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Workshop 11: Metagenomics Analysis

q Ini?al 16S & mWGS metagenomic studies to generate an es?mate of the complexity of the microbial community at each body site, providing ini?al answers to the ques?ons of whether there is a "core" microbiome at each site q Demonstraon projects to determine the relaonship between disease and changes in the human microbiome

Meta'omic Analysis with MetaPhlAn & LEfSe

Meta'omic Analysis with MetaPhlAn & LEfSe Eric Franzosa for Phylogenomics and Metagenomics The University of Texas at Austin 17 February 2013 Metagenomic Phylogenetic Analysis Fast and accurate metagenomic profiling of microbial community composition using unique 16S-based estimation • v13 (+) & v35 (x) regions 49

Vegan: an introduction to ordination

correspondence analysis as an example It is rst shown how a model is de ned, then the document discusses model building and sign cance tests of the whole analysis, single constraints and axes

Mining EBI Metagenomics result output files

Mining EBI Metagenomics result output files 2 Tutorial learning objectives After completing this course, you should: • understand the format of the EMG result files • be able to extract information from the result files available on the EMG website using open source tools (The R statistical environment)

!diversity*metrics - Evolutionary Biology

Alpha&Diversity:*within*sample*diversity* Sample1 & Sample2 & Sample3 & Sample4 & Marker!based*metagenomic*tutorial* 2*

There are many reasons for studying bacteria

the efficient management and processing of both small-scale and large-scale datasets and for the analysis of various types of data produced from expression profile analysis, metagenomic and metatranscriptomic analysis, and so on Learn more » Recent Highlights 'Whole exome sequencing in Thai patients with retinitis pigmentosa reveals novel

Ecotoxicology and Environmental Safety

analysis was performed using 16S rRNA gene sequences The rhizosphere bacteria were divided into 33 major Ecotoxicology and Environmental Safety 145 (2017) 111-118 Available online 13 July 2017 Zhengdan-958 and soybean plants (Glycine max) Zhonghuang-57 were used in the phytoremediation experiment In the pot experiment, there

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MG Rast workshop - Netherlands Bioinformatics Centre

Extract species information from MG-RAST based of shotgun reads (non-16s) Extract functional annotation Multiple metagenomes Compare metagenomes using the analysis toolkit of MG-RAST Interact with MG-RAST using R Introduction In this workshop we will a short overview of the MG-RAST metagenomics annotation pipeline

NON METRIC MULTIDIMENSIONAL SCALING MDS

Nonmetric multidimensional scaling (MDS, also NMDS and NMS) is an ordination tech-nique that differs in several ways from nearly all other ordination methods In most ordina-tion methods, many axes are calculated, but only a few are viewed, owing to graphical limita-tions

GutCyc: a Multi-Study Collection of Human Gut Microbiome ...

Jul 31, 2016 · GutCyc: a Multi-Study Collection of Human Gut Microbiome Metabolic Models Aria S Hahn1,2+ Tomer Altman3,4+ Kishori M Konwar1,2,5+ Niels W Hanson1 Dongjae Kim6 David A Relman7,8,9 David L Dill10 Steven J Hallam1,2,11* July 31, 2016 1 Department of Microbiology and Immunology, University of British Columbia, Vancouver, BC Canada 2

INTRODUCTION Open Access Education, collaboration, and ...

INTRODUCTION Open Access Education, collaboration, and innovation: intelligent biology and medicine in the era of big data Jianhua Ruan1*, Victor Jin2, Yufei Huang3, Hua Xu4, Jeremy S Edwards5, Yidong Chen6,7, Zhongming Zhao8,9* From The International Conference on ...