



Apr 16, 2020

# The calculation of gut metabolic modules form gene profile

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## ABSTRACT

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## GUIDELINES

The calculation of gut metabolic modules form gene profile

## BEFORE STARTING

The input is the gene profile

- 1 Step 1: the putative amino acid sequences were translated from the gene catalogues and aligned against the proteins/domains in the KEGG databases (release 79.0, with animal and plant genes removed) using BLASTP (v2.2.26, default parameter except that -e 0.01 -b 100 -K 1 -F T -m 8). Each protein was assigned to the KO group by the highest scoring annotated hit(s) containing at least one HSP scoring >60 bits. The relative abundance profile of KOs was determined by summing the relative abundance of genes from each KO.
- 2 Step 2: The calculation of gut metabolic modules by one command:  
`'java -jar gmms.jar -a 2 -d GMMs.v1.07.txt -i input_KO_profile -s average -o index'`  
You could refer to the <http://www.raeslab.org/companion/gmms/> for 'gmms.jar' and 'GMMs.v1.07.txt'.



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