Biodiversity. Bioinformatics. Biotechnology.

Consortium MicroB3, Co-ordinator, Uni Jacobs (Bremen)

- Max Planck Institute for Marine Microbiology (Lead WP5)
- University of Oxford (Lead WP2)
- Institute of Marine Biology, Biotechnology and Aquaculture, Hellenic Center for Marine Research
- Alfred Wegener Institute for Polar and Marine Research
- Centre National de la Recherche Scientifique (Lead WP6)
- Institute of Marine Sciences (CSIC)
- Stazione Zoologica Anton Dohrn
- Marine Biological Association
- Flemish Institute for Biotechnology
- The Scientific and Technological Research Council of Turkey
- Marine Information Service (Lead WP3)
- International Council for the Exploration of the Sea
- Flanders Marine Institute
- French Research Institute for Exploration of the Sea
- European Bioinformatics Institute (Lead WP4)
- CEA - Genoscope
- University Bremen
- University of Groningen (Lead WP7)
- National University of Ireland, Cork
- School of Biological Sciences, Bangor University
- Institute for Coastal Marine Environment
- Université catholique de Louvain (Lead WP8)
- The Mediterranean Science Comission
- International Union for Conservation of Nature
- Environmental & Marine Project Management Agency (Lead WP9)
- Matís ltd. - Icelandic Food and Biotech R&D
- BIO-ILIBERIS R&D
- InterWorks
- Ribocon
- Bio-Prodict
- PharmaMar, S.A.

Why study the Marine Environment?

What Do we Need for a Better Understanding?

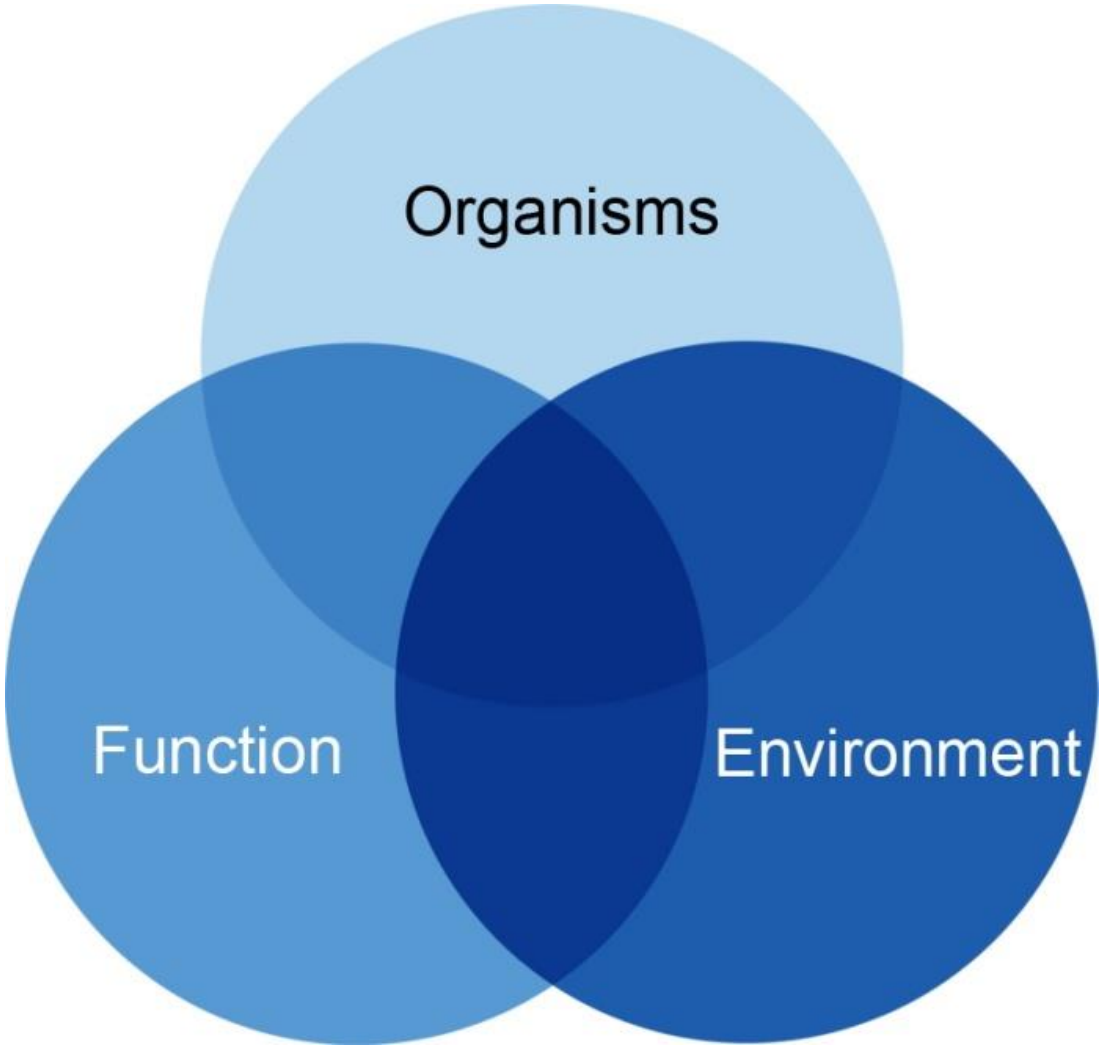
Who is out there and

How much of which kind?

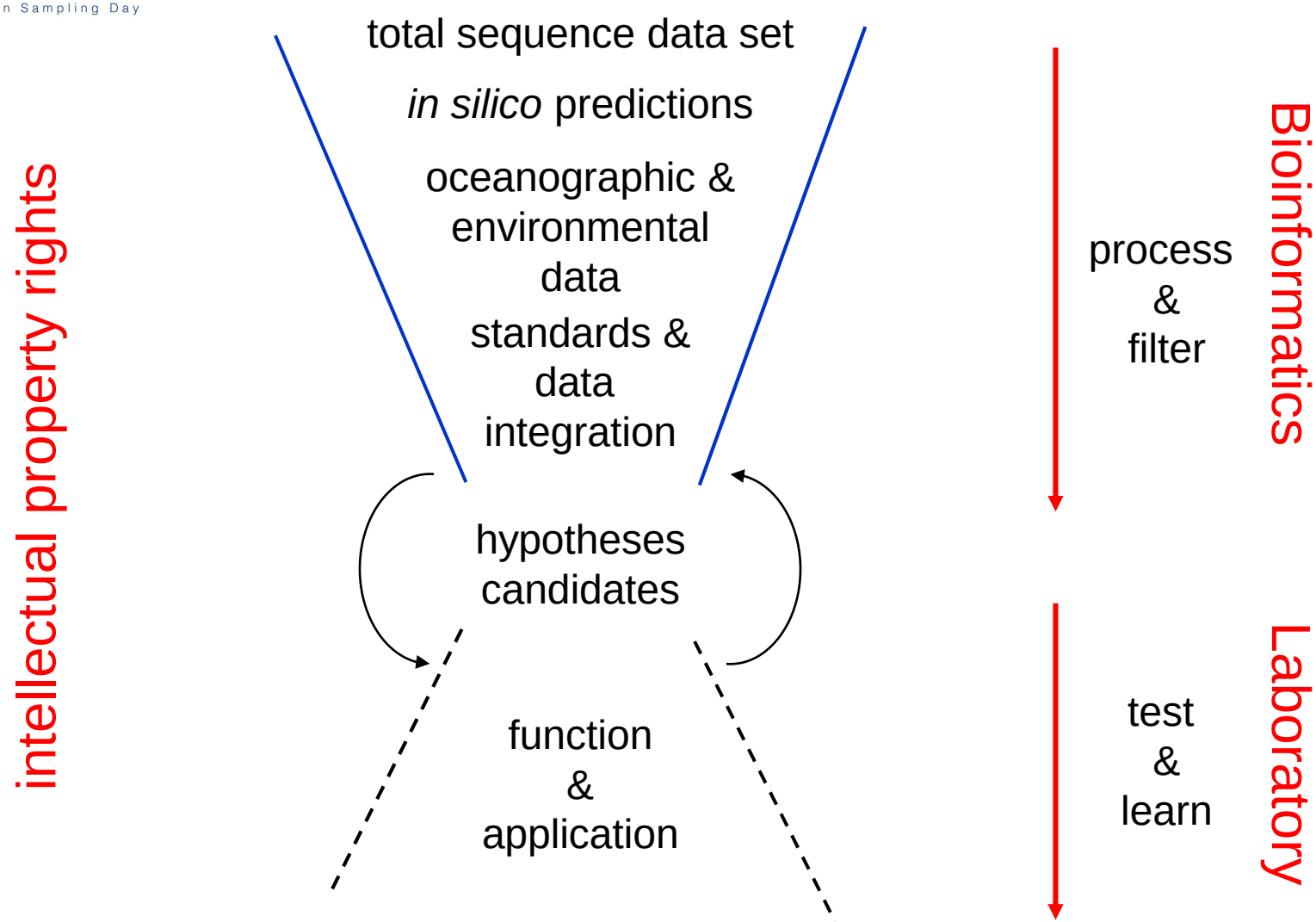
What are they doing and

How is their relationship to the environment?

Data Integration



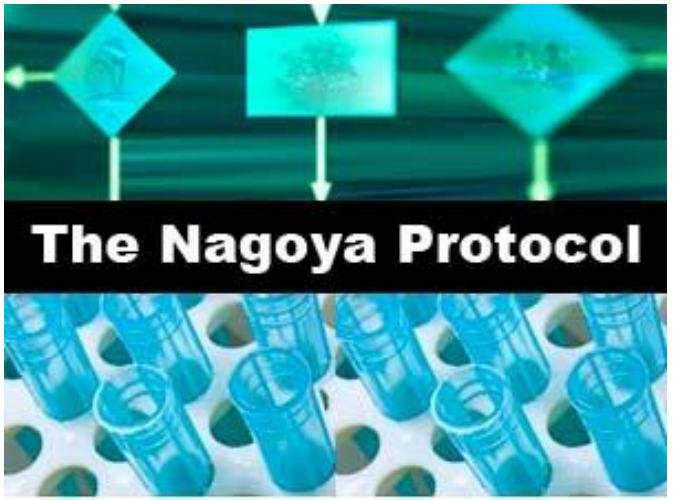
small and large scale study sites



ecosystems biology & biotechnology

The Nagoya Protocol

The Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits (ABS) Arising from their Utilization to the Convention on Biological Diversity is an international agreement which aims at sharing the benefits arising from the utilization of genetic resources in a fair and equitable way. It entered into force on 12 October 2014, 90 days after the date of deposit of the fiftieth instrument of ratification.



Intellectual Property (IP) Management for Marine Bioprospecting

Tom Dedeurwaerdere,
Univ. Louvain

Arianna Broggiato,
Univ. Louvain

Michele Barbier,
CIESM

Create a global microbiome effort

Understanding how microbes affect health and the biosphere requires an international initiative, argue **Nicole Dubilier**, **Margaret McFall-Ngai** and **Liping Zhao**.

Microbes have been discovered on Earth wherever anyone has looked for them, from the boiling waters of Yellowstone's hot springs in Wyoming to the depths of cold, dark Antarctic lakes under 800 metres of ice. A holistic understanding of the role of Earth's microbial community and its genome — its microbiome — in the biosphere and in human health is key to meeting many of the challenges that

…tance of the microbial world. This is thanks to developments such as low-cost high-throughput sequencing; advances in sample preparation that allow researchers to sequence genomes from individual cells as well as from microbial communities; improvements in computing power and imaging technologies; and the development of bioinformatics tools to help make sense of the data.

Thus biologists are gaining insight into the identity and function of microbes that cannot be grown in the laboratory — the vast majority of Earth's microbiome. Currently only 35 bacterial and archaeal phyla are recognized on the basis of classical approaches to microbial taxonomy. Sequencing efforts in the past few years have pushed the number closer to 1,000 (ref. 2).

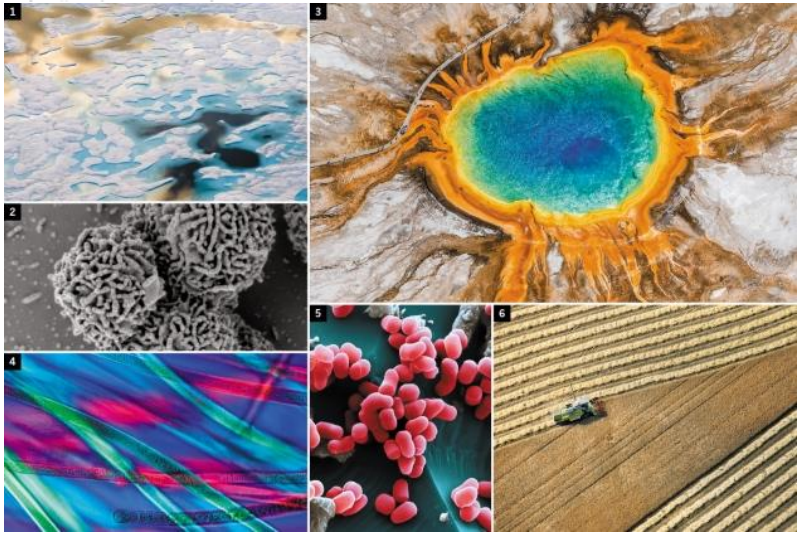
Newfound groups of bacteria are throwing old assumptions about the tree of life into question, and revealing vast holes in our ▶

nature International weekly journal of science

Home | News & Comment | Research | Careers & Jobs | Current Issue

Archive > Volume 526 > Issue 7575 > Comment > Article

NATURE | COMMENT



The Genomic Standards Consortium

Innovation through Collaboration

- Established in September 2005
- Governed by a Board
- 100+ members
- Representatives from:

  INSDC (EMBL-EBI/DDBJ/GenBank), Sanger, JGI, JCVI, GOLD, CAMERA, MG-RAST, RDP, SILVA, VAMPS and many more
- Open membership defined by participation

GSC 10, Argonne, 2010

GSC 12, Bremen, 2011

GSC 13, BGI 2012

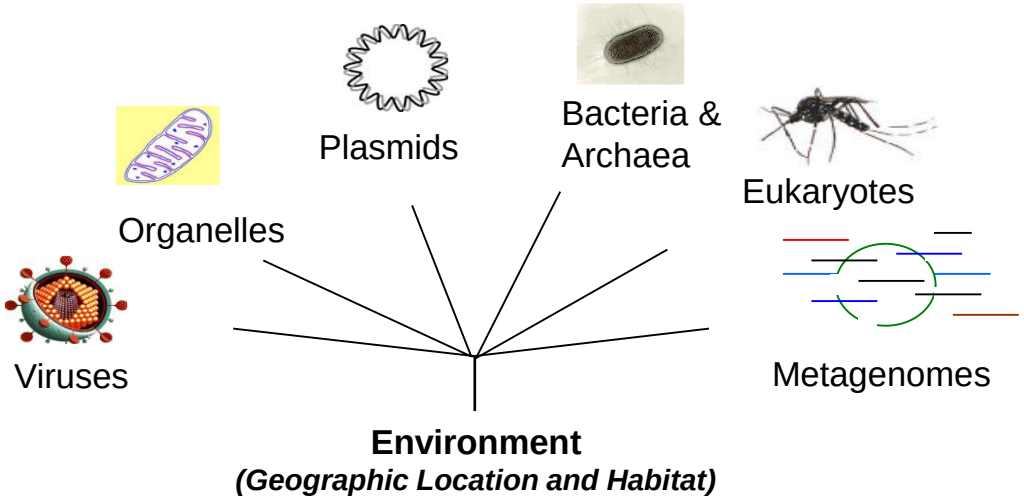
GSC 14, NIH 2013

GSC 17, JGI 2015

gsc genomic STANDARDS consortium

GSC Goals

- Promote mechanisms that standardize
  - the description of genomes, metagenomes, marker genes
  - and the exchange and integration of contextual (meta)data



Field et al., 2008, Nat Biotechnology, 26(5):541

SIGS Standards in Genomic Sciences
An Open Access Journal of the Genomic Standards Consortium

Global Sampling Event

Orchestrated

Contexual Data

Microbial Diversity & Function

Standardized Protocols

Fixed in Time June 21st

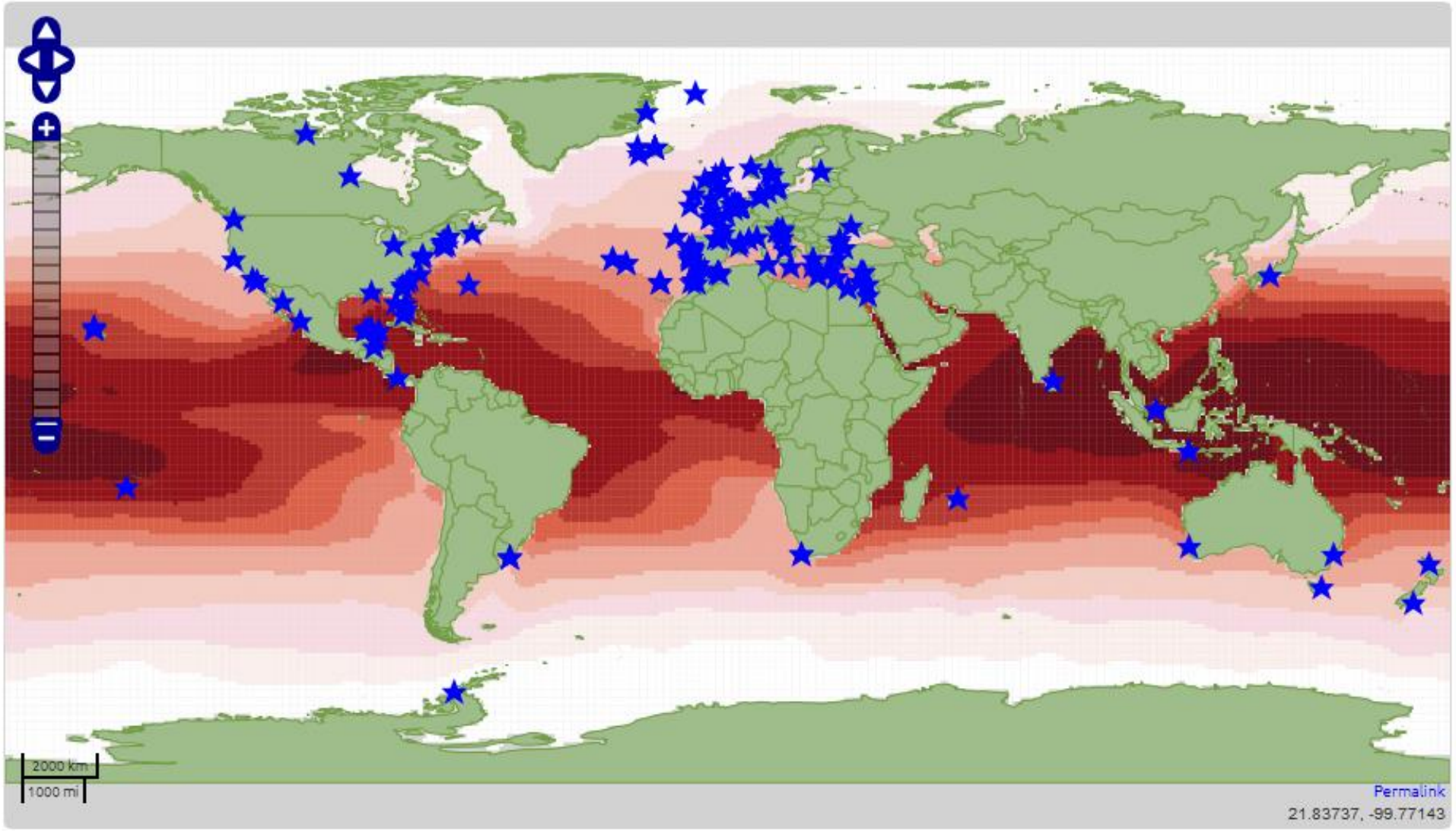
OSD

Ocean Sampling Day

www.oceansamplingday.org

Legal Framework
ABS, MTA, DTA

Map of OSD sites (191)



www.oceansamplingday.org

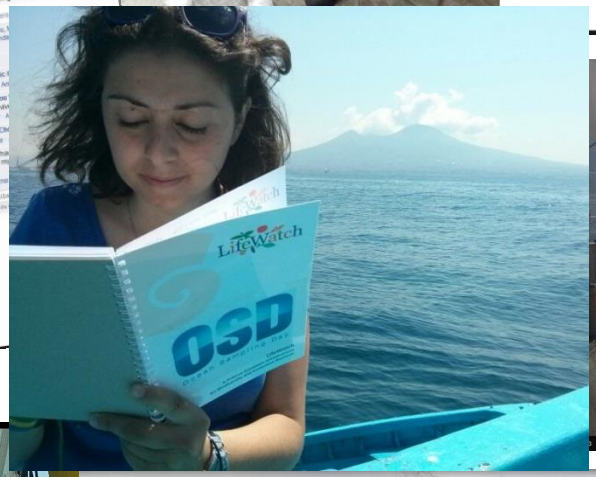

GREETINGS FROM THE AZORES!
#osd2014

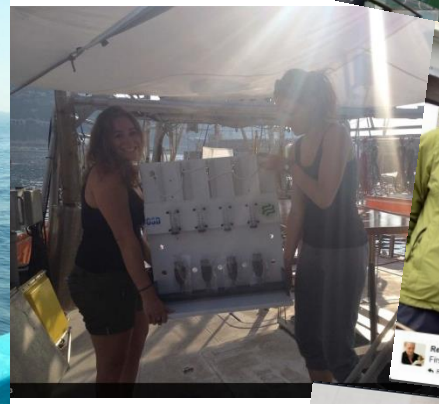

2015
OSD
OSD
BONE!


OSD


Cefas
OSD 2014


OSD
MOROCCO


LifeWatch
OSD

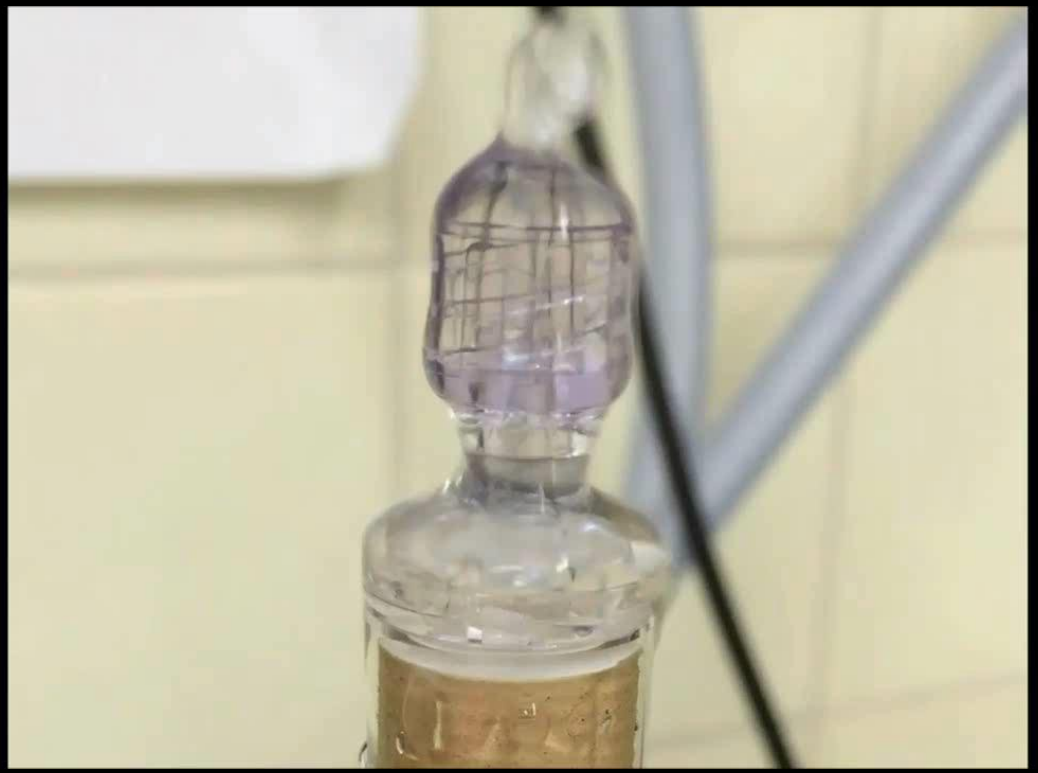



Rebecca Thomas
First boat team of our #icelP14 students taking part in #OSD2014 in Iceland


OSD


OSD


CIMAR
OSD
climar



Portugal and Helgoland

Citizen Science Project MyOSD

MY OSD
Ocean Sampling Day

www.my-osd.org

MyOSD Sampling Kit 2015

MyOSD Log sheet

MyOSD Handbook

Sterivex filters

Thermometer

Big falcon tubes (*to store the Sterivex filters*)

Labels and plastic bag

Small falcon tube (*to collect the sample for salinity*)

Ethanol (*to clean the bucket*)

RNAlater tubes (*to stabilize the sample after the filtration*)

Big syringes 50ml

Small syringe 3ml

Blu tack

Gloves

MyOSD Hubs 2015

270 kits

MyOSD 2015

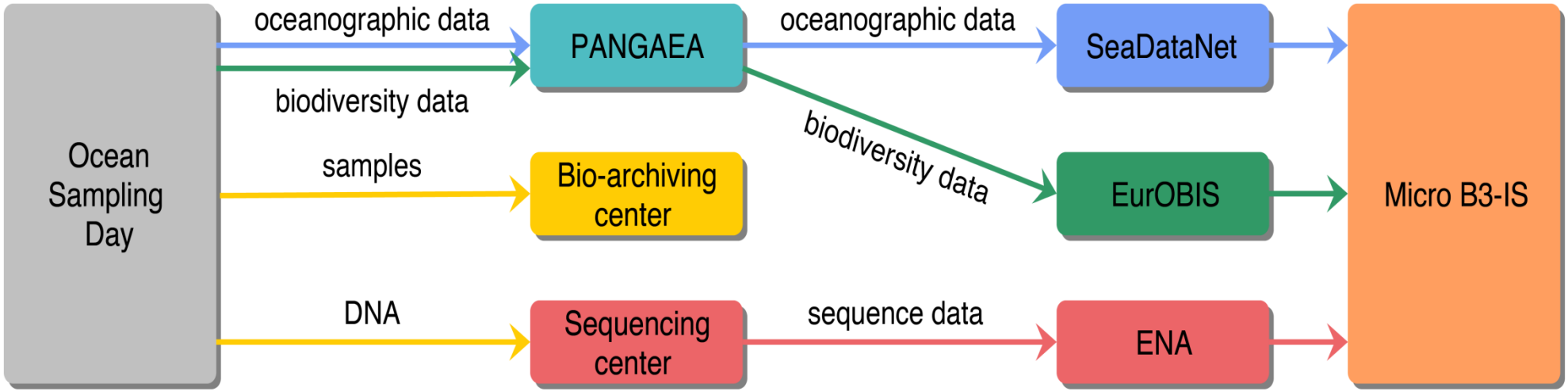
More than 1000 filters

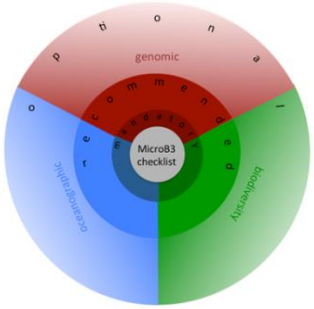
Sequencing with LGC genomics

- 16S rRNA gene amplicon data
  - 40,000 to 50,000 amplicon tags (2x 300 bases)
  - 6,038,864 reads, 276,323 control reads
- 18S rRNA gene amplicon data
  - 40,000 to 50,000 amplicon tags (2x 300 bases)
  - 5,089,384 reads
- Metagenome
  - 1,000,000 reads (2x 300 bases) for 150 metagenomes
  - 149,520,184 reads


Image courtesy of JohnGoode

Sample and Data Workflow for OSD



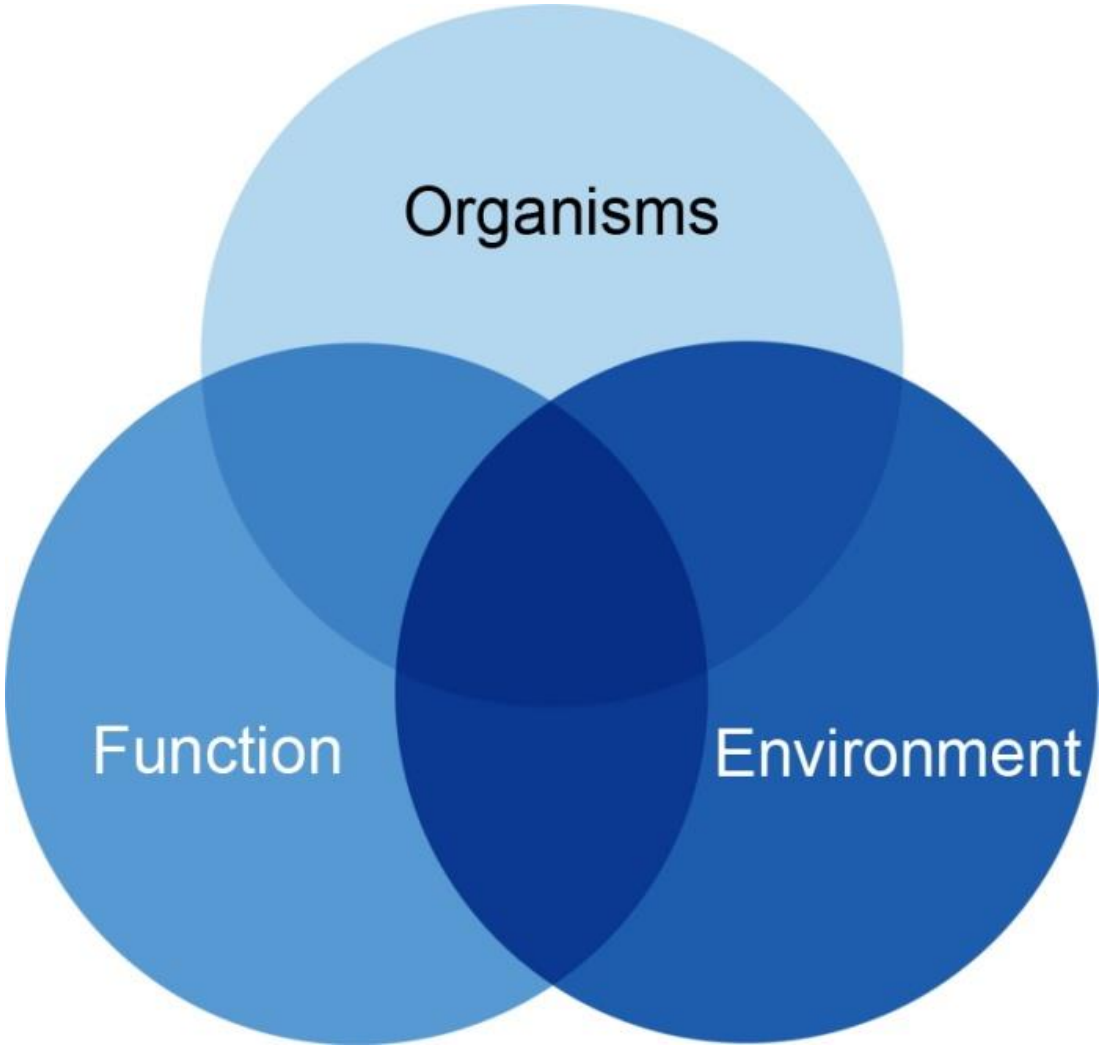


PACIFIC BIOSCIENCES

LIFEWATCH

Smithsonian

Data Analysis & Integration



The Ocean Resistome

DANTAS LAB

Washington University in St.Louis

The ISME Journal (2015) 9, 207–216

www.nature.com/ismej

ORIGINAL ARTICLE

Improved annotation of antibiotic resistance determinants reveals microbial resistomes cluster by ecology

Molly K Gibson[1], Kevin J Forsberg[1] and Gautam Dantas[1,2,3]
[1]*Center for Genome Sciences and Systems Biology, Washington University School of Medicine, St Louis, MO, USA;* [2]*Department of Pathology and Immunology, Washington University School of Medicine, St Louis, MO, USA and* [3]*Department of Biomedical Engineering, Washington University, St Louis, MO, USA*

Resfams

a curated database of protein families and associated profile hidden Markov models (HMMs), confirmed for antibiotic resistance function

http://www.dantaslab.org/resfams/

Biosynthetic Gene Clusters

Classification of OSD and TARA reads (~64 billion reads) using the 158 BGC signatures of antiSMASH

Identified 1,176,640 contigs with BGC signatures and analysed using antiSMASH

➞ 84,008 contigs in OSD
➞ 1,092,632 contigs in TARA

In collaboration with Marnix Medema

Slide by Antonio Fernandez-Guerra

Frank Oliver Glöckner <fog@mpi-bremen.de>

www.facebook.com/microb3osd

www.microb3.eu

JACOBS UNIVERSITY