

January 14-18, 2012

San Diego, CA

[www.intl-pag.org](http://www.intl-pag.org)



P L A N T & A N I M A L G E N O M E X X

The Largest Ag-Genomics Meeting in the World.

[Home/Search](#)

[Browse by Day](#)

[Browse by Type](#)

[Author Index](#)

[Poster Categories](#)

**P0992 Expanding Enrichment Analysis to the Evolutionary Space: Development and Validation of Kegg Orthology enrichMent - Online DetectiOn (KOMODO) to Detect Biased Distribution of Enzymatic Activities in Monophyletic Taxa**

**Francisco P. Lobo** , EMBRAPA - Brazilian Agricultural Research Corporation, Campinas, Brazil

Maíra Ribeiro Rodrigues , Federal University of Minas Gerais

Glória Regina Franco , Federal University of Minas Gerais

High-throughput experiments are central to understand complex biological systems. However, the results usually obtained in "omics" experiments, such as varying genes in microarrays, are not directly biologically meaningful. They must be annotated using dictionaries of biological terms to allow the automatic extraction of relevant biological information. An established procedure in this direction is the use of enrichment analysis to evidence non-random distribution of biological properties across experiments. Despite the huge success of enrichment analysis to interpret microarray experiments, it is almost not used in other categories of "omics" data. In this study we used enrichment analysis to study an important biological entity never contemplated before: the monophyletic taxon. We developed KOMODO (Kegg Orthology enrichMent - Online DetectiOn), a web tool to detect significantly biased distribution of homologous genes across taxa. KOMODO also displays the results as KEGG pathways, allowing users to query their own taxa and pathways of interest in a visual and explorative way. To validate KOMODO we analyzed portions of central carbon metabolism in two taxa extensively characterized regarding their carbon metabolism profile (*Enterobacteriaceae* family and *Lactobacillales* order). We found that virtually all the enzymatic activities differentially represented were directly related to already known key metabolic traits in these taxa, such as lactate production in *Lactobacillales*. The results found for these well-characterized taxa suggest that KOMODO is capable of detecting biologically meaningful biases in the distribution of homologous genes, and demonstrates enrichment analysis as a tool to characterize taxons under the "omics" paradigm. KOMODO is available at <http://pggenetica.icb.ufmg.br/komodo/>.

[Back to: Poster Abstracts](#)

[<< Previous Abstract](#) | [Next Abstract >>](#)