Jianying Li joined CHGV as a bioinformatician at Center for Human Genome Variation. He oversees a team of CHGV Bioinformaticians that focuses on new software development as well as development and maintenance of specific areas of the analysis pipeline; develops and implements innovative computational approaches for the analysis of large sequenced datasets from NGS technologies; collaborates and consults with CHGV researchers to analyze problems and recommend solutions to meet the computational needs for a wide range of biological research.

Selected recent publications:

J Huang, W Shi, J Zhang, J W Chou, R S Paules, K Gerrish, J Li, et al on the MAQC consortium, (2010) Genomic indicators in the blood predict a drug-induced liver injury response The Pharmacogenomics Journal (2010) 10, 267–277

Co-author on the MAQC consortium, (2010) “The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models” Nature Biotechnology (advance online access: 10.1038/nbt.1665)

Cabanski CR, Qi Y, Yin X, Bair E, Hayward MC, **Li J**, et al. **(2010)** SWISS MADE: Standardized WithIn class Sum of Squares to evaluate Methodologies And Dataset Elements **PloS ONE** 5(3): e9905

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**Song, M.O., J. Li, and J.H. Freedman** **(2009)** Physiological and Toxicological Transcriptome Exposure Levels Changes in HepG2 Cells Exposed to Copper” **Physiol. Genomics.** 38: 386-401.

P. R. Bushel, A. N. Heinloth, **J. Li**, et al **(2007)** “Blood Gene Expression Signatures Predict Exposure Levels” **PNAS.** v.104, no. 46: 18211-18216