

## List of publications

1. Yanju Zhang, Elia Stupka, Christiaan V. Henkel, Hans J. Jansen, Herman P. Spaink and Fons J. Verbeek. Identification of Common Carp Innate Immune Genes with Whole-Genome Sequencing and RNA-Seq Data. *Journal of Integrative Bioinformatics*, 8(2):169, 2011. Online Journal: [http://journal.imbio.de/index.php?paper\\_id=169](http://journal.imbio.de/index.php?paper_id=169)
2. Yanju Zhang and Fons J. Verbeek. Comparison and Integration of Target Prediction Algorithms for microRNA Studies. *Journal of Integrative Bioinformatics*, 7(3):127, 2010. Online Journal: [http://journal.imbio.de/index.php?paper\\_id=127](http://journal.imbio.de/index.php?paper_id=127)
3. Yanju Zhang, Jeroen S. de Bruin and Fons J. Verbeek. Specificity Enhancement in microRNA Target Prediction through Knowledge Discovery. *Chapter 20 In: Machine Learning*, Eds. Yagang Zhang, ISBN: 978-953-307-033-9, INTECH, February 2010
4. Yanju Zhang, Jeroen S. de Bruin, Fons J. Verbeek. miRNA target prediction through mining of miRNA relationships. *Proceedings of the 8th IEEE International Conference on Bioinformatics and Bioengineering*. ISBN: 978-1-4244-2844-1, 1-6, 2008
5. Yanju Zhang, Joost M. Woltering, Fons J. Verbeek. Screen of microRNA targets in zebrafish using heterogeneous data sources: a case study for dre-miR-10 and dre-miR-196. *International Journal of Mathematical, Physical and Engineering Sciences*, Vol. 2 (1), 10-17, 2007
6. Gihan Dawelbait, Christof Winter, Yanju Zhang, Christian Pilarky, Robert Grtzmann, Jrg-Christian Heinrich and Michael Schroeder. Structural templates predict novel protein interactions and targets from pancreas tumour gene expression data. *Bioinformatics*, 23:i115–24, 2007
7. Gihan Dawelbait, Christian Pilarsky, Yanju Zhang, Robert Grtzmann and Michael Schroeder. Structural protein interactions predict kinase-inhibitor interactions in upregulated pancreas tumour genes expression data. In Kay Diederichs, Robert Glen, and Oliver Kohlbacher, editors, *Proceedings of the 1st International Symposium on Computational Life Science*. Springer LNBI, 2005



## Curriculum Vitae

Yanju Zhang was born on 11 June 1980 in Guilin, Guangxi, China. She studied Computer Science at Guilin University of Electronic Technology, China and received the bachelor degree in 2002. After that she worked as a teaching assistant at this university for one year. From 2003 to 2005, she studied Molecular Bioengineering at Technological University Dresden, Germany. She obtained her master degree with a thesis on bioinformatics, i.e. *using protein-protein interactions and metabolic pathways to interpret tumor gene expression data*. Since 2006, she started her PhD at the Leiden Institute of Advanced Computer Science, Leiden University in the section Imaging and BioInformatics under the supervision of Dr. Ir. Fons J. Verbeek. This project was part of the BioRange project, a large national BioInformatics programme under the supervision of the Netherlands BioInformatics Centre. The focus of her research has been heterogeneous data integration and methodology development for the analysis of biological data. Her research interests include applying machine learning algorithms and visualization in bioinformatics, pathway and interaction network modeling, sequencing analyses and comparative genomics. In March 2010, she was selected for a Frontiers of Functional Genomics grant award and did her internship at the group of Dr. Elia Stupka in the Cancer Institute of London, UK. Here she elaborated on a carp genome sequencing, assembly and annotation project that was initiated at the Molecular Cell Biology of the Leiden Institute of Biology. From 2010 until now, she has been working in the lab of Prof. dr. Eline P. Slagboom in department of Molecular Epidemiology at Leiden University Medical Center. Her research work concerns methodology and algorithm development for RNA-Seq data and methylation arrays.



## Acknowledgements

Wrapping up all my research into this small thesis has not been an easy job. This dissertation would not have been possible without the support, inspiration and help from all the kind people around me.

I enjoyed talking to Dr. Erno Vreugdenhil who patiently explained the background and biological function of microRNA to me. Thanks, also, to Prof. Herman P. Spaink for getting us involved in the carp genome project. This next-generation sequencing project has had a great impact on my subsequent research.

I am very grateful to Dr. Christiaan Henkel who showed me lots of techniques and approaches for analyzing sequencing data. Chris, your suggestions and inspiration played an important role in developing my approach to the carp project.

I would like to thank Elia Stupka for hosting my internship at UCL, London. Elia, I learned a lot from you and I had a great time.

Many thanks to my colleagues at the LIACS. It has been a pleasure working with you. In particular, I am indebted to Amalia, Laura and Joris for helpful suggestions in English writing. As friends, you guys always comforted and encouraged me at times I was struggling which I have appreciated very much. Kuan, I would specifically like to thank you for criticizing my work and thereby encouraging me to consider every analysis critically. And I am grateful to Julia, Peng, Dome and Zi for being kind to me and giving me support in both science and life. Thanks, Yun, for me you are like a sister.

I would like to thank Fabrice who shared the office with me during the first three years of my PhD. Your quick completion of your PhD study set an example for us and your positive attitude towards research affected me a lot. And thanks, Juan, for inviting me to the Dutch Conversation Night and showing me many weird and funny things in Holland.

I owe a debt of gratitude to Eline and Kai for giving me an opportunity to work in the MolEpi group at the LUMC after my PhD studies. Thanks Steffan and Eric-Wubbo for offering me all kinds of help to finish up this thesis.

Thanks Xiaohong and Lu for being my paranymphs. Xiaohong, we have known each other for almost five years. You are such a good friend and secret keeper with whom I can

share both happiness and sadness. Lu, such a nice girl living upstairs of my apartment, I always enjoy having tea or dinner with you at your place when I feel tired and lonely downstairs.

I also would like to thank my badminton friends, especially Hying, Richard and Kian. Playing badminton has been my major way to release stress. I am also glad that we are friends beyond the badminton courts. It was fun having dinner and boat trips with you. Thanks Elise, Xiaodong and Gary for your company.

I owe my deepest gratitude to my dear brother Fulin. Thanks for taking good care of our parents. You are also a good brother whom I can always count on. I thank my sister-in-law Aiqiong and my niece Wenjia for bringing so much happiness to our family.

Finally, millions of thanks to my parents. Dad and Mom, you are the best in the world. Your kindness, persistence and other good traits set me a good example. Thank you for supporting me in studying abroad, for always being there for me whatever happened, for sending all kinds of good food to me from many miles away. I will be very grateful to you for all my life.

Yanju Zhang, October 2011