

CMEIAS® v3.10: ADVANCED COMPUTATIONAL TOOLS OF IMAGE ANALYSIS SOFTWARE DESIGNED TO STRENGTHEN MICROSCOPY-BASED APPROACHES FOR UNDERSTANDING MICROBIAL ECOLOGY

FRANK B. DAZZO, J. LIU, K. KWATRA, C. GROSS, N. PHILIPS, C. MONOSMITH, K. KLEMMER, Z. JI, C. GIDCUMB, R. SHAH, D. MCGARRELL, I. FOLLAND, I. GANESAN, P. SMITH, Y. YANNI, S. GANTNER, P. JHA, K. CARD, S. LUNDBACK, B. NICCUM, S. ZAMANI, I LEADER, D. STAWKEY, B. PATEL, A. JONES, T ABUKAR MSU EAST LANSING, MI

Information from Digital Images of Microbial Communities

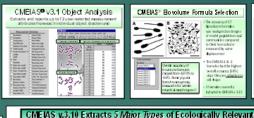
Morphological Diversity

A major challenge in microbial ecology is to develop computing tools that can extract ecologically important information from digital images of microbial populations and communities at single cell resolution, and analyze their structure in situ without cultivation. Several microbial ecologists, mathematicians and computer scientists are addressing this challenge by developing a software package called CMEIAS (Center for Microbial Ecology Image Analysis System), CMEIAS applies pattern recognition algorithms to classify microbial morphotypes with 97% accuracy, A CMEIAS-IT v3.10 upgrade is being developed to analyze microbial (i) morphological diversity related to the database of currently described bacteria; (ii) abundance (cell density, biovolume, biomass carbon, biosurface area, cumulative length); (iii) metabolic activity, autecology and phylogeny using color segmentation of fluorescent molecular probes, and (iv) in situ patterns of spatial distribution during surface colonization of biofilm landscapes. CMEIAS includes plugins with many new object analysis/classification features, new tools to help edit images before analysis (Object Separation, Color Segmentation), Excel Com Add-Ins that compile & analyze CMEIAS ecological data, a fractal dimension analyzer, new exploratory cluster analysis tools to optimize the decision boundaries for classification of the operational morphological units with unlimited morphological diversity, and a Quadrat Maker tool for spatial distribution analyses of microbial colonization. CMEIAS is currently being used to analyze spatial patterns of microbial colonization on plant roots, freshwater biofilm communities on surface polymers on glass, shifts in vaginal microflora in health and BV disease, and the in situ spatial scale of bacterial cell-to-cell communication at single cell resolution. These CMEIAS-based applications can facilitate research designed to enhance our understanding of microbial ecology by providing well-documented, accurate, robust and user-friendly computing tools that extract important, quantitative information from digital images of microbes at multiple spatial scales relevant to their in situ ecological behavior in various habitats. CMEIAS computer-assisted microscopy adds an exciting new dimension of awesome computational power to many types of quantitative microbial ecology research, and is especially valuable when combined with molecular-based and other methods of polyphasic community analysis.





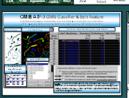














Size Border Cluster Analysis



extracts 3 types of data for spatial ecology analysis:

CMEIA 8 computing tools:







Human Vaginal Microflora: "Normal" vs. Bacterial Vaginosis The morie dictory is in microbial common by the they rever be day light microscopy mary his or like all made Tyrk m for exploring medical microbials groupplications of CHLIAS compates an object on a corpose to flower.







