Heterogeneous data analysis for annotation of microRNAs and novel genome assembly

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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

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

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, Chrisitan Pilarky, Robert Grtzmann, Jrg-Chrisitan 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 Ccancer 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.

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