Xi Zhao

March 27, 2013

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Education

2007-2011 **Ph.D. (Bioinformatics and Statistics)**. University of Oslo, Norway.

"Systems Biology and Genomics of Breast Cancer through mining multi-level molecular profiles."

2006 **M.Sc. (Applied Statistics)**. *Magna Cum Laude*. Universiteit Hasselt, Belgium & Universiteit Maastricht, the Netherlands.

"Assessing Global Normalization Assumption in Preprocessing Analysis of Two-Color Microarray Expression Data."

2005 **M.Sc. (Bioinformatics)**. *Cum Laude*. Katholieke Universiteit Leuven, Belgium.

"Bioinformatics strategy for classification of serological specificities in Human Leukocyte Antigen Systems."

2004 **B.Sc. (Electrical Engineering)**. *Honors*. Dalian Maritime University, China.

Work experience

2012- Postdoctoral scholar. Stanford University, School of Medicine, Center for Cancer Systems Biology. Advisor: Sylvia Plevritis.

06-12/2011 Research associate. Institute for Clinical Medicine, Faculty of Medicine, University of Oslo, Oslo, Norway.

2006-2007 Research associate. Oslo University Hospital, Radiumhospital. Anne-Lise Børresen-Dale's lab, Oslo, Norway.

2006 Internship. Center of Microbial and Plant Genetics, K.U.Leuven, Belgium.

2005 Internship. Algonomics, Gent, Belgium.

2004 Internship. Panasonic, Dalian, China.

Research activities

12/2009 - Visiting research student in Chris Sander´s lab, Computational biology center, Memorial

02/2011 Sloan-Kettering Cancer Research Center, New York, USA. *Pathway analysis in high-throughput genomic data.*

11/2007 Scientific visit at Department of Statistics, Stanford University, Stanford, California, USA (Rob Tibshirani, Trevor Hastie).

10/2007 Scientific visit at Bioinformatics & Functional Genomics lab, Princeton University, Princeton, New Jersey, USA (Olga Troyanskaya).

Grants & Fellowships

2010 Travel grant. UNIFOR fund, University of Oslo.

2010 Travel grant. Den Norsk Hydros Fond, Oslo University Hospital.

2010 PhD Fellowship. Cancer program, The Norwegian Research Council.

2007-2009 PhD Fellowship. FUGE program, The Norwegian Research Council.

Patent

2012 US patent application for methodology in Zhao *et. al* 2011, PLoS ONE. *Submitted.*

Skills

Comprehensive knowledge in Statistics, Bioinformatics & Biology:

- Survival analysis, multivariate analysis, Bayesian statistics, non-linear modelling, longitudinal analysis, machine learning, data mining techniques.
- Design and implement computational algorithms in programming languages.
- Process, analyze & visualize high-throughput genomic data (mRNA, aCGH, SNP, RNA-Seq), pathway/module analysis, motif finding, sequence alignment, phylogenetics.
- Microarray technology, whole genome sequencing technology, cancer biology, molecular biology, network biology, immunology, protein technology.

Good programming skills:

- Highly skilled in R/S-plus and building R/Bioconductor package.
- Skilled in SAS, MatLab, Perl/BioPerl, Shell script.
- Familiarity with JavaScript, C/C++, XML, assembly language.
- Proficient skills with Macintosh, UNIX/Linux, shell environment, Windows.

Broad understanding of Bioinformatics tools & common Statistical softwares

- Open souce: Gephi, Cytoscape, IGV, GenePattern, UCSC Genome Browser, Blast...
- Biological database: BioMart, SMD, NCBI, PDB, Swiss-Prot, GO, ...
- Gui-based tools: SPSS, WINBUGS, StatXact, ...

Conferences

09/2010 Cold Spring Harbor Asia conference on Computational Biology 2010, Suzhou. *Poster.*

06/2010 21st meeting of the European Association for Cancer Research. Oslo. *Poster.*

06/2010 RECOMB Computational Cancer Biology 2010. Oslo. *Poster.*

09/2009 ECCO 15 - 34th ESMO Multidisciplinary Congress. Berlin. *Poster.*

Publications

Edvardsen, H., Landmark-Høyvik, H., Reinertsen, K.V., **Zhao, X.**, Grenaker-Alnæs, G.I., Nebdal, D., Syvanen, A.C., Rødningen, O., Alsner,J., Overgaard, J., Børresen-Dale, A.L., Fossa,S.D. and Kristensen, V.N. (*In press*). SNP in TXNRD2 Associated to Radiation-Induced Fibrosis: A Study of Genetic Variation in Reactive Oxygen Species Metabolism and Signaling. *International Journal of Radiation Oncology.*

Riis, M.L., **Zhao, X.**, Kaveh, F., Vollan, H.S., Nesbakken, A.-J., Solvang, H.K., Lüders, T., Bukholm, I.R., and Kristensen, V.N. (2013). Gene Expression Profile Analysis of T1 and T2 Breast Cancer Reveals Different Activation Pathways. *ISRN Oncology* vol. 2013.

Freed-Pastor, W.A, Mizuno, H., **Zhao**, **X.,** Langerød, A., Chicas, A., Li, W., Polotskaia, A., Bissell, M.J., Tian, B., Lowe, S.W., Børreson Dale, A.L., Levine, A.J., Bargonetti, J., and Prives, C. (2012). Mutant p53 Disrupts Mammary Tissue Architecture via the Mevalonate Pathway. *Cell*, 148, 244-258.

Zhao, X., Rødland, E.A., Sørlie, T., Naume, B., Langerød, A., Frigessi, A., Kristensen, V.N., Børresen-Dale, A.L., and Lingjærde, O.C. (2011). Combining Gene Signatures Improves Prediction of Breast Cancer Survival. *PLoS One 6*, e17845.

Sørlie, T., Borgan, E., Myhre, S., Vollan, H.K., Russnes, H., **Zhao, X.**, Nilsen, G., Lingjærde, O.C., Børresen-Dale, A.L., and Rødland, E. (2010). The importance of gene-centring microarray data. *The Lancet Oncology* 11, 719-720.

Naume, B., **Zhao, X.**, Synnestvedt, M., Borgen, E., Russnes, H., Lingjærde, O., Strømberg, M., Wiedswang, G., Kvalheim, G., Kåresen, R., Nesland, J., Børresen-Dale, A.L., and Sørlie, T. (2007). Presence of bone marrow micrometastasis is associated with different recurrence risk within molecular subtypes of breast cancer. *Molecular Oncology* 1, 160-171.

Zhao, X., Rødland, E.A., Sørlie, T., Kristensen, V.N., Lingjærde, O.C., and Børresen-Dale, A.L. (*Under revision*). Systematic assessment of prognostic gene signatures for breast cancer shows distinct influence of time and ER status. *BMC Cancer.*

Yamamoto S., Wu Z., Russnes H.G., Takagi S, Vaske C., Sun H., Kim J.H., Carver K., **Zhao X.**, Vollan H.K.M, Maruyama R., Almendro V., Bessarabova M., Rueda O., Nikolsky Y., Caldas C., Liu X.S., Polyak K. (*Under revision*). The JARID1B/KDM5B histone demethylase is a luminal lineage-driving oncogene in breast cancer. *Science.*

Aarøe, J., Myhre, S., Haakense, V., Helland, Å., **Zhao**, **X.**, Vollan, H.K., Russnes, H., Due, E.U., Baumbusch, L., Wärnberg, F., Botling, J., Alsner, J., Overgaard, J., Sørlie, T., Lingjærde, O.C., Børresen-Dale, A.L. *(Under review).* Regional complexity in breast tumors reveals patterns of prognostic value. *Genome Medicine.*

Sternemalm J, Russnes H, **Zhao X**, Risberg B, Nord SH, Caldas C, Børresen-Dale AL, Stokke T, Patzke S. (*Under review*). Nuclear CSPP1 expression defines subtypes of basal-like breast cancer. *Cancer research.*

Anchang B., Do M., **Zhao X**., Plevritis S. (*Submitted*). An optimal non-parametric gating strategy to isolate pure subpopulations in heterogeneous single cell data.

Zhao, X., Plevritis, S. *(Manuscript).* Molecular classification on clinically defined breast cancer cohorts.

Zhao, X., Ciriello, G., Schultz, N., Rødland, E.A., Taylor, B.S., Cerami, E., Socci, N.D., Baumbusch, L.O., Kristensen, V.N., Lingjærde, O.C., Sander, C., and Børresen-Dale, A.L. (*Manuscript*). Integrative genomic profiling identify different tumorigenic mechanisms driving progression in luminal A and basal breast cancers.

Invited book chapter

Zhao, X., Lingjærde, O.C., Børreson Dale, A.L. (2012). Breast cancer prognostication and risk prediction in postgenomic era. *In The Continuum of Health Risk Assessments*. InTech, ISBN: 980-953-307-582-7.

Posters

Zhao, **X.,** Schultz, N., Taylor, B.S., Cerami, E., Baumbusch, L.O., Haakensen, V.D., Lingjærde, O.C., Kristensen, V.N., Sander, C., Børresen-Dale, A.L. (2010). Pathway signatures in breast cancer progression – A genome-scale study based on integration of biology networks, DNA copy number, gene expression and mutations. *21st meeting of the European Association for Cancer Research (EACR-21)*. Oslo.

Zhao, **X.,** Schultz, N., Taylor, B.S., Nebdal, D., Cerami, E., Baumbusch, L.O., Sander, C., Børresen-Dale, A.L. (2010). Pathway signatures in breast cancer progression – A genome-scale study based on integration of biology networks, DNA copy number, gene expression and mutations. *Cold Spring Harbor Conferences Asia Meeting on Computational Biology 2010*, Suzhou.

Zhao, **X.,** Sørlie, T., Naume, B., Langerød, A., Frigessi, A., Kristensen, V.N., Børresen-Dale, A.L., Lingjærde. O.C. (2010). A multivariate Cox framework for prediction of breast cancer survival based on combined gene signatures. *RECOMB Computational Cancer Biology 2010*, Oslo.

Zhao, **X.,** Sørlie, T., Naume, B., Langerød, A., Børresen-Dale, A.L., Lingjærde, O.C. (2009). Comparison and combination of gene-set classifiers for prediction of localized breast cancer survival. *ECCO 15 - 34th ESMO Multidisciplinary Congress*. Berlin.

Peer-Reviews

Journal reviewer for Expert Opinion On Therapeutic Targets.

Journal reviewer for Journal of Biomedical Informatics.

Conference reviewer for the 17th International Conference on Research in Computational Molecular Biology (RECOMB).