission FP7 |
| 2008-2013 | Project manager
ATHEROREMO (European collaborative project on inflammation and vascular wall remodeling in Atherosclerosis), European Commission FP7 |
| 2008-2010 | Project manager
HEPADIP (Hepatic and adipose tissue in the metabolic syndrome), European Commission FP6 |

Research mobility

- | | |
|-----------|--|
| Oct. 2013 | Visiting researcher, European Bioinformatics Institute (with Dr. Julio Saez-Rodriguez), Hinxton, UK |
| Nov. 2009 | Visiting researcher, Blavatnik School of Computer Science and the Department of Molecular Microbiology and Biotechnology (with Dr. Eran Halperin), Tel-Aviv University, Israel |

PhD thesis supervision

- | | |
|-----------------|--|
| Alok Jaiswal | 2013 – 2018
Faculty of Biological and Environmental Sciences (together with Prof. Tero Aittokallio)
Title: Integrative modeling of functional and genomic landscapes for effective anti-cancer treatment |
| Liye He | 2015 - present
Faculty of Biological and Environmental Sciences (together with Prof. Tero Aittokallio)
Title: Network-based drug combinations for personalized medicine: From computational modelling to experimental design |
| Alina Malyutina | 2017 – present
Institute for Molecular Medicine Finland (together with Dr. Caroline Heckman)
Title: Predicting personalized drug combinations for multiple myeloma patients through integration of drug sensitivity and molecular profiles at the cell lineage level |
| Yinyin Wang | 2017 – present
Institute for Molecular Medicine Finland
Title: Discovery of therapeutic targets of natural products using network pharmacology modeling approaches |
| Wenyu Wang | 2018 – present
Institute for Molecular Medicine Finland
Title: Functional screening data analysis for cancers |

Bulat Zagidullin 2018 – present
 Institute for Molecular Medicine Finland
 Title: Drug combination predicting and testing using informatics approaches

Master thesis supervision

Muhammad 2017
 Khan Department of Computer Science, Aalto University, Finland (together with Prof. Samuel Kaski)
 Title: Computational drug-repositioning in cancer using machine learning approaches

Joseph Saad 2017- present
 Institute of Biomedicine, University of Turku, Finland (together with Dr. Caroline Heckman)
 Title: Personalization of acute myeloid leukemia treatment: predictive response biomarkers to JQ1

PhD thesis pre-examiner

Alberto Pessia Department of Mathematics and Statistics, University of Helsinki
 Thesis: Bayesian cluster analysis with applications to pathogen population genomics
 28.08.2017

Minna Vehkala Department of Mathematics and Statistics, University of Helsinki
 Thesis: Statistical Analysis Tools for Metabolic and Genomic Bacterial Data
 24.10.2016

Software development

SynergyFinder Analyzing drug combination dose-response matrix data (Web application & R)
<http://synergyfinder.fimm.fi>
<https://bioconductor.org/packages/release/bioc/html/synergyfinder.html>

TIMMA Target inhibition network analysis using Minimization and Maximization Averaging (R)
<https://cran.r-project.org/web/packages/timma/index.html>

T-BAPS T-RFLP Bayesian Analysis of Population Structures (Matlab)
www.helsinki.fi/bsg/software/T-BAPS/

BAPS Bayesian Analysis of Population Structure (Matlab)
www.helsinki.fi/bsg/software/BAPS/

Teaching qualifications

Invited lectures

04-05/2018 Principles of Bioscience Omics

09/2017 Summer School on Ecological Network Inference and Analysis, Leuven, KU Leven, Belgium

04/2014 Protein interaction biochemistry – lecture and practical course, Haartman Institute, University of Helsinki, Finland

10/2013 Systems biology seminar course, Biomedicum, University of Helsinki, Finland

- 12/2012 Microarray and next generation sequencing, Biomedicum, University of Helsinki, Finland
- 09/2011 The European Atherosclerosis Society advanced course in metabolomics for clinical research, VTT Technical Research Centre of Finland, Finland
- 03/2009 The EU training for EU FP7 ETHERPATHS consortium (Characterization and modeling of dietary effects mediated by gut microbiota on lipid metabolism) in bioinformatics and systems modeling, University of Barcelona, Spain

Publications

Summary

- ü 38 articles in refereed international journals
- ü 16 of which are with first or correspondence authorship
- ü Total citations: 2087 (Google scholar)
- ü H-index: 19 (Google scholar)
- ü Total impact factors: 280
- ü 6 under review

Manuscripts under review

- [1] Ma, L., Li, Z., Piepponen, P., Pongratz, G., Piirainen, S., Tang, J., Rauvala, H., and Tian, L. Syndecan-3 regulates the sympathetic response and innate immunity associated with prostate cancer development.
- [2] Malyutina, A., Majumder, M.M., Wang, W., Pessia, A., Heckman, C. and Tang, J. Drug combination sensitivity scoring facilitates the discovery of synergistic and efficacious drug combinations in cancer.
- [3] Wang, W., Malyutina, A., Pessia, A., Heckman, C. and Tang, J. Improving the consistency of functional genomics screens using molecular features - a multi-omics, pan-cancer study.
- [4] Majumder, M.M., Leppä, A.M., Hellesøy, M., Dowling, P., Malyutina, A., Bazou, D., Andersson, E., Parsons, A., Tang, J., Mustjoki, S., Gorman, P.O., Wennerberg, K., Porkka, K., Gjertsen, B.T. and Heckman, C. High content multi-parametric single cell assay defines distinct drug effects in healthy hematological cell lineages that are retained in malignant counterparts.
- [5] Younsi, R., Tang, J. and Holm L. pi-cyc: a reference-free SNP discovery application using parallel graph search.
- [6] Cazaly, E., Saad, J., Wang, W., Heckman, C., Ollikainen, M., and Tang, J. Making sense of the epigenome using data integration approaches.

Publications (in chronological order with ten most important publications highlighted)

- [1] Tang, J., Gautam, P., Gupta, A., He, L., Timonen, S., Akimov, Y., Szwajda, A., Jaiswal, A., Turei, D., Yadav, B., Kankainen, M., Saarela, J., Saez-Rodriguez, J., Wennerberg, K. and Aittokallio, T. Network pharmacology modeling identifies Aurora B and ZAK as synergistic partners in triple negative breast cancer. Conditionally accepted.

- [2] Zheng, Y., Liu, C., Li, Y., Jiang, H., Yang, P., Tang, J., Xu, Y., Wang, H., and He, Y. (2018) Loss-of-function mutations with circadian rhythm regulator Per1/Per2 lead to premature ovarian insufficiency. *Biol. Reprod.* doi: 10.1093/biolre/iy0245 (Impact factor: 3.5).
- [3] Tanoli, Z.R., Alam, Z., Vähä-Koskela, M., Ravikumar, B., Malyutina, A., Jaiswal, A., Tang, J., Wennerberg, K. and Aittokallio, T. (2018) Drug Target Commons 2.0: a community-platform for systematic analysis of drug-target interaction profiles. *Database.* 2018, bay083. doi: 10.1093/database/bay083 (Impact factor: 4.0).
- [4] He, L.* , Tang, J.* , Andersson, E., Timonen, S., Wennerberg, K., Mustjoki, S. and Aittokallio, T. (2018) Patient-customized drug combination prediction and testing for T-cell prolymphocytic leukemia patients. *Cancer Res.* 78, 2407-2418 (Impact factor: 9.3).
- [5] Tang, J., Zia-ur-Rheman, T., Ravikumar, B., Alam, Z., Rebane, A., Vähä-koskela, M., Peddinti, G., van Adrichem, A.J., Wakkinen, J., Jaiswal, A., Karjalainen, E., Gautam, P., He, L., Parri, E., Khan, S., Gupta, A., Ali, M., Yetukuri, L., Gustavsson, A., Seashore-Ludlow, B., Hersey, A., Leach, A.R., Overington, J.P., Repasky, G., Wennerberg, K. and Aittokallio, T. (2018) DrugTargetCommons: a community-effort to build a consensus knowledgebase for drug-target interactions. *Cell Chem. Biol.* 25, 224-229 (Impact factor: 5.6).
- [6] Azencott, C.A., Aittokallio, T., Roy, S., Agrawal, A., Barillot, E., Bessonov, N., Chasman, D., Czerwinska, U., Siahpirani, A.F., Greenberg, J., Huber, M., Kaski, S., Kurz, Christoph, Mailick, M., Merzenich, M., Morozova, N., Movaghar, A., Nahum, M., Nordling, T.E.M., Penner, R., Roy, S., Saha, K., Salim, A., Sorooshyari, S., Soumelis, V. Stark-Invar, A., Sterling, A., Tang, J., Tosenberger, A., van Vieet, T., Wennerberg, K., Zinovyev, A., Norman, T., Friend, S., Stolovitzky, G. and Goldenberg, A. (2017) The inconvenience of data of convenience: Computational research beyond post-mortem analyses. *Nat. Methods.* 14, 937-938 (Impact factor: 25.1).
- [7] Gönen, M., Weir, B.A., Cowley, G.S., Vazquez, F., Guan, Y., Jaiswal, A., Karasuyama, M., Uzunangelov, V., Wang, T., Tsherniak, A., Howell, S., Marbach, D., Hoff, B., Norman, T.C., Airola, A., Bivol, A., Bunte, K., Carlin, D., Chopra, S., Deran, A., Ellrott, K., Gopalacharyulu, P., Graim, K., Kaski, S., Khan, S.A., Newton, Y., Ng, S., Pahikkala, T., Paull, E., Sokolov, A., Tang, H., Tang, J., Wennerberg, K., Xie, Y., Zhan, X., Zhu, F., Aittokallio, T., Mamitsuka, H., Stuart, J.M., Boehm, J.S., Root, D.E., Xiao, G., Stolovitzky, G., Hahn, W.C. and Margolin, A.A. (2017) A Community challenge for inferring genetic predictors of gene essentialities through analysis of a functional screen of cancer cell lines. *Cell Syst.* 5, 485-497 (Impact factor: 9.0).
- [8] Andersson, E.I., Pützer, S., Yadav, B., Dufva, O., Khan, S., He, L., Sellner, L., Schrader, A., Crispatzu, G., Oleś, M., Zhang, H., Adnan-Awad, S., Lagström, S., Bellanger, D., Mpindi, J.P., Eldfors, S., Pemovska, T., Pietarinen, P., Lauhio, A., Tomska, K., Cuesta-Mateos, C., Faber, E., Koschmieder, S., Brümmendorf, T.H., Kytölä, S., Savolainen, E.R., Siitonen, T., Ellonen, P., Kallioniemi, O., Wennerberg, K., Ding, W., Stern, M.H., Huber, W., Anders, S., Tang, J., Aittokallio, T., Zenz, T., Herling, M. and Mustjoki, S. (2017) Discovery of novel drug sensitivities in T-PLL by high-throughput ex vivo drug testing and mutation profiling. *Leukemia.* 32, 774-787 (Impact factor: 12.0).
- [9] Jaiswal, A., Gopalacharyulu, P., Wennerberg, K., Kuznetsov, S., Tang, J., and Aittokallio, T. (2017) Seed-effect modeling improves the consistency of genome-wide loss-of-function screens and identifies synthetic lethal vulnerabilities in cancer cells. *Genome Med.* 9, 51 (Impact factor: 8.9).

- [10] Khan, M.S.S., Asif, M., Basheer, M.K.A., Kang, C.W., Al-Suede, F.S., Ein, O.C., Tang, J., Majid, A.S.A., Majid, A.M.S.A. (2017) Treatment of novel IL17A inhibitor in glioblastoma implementing 3rd generation co-culture cell line and patient-derived tumor model. *Eur. J. Pharmacol.* 803, 24-38 (Impact factor: 2.9).
- [11] Ianevski, A., He, L., Aittokallio, T. and Tang, J. (2017) SynergyFinder: a web application for analyzing drug combination dose-response matrix data. *Bioinformatics.* 33, 2413-2415 (Impact factor: 5.5).
- [12] Haltia, U.M., Andersson, N., Yadav, B., Färkkilä, A., Kuleskiy, E., Kankainen, M., Tang, J., Bützow, R., Riska, A., Leminen, A., Heikinheimo, M., Kallioniemi, O., Unkila-Kallio, L., Wennerberg, K., Aittokallio, T. and Anttonen, M. (2017) Synergistic inhibition of ovarian granulosa cell tumors by combining dasatinib or mTOR-inhibitors with taxane treatment. *Gynecol. Oncol.* 144, 621-630 (Impact factor: 4.5).
- [13] Karjalainen, R., Pemovska, T., Popa, M., Liu, M., Javarappa, K.K., Majumder, M.M., Yadav, B., Tamborero, D., Tang, J., Bychkov, D., Kontro, M., Parsons, A., Suvela, M., Mayoral, Safont M., Porkka, K., Aittokallio, T., Kallioniemi, O., McCormack, E., Gjertsen, B.T., Wennerberg, K., Knowles, J. and Heckman, C.A. (2017) JAK1/2 and BCL2 inhibitors synergize to counteract bone marrow stromal cell-induced protection of AML. *Blood.* 130, 789-802 (Impact factor: 13.2).
- [14] Tang, J. (2017) Informatics approaches for predicting, understanding and testing cancer drug combinations. *Methods Mol. Biol.* 1636:485-506. Book chapter in *Kinase Signaling Networks*, Springer.
- [15] He, L., Kuleskiy, E., Saarela, J., Turunen, L., Wennerberg, K., Aittokallio, T. and Tang, J. (2017) Methods for high-throughput drug combination screening and synergy scoring. *Methods Mol. Biol.* Book chapter in *Cancer Systems Biology*, Springer.
- [16] Sieberts, S.K., Zhu, F., García-García, J., Stahl, E., Pratap, A., Pandey, G., Pappas, D., Aguilar, D., Anton, B., Bonet, J., Eksi, R., Fornés, O., Guney, E., Li, H., Marín, M.A., Panwar, B., Planas-Iglesias, J., Poglayen, D., Cui, J., Falcao, A.O., Suver, C., Hoff, B., Balagurusamy, V.S., Dillenberger, D., Neto, E.C., Norman, T., Aittokallio, T., Ammad-Ud-Din, M., Azencott, C.A., Bellón, V., Boeva, V., Bunte, K., Chheda, H., Cheng, L., Corander, J., Dumontier, M., Goldenberg, A., Gopalacharyulu, P., Hajiloo, M., Hidru, D., Jaiswal, A., Kaski, S., Khalfaoui, B., Khan, S.A., Kramer, E.R., Marttinen, P., Mezlini, A.M., Molparia, B., Pirinen, M., Saarela, J., Samwald, M., Stoven, V., Tang, H., Tang, J., Torkamani, A., Vert, J.P., Wang, B., Wang, T., Wennerberg, K., Wineinger, N.E., Xiao, G., Xie, Y., Yeung, R., Zhan, X., Zhao, C.; Members of the Rheumatoid Arthritis Challenge Consortium, Greenberg, J., Kremer, J., Michaud, K., Barton, A., Coenen, M., Mariette, X., Miceli, C., Shadick, N., Weinblatt, M., de Vries, N., Tak, P.P., Gerlag, D., Huizinga, T.W., Kurreeman, F., Allaart, C.F., Louis, Bridges, S. Jr., Criswell, L., Moreland, L., Klareskog, L., Saevarsdottir, S., Padyukov, L., Gregersen, P.K., Friend, S., Plenge, R., Stolovitzky, G., Oliva, B., Guan, Y., Mangravite, L.M., Bridges, S.L., Criswell, L., Moreland, L., Klareskog, L., Saevarsdottir, S., Padyukov, L., Gregersen, P.K., Friend, S., Plenge, R., Stolovitzky, G., Oliva, B., Guan, Y. and Mangravite, L.M. (2016) Crowdsourced assessment of genetic contribution to predicting disease lowering response of anti-TNF treatment in rheumatoid arthritis. *Nat. Commun.* 7, 12460 (Impact factor: 12.4).

- [17] Yadav, B., Wenerberg, K., Aittokallio, T. and Tang, J. (2015) Searching for drug synergy in complex dose-response landscapes using an interaction potency model. *Comput. Struct. Biotechnol. J.* 13, 504-513 (Impact factor: 4.1).
- [18] Tang, J., Wennerberg, K. and Aittokallio, T. (2015) What is synergy? The Saariselkä agreement revisited. *Front. Pharmacol.* 6, 181 (Impact factor: 3.8).
- [19] He, L., Wennerberg, K., Aittokallio, T., and Tang, J. (2015) TIMMA-R: an R package for predicting synergistic multi-targeted drug combinations in cancer cell lines or patient-derived sample. *Bioinformatics.* 31, 1866-1868 (Impact factor: 5.8).
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- [21] Szwajda, A., Gautam, P., Karhinen, L., Jha, SK., Shakyawar, S., Yadav, B., Tang, J., Wennerberg, K., and Aittokallio, T. (2015) Systematic mapping of kinase addiction combinations in breast cancer cells by integrating drug sensitivity and selectivity profiles. *Chem. Biol.* 22, 1144-1155 (Impact factor: 6.6).
- [22] Kibble, M., Saarinen, N., Tang, J., Wennerberg, K., Mäkelä, S., and Aittokallio, T. (2015) Network pharmacology applications to map the unexplored target space and therapeutic potential of natural products. *Nat. Prod. Rep.* 32, 1249-1266 (Impact factor: 11.0).
- [23] Tang, J., Szwajda, A., Shakyawar, S., Xu, T., Hintsanen, P., Wennerberg, K., and Aittokallio, T. (2014). Making sense of large-scale kinase inhibitor bioactivity data sets: a comparative and integrative analysis. *J. Chem. Inf. Model.* 54, 735–743 (Impact factor: 3.8).
- [24] Tang, J., and Aittokallio, T. (2014). Network pharmacology strategies toward multi-target anticancer therapies: from computational models to experimental design principles. *Curr. Pharm. Des.* 20, 23–36 (Impact factor: 4.4).
- [25] Blomstedt, P., Tang, J., Xiong, J., Granlund, C., and Corander, J. (2014) A Bayesian predictive model for clustering data of mixed discrete and continuous type. *IEEE Trans. Pattern Anal. Mach. Intell.* 37, 489-498 (Impact factor: 9.5).
- [26] Pahikkala, T., Airola, A., Pietilä, S., Shakyawar, S., Szwajda, A., Tang, J., and Aittokallio, T. (2014) Toward more realistic drug-target interaction predictions. *Brief. Bioinform.* 16, 325-337 (Impact factor: 5.1).
- [27] Tang, J., Karhinen, L., Xu, T., Szwajda, A., Yadav, B., Wennerberg, K., and Aittokallio, T. (2013) Target inhibition networks: predicting selective combinations of druggable targets to block cancer survival pathways. *PLoS Comput. Biol.* 9, e1003226 (Impact factor: 4.0).
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- Lönnqvist, J. and Cannon, T.D. (2012) Phospholipids and insulin resistance in psychosis: a lipidomics study of twin pairs discordant for schizophrenia. *Genome Med.* 4, 1 (Impact factor: 8.9).
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- [32] Tang, J., Tan, C.Y., Oresic, M., and Vidal-Puig, A. (2009). Integrating post-genomic approaches as a strategy to advance our understanding of health and disease. *Genome Med.* 1, 35 (Impact factor: 8.9).
- [33] Hanage, W.P., Fraser, C., Tang, J., Connor, T.R., and Corander, J. (2009) Hyper-recombination, diversity, and antibiotic resistance in pneumococcus. *Science* 324, 1454–1457 (Impact factor: 37.2).
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- [35] Tang, J., Hanage, W.P., Fraser, C., and Corander, J. (2009) Identifying currents in the gene pool for bacterial populations using an integrative approach. *PLoS Comput. Biol.* 5, e1000455 (Impact factor: 4.0).
- [36] Corander, J., Marttinen, P., Sirén, J., and Tang, J. (2008) Enhanced Bayesian modelling in BAPS software for learning genetic structures of populations. *BMC Bioinformatics* 9, 539 (Impact factor: 2.2).
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