# An online integrated system for the genome-wide co-expression study by liquid association

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## Abstract

Nowaday, simple similarity analysis has been applied in almost all microarray data analysis. The working assumption is that the co-reguated genes are functionally related. This assumption, however, does not hold for most of functionally related genes. Liquid association (LA) is a more advanced notion for describing the interaction between two genes as mediated by a third gene. In this talk, I will explain the concepts and applications of LA using examples from the paper to appear in Nature pharmacogenomics (Li and Yuan). In addition, I will share you with my experience in developing online integrated system to manage the enormouse amount of information distilled by LA and a growing number of microarray and other biological databases available in public. Up to date, we have installed many microarray datasets for Yeast, Human Cell Lines, Lung Cancers, C elegant, E coli and more. The output of LA are successfully linked to global genomic databases such as UniGene, LocusLink, Ligand, Go, SwissProt, SGD and Sequence data for the limited species. Finally, I will explain my ideas behind the system construction and demonstrate how to use our website.