OPEN /

ACCESS

Conference Abstract

Planning for Field Based Biological Sample Collection: Using the Genomic Observatories Metadatabase Project Interface

John Deck[‡], Michelle Gaither[§], Rodney Ewing^I, Christopher Bird[¶], Neil Davies^{‡,#}, Chistopher Meyer^a, Cynthia Riginos[«], Robert J Toonen[»], Eric Crandall[^]

‡ University of California at Berkeley, Berkeley, United States of America

§ University of Central Florida, Orlando, United States of America

| Biocode, LLC, Junction City, United States of America

¶ Texas A&M, Corpus Christi, United States of America

University of California, Moorea, French Polynesia

Department of Invertebrate Zoology, U.S. National Museum of Natural History, Smithsonian Institution, Smithsonian Institution, United States of America

« University of Queensland, Brisbane, Australia

» Hawai'i Institute of Marine Biology, University of Hawai'i at Mānoa, Kāne'ohe, United States of America

^ California State University Monterey Bay, Monterey, United States of America

Corresponding author: John Deck (jdeck88@gmail.com)

Received: 09 Apr 2018 | Published: 05 Jul 2018

Citation: Deck J, Gaither M, Ewing R, Bird C, Davies N, Meyer C, Riginos C, Toonen R, Crandall E (2018) Planning for Field Based Biological Sample Collection: Using the Genomic Observatories Metadatabase Project Interface. Biodiversity Information Science and Standards 2: e25651. https://doi.org/10.3897/biss.2.25651

Abstract

BISS Biodiversity Information Science and

The Genomic Observatories Metadatabase (GeOMe, <u>http://www.geome-db.org/</u>) is an open access repository for geographic and ecological metadata associated with biosamples and genetic data. It contributes to the informatics stack – Biocode Commons – of the Genomic Observatories Network (<u>https://gigascience.biomedcentral.com/articles/10.1186/2047-217X-3-2</u>). The GeOMe project interface enables administrators to plan and execute field based sample collection efforts. GeOMe projects specify a core set of sample metadata fields based on community standard vocabularies and also includes plugins for associating samples with photos, subsamples, NextGen sequence metadata, and permits. Users can upload their own expedition-specific metadata, which contributes to the overall project dataset while providing the user a convenient method for updating and

This is an open access article distributed under the terms of the CC0 Public Domain Dedication.

refining their contributed data. GeOMe provides connection points to the Global Biodiversity Information Facility and archived genetic data stored in the National Center for Biotechnology Information's (NCBI's) Sequence Read Archive (SRA), linking specimens and sequences via unique persistent identifiers.

Presenting author

John Deck