

## RECONSTRUCTION OF A KEGG-BASED *Mus musculus* METABOLIC NETWORK TO BE USED IN FBA MODELS.

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Although several works of metabolic dynamics exist for E Coli and other bacterial cells the research in metabolic dynamics of mammalian cells is still insufficient. In Nielsen and coworkers work a *mus musculus* network, designed to be used by FBA models, was developed but this network resulted difficult to update and compare because of the particular labeling of metabolites and reactions used herein. In other hand, a large research effort has been made in the analysis of the topology of metabolic networks, but these analyses are meaningless for the understanding of the system dynamics. In this fashion Ma and Zeng organize metabolic networks for several organisms using KEGG database, but these networks were designed to be studied by topology measures and not by FBA models. In this work we extend this KEGG based metabolic model to be used in FBA models. First, a revision of specific reactions and enzymes of mmu is made using the last KEGG releases. Second, a mitochondrial sub-network is added using databases of cellular localization. Third, reactions reversibility, one of the key points in FBA, is revised computationally and manually. Fourth, transport reactions of input and output metabolite were added for both external metabolites and mitochondrial metabolites. This new network is analyzed by FBA model, characterized and compared by topology measures. The fraction of active metabolites in steady state is analyzed using an algorithm to reduce the entire network to the functional relevant component in steady state. Finally a lethality analysis was made comparing the lethal enzymes with those published in Nielsen work. Additionally a KEGG dictionary to translate and compare the network is supplied.

