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Towards Standards For Sequencing and Bioinformatic Analysis Quality Control when using eDNA for Metabarcoding and Taxonomic Identification

Joshua A. Steele, Susanna Theroux, Dovi Kacev, Raphael D. Mazor, Yiping Cao, John F. Griffith, and Eric D. Stein

Southern California Coastal Water Research Project Authority, Costa Mesa, CA, USA

Abstract

With the emergence of next generation sequencing technology (NGS), it has become possible and practical to sequence whole communities of organisms for environmental exploration and assessment. The copious sequence data generated provides the sensitivity and depth to allow the use of environmental DNA to answer questions about the health of an ecosystem or the populations present. Analyzing this abundance of information requires bioinformatic tools to perform quality control, sequencing processing, and assignment of sequence identity. We have begun applying these new sequencing technologies to metabarcoding for characterization of vertebrate, invertebrate, algal, and microbial assemblages in freshwater, estuarine, and marine ecosystems, in collaboration with management and research agencies at the state, federal, and international level. For NGS to be useful for management or regulatory applications, it will be critical to develop standards that will ensure the quality of the data produced and the reliability of the data analyses. Building on other large collaborative sequencing projects (e.g. the Barcode of Life or the Human Microbiome Project), processes that can affect the outcomes of the study (such as sequence quality [including idiosyncrasies of the sequencer platform], sequence clustering, and taxonomic classification) should be standardized where possible. The reliance on gene databases also requires both standardization and coordination across the research and management communities to ensure the best possible information is used for identification and classification of sequences. Development of standards has begun nationally and internationally; and we will present approaches to incorporate the needs of research groups, management agencies, regulators, and regulated agencies into these guidelines.