

I am participating at [PSB 2014, Pacific Symposium on Biocomputing](http://psb.stanford.edu), an international conference of current research in the theory and application of computational methods in problems of biological significance, which is held on the Big Island of Hawaii.

We got accepted a paper on [Matrix factorization-based data fusion for gene function prediction in baker's yeast and slime mold](http://psb.stanford.edu/psb-online/proceedings/psb14/zitnik.pdf) to PSB. In the paper, we have examined the applicability of our recently proposed matrix factorization-based data fusion approach on the problem of gene function prediction. We studied three fusion scenarios to demonstrate high accuracy of our approach when learning from disparate, incomplete and noisy data. The studies were successfully carried out for two different organisms, where, for example, the protein-protein interaction network for yeast is nearly complete but it is noisy, whereas the sets of available interactions for slime mold are rather sparse and only about one-tenth of its genes have experimentally derived annotations.