CMEIAS© v4.0: ADVANCED COMPUTATIONAL TOOLS OF BIOIMAGE INFORMATICS SOFTWARE DESIGNED TO STRENGTHEN MICROSCOPY-BASED APPROACHES FOR UNDERSTANDING MICROBIAL ECOLOGY

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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 upgrade is being developed to analyze microbial (i) morphological diversity related to the database of currently described bacteria; (ii) abundance (e.g., cell density, biovolume, biomass carbon, biosurface area, cumulative length); (iii) ecophysiology (e.g., metabolic activity, autecology and phylogeny using color segmentation of fluorescent molecular probes), and (iv) *in situ* spatial / landscape ecology. CMEIAS includes plugins with many new object analysis/classification features, new tools to help edit images before analysis (Object Separation, Color Segmentation), Excel add-Ins that prepare, 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 plot-based spatial distribution analyses of microbial colonization patterns. CMEIAS is currently being used to analyze microbial colonization patterns and intensity 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 interactions 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 bioimage informatics software is released at our project website <http://cme.msu.edu/cmeias/>, adds computational power to many types of quantitative microbial ecology research, and is especially valuable in filling gaps when combined with molecular-based and other methods of polyphasic community analysis.