

# 16s Metagenomic Analysis Tutorial Max Planck Society

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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)

**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

**!diversity\*metrics - Evolutionary Biology**

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

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METHODOLOGY ARTICLE Open Access All-Food-Seq (AFS): a quantifiable screen for species in biological samples by deep DNA sequencing Fabian Ripp1†, ...

**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

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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

**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 ...

**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