Software for Metagenomics and Metadata Standards

Iddo Friedberg
CAMERA / CALIT2
University of California San Diego

camera Marine Microbial Ecology

it2

Gordon and Betty MOORE FOUNDATION

UCSD

What is Metagenomics?

- Culture-free approach to study microbial communities
  - < 1% of microbes can be cultured
  - DNA directly isolated from environmental sample and sequenced
- Examining genomic content of organisms in community/environment to better understand:
  - Diversity of organisms
  - Their roles and interactions in the ecosystem

Metagenomics: Appy Genomics to Populations & Communities

	 Individual	 Population	 Community
Ecology	**Physiology:** Differential gene expression in response to change	**Demographics:** Birth, death, immigration, emigration	**Community ecology:** Interspecific interactions that shape community structure and function
Genomics	Fine-scale mapping of individual genomes	**Population genomics:** Comparative genomic analyses to assess variation	**Metagenomics:** Genetic potential of collective members of community
Genetics	**Bacterial genetics:** Role of genes under various conditions	**Population genetics:** Allele frequency distribution	**Community genetics:** Interplay between genetic composition of community and ecological community properties

Little AEF, et al. 2008.
Annu. Rev. Microbiol. 62:375–401

camera Marine Microbial Ecology

MOORE FOUNDATION

UCSD

What Can We Learn?

- **Taxonomic content**: Taxon diversity in a habitat (using taxonomic markers)
- **Functional content**: biological functions, qualitative and quantitative profiles
- **Coping with the environment**: differences in functional content between habitats
- **Decompose the biotic / abiotic elements in a habitat**: metadata analysis
- …

Some Metagenomic Studies

- **Bacterial rhodopsins** (Beja *et al.* 2000)
- **Acid mine drainage study** (Tyson *et al.* 2004)
- **Sargasso sea study** (Venter *et al.* 2004)
- **Wisconsin soil study** (DeLong *et al.* 2006)
- **Termite Hindgut** (Warnecke *et al.* 2007)
- **Human Obesity** (Turnbaugh *et al.* 2006)

… and many, many others

What is CAMERA?

- Community Cyberinfrastructure for Advanced Marine Microbial Research and Analysis
- 7 year $24.5 mil grant from the Moore foundation
- Goal: build a community computational resource for researchers in metagenomics
- ”Cyberinfrastrcture”: hardware, software & data

camera Marine Microbial Ecology

it²

Gordon and Betty MOORE FOUNDATION

UCSD

What is CAMERA? Hardware

camera
Marine Microbial Ecology

it²

Gordon and Betty
MOORE
FOUNDATION

UCSD

What is CAMERA? Hardware

512 CPU, 200 TB, 5 TFlops

camera Marine Microbial Ecology

it²

Gordon and Betty MOORE FOUNDATION

UCSD

What is CAMERA? Data

- Metagenomic sequence data are:
  - Voluminous
  - Noisy
  - Partial
- At the very least they should be:
  - Standardized for processing
  - Associated with Metadata

Why Metadata?

- Microbial communities are affected by and affect their habitats
- Therefore habitat data, in addition to sequence data, is crucial for an **environmental** genomic picture
- Also, sample condition data is needed for reproducibility

camera Marine Microbial Ecology

it2

Gordon and Betty MOORE FOUNDATION

UCSD

Why Metadata?

- Microbial communities are affected by and affect their habitat
- Sequence information + metadata = whole picture

- Habitat Type
- Geographic Location (large area)
- Sample Location (smaller area)
- Country
- Filter Size
- Latitude (exact location)
- Longitude (exact location)
- Depth
- Wat. Dep.
- Chlorophyll
- Oxygen
- Fluor.
- Salin.
- Temp
- Trans.
- BioMass
- Inorg. Carbon
- Inorg. Phospate
- Org. Carbon
- Nitr.
- # Pooled
- # Sampled
- Volume
- Coll. Date

Why Metadata?

- Microbial communities are affected by and affect their habitat
- Sequence information + metadata = whole picture

Habitat

Country

Altitude

Temperature

pH

Filter size

camera Marine Microbial Ecology

it2

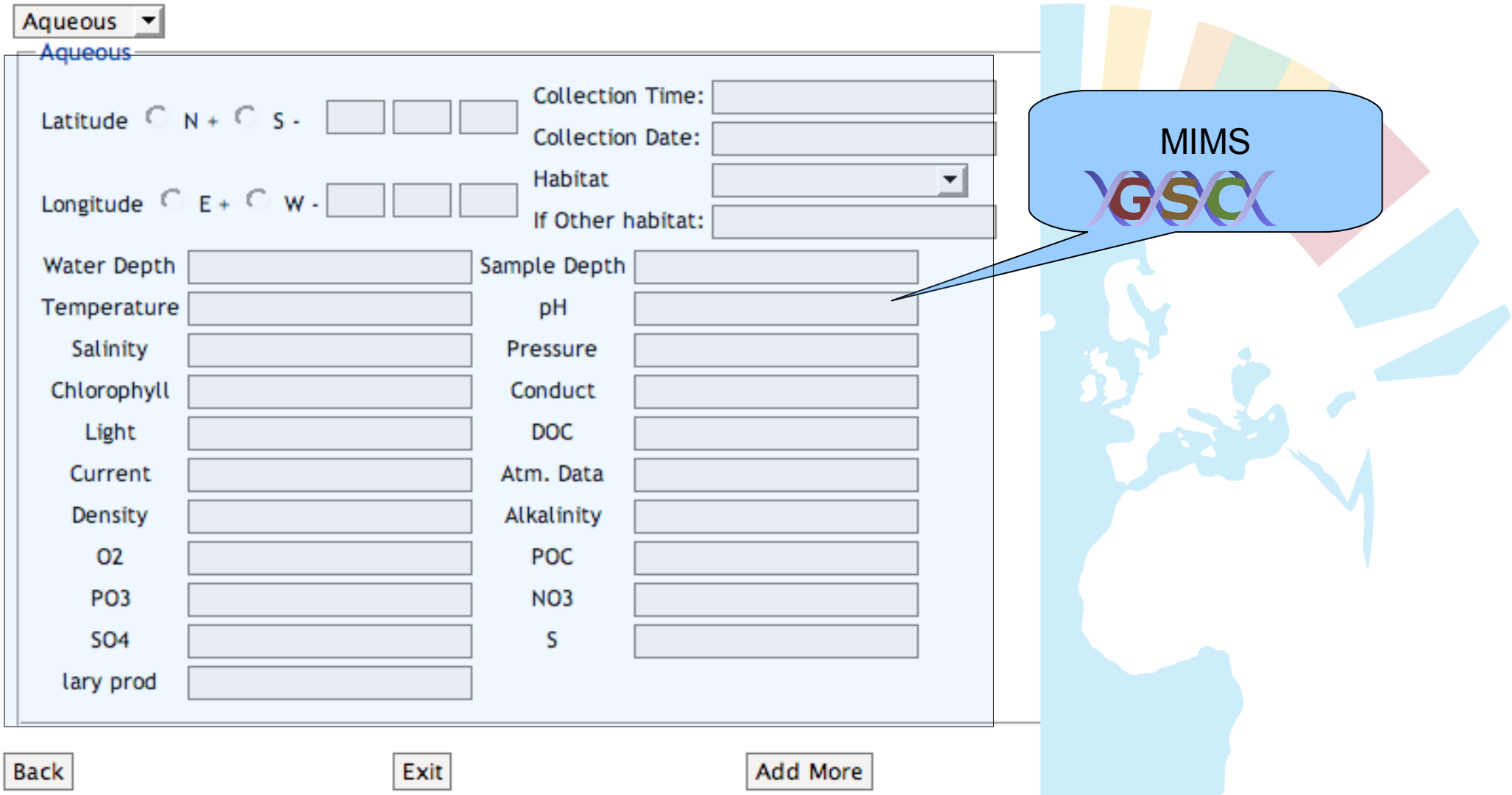
Gordon and Betty MOORE FOUNDATION

UCSD

Data Standards and Data Acquisition

- Minimal Information for (Meta)Genomic Sequences: MIGS/MIMS
- A Metadata standard, developed by the Genomics Standards Consortium
  - Controlled vocabularies e.g. EnvO, PATO, CABRI
  - Common language: GCDML
- Submissions shall comply with a MIMS/MIGS core, but any metadata can be entered via keywords and free text
- Different metadata submission forms for different habitats: (water, soil, air, hosts)

Standards Compliance: MIMS/MIGS



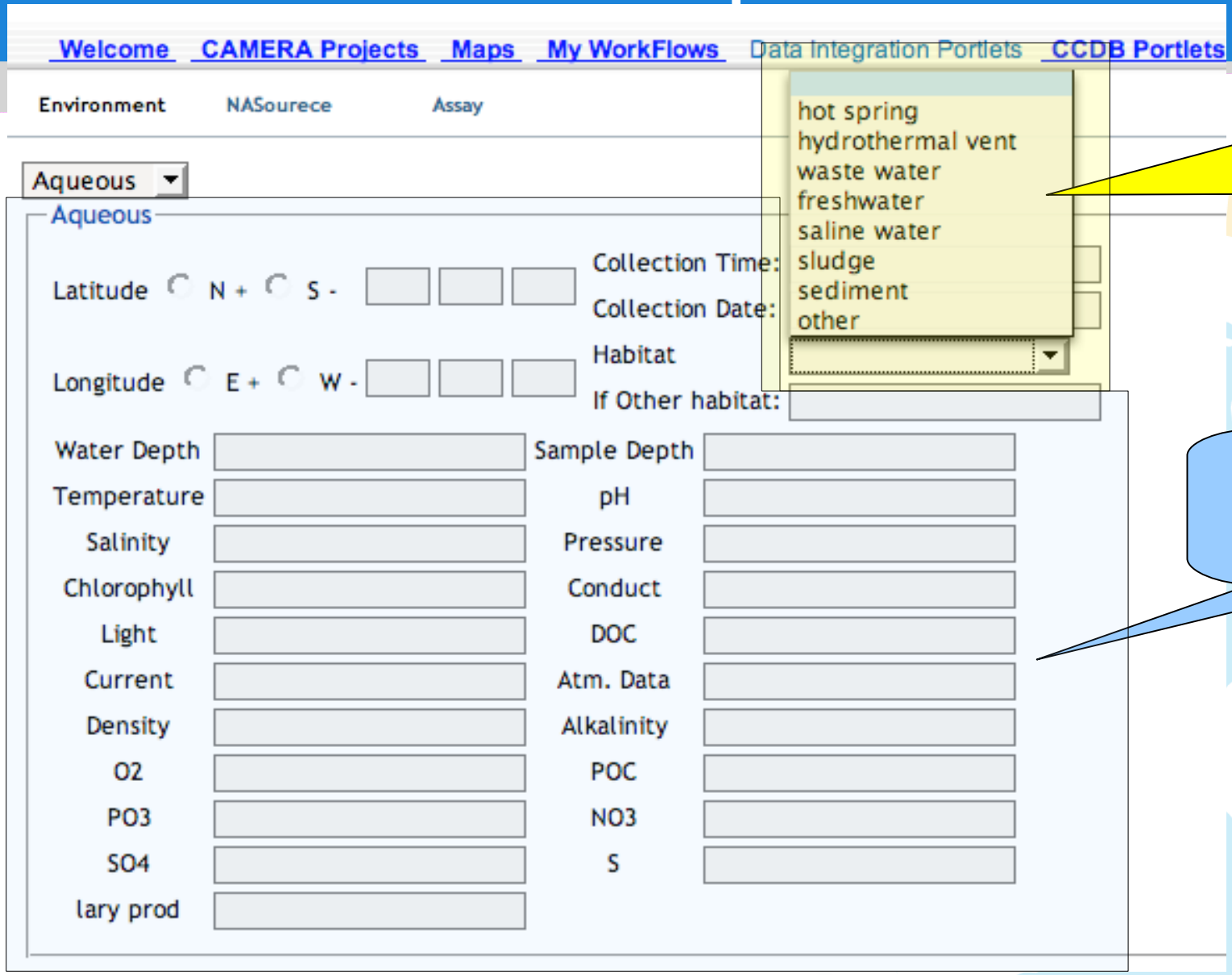
camera Marine Microbial Ecology

it2

Gordon and Betty MOORE FOUNDATION

UCSD

Standards Compliance: MIMS/MIGS



Environmental Ontology

Envo

MIMS

GSC

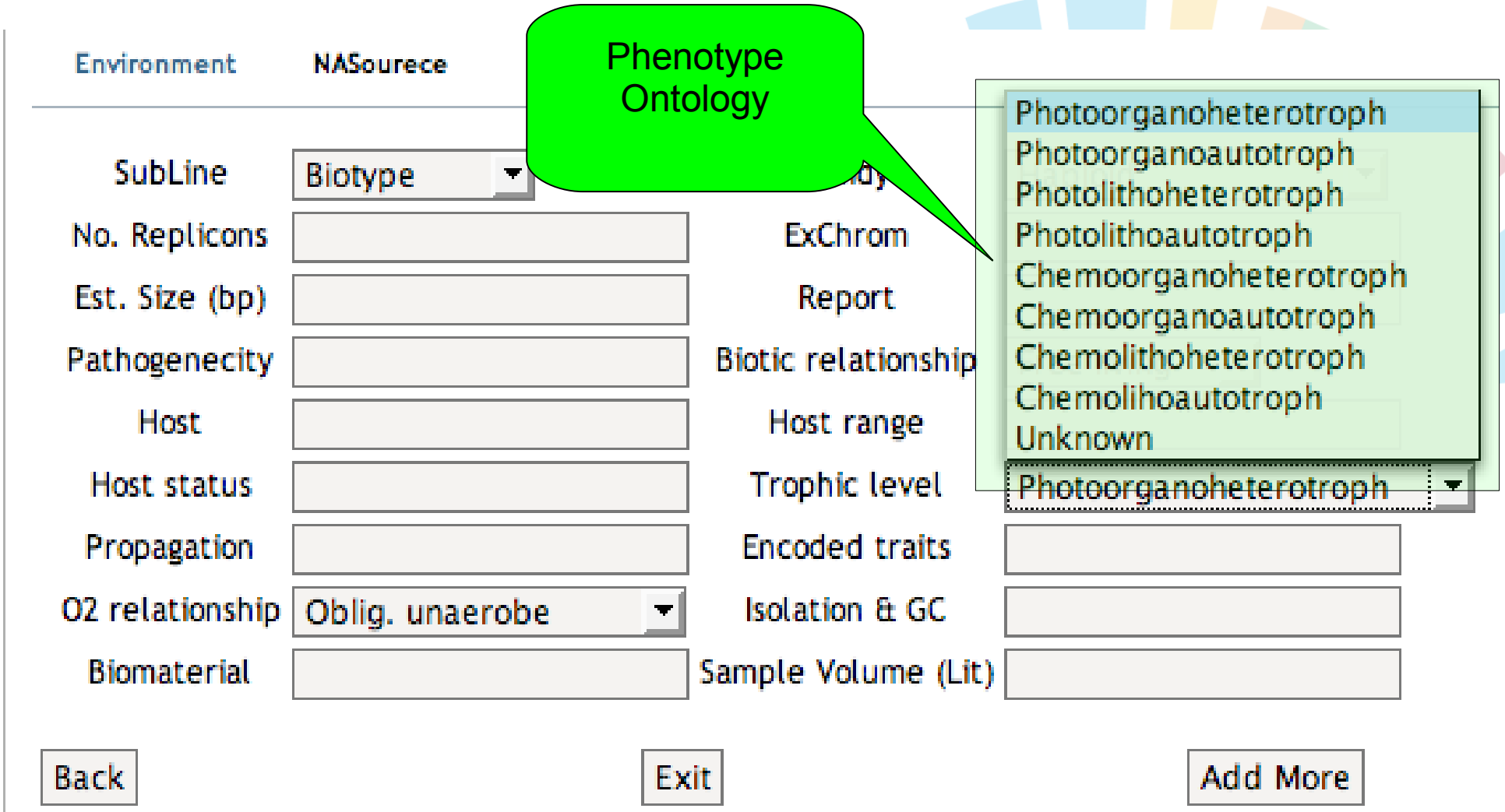
camera Marine Microbial Ecology

it2

Gordon and Betty MOORE FOUNDATION

UCSD

Standards Compliance: PATO



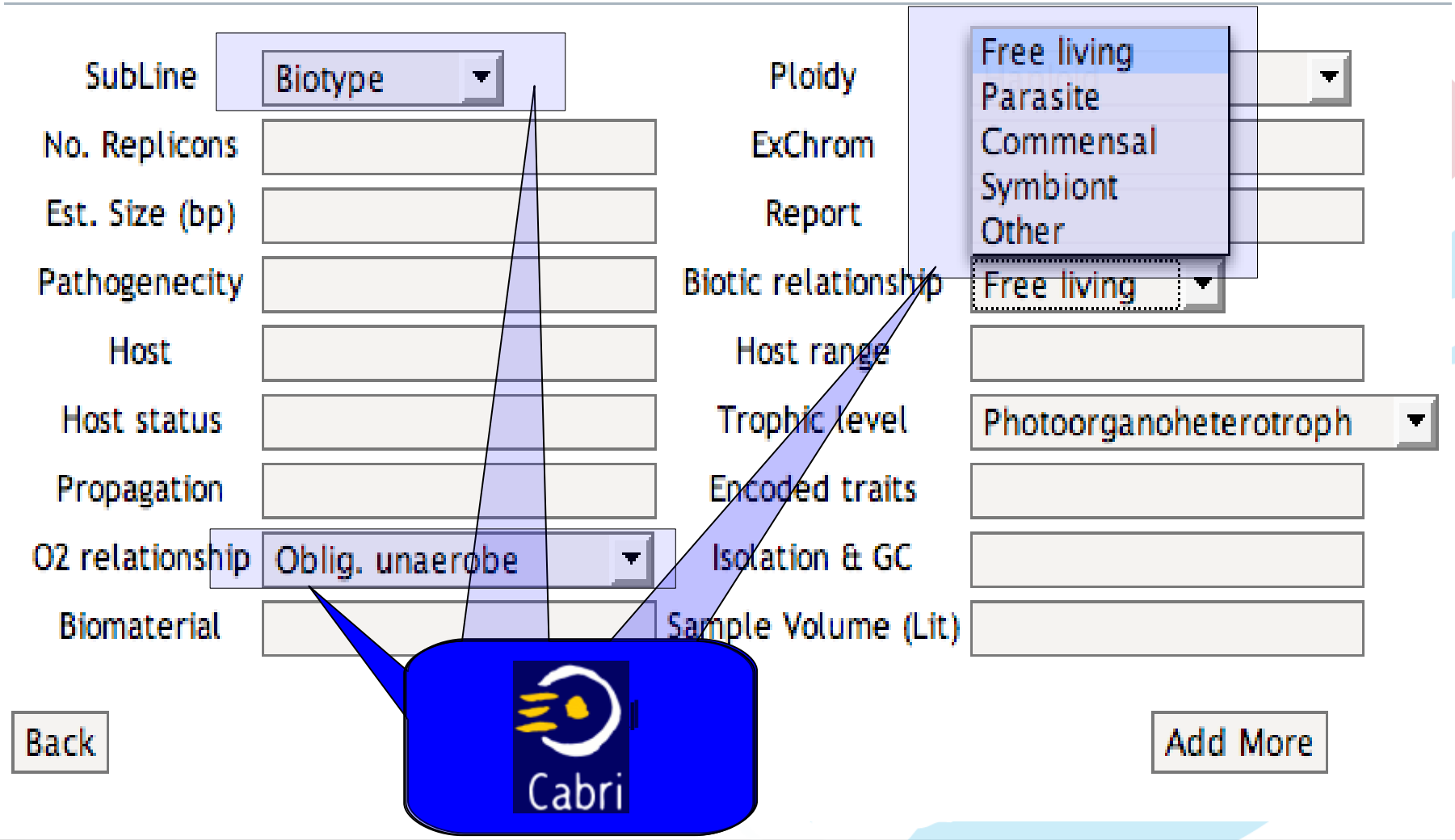
camera Marine Microbial Ecology

it2

Gordon and Betty MOORE FOUNDATION

UCSD

Standards Compliance: Controlled Vocabularies



camera
Marine Microbial Ecology

Things to Think About

- Visualization:
  - How do we look at ”disembodied” sequence data?
  - ”Fragment recruitment” track
  - Visualization of sequence data <--> metadata associations
- Database: association of metadata and sequence data; queries by metadata
-

Would you Like to Know More?

- The Genomic Standards Consortium. MIMS & GCDML: http://gensc.org
- BioMIST (soon): http://sourceforge.net/projects/biomist/
- CAMERA: http://camera.calit2.net
- Me: http://iddo-friedberg.net

Would you Like to Know More?

- The Geno nsortium. MIMS & G http://gens
- BioMIST (http://sour ts/biomist/
- CAMERA: t2.net
- Me: http://

camera Marine Microbial Ecology

it2

Gordon and Betty MOORE FOUNDATION

UCSD

Thanks

- CAMERA data acquisition team:
  - Brian Fox
  - Shulei Sun
  - Jing Chen
  - Laurence Bohannan
  - Jeffrey Grethe
- Genomic Standards Consortium
  - Dawn Field
  - George Garrity
  - Renzo Kottman