Title: Construction of a DNA distinguishable community

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Abstract:

Background:

Multicellular eukaryotes are associated with complex communities of microorganisms. These host associated communities provide many beneficial functions for the host organism including, nutrient acquisition, pathogen defense, and buffering against abiotic stresses. Although, sequencing based approaches have given insight into determining who is present in the community and functional potential, interpretation of these results may be extremely difficult. Some researchers have shifted approaches to synthetic or constructed based microbial communities’ experiments to unravel host-microorganism interactions. This method involves adding known microbial strains to a host organism

In this paper, we describe a new software program, NAME, which will create a diverse community of organisms that can be distinguished through DNA sequencing technology.

Implementation:

Results and Discussion:

References:

Availability and requirements

Lists the following:

Project name: e.g. My bioinformatics project

Project home page: e.g. http://sourceforge.net/projects/mged

Operating system(s): e.g. Platform independent

Programming language: e.g. Java

Other requirements: e.g. Java 1.3.1 or higher, Tomcat 4.0 or higher

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Abbreviations:

DNA: Deoxyribonucleic acid

FASTA: Fast-all (file format)