Jan 05, 2021

The calculation of gut metabolic modules from gene profile

Forked from The calculation of gut metabolic modules form gene profile

In 2 collections

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[1]BGI

1 *Works for me*   dx.doi.org/10.17504/protocols.io.bq6gmzbw

BGI   GIGA   1 more workspace

wangqi

ABSTRACT

The calculation of gut metabolic modules from gene profile

DOI

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PROTOCOL CITATION

COLLECTIONS ⓘ

Protocols for "Shotgun Metagenomics of 361 elderly women reveals gut microbiome change in bone mass loss"

Protocols for "Linking gut microbiome to bone mineral density: a shotgun metagenomic study of 361 eldly women"

FORK NOTE

FORK FROM

Forked from The calculation of gut metabolic modules form gene profile, Qi Wang

KEYWORDS

gut metabolic modules, Metagenomics data, KO profile

LICENSE

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PARENT PROTOCOLS

Part of collection

Protocols for "Shotgun Metagenomics of 361 elderly women reveals gut microbiome change in bone mass loss"

Protocols for "Linking gut microbiome to bone mineral density: a shotgun metagenomic study of 361 eldly women"

GUIDELINES

The calculation of gut metabolic modules form gene profile

ABSTRACT

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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'.