



# Marine Microbial Biodiversity, Bioinformatics & Biotechnology



Grant agreement n°287589

Acronym: Micro B3

Start date of project: 01/01/2012, funded for 48 month

## Deliverable 9.10

# Final overall report on bioinformatic training pipeline and on the final conference

Version: 1.0

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Approved by: Prof. Frank Oliver Glöckner, 15/12/2015

Expected Submission Date: 31/12/2015

Actual Submission Date: 15/12/2015

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The Micro B3 project has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement no 287589 (Joint Call OCEAN.2011-2: Marine microbial diversity – new insights into marine ecosystems functioning and its biotechnological potential).

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## Summary

The deliverable N° 9.10 “Final Overall Report on Bioinformatic Training Pipeline and on the Final Conference” deals in detail with results of task 9-4 on training and of task 9-5, the final Micro B3 conference from the last two years. In the first period one bioinformatics and one biostatistics courses were performed, which were reported on in detail in D9.6; in the third period - besides the courses detailed below - a dedicated OSD annotation jamboree was performed in March 2015, which is only summarized here as it was already fully reported on in D9.8. Therefore this report covers in more detail courses numbered 3, 4 and 6 (held in March 2014, May/June 2014 and April 2015) and an overall evaluation of the total of five courses forming the original training pipeline and one additional biotechnologically focussed one.

### **Overview of all Micro B3-related training courses with numbers of trainees**

1. Bioinformatics for Beginners (2012, Bremen, DE, 11 trainees)
2. Biodiversity Statistics (June 2013, Bremen, DE, 21 trainees)
3. Marine Metagenomics Bioinformatics (Spring 2014, EBI Training Centre, UK, 24 trainees)
4. Multi-disciplinary Summer School (May/June 2014, Crete, GR, 21 trainees, four local tutors)
5. Micro B3 OSD Analysis Workshop/Jamboree (March 2015 at EBI Training Centre, UK, 30 trainees)
6. KyroBio Masterclass Computational Approaches for Discovery and Engineering of Enzymes for Biocatalysis and Synthetic Biology (Spring 2015, Univ. Groningen, NL, 28 trainees)

The third bioinformatics course Marine Metagenomics Bioinformatics brought together 26 participants with 13 lecturers/organizers. The event, hosted by the EMBL-EBI on the Hinxton Genome Campus in Cambridge UK, took place from March 24<sup>th</sup> through to March 28<sup>th</sup> 2014. The course provided marine biologists, particularly those preparing for Ocean Sampling Day, with training to use publicly available resources to manage, share, analyse and interpret amplicon and metagenomics data. Attendees were trained in a range of metagenomics analysis methods and prepared to manage the arrival of subsequent OSD data.

The Micro B3 summer school, held on Crete at the HCMR marine station took place from 26 May to 6 June 2014. 25 participants attended for the full duration, with one additional Norwegian candidate visiting for the first week, all from OSD participating parties. The first week dealt with standardized sampling and sample extraction, as well as covering the legal aspects of ABS-conform sample taking. In the second week the OSD handbook was tested and refined, including real data submission and details of bioinformatic and statistical

analyses of amplicon and metagenomics data analyses practiced, with a view to the upcoming OSD 2014.

The Micro B3 OSD Analysis Workshop was again held at EMBL-EBI, from 9 to 13 March 2015. Twenty-eight researchers from across Europe and worldwide took part. The event was partially a training course, and partially a data analysis 'jamboree', collaboratively organised by EMBL-EBI, CNRS and Jacobs University Bremen. Training focused on hands-on work, like tutorials how to submit and access OSD data, how to perform QC and how to conform to common metagenomics standards. (Note: this course was already reported on in D9.8.)

Additionally to the original training plan, a sixth course called 'Masterclass Computational Approaches for Discovery and Engineering of Enzymes for Biocatalysis and Synthetic Biology' was held in Groningen from April 20-24, 2015. It aimed mainly at teaching biochemists and biotechnologists to become more familiar with and use bioinformatic approaches to facilitate their laboratory work. It was done under the auspices of the KyroBio project with support from the BE Basic and the Micro B3 projects by partner Dick Janssen from UGRO.

The long-term survey highlighted the network building aspects of a training pipeline, i.e. when trainees have the chance to take part in more than one course (10 attended two, three postdocs attended three courses) and when the courses build on each other, at least partially. As there were not many Micro B3 PhD students the concept to train them from their starting year all the way to joint papers in their final year did not materialize. However, many of the Postdocs, who attended more than one course, did mention papers done or in planning for which the new knowledge obtained through the trainings helped. All of the 16 trainees asked to fill in the survey (including three more senior PIs) handed over knowledge gained to other scientists in formal or more often in informal ways.

In total six courses were held (see box above) and 135 trainees profited formally and directly, spreading the information obtained through embedding it in courses or seminars as well as personally to at least further 161 scientists.

Overall 30 Micro B3 partners were involved in dissemination and training and many trainers were teaching in several courses, which was very helpful for the training pipeline concept. At least 18 out of 32 partners sent trainees, some to almost all of the courses. Repetitions of some courses are planned.

The Micro B3 Final Conference, organized by the Micro B3 partner Jacobs University, was held in Brussels, at the Flemish Academy of Science and the Arts, from 2nd to 5th November 2015. The objective of the Micro B3 Final Conference was to bring together policy and biodiversity stakeholders from Europe and overseas to present the project results, discuss on the project perspectives and provide key recommendations and inputs from Micro B3 researchers to the European Commission.

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## **Introduction**

As planned in the “*Updated Dissemination & Training Plan*” (D9.22), three training courses were carried out in the years 2014 and 2015.

Once the programmes were arranged, all courses were promoted via mailing lists (including an invitation to all OSD sampling site participants), via the Micro B3 website (<https://www.microb3.eu/events/workshops>) and the two held at EBI also via the EMBL-EBI website.

## **Marine Metagenomics Bioinformatics**

### **Course Preparation and Implementation**

The first course in the second period of Micro B3 was held at EBI in March 2014. This training course preceded the Ocean Sampling Day, and therefore the course objectives focused on developing the skills of site representatives as preparation. The learning outcomes for the course were:

- Identify marker gene and metagenomics data with the minimum standards required for submission to comply with the Genomic Standards Consortium (GSC)
- Discuss the merits and drawbacks of using a range of amplicon based (marker genes) and metagenomics tools including the EBI metagenomics portal
- Submit marker genes metagenomics data to public repositories
- Use bioinformatics tools to create own marine metagenomics pipelines
- Interpret results and compare them with other metagenomics datasets.

The course was organised by Jörg Peplies (Ribocon GmbH, Germany) and Laura Emery (EMBL-EBI, UK), with input from numerous other members of the Micro B3 project as well as input from members of the EMBL-EBI metagenomics team. Several teleconferences were held to discuss the focus and design of the course, and productive input was made by (Peter Sterk, EMBL-EBI, UK), Renzo Kottmann (and Antonio Fernandez – (MPI for Marine Microbiology, Germany). The EMBL-EBI host was also in charge of the logistics of the event.

The programme was designed so that approximately half of the time was dedicated to practical hands-on data analysis, with the remaining time spent on theoretical aspects of the analysis. The first day was dedicated to data submission and an introduction to Ocean Sampling Day. The second and third days were dedicated to initial data analysis of metagenomics samples, including pre-processing of NGS data, taxonomic analyses, submission to the EBI Metagenomics Portal, interpretation of results and some subsequent downstream analyses. The fourth and fifth days were devoted to downstream analyses in an ecological context, and included the use of SILVAngs, ecological analyses including

multivariate statistics, OTU networks, exploring unknown sequences and the analysis of traits.

As more applicants applied for the course than could be accommodated participants were selected on the basis of their involvement in OSD as well as on the relevance and quality of their application. Gender balance was achieved during the selection process with 14 females and 12 males accepted. The applicants that were selected also represented diverse sampling sites and nationalities; representing a total of 15 countries, including 11 from the EU.

Trainers were: Laura Emery, Petra Ten Hoopen, Alex Mitchell, Hubert Denise, Peter Sterk, Rajesh Radhakrishnan, Marc Rossello from EMBL-EBI, UK; Frank Oliver Glöckner, Jacobs University, Germany; Dawn Field, University, Oxford, Biodiversity Institute UK; Pier Luigi Buttigieg, Antonio Fernandez Guerra and Renzo Kottmann, MPI for Marine Microbiology, Germany and Jörg Peplies, Ribocon GmbH, Germany.

### **Evaluation of the 2014 Marine Metagenomics Bioinformatics Course**

All of the participants who attended the event completed the end of course survey of the event by the EMBL-EBI (Annex 1). The overall rating for the event was excellent, with 88.5% percent of participants having rated the course as either “good” or “excellent”. The session on “Ecological analyses” led by Pier Luigi Buttigieg (MPI for Marine Microbiology, Germany) was particularly well received, with 53.8% of participants having rated it as “excellent”. More than 92% of respondents stated that they will use the resources and tools presented in the future, indicating that the course content effectively covered future needs of the participants.

There were few criticisms reported by multiple participants (A1 – Q7, see Annex 1) concerning the “data submission” session which was believed to be difficult to follow. A couple of participants commented that they would have liked to spend more time on practical work. When commenting on positive aspects of the course, participants cited the ecological and statistical analyses as a particular highlight as well as the interactions with other delegates, the QIIME taxonomic analysis, and the range of tools and databases covered.

Following the course, the course materials were uploaded online to be made publically available, thus increasing the impact of the course. The materials are available via the EBI training FTP site:

[ftp://ftp.ebi.ac.uk/pub/training/2014/Micro\\_B3\\_Marine\\_Metagenomics\\_Bioinformatics](ftp://ftp.ebi.ac.uk/pub/training/2014/Micro_B3_Marine_Metagenomics_Bioinformatics)

More detail, can be found under the following link(s):

<https://www.ebi.ac.uk/training/events/2014/micro-b3-marine-metagenomics-bioinformatics>



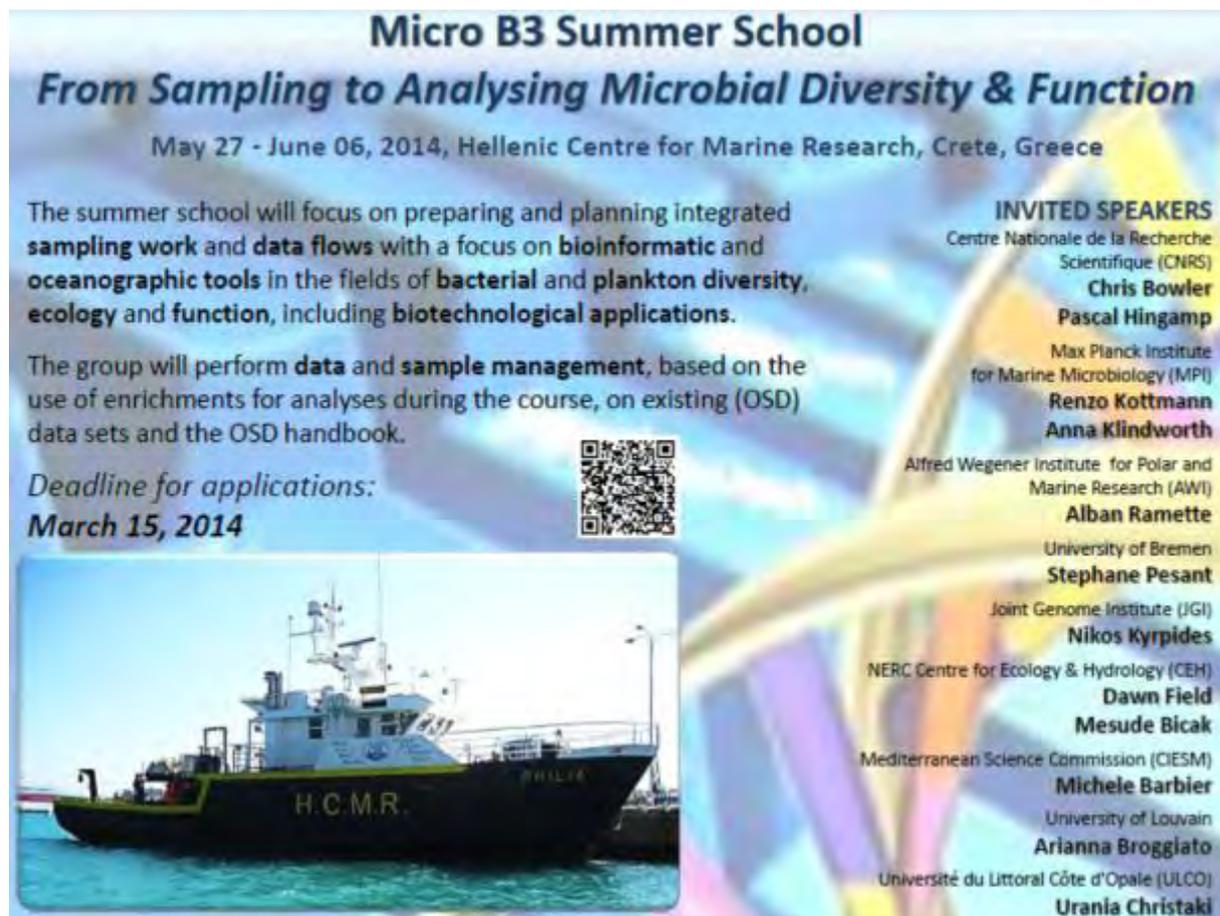
**Figure 1:** Antonio Fernàndez-Guerra's session in the EMBL-EBI computer room

## Summer School

### Course Preparation

The preparation of this two-week course started already one year before with a visit of Johanna Wesnigk, Leader of WP 9 to the HCMR host. A whole team at HCMR was committed to make the school as practical and hands-on as possible, with a mesocosm experiment set up for taking large amounts of sea water samples for filtration as well as a ship cruise to practice sampling and filtration of smaller sample sizes on board. The lab work was planned in much detail with up to three groups working in parallel and some sequencing done of samples taken during the school, by the experienced lab technician of HCMR.

The schedule or programme then went through many iterations, until all key lecturers had provided input to the content, the titles and the timing (for the final version see [www.microb3.eu/events/workshops/micro-b3-summer-school-crete/agenda](http://www.microb3.eu/events/workshops/micro-b3-summer-school-crete/agenda)). Besides lecturers from many Micro B3 partners, invited speakers from JGI in the USA, as well as CNRS- and Greek partner institutes could be committed to contribute.



**Micro B3 Summer School**  
**From Sampling to Analysing Microbial Diversity & Function**  
May 27 - June 06, 2014, Hellenic Centre for Marine Research, Crete, Greece

The summer school will focus on preparing and planning integrated **sampling work** and **data flows** with a focus on **bioinformatic** and **oceanographic tools** in the fields of **bacterial** and **plankton diversity**, **ecology** and **function**, including **biotechnological applications**.

The group will perform **data** and **sample management**, based on the use of enrichments for analyses during the course, on existing (OSD) data sets and the OSD handbook.

*Deadline for applications:*  
**March 15, 2014**



**INVITED SPEAKERS**

- Centre Nationale de la Recherche Scientifique (CNRS)  
**Chris Bowler**  
**Pascal Hingamp**
- Max Planck Institute for Marine Microbiology (MPI)  
**Renzo Kottmann**  
**Anna Klindworth**
- Alfred Wegener Institute for Polar and Marine Research (AWI)  
**Alban Ramette**
- University of Bremen  
**Stephane Pesant**
- Joint Genome Institute (JGI)  
**Nikos Kyrpides**
- NERC Centre for Ecology & Hydrology (CEH)  
**Dawn Field**  
**Mesude Bicak**
- Mediterranean Science Commission (CIESM)  
**Michele Barbier**
- University of Louvain  
**Arianna Broggiato**
- Université du Littoral Côte d'Opale (ULCO)  
**Urania Christaki**



University of Crete (UOC)  
**Ioannis Karakassis**

Technical University of Crete (TUC)  
**Nikos Paranychianakis**

Hellenic Centre for Marine Research (HCMR)  
**Christos Arvanitidis**  
**Matina Nikolopoulou**  
**Anastasis Oulas**  
**Evangelos Pafillis**  
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**OSD**  
Ocean Sampling Day

**hcmr**  
Hellenic Centre for Marine Research

The Micro B3 project is funded from the European Union's Seventh Framework Programme (Joint Call OCEAN 2011-2: Marine microbial diversity – new insights into marine ecosystems functioning and its biotechnological potential) under the grant agreement no 227569. The Micro B3 project is solely responsible for this publication. It does not represent the opinion of the EU.

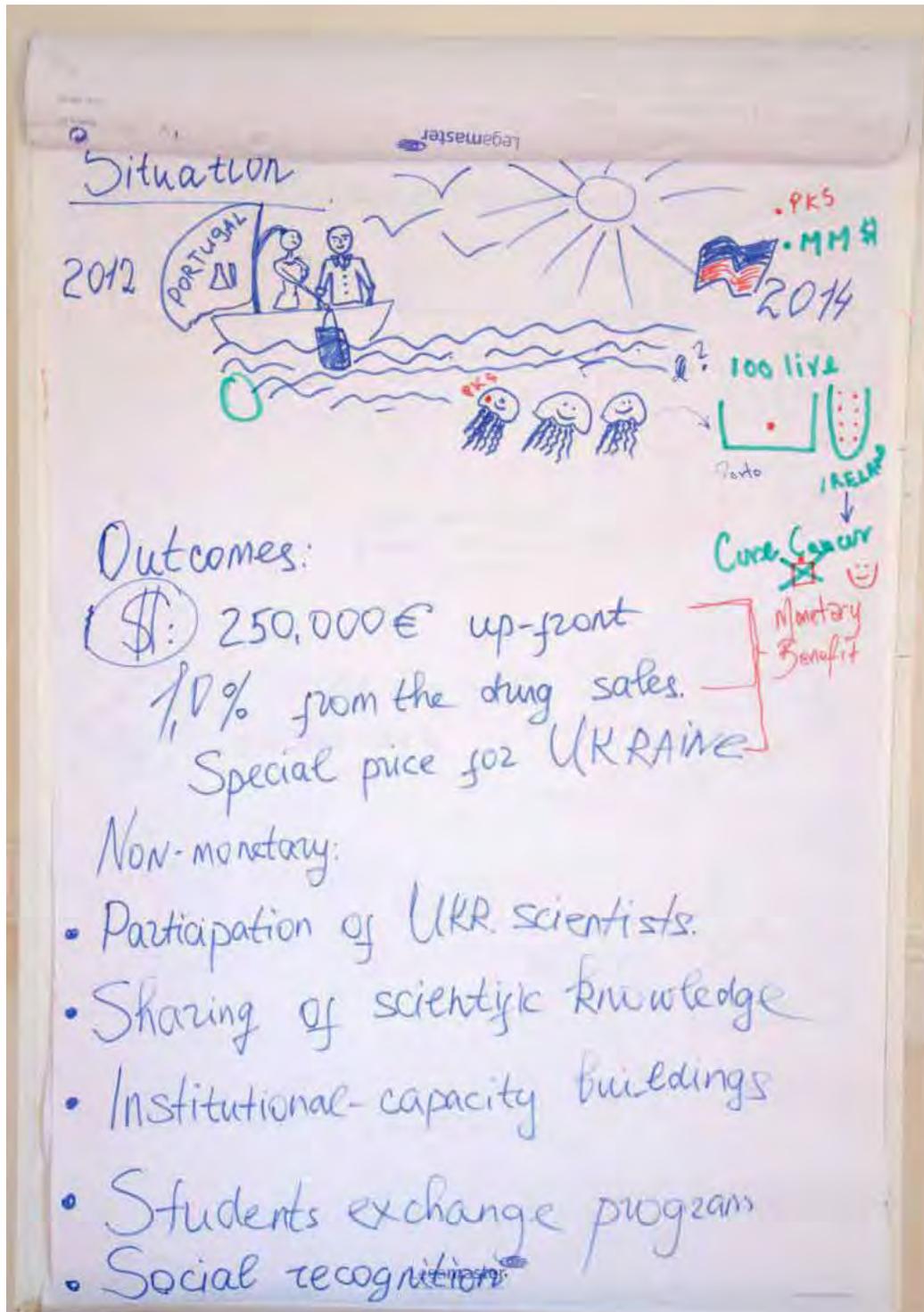
The recruitment process for trainees was done as described before with registration for the OSD running in parallel. Therefore many final adjustments had to be made. In the end 25 trainees were chosen with a gender bias towards females, as many more had applied than males, also there was a bias toward trainees from Italy, which was thought helpful as Micro B3 had only one Italian partner and thus more OSD sampling sites in the Mediterranean as well as many sites in Portugal, where Micro B3 has no partner, could be secured. Five places - on top on the originally planned 20 - were reserved for HCMR trainees, with some of them actively tutoring during the lab work and some former trainees lecturing in the bioinformatics part. In total 21 trainees attended, from several Micro B3 partners (excluding four HCMR tutors) and from the non EU-countries Turkey, Israel, Morocco and Mexico.

## Implementing the Summer School

The course ran exceedingly well with the first week packed with research activities like sampling the mesocosms, the short research cruise into Cretan waters with samples taken from two depth, an interactive role play on ABS (for one example of the four scenarios dealt with, see picture below) and lab work in two and three parallel groups on sample filtration, flow cytometry and molecular work in the afternoons. One lecturer per day set the scene and additional invited lecturers in the evenings provided further perspectives, focussing on biodiversity and biotechnological issues.

The trainees were also active in presenting posters they brought along, which explained their research and their OSD sites. A great weekend trip and a beach party helped to form a

close community, which went to many meals together and exchanged many scientific details (see final overall survey for more networking aspect).



In the second week the OSD team arrived and intertwined lectures with hands-on exercise. Especially S. Pesant from Uni Bremen /PANGAEA bridged the topics of both weeks by safeguarding that environmental data were taken, understood and entered into the OSD logsheets and databases, all based on his ample experience with the Tara Oceans cruise. P. Hingamp and Alban Ramette connected to the earlier training courses on bioinformatics and

biostatistics. They, together with Chris Bowler, who lectured in the first week, ensured a continuum between classical biodiversity research and novel tools (like MetaG, MetaT, MASAME) to understand taxonomical, ecological and functional traits.

The large OSD team ensured that relevant bioinformatics standards were understood and practiced, for example BioSharing, QIIME and SILVAngs. Also this week included reviews of the OSD handbook chapters by groups of trainees. Nikos Kyrpides, the invited speaker from the JGI, USA provided two lectures on

1. The future of microbial genomics
2. Comparative analysis methods for microbial (meta)genomes

and also discussed further cooperation options with the HCMR.

Finally an outlook on the organisation of the upcoming OSD and annotation jamboree was provided (see D9.8 for details on the Jamboree, which formed the last course of the training pipeline).

## **Evaluation of the Summer School**

For this course a similar questionnaire was used as in the first two courses, held in Bremen and reported on in D 9.6, which contains an example in its annex. The graphic results can be found in annex 2 to this deliverable. Overall 93 percent rated the summer school as meeting their expectations (to 90 or even 100 %) and as very good or excellent, only 5 % chose 70 respectively 80 %. –nevertheless the remaining and 7 % rated the overall course as good. The course length was appreciated by 85% but 10% found it only good and 5 % sufficient.

This 90 % rating was maintained throughout most of the more detailed questions on quality of presentations, course content, comparison to other courses, whereas the handouts – of which there were not that many, got 5 % poor, 15 % only good, 20 % very good and 60 % excellent. Finally, the instructors got excellent from 75 % and very good from the remaining 35 %.of the trainees, totally 100 %.

## Additional Training Course (lead UGRO)



The poster features logos for KYROBIO, Biodiversity Bioinformatics Biotechnology, and the University of Groningen. The background is a stylized molecular structure with various colored atoms.

**Masterclass "Computational Approaches for Discovery and Engineering of Enzymes for Biocatalysis and Synthetic Biology"**  
April 20-24, 2015  
University of Groningen  
Linnaeusborg, Nijenborgh 7, Groningen, The Netherlands

**Goal**  
The course aims to make students familiar with the use of computational and bioinformatics tools for engineering the biocatalytic performance of enzymes that are relevant for applied biocatalysis and synthetic biology. The course provides both a sound theoretical background on computational methods relevant to enzyme engineering (homology modeling, energy calculations, protein design, bioinformatics), and hands-on computer exercises on visualization and analysis of enzymes structures, including docking simulations. The theoretical and practical parts are integrated in a few problem-solving modules.

**Topics**  
Discovery of enzymes and design of pathways by bioinformatics approaches  
Enzyme engineering and kinetics  
Modeling and visualization of protein structures  
Use of docking and molecular dynamics simulations  
Computational enzyme (re)design  
Directed evolution with use of structural information  
Sequence- and structure-based smart libraries  
Thermostability and stereoselectivity engineering  
Industrial examples of enzyme engineering  
Short participant presentations (10-15 min)

**Tutors and teachers**  
Tom van den Bergh, Bio-Product, The Netherlands  
Jiri Damborsky, Masaryk University, Czech Republic  
Dick Janissen, University of Groningen, The Netherlands  
Rene de Jong, DSM, The Netherlands  
Marcelo Masman, University of Groningen, The Netherlands  
Marrix Modama, MPI Bremen, Germany/University of Wageningen, The Netherlands  
Nick Turner, University of Manchester, United Kingdom  
Hein Wijma, University of Groningen, The Netherlands

**Masterclass coordination**  
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Sandra Haan & Tamara Hummel, GBB, University of Groningen, The Netherlands

[Further information and application](#)  
Deadline application March 1, 2015

The one-week course aimed to make students familiar with the use of computational and bioinformatics tools for engineering the performance of enzymes that are relevant for applied biocatalysis and synthetic biology. This is done in order to promote better use of bioinformatics and computational tools in a biochemistry laboratory environment and to stimulate the development and use of (better) prediction tools for improving biocatalyst performance, based on functional screening, genome mining and gene synthesis. The overall programme consisted of lectures in the morning by various speakers who presented the essential principles of computational methods and recent highlights from their own research. Speakers were affiliated to the EU project KyroBio (FP7; <http://www.kyrobio.eu/>; KyroBio Deliverable Report D.6, submitted), Micro B3 (FP7), ROBOX (from the H2020

program; <http://www.h2020robox.eu/>), BE-Basic (an international Dutch program; <http://www.be-basic.org/>), or to other networks, and their partner organizations, both from industry and academia. The KyroBio coordinator Prof. Nick Turner gave a keynote lecture in which the great opportunities and future prospects of biocatalysis were well explained for a large audience of biochemists and organic chemists.

The afternoon sessions were computer exercises on visualisation of protein structures, performing molecular docking simulations, computational design of stabilizing disulfide bonds, and running MD simulations (given by Dr. Marcelo Masman and Dr. Hein Wijma, Micro B3 partner UGRO) and the use of the 3DM database (given by Tom van den Bergh, Micro B3 partner BioProduct), in part supported by Dr. Rene de Jong (DSM). Dr. de Jong also provided detailed insight in the use of computational tools for enzyme engineering in an industrial setting.

## Use of bioinformatics and computational tools in a biochemistry laboratory environment



### Finding a new/better biocatalyst

- Blast: thermophilic and marine sequences, PDB
- Multiple sequence alignments
- Homology modeling
- Docking
- Molecular dynamics

- ▶ uncertainty of project outcomes
- ▶ to be used by non-specialists

- a.m. lectures
- p.m. hands-on computer classes
- Practical examples: convincing
- Biophysics: basic
- Awareness
- Usability

### IGEM competition



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In total 29 trainees (PhD students and postdocs) attended this course. All participants but one (illness) completed the theoretical and practical parts of the course and received on day 5 an official University of Groningen (GBB) certificate.

The course was well appreciated, as indicated by the scores collected from the evaluation forms (see below). Some comments and hints of the participants for future editions included:

- Positive comments about the masterclass (8);
- Improve instructions for using Linux (7);

- Improve support with computer training (2); Positive comments about MD, docking (2); and Discuss answers to exercises (2);
- Provide info on suggested reading.

The hints will be carefully considered for future editions of this course. It will likely be offered on a 2-year basis.

		Poor	Neutral	Good	Very good	Excel				
Bioinformatic tools for enzymatic pathway discovery										
	Content	0	0	6	14	6				
Computational tools for the synthetic biology design of metabolic pathways										
	Content	0	0	9	12	5				
Structure-based engineering										
	Content	0	0	9	14	4				
Molecular dynamics										
	Content	0	1	3	14	8				
Computer training: Visualisation disulfide bond design (Monday, April 20)										
	Content	0	3	10	11	3				
	Support	0	2	10	11	3				
Concept of modeling and prediction										
	Content	0	0	1	15	10				
Software tools for tunnels and hot spots										
	Content	0	0	2	13	12				
Docking simulations										
	Content	0	0	5	14	7				
Computer training: Docking simulations (Tuesday, April 21)										
	Content	0	10	4	12	10				
	Support	0	0	6	12	9				
Computational Design										
	Content	1	5	14	6	1				
Computer training: Enzyme stability engineering										
	Content	0	3	11	7	5				
	Support	0	3	9	11	2				
Directed evolution for biocatalysis										
	Content	1	1	5	12	9				
Biocatalytic retrosynthesis										
	Content	3	2	5	11	7				
Engineering nature's enzyme repertoire for food and pharma										
	Content	0	1	7	14	5				
Enzyme specificity redesign using coupled protein side-chain and backbone flexibility										
	Content	0	1	8	12	6				
Computer training: Selectivity engineering and MD simulations (Thursday, April 23)										
	Content	0	2	8	15	3				
	Support	1	3	4	15	5				
Sequence and structure-inspired protein engineering using 3DM databases										
	Content	0	1	8	14	4				
Computer training: 3DM databases										
	Content	0	1	11	10	1				
	Support	1	2	6	11	2				
Computer training: 3DM databases Wrap up (Friday, April 24)										
	Content	0	1	8	6	0				
	Support	0	3	2	7	2				
Lecture room										
	Facilities	0	1	4	14	7				
	Convenience	1	3	3	14	6				
Computer room										
	Facilities	0	1	3	13	11				
	Convenience	0	2	4	12	10				
The course was well organized										
	Content	0	0	3	12	13				
The syllabus was clear										
	Content	1	1	4	12	10				
Catering lunch										
	Quality	0	2	4	15	6				
	Convenience	0	0	3	17	7				
Catering dinner										
	Quality	0	0	1	12	14				
	Convenience	0	0	3	10	14				
In general I would give this course the following mark										
	1	2	3	4	5	6	7	8	9	10
	0	0	0	0	0	0	4	9	10	4

## **Overall Evaluation of the Training Pipeline**

In the last months of the Micro B3 project a short questionnaire, based on EBI experience and adapted to Micro B3 needs, was circulated to all trainees who had attended two courses or more as well to a few who attended only one course, but whose feedback was deemed interesting (see annex 3 for the questionnaire).

Most of them replied in a rather enthusiastic way, showing how they used the knowledge for further training, mainly in their native languages and that the networking was working. A few more senior trainees who had only attended one course were contacted from Mexico, Ukraine and Italy, to find out how they used the knowledge obtained for further spreading. In the table below all replies are listed, split into two groups, first the Post Docs and senior investigators (PI) then the PhD students. The courses they attended were numbered 1 – 5 according to this order:

1. Bioinformatics for beginners (2012, Bremen, DE)
2. Biodiversity statistics (June 2013, Bremen, DE)
3. Metagenome analyses (Spring 2014, EBI Training Centre, UK)
4. Interdisciplinary summer school (May/June 2014, Crete, GR)
5. Micro B3 OSD Analysis Workshop/Jamboree (March 2015 at EBI Training Centre, UK)

Most of the 13 persons who replied attended two of the courses 3 to 5, or, in three cases, even all three. Only two persons attended the first and the second course and one person the first and third training. Three persons who had attended only the summer school were additionally asked to fill in the survey, as they were experienced PIs and one had come to support her PhD student and thus ensure better spreading. In total 17 persons were contacted and 16 replied.

Most had been working in both or one of the research fields marine ecology and/or bioinformatics before, but a few started to work more in one or both of this fields after attending the training, so the training helped two PhD students and one classical, more senior marine ecologist to get more familiar with bioinformatics (with NGS protocols explicitly mentioned in one case). With one exception, 15 trainees keep using the resources presented and taught.

Asked about publications, also in planning, or grant proposals accomplished as result of course attendance in total 13 grant proposals were listed with relation to the Micro B3 trainings, some as travel grants, some in collaboration, and not all had been successful. 10 papers were published and one poster, and at least four further publications are in planning – sometimes the replies were not quantitative and also, papers on the OSD results were mentioned several times.

Even if only 50 % of the Postdocs had already published papers based on the experience gained through the courses, many including the PhD students, assured that the knowledge

gained was useful to them and to colleagues and would lead to publications eventually. Especially noteworthy are the many mentioning of different informal ways in which the knowledge was handed over to colleagues and staff in the home institutions which included individual tutoring and well as an one-hour seminar for the working group. In total at least 67 persons were trained informally (12 replies) and 63 formally (4 replies), some did not specify the exact number. Some more senior trainees used the knowledge obtained for training their whole group or inserting it into curricula of regularly held MSc courses, and very often the dissemination was done in the native language. One Postdoc had even used the knowledge in an outside training in Vietnam he was involved in directly after the summer school.

The network formed between trainees and with several lecturers was very active, with some visits made by HCMR trainees, i.e. to the MPIMM in Bremen, PhD student exchanges planned and one Postdoc from Italy now based in Spain, as well as other links between trainees, who are planning or doing joint research (within Portugal, between Italy and Israel) and with lecturers.

14 of the 16 pipeline trainees replied positively about the need for additional or repeat training courses, two did not reply to this question, and nobody said no. Further topics in which training might be useful could be: (meta)transcriptomics, ecological statistics (training on 'R' was mentioned several time as being highly useful) and further jamboree-style work on the 2015 OSD data or a hackathon.

Several persons showed their willingness to organize a similar training in coming years, if funding can be found. Some quotes from trainees are shown in the text box and a systematic overview can be found in the table below.

With these courses we were actually able to start analysing NGS data that we were not able before!  
I published a paper and another has been submitted (OSD-unrelated) also due to these precious information (stats, R).  
We included in the marine microbiology course, OSD protocols for sampling and sending samples for metagenomics.

### Micro B3 Training Pipeline Evaluation Survey Feedback (Summary)

Name, country	Courses	Working in fields of mar. ecol./ bioinfo)	Use of resources to date	Publish or write Grant	Formal training home-lab	Informal training home-lab	Collaborations with other participants or lecturers	Wish for additional / repeat trainings	Other important details
		<i>Before / after</i>	<i>Yes, b, c, d</i>	<i>P, G, P.i.pl.</i>	<i>No of persons</i>	<i>No of persons</i>	<i>Including informal networking</i>	<i>Yes /No, topic</i>	
<b>Postdoc, PI:</b>									
Male, Greece	1, 2	Yes for both	No	No	-	5	-	Yes	Was not able to use tools as not available in the internet
Male Iceland	1, 2	Yes for both	Yes	P.i.pl.	-	5	Yes	-	
Male, Italy	4, 5	Yes for both	Yes	2 P; Several P.i.pl.	-	3	only informal networking	Yes, ecology & statistics	Used knowledge for bioinfo. MSc course in Vietnam; R especially useful
Female, Portugal	4, 5	Yes for both	Yes	3 P, 6 G	-	5 colleagues & at least 4 students	Formally (planned PhD supervisor) PhD student exchanges	Yes, transcriptomics	Started NGS data analysis pipeline; Increasing possibilities for publication
Female, Italy	3, 4, 5	Yes for both	Yes	2 P.i.pl. 1 Poster	-	1	Part of OSD analysis proposal group	Yes	Now working on DNA-meta barcoding
Female, Italy	3, 4, 5	Yes for both	Yes	Several P.i.pl.	-	10	only informal networking	Yes, meta-transcriptomics	
Male, Greece	3, 4, 5	Yes for both	Yes	2 P, 1 G	10	-	Semi-formal network established (grant); conference contribution	Yes	
<i>Male, Italy (PostDoc)</i>	4	-	Yes	1 P, 1 G, 1 P.i.pl.	-	6	<i>Only informal networking</i>	-	<i>Joint research with trainee from Israel</i>
<i>Female, Ukraine (PI)</i>	4	<i>Yes for both</i>	Yes	1 G	-	40 (only 1 hour)	Yes	Yes	
<i>Female Mexico (PI)</i>	4	-	Yes	1 G, 1 P	13		<i>only informal networking</i>	<i>Yes, ecol. microbio. &amp; bioinfo.</i>	<i>Elements of summer school included in regular courses</i>
<b>Subtotals (10 persons)</b>	-	<b>8 yes for both</b>	<b>9 yes 1 no</b>	<b>9 papers 10 grants min. 4 P.i.pl.</b>	<b>23 persons (2 replies)</b>	<b>79 Persons (8 replies)</b>	<b>2 yes 4 informal networking 1 (semi)-, 2 formal collab.</b>	<b>8 yes</b>	

Name, country	Courses	Working in fields of mar. ecol./ bioinfo)	Use of resources to date	Publish or write Grant	Formal training home-lab	Informal training home-lab	Collaborations with other participants or lecturers	Wish for additional / repeat trainings	Other important details
<b>PhD-Students:</b>									
Female Great Britain	1, 3	Yes for both	Yes	No	No	4	No	Yes	Initial assessment of raw data
Female, Greece	3, 4	No before Yes afterwards	Yes	No	-	Yes only basic	only informal networking	Yes, hackathon	
Female, Morocco	3, 4	No before Yes afterwards	Yes	3 G	40 (for 3 hours)		only informal networking	Yes, for extended summer school	Did 3 presentations during a conference in Morocco; wish for longer courses
Male, Belgium	3, 5	Yes for both	Yes	1 P	-	1	only informal networking	Yes	
Female Turkey	4, 5	-	Yes	-	-	5	only informal networking	Yes	Asks for Jamboree on 2015 OSD data
Female Portugal	4, 5	Yes for both	Yes	-	9	-	Yes with 3 scientists	Yes	Will compare OSD data with regional data in PhD
<b>Subtotals (6 persons)</b>	-	<b>3 yes for both 2 no before/yes after</b>	<b>6 yes</b>	<b>1 Paper 3 Grants 2 no</b>	<b>49 (2 replies)</b>	<b>Min. 10 (4 replies)</b>	<b>1 formal collaboration 4 informal networking 1 no</b>	<b>6 yes</b>	
<b>Totals (16 persons)</b>	-	<b>11 yes for both 3 no before/yes after</b>	<b>15 yes 1 no</b>	<b>10 Papers 13 Grants Min. 4 P.i.pl. 1 Poster</b>	<b>72 persons (4 replies)</b>	<b>89 persons (12 replies)</b>	<b>3 formal collaborations 1 semi-formal collaboration 8 informal networking 2 yes 1 no</b>	<b>14 yes, different topics provided</b>	

**Legend: P = Publication; G = Grant P.i.pl. = Publication in planning**

Note: if a trainee has published a paper this does not mean that the paper is related to the Micro B3 project

## **Final Overview**

In total six courses were held in which 135 trainees were trained formally and directly (equalling 17 persons less, due to the pipeline concept). At least 161 more profited from the Micro B3 training, in an indirect way, as described above, informally and formally (72 persons were formally trained and 89 persons informed through seminars, workshops or other means). A precise number is hard to establish, as for example during the summer school two PhD students and two Postdocs contributed to the training as well as being trained themselves. Also, during the final jamboree, there was a training team of 11 persons training 29 jamboree participants, some of them rather experienced persons from partners and even including a member of the Micro B3 advisory board.

1. Bioinformatics for Beginners (2012, Bremen, DE, 11 trainees)
2. Biodiversity Statistics (June 2013, Bremen, DE, 21 trainees)
3. Marine Metagenomics Bioinformatics (Spring 2014, EBI Training Centre, UK, 24 trainees)
4. Multi-disciplinary Summer School (May/June 2014, Crete, GR, 21 trainees, four local tutors)
5. Micro B3 OSD Analysis Workshop/Jamboree (March 2015 at EBI Training Centre, UK, 30 trainees)
6. KyroBio Masterclass (Spring 2015, Univ. Groningen, NL, 28 trainees)

Overall 30 Micro B3 partners were involved in dissemination and training and many trainers were teaching in several courses, which was very helpful for the training pipeline concept:

- A large team from the EMBL-EBI, led by Laura Emery
- Pascal Hingamp, Chris Bowler (CNRS) , Stephane Pesant (Uni Bremen)
- Pier Luigi Buttigieg & Alban Ramette
- Renzo Kottmann & Antonio Fernandez-Guerra and more persons from the MPI & Jacobs teams (also for industry workshops)

At least 18 out of 32 partners sent trainees, some to almost all of the courses (CNRS; CSIC, HCMR, SZN/CNR). This is a high number as not all partners have staff for which the course topics were useful, for example the legal team.

A repeat of the summer school would be possible, for example at HCMR but also other trainees showed interest, if funding can be found. Further OSD data analysis meetings are in the pipeline around OSD analysis teams which formed as one result of the 2015 course.

## **Micro B3 Final Conference**

The Micro B3 Final Conference, organized by the Micro B3 partner Jacobs University, was held in Brussels, at the Flemish Academy of Science and the Arts, from 2<sup>nd</sup> to 5<sup>th</sup> November 2015. The objective of the Micro B3 Final Conference was to bring together policy and biodiversity stakeholders from Europe and overseas to present the project results, discuss on the project perspectives and provide key recommendations and inputs from Micro B3 researchers to the European Commission.

The conference brought together people from 46 institutions, including high-level guests and invited speakers. The Conference programme included six sessions, with a total of 35 talks (8 from invited speakers). The full reader of the conference, including the programme, abstracts of all talks and other information are available in the Annex 4.

## **Planning Phase and Development of Content**

The Organization Committee was composed of:

Frank Oliver Glöckner, Jacobs University

Marianna Mea, Jacobs University

Sandra Nowack, Jacobs University

The first outline of the Conference was presented to the Micro B3 partners during the EEB Meeting that took place on 13-14 January 2015, in Bremen (Germany). The Committee, took into account the feedback from the EEB and the Advisory Board, and set a doodle poll to identify the more suitable dates. The Committee selected the venue after a visit in Brussels in April.

## **Organization**

With the support of M. Barbier (CIESM) and R. Kottmann (MPIMM), and feedback from the WP leaders, the Committee selected the invited speakers and defined the final programme. It was decided to embed the Third Industry Workshop into the Conference to use the forum of the final conference as an outreach platform. The programme included also the showcase of the Micro B3 documentary film and the OSD movies.

Jacobs University planned and managed all local elements in Brussels (venue logistic and meals) and took care of collecting detailed information of speakers and abstracts of talks for the reader to be distributed to all participants at the meeting (available for download at the following link

[https://microb3.eu/sites/default/files/pdf/Micro%20B3%20Final%20Conference%20Reader\\_low%20res.pdf](https://microb3.eu/sites/default/files/pdf/Micro%20B3%20Final%20Conference%20Reader_low%20res.pdf) and included in this report as Annex 4. EMPA was in charge of the press work for the entire conference and for the workshop.

## Promotion Phase

The promotion of the Conference has been done through the following channels:

- The programme was published on the Micro B3 website under “events” and “meetings” and the registration was open on the Micro B3 website dedicated section from July 2015 on.
- Jacobs University sent personal invitations for the Micro B3 Final Conference and the workshop to other EU projects, members from the EU parliament (Industry, Research and Energy Committee), representatives of the European Commission
- The Conference (and the workshop) announcement was also sent to different EU-associations and networks: European Science Foundation, European Network of Marine Research Institute and Stations, European Society for Biotechnology, EuropaBio, EuroMarine, European Marine Biotechnology ERA Net
- The announcement was published on Micro B3 project website and social networks, and was sent via email to all Micro B3 partners and AB members.
- Jacobs University announced the conference on the CORDIS website

[http://cordis.europa.eu/event/rcn/143655\\_en.html](http://cordis.europa.eu/event/rcn/143655_en.html) (Annex 5) and on the University website: <https://www.jacobs-university.de/news/bremen-brussels-micro-b3-final-conference>

- It also appeared on websites from SubMariner Network, EurOcean event section and of the German Federal Ministry of Education and Research
- EMPA compiled a media contact list, focussing on German and other media representatives in Brussels who were informed on the project, the conference and the workshop, based on the press releases, including one reminder
- A press release in English and German (Annex 6) for the Micro B3 final conference was spread to IDW, a German-based scientific bi-lingual information service with the objective to promote the presence of science and research in public and in the media. The English version: **Tracking and Tracing the Smallest Marine Life Forms"** <http://idw-online.de/en/news638455> was actively sent to **11588** subscribers of this list, thereof **2910** classified as media, and 208 thereof as journalists, specially accredited with IDW. The German version: **Konferenz in Brüssel: Auf den Spuren kleinster Meereslebewesen"** <http://idw-online.de/de/news638453> was actively sent to **15913** subscribers of this list, thereof **3920** classified as media, and 288 thereof as journalists, specially accredited with IDW. Probably there is a strong overlap between the two lists.
- Jacobs published a news and press release on the Final Conference and the workshop on 27<sup>th</sup> October and 25<sup>th</sup> November 2015  
<https://www.jacobs-university.de/news/bremen-brussels-micro-b3-final-conference>  
[https://www.microb3.eu/sites/default/files/media\\_material/press\\_release/Pressemitteilung%20-%20Medizin%20aus%20dem%20Meer\\_0.pdf](https://www.microb3.eu/sites/default/files/media_material/press_release/Pressemitteilung%20-%20Medizin%20aus%20dem%20Meer_0.pdf)

## **Implementation phase**

During the Conference, Micro B3 members highlighted the worldwide attention the project has already received and reported the achievements of each Work Package.

- The 80 plus peer-reviewed publications from the project reflect its significant contribution to the advancement of science
- The Micro B3/OSD aligns nicely with the ongoing discussions on creating the Unified Microbiome Initiative (UMI) or an International Microbiome Initiative (IMI)
- Micro B3's two world-wide Ocean Sampling Days (OSD) and its citizen science campaign MyOSD can be considered a proof of concept for the main issues denoted, like standardisation for comparative data analysis and data sharing, internationality, interdisciplinary, training, as well as a solid legal framework with respect to the recently ratified Nagoya Protocol to the Convention on Biological Diversity
- This Protocol is an important cornerstone to provide a solid legal framework on Access to and Benefit Sharing (ABS) of marine genetic resources as outlined and emphasized by an illustrative talk by Chris Lyal from the Natural History Museum, London
- As invited speaker and Advisory Board Member Linda Amaral Zettler (Woods Hole, USA) highlighted promising US-American initiatives dealing with the high diversity of marine microorganisms - some finished, and some running in parallel - but all fuelling world-wide microbiome data comparisons for better understanding biodiversity and functions. This was complemented by a fascinating talk of Colomban de Vargas (CNRS, Roscoff) on results of the TARA Oceans circumnavigations, which brought to our attention the incredible biodiversity within the marine micro-, phyto- and zooplankton
- Tom Redd from the European Joint Programming Initiative JPI Oceans presented their wide-ranging pilot actions, into which future OSDs might fit well. Simon Claus and Angel Borja outlined how Micro B3 integrates well with the ongoing DEVOTES project and the recently started infrastructure project AtlantOS
- Kicked off by Torger Børresen from the ERA-NET Marine Biotech the conference continued with presenting many biotechnological results relevant for blue growth
- The embedded third industrial expert workshop of Micro B3 with invited speakers from several successful SME's and industry (reported in the Deliverable 9.9) paved the way on how to collaborate to better exploit diverse value chains with marine inputs.



### **Follow-up**

- A “Thank you” note was sent after the Conference to all the attendees, highlighting the success of the event.
- Pictures and pdf version of the presentations given during the Conference are available at the link:

<https://owncloud.mpi-bremen.de/index.php/s/p9i8lr5NU7GPgv5>

- A press release was published by Jacobs University on Cordis:  
[http://cordis.europa.eu/news/rcn/129194\\_en.html](http://cordis.europa.eu/news/rcn/129194_en.html) (Annex 7).

All abstracts and further information were made available as a reader for all participants of the final conference (Annex 4).

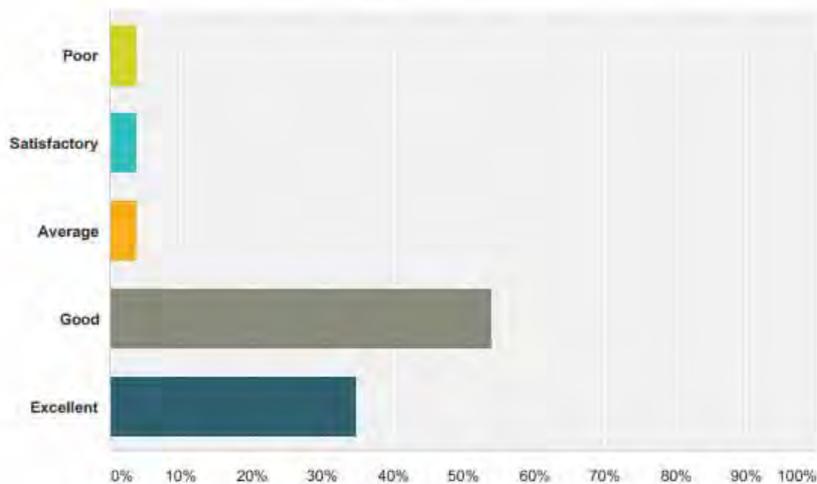
## Annexes

### Annex 1: Evaluation of the EBI Metagenomics Bioinformatic Analysis Course

Questions 1 to 3 pertain to administrative matters (Q1 “Name”, Q2 “Email”, Q3 “May we contact you by email in future to take part in usability testing / interviews/surveys or other user research activities?”). Results for questions Q4 to Q11 were the following:

#### Q4 Please tell us your overall rating for the entire course.

Answered: 26 Skipped: 1



Answer Choices	Responses	
Poor	3.85%	1
Satisfactory	3.85%	1
Average	3.85%	1
Good	53.85%	14
Excellent	34.62%	9
<b>Total</b>		<b>26</b>

#### Q5 Please rate each section of the course.

Answered: 26 Skipped: 1

Marine Microbial Biodiversity, Bioinformatics and Biotechnology

D9.10: Final Overall Report on Bioinformatic Training Pipeline and on the Final Conference

	Did not attend	Poor	Satisfactory	Average	Good	Excellent	Total
Day 1: Course introduction and case study with ribosomal RNA diversity analysis(lecture and hands-on, SILVA & SILVAngs)	0.00% 0	0.00% 0	0.00% 0	0.00% 0	69.23% 18	30.77% 8	26
Day 1: Keynote about Ocean Sampling Day and Genomic Observatories	0.00% 0	0.00% 0	3.85% 1	7.69% 2	61.54% 16	26.92% 7	26
Day 1: Standards for data submission including the Ocean Sampling Day handbook	0.00% 0	0.00% 0	3.85% 1	34.62% 9	38.46% 10	23.08% 6	26
Day 2: Introduction to NGS (Lecture)	0.00% 0	0.00% 0	3.85% 1	15.38% 4	42.31% 11	38.46% 10	26
Day 2: Considerations for metagenomics data analysis	0.00% 0	0.00% 0	3.85% 1	15.38% 4	46.15% 12	34.62% 9	26
Day 2: Command line warm up	0.00% 0	3.85% 1	7.69% 2	11.54% 3	34.62% 9	42.31% 11	26
Day 2: Quality control (Lecture) + Quality control (trimming, primers, FASTQC) (hands-on)	0.00% 0	0.00% 0	11.54% 3	19.23% 5	46.15% 12	23.08% 6	26
Day 2: Taxonomic analysis of amplicon and shotgun data (lecture)	0.00% 0	0.00% 0	3.85% 1	11.54% 3	57.69% 15	26.92% 7	26
Day 2: Taxonomic analyses: Qiime tutorial 1 (Hands-on)	0.00% 0	0.00% 0	15.38% 4	7.69% 2	50.00% 13	26.92% 7	26
Day 2: Taxonomic analyses: Qiime tutorial 2 (Hands-on)	0.00% 0	7.69% 2	7.69% 2	7.69% 2	50.00% 13	26.92% 7	26
Day 2: Data visualization using emperor (Hands-on)	3.85% 1	7.69% 2	7.69% 2	7.69% 2	57.69% 15	15.38% 4	26
Day 3: Metagenome assembly (Lecture/hands-on)	0.00% 0	7.69% 2	7.69% 2	26.92% 7	42.31% 11	15.38% 4	26
Day 3: An introduction to the EBI Metagenomics portal (EMG)	0.00% 0	0.00% 0	7.69% 2	23.08% 6	46.15% 12	23.08% 6	26
Day 3: InterPro and GO for functional analysis of metagenomic data (Lecture)	0.00% 0	3.85% 1	0.00% 0	23.08% 6	50.00% 13	23.08% 6	26
Day 3: Functional analysis using EMG (Hands-on)	0.00% 0	7.69% 2	3.85% 1	15.38% 4	50.00% 13	23.08% 6	26
Day 3: Analysis of metagenomics data using R (hands-on)	3.85% 1	3.85% 1	7.69% 2	23.08% 6	38.46% 10	23.08% 6	26
Day 3: Introduction to ENA	0.00% 0	0.00% 0	7.69% 2	26.92% 7	42.31% 11	23.08% 6	26
Day 3: Using Webin for online data submission (hands-on)	0.00% 0	3.85% 1	3.85% 1	30.77% 8	46.15% 12	15.38% 4	26
Day 3: Data retrieval	0.00% 0	11.54% 3	3.85% 1	15.38% 4	53.85% 14	15.38% 4	26
Day 4: Exploring results from SILVAngs taxonomic analysis (hands-on)	0.00% 0	7.69% 2	7.69% 2	11.54% 3	38.46% 10	34.62% 9	26
Day 4: Bringing data into environmental context: the Micro B3 Information System (lecture and hands-on)	0.00% 0	3.85% 1	3.85% 1	23.08% 6	38.46% 10	30.77% 8	26
Day 4: We have the OTUs, so what now? Ecological analysis (lecture and hands-on)	0.00% 0	3.85% 1	3.85% 1	15.38% 4	23.08% 6	53.85% 14	26
Day 4: We have the OTUs, so what now? Building and exploring OTUs co-occurrence networks (lecture and hands-on)	0.00% 0	7.69% 2	3.85% 1	19.23% 5	30.77% 8	38.46% 10	26
Day 5: Exploring the dark side of the metagenomes: a look at the unknowns (lecture and hands-on)	0.00% 0	7.69% 2	7.69% 2	15.38% 4	46.15% 12	23.08% 6	26
Day 5: Taverna workflows: Trail-based ecology and metagenomes (lecture and hands-on)	0.00% 0	7.69% 2	11.54% 3	11.54% 3	50.00% 13	19.23% 5	26

### Q6 What was the best part of the course?

Answered: 26 Skipped: 1

#	Responses	Date
1	the interaction with the rest of the people, the wonderful environment at EBI.	3/15/2015 11:54 PM
2	SILVA and NGS software, Metagenome assembly also the lecture about OSD	3/29/2014 5:07 PM
3	Qimme hands-on	3/28/2014 2:38 PM
4	The reference materials, take home files, tutorials, etc.	3/28/2014 2:05 PM
5	The best part for me was the statistical analyses of the OTUS, Best lecture by Pier.	3/28/2014 1:58 PM
6	Taxonomic analyses with Qiime (tutorials)	3/28/2014 1:57 PM
7	Use of QIIME Explanation of R potential for ecological analysis when you have the OTUs	3/28/2014 1:56 PM
8	The best part of the course was the hands on experience with QIIME	3/28/2014 1:56 PM
9	The overall view about what can be done with our data in several software's and tools of data analysis. The ambience was very good and the hospitality	3/28/2014 1:56 PM
10	I would say the Silvangs	3/28/2014 1:56 PM
11	d	3/28/2014 1:54 PM
12	Having pipelines, workflows, scripts and data examples I can take back to my institute to analyze and continue learning. It was a great kickstart to all the techniques and analysis tools I need to do my pHd thesis. I specially liked the part from Pier-Luigi Bersani, and the topics covered by Antoni (Network Analyses).	3/28/2014 1:54 PM
13	Multivariate statistics and network analysis lectures.	3/28/2014 1:54 PM
14	The stats for PCA plots and the networks anlysis	3/28/2014 1:54 PM
15	I especialtz liked the first part when we realiz worked with the raw sequence data.	3/28/2014 1:53 PM
16	Organisation was fantastic.	3/28/2014 1:53 PM
17	The data preparation with R comands.	3/28/2014 1:52 PM
18	Ecological, Taxonomical and statistical and analysis parts	3/28/2014 1:52 PM
19	Having the possibility to get a deeper knowledge regarding some already known frameworks and having the possibility of digging deep into the use of Qiime, for instances, which I personaly did not know. Also, I found the Quality Control part of the course very useful.	3/28/2014 1:51 PM
20	The introduction to various tools that are commonly used in metagenomic analysis.	3/28/2014 1:51 PM
21	the big range of available databases shown and explained	3/28/2014 1:50 PM
22	balance between lectures and tutorials	3/28/2014 1:49 PM
23	The part related to the statistical analyses	3/28/2014 1:49 PM
24	Statistical Analysis	3/28/2014 1:47 PM
25	statistics using R	3/28/2014 1:46 PM
26	Statistical Analysis	3/28/2014 8:48 AM

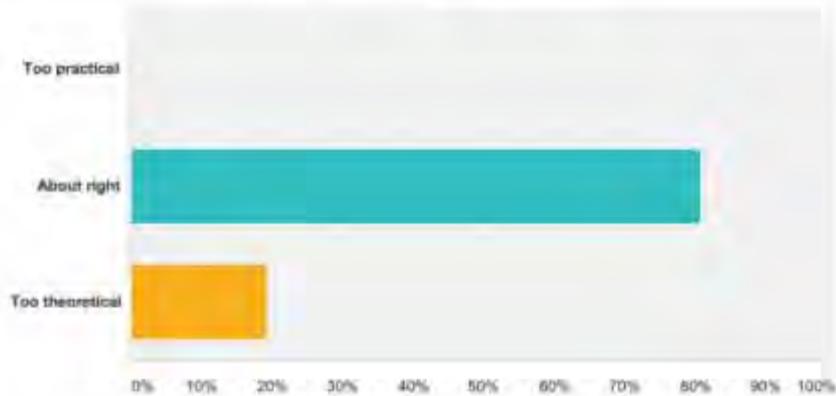
Q7 What was the worst part of the course?

Answered: 26 Skipped: 1

#	Responses	Date
1	I would have liked more hands-on than lectures.	3/15/2015 11:54 PM
2	There was no worst part, just at the end of the course, it was a bit hard to follow the professor and unfortunately it was a very important hand on to do.	3/29/2014 5:07 PM
3	Assembly hands-on	3/28/2014 2:38 PM
4	the limited time and rapid pace of the hands-on computer work, especially, with R, cytoscape, Taverna, etc.	3/28/2014 2:05 PM
5	I think some tools were a bit confusing because not enough background was provided. Some sessions were just a sequence of command lines (sometimes too fast) without much reasoning about why and what exactly we were doing. The lecturers know a lot, but sometimes they have a bad time putting themselves in our place! If I may suggest something, it would be to use a simple, small subset of a real data set and go through the course with it. I am a little disappointed because I thought I would have this type of notion - from raw data to the statistical analysis and presentation.	3/28/2014 1:58 PM
6	Metagenome assembly (Lecture/hands-on)	3/28/2014 1:57 PM
7	Metagenome assembly Analysis of metagenomics data using R	3/28/2014 1:56 PM
8	The worst part of the course was the ENA/data submission/date retrieval part, as it was too explanatory with too many details	3/28/2014 1:56 PM
9	Don't have the opportunity of discuss our results in detail with the speakers, and don't use the examples of our own data. I was rdesapointed for sometimes don't have the opportunity to submit my data.	3/28/2014 1:56 PM
10	It was a pity that towards the end of course some of the lectures were already not in place to help around with some questions, it was just at the very end that I got to analyse my data and thus nobody to explain me all sorts of errors popping out!!!	3/28/2014 1:56 PM
11	d	3/28/2014 1:54 PM
12	I believe the introduction was too long .Specially since it didnt covered pros and cons of using different approaches and techniques, something I would really have found usefull.	3/28/2014 1:54 PM
13	There could be a bit more explained on the recent metagenomic assembly tools and benchmark results to pick up the current best.	3/28/2014 1:54 PM
14	too much info on ocean sampling data submission, not enough time for stats and networks	3/28/2014 1:54 PM
15	All the dataset we explored were tested and curated in a way that they were guaranteed to work. However, data usually doesn't look like this. I was missing the part of how to generate the right input files (especially for the sessions during the last 2 days of the course). Besides, it would have been nice to really go from A to Z of the analysis on one dataset - and to learn how to deal with arising problems. Sometimes the workflow seemed a bit fragmented. It would be a good idea to include the option of having some time to analyse your own data (maybe as an extra course or an extension to the course - I know that time is always a limiting factor)	3/28/2014 1:53 PM
16	found everything was ok.	3/28/2014 1:53 PM
17	In the case of the workflows, we haven't a time to make the correct learning.	3/28/2014 1:52 PM
18	Submission data part not exiting	3/28/2014 1:52 PM
19	I do not have a lot of experience neither with the Unix command line and R, but I found it harder to keep up with the tutorials involving R than with the command line. Maybe if I had more experience, I'd have absorbed much more from that part, but other than that, I think the course was very well structured.	3/28/2014 1:51 PM
20	Some software issues	3/28/2014 1:51 PM
21	hard to comprehend the scripts if unix/R level is not very high	3/28/2014 1:50 PM
22	NA	3/28/2014 1:49 PM
23	I do think there were no "worst parts"	3/28/2014 1:49 PM
24	Data submission is complicated, time consuming and gives little credit. However, I understand that it is essential in science. Therefore this part was the worst, which is however related to the subject itself and not to the presenters who did a very good job in presenting the topic.	3/28/2014 1:47 PM
25	Too much presentation of NGS principles	3/28/2014 1:46 PM
26	Data submission is complicated, time consuming and gives little credit. However, I understand that it is essential in science. Therefore this part was the worst, which is however related to the subject itself and not to the presenters who did a very good job.	3/28/2014 8:48 AM

**Q8 The balance of theoretical and practical content across the course was**

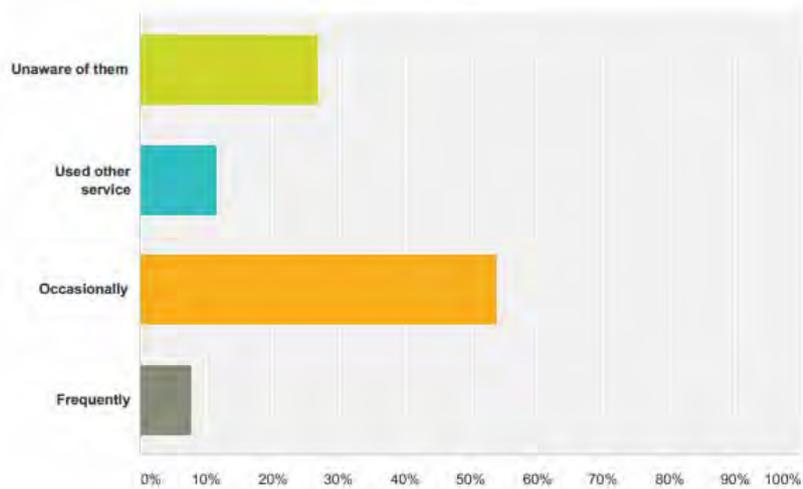
Answered: 26 Skipped: 1



Answer Choices	Responses
Too practical	0.00% 0
About right	80.77% 21
Too theoretical	19.23% 5
<b>Total</b>	<b>26</b>

**Q9 Have you used the resources covered in the course before?**

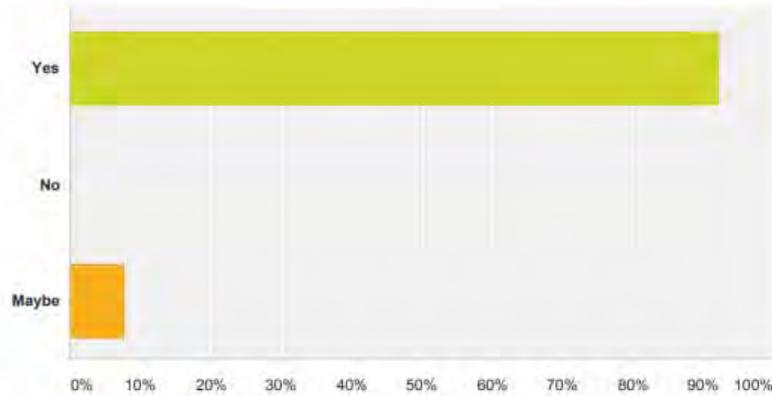
Answered: 26 Skipped: 1



Answer Choices	Responses
Unaware of them	26.92% 7
Used other service	11.54% 3
Occasionally	53.85% 14
Frequently	7.69% 2
<b>Total</b>	<b>26</b>

**Q10 Will you use the tools/resources covered in the course in your future work?**

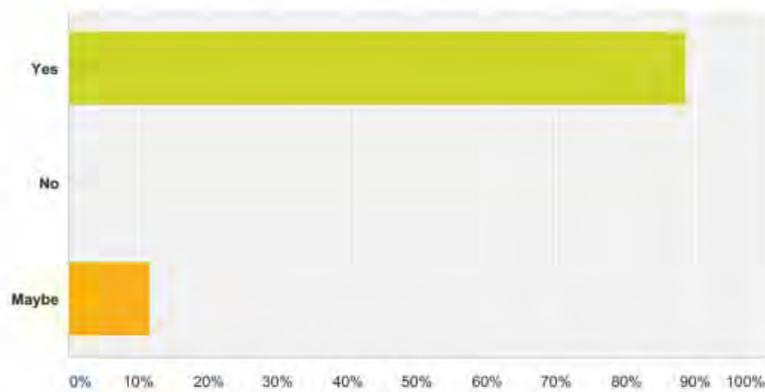
Answered: 26 Skipped: 1



Answer Choices	Responses	
Yes	92.31%	24
No	0.00%	0
Maybe	7.69%	2
<b>Total</b>		<b>26</b>

**Q11 Would you recommend this course?**

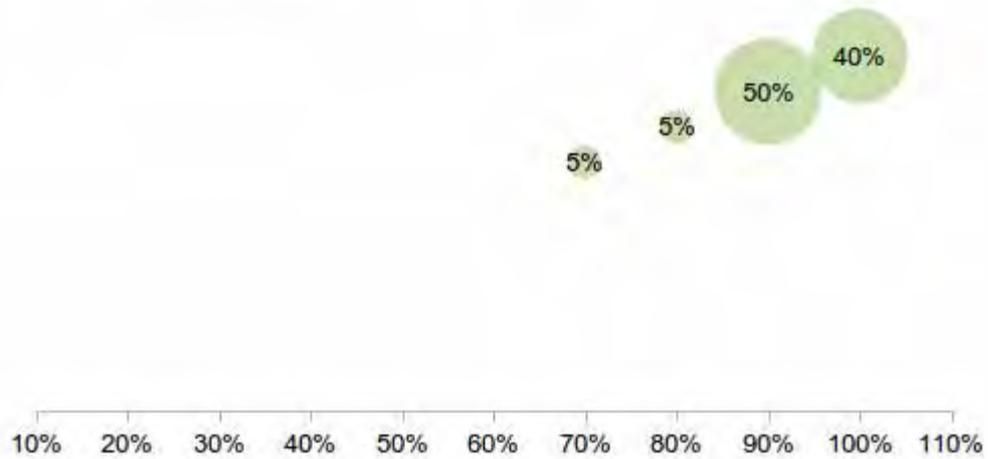
Answered: 26 Skipped: 1



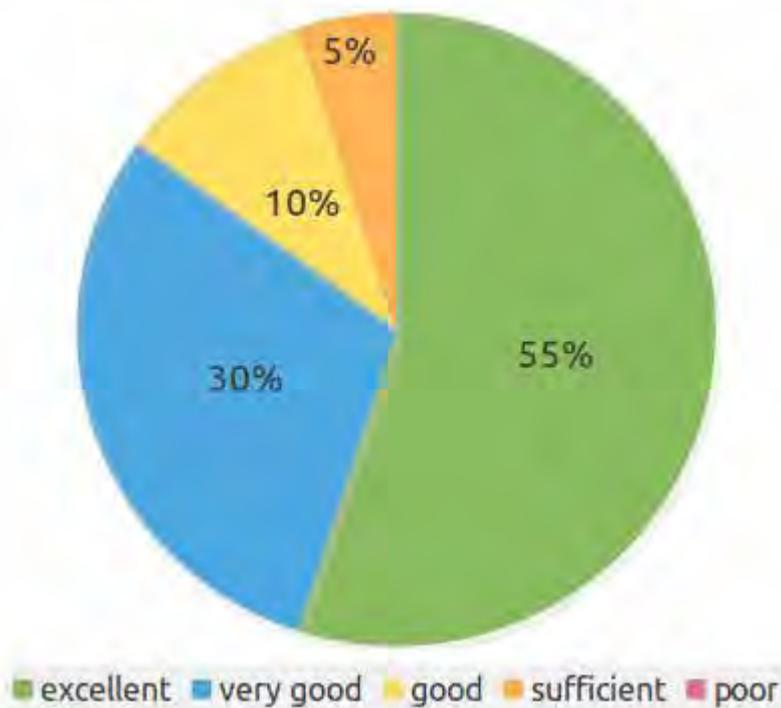
Answer Choices	Responses	
Yes	88.46%	23
No	0.00%	0
Maybe	11.54%	3
<b>Total</b>		<b>26</b>

**Annex 2: Evaluation results of the Micro B3 Summer School**

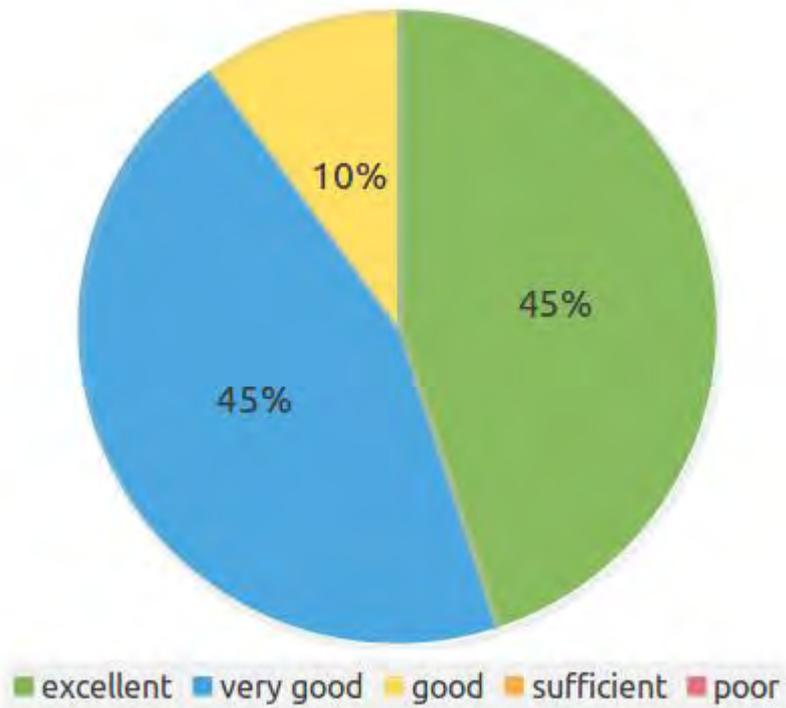
**My expectation for this course was met (0-100%)**



**1. The course length was**



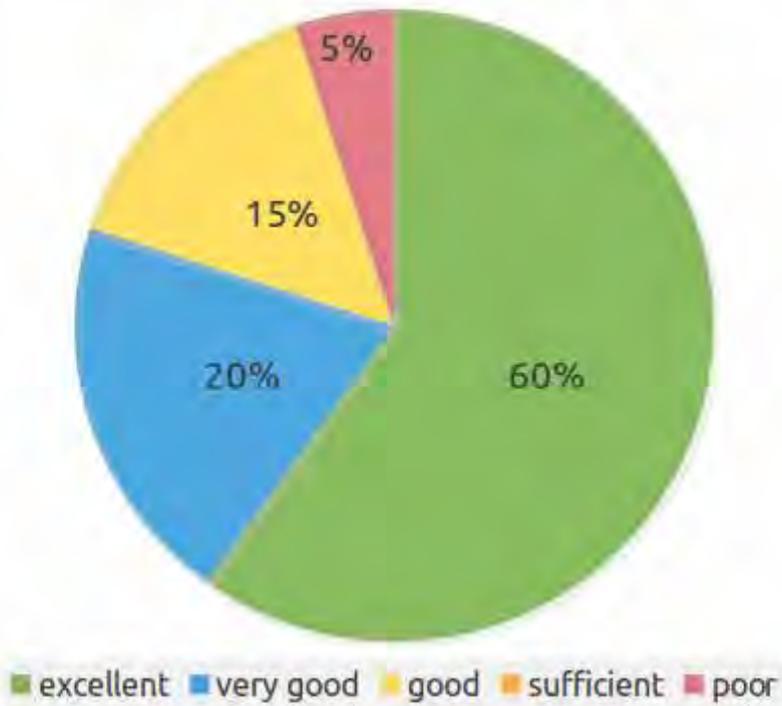
### 3. The presentations were



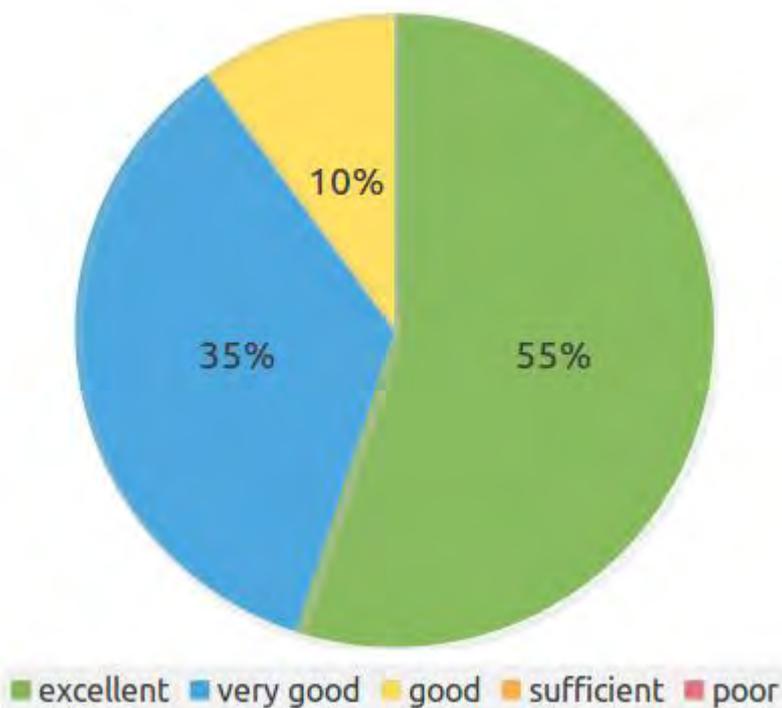
### 4. The instructors were



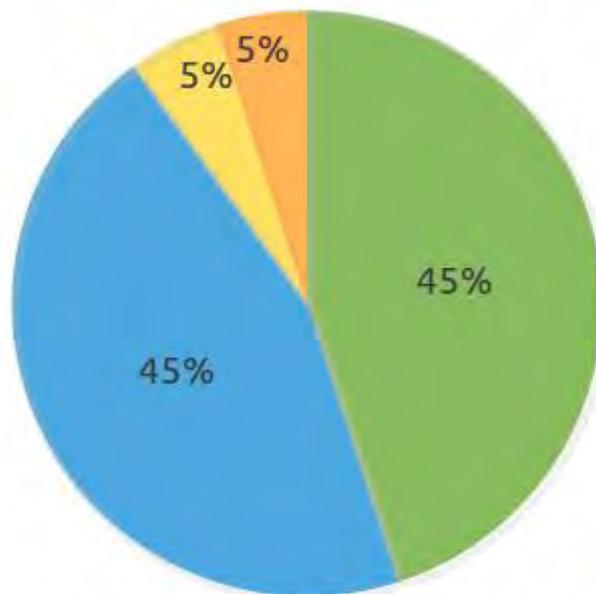
### 5. The handouts were



### 6. The course content was

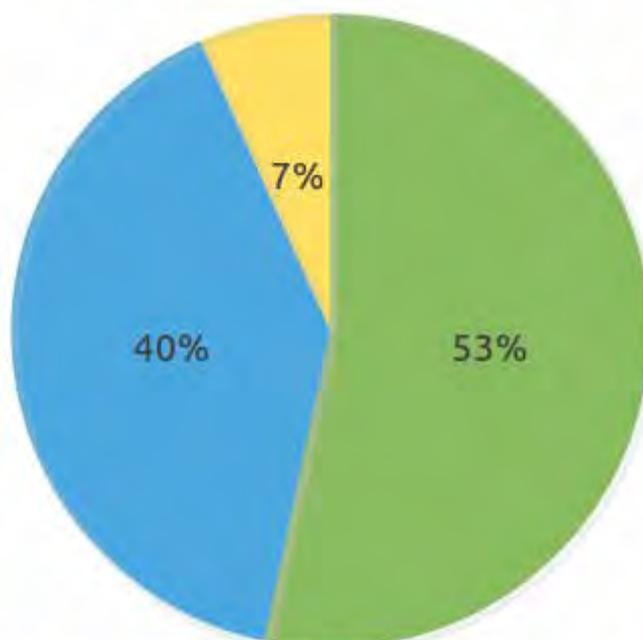


### 7. How was this course in comparison to other courses you have participated



■ excellent ■ very good ■ good ■ sufficient ■ poor

### 8. In general the course was



■ excellent ■ very good ■ good ■ sufficient ■ poor

### Annex 3: Long -Term Feedback Survey

As someone who has previously attended more than one Micro B3-funded and organized course (including two under the lead of EMBL-EBI), we would like to ask you some questions about the impact that the training had on your work, considering the skills and knowledge you gained.

The following survey consists of 8 questions and should take approximately no more than 10 minutes to complete. All data collected is anonymous and will be used for our report to the Commission and for better designing future courses.

1. Which of the following courses did you attend?  
(delete the ones you did not attend)
  1. Bioinformatics for beginners (2012, Bremen, DE)
  2. Biodiversity statistics (June 2013, Bremen, DE)
  3. Metagenome analyses (Spring 2014, EBI Training Centre, UK)
  4. Interdisciplinary summer school (May/June 2014, Crete, GR)
  5. Micro B3 OSD Analysis Workshop/Jamboree (March 2015 at EBI Training Centre, UK)
  
2. Were you working in the fields of bioinformatics and/or marine ecology:
  - a. Before attending the courses?
  
  - b. After attending the courses?
  
3. Do you still use the resources taught?
  - a. Yes, I use the same or similar resources from EMBL-EBI /Micro B3
  
  - b. I don't use the EMBL-EBI /Micro B3 resources, but I use ones in the same area from other providers
  
  - c. I don't use the resources in this area any more
  
  - d. I rarely/never used the resources in this area

4. As a result of your attendance, did you:
  - a. Publish a journal article
    - Please provide details
  - b. Publish a book chapter
    - Please provide details
  - c. Write a grant proposal
    - Please provide details
  - d. Author software
    - Please provide details
  - e. Other \_\_\_\_\_
  
5. Have you helped anyone else learn about the course topics / use the resources mentioned since you attended?  
*(formally, as training, in English/your native language, or informally, if possible, tell us how many persons)*
  
6. Did you establish any collaborations with participants or lecturers on the course?  
*(If yes, please provide some details)*
  
7. Would you like additional / repeat training in the areas taught on the courses or in related ones?
  
8. Any other comments:

**Annex 4: Final Conference Reader**



## Micro B3 Final Conference

&

# Industry Workshop “Collaboration between Academia, SMEs, and Industry - Transforming Inventions into Innovations in the fields of Bioinformatics and Biotechnology”

November 2-5, 2015, Brussels, Belgium



## Welcome to the Micro B3 Final Conference

As the coordinator it is my pleasure to welcome all partners, Ocean Sampling Day and MyOSD participants, industry representatives, members of the European Commission as well as guests to the Final Conference of the Marine Microbial Biodiversity, Bioinformatics and Biotechnology (Micro B3) EU-project at the Royal Flemish Academy of Belgium for Science and the Arts in Brussels.



The intention of the conference is to bring together policy and biodiversity stakeholders from Europe and overseas to present our project results, discuss on the project perspectives and provide key recommendations and inputs from Micro B3 researchers to industry and the European Commission.

The agenda represents the three main pillars of Micro B3: Biodiversity, Bioinformatics and Biotechnology, highlighting the outcomes of the operational Work Packages of Micro B3, including a showcase for the two movies produced during the project.

Embedded in the Micro B3 Final Conference is our Third Industry Expert Workshop: "Collaboration between Academia, SMEs, and Industry - Transforming Inventions into Innovations in the fields of Bioinformatics and Biotechnology".

This Expert Workshop brings together managers of various backgrounds within and outside of the Micro B3 consortium to illuminate different strategies for knowledge and technology transfer between the public and private sector and corresponding experiences, based on use cases in bioinformatics and (marine) biotechnology.

I am looking forward to three exciting days of great science and how to transfer our data, information and knowledge gained into applications.

Thank you for being with us in Brussels.



Frank Oliver Glöckner  
Coordinator of Micro B3

My special thanks goes to Sandra Nowack and Marianna Mea who did a fantastic job in getting this conference organized.



Sandra Nowack



Marianna Mea



## **The Project Micro B3: MARINE MICROBIAL BIODIVERSITY, BIOINFORMATICS AND BIOTECHNOLOGY**

**Technological advances in the fields of 'Omics have enabled marine scientists to realise projects they only dreamt of 10 years ago. Large amounts of next generation sequencing data stand in contrast to the small amount of data management infrastructure with integrated analysis software currently available. Micro B3 is improving Europe's capacity for bioinformatics and marine microbial data integration for the benefit of a variety of disciplines in biosciences, technology, computing and law. Micro B3 is developing an innovative, transparent and user-friendly Information System for seamless, integration, and visualisation of huge amount of marine data from past and on-going biodiversity sampling campaigns like the Global Ocean Sampling, Tara Oceans and Malaspina expeditions, long-term ecological research stations, and from Micro B3's novel Ocean Sampling Days, which perform global snapshots of marine microbial plankton diversity.**

The 9 million Euro project Micro B3, involves 32 partners from 14 European countries and three international organisations. It works in interdisciplinary teams of experts in bioinformatics, computer science, biology, ecology, oceanography, biotechnology, ethics and law. From 2012 until end of 2015 Micro B3 is implementing its primary objective to develop and provide integrated access to biodiversity, genomic, oceanographic and earth-observation databases. It is building on global standards for sampling and data processing like the Minimum Information about any (x) Sequence (MIxS) standard and checklist. For Micro B3's multidisciplinary approach interoperability is a key feature.

### **Key Objectives**

The combined approach within Micro B3 facilitates the whole process of knowledge generation and its use: from legal and technical aspects of sampling and data acquisition all the way to integrated data analysis, sound statistics and to testing of applications within selected biotechnology value chains. The innovative joint analysis of genomic and ecological information is generating new knowledge and provides new perspectives for the modelling and exploration of marine microbial communities. This will also provide new targets for biotechnological applications. Most of Micro B3's results are documented in peer-reviewed publications with full texts available through OpenAire.

### **Biodiversity, Bioinformatics, Biotechnology and the Ocean Sampling Day**

Work has focused on mobilizing the larger marine research community for sampling of the world's ocean, which was accomplished by two global Ocean Sampling Days (OSDs) on 21<sup>st</sup> June 2014 and 2015. Their success was largely due to the engagement of a network of over 150 marine sites and their in-kind contributions of samples and expertise. In addition to the Micro B3-funded sequencing of 500 amplicon profiles and 150 metagenomes, eukaryotic samples from 33 sites were sequenced through a LifeWatch fund. OSD included the citizen science campaign MyOSD, based on a Smartphone App and sampling kit, to raise awareness for marine microbes and their ecological roles, with resulting data immediately shown in a global map.

A data-flow model was implemented between four European infrastructures (SeaDataNet, EurOBIS, EMBL-EBI/ENA and PANGAEA). It allows for direct sharing of metadata and provides access to important contextual data. The published Micro B3 Standard Operating Procedures and Reporting Standards allow marine data to be collected in an orchestrated way and consistently with national and international legal commitments.

Together with the Micro B3-inspired MIBiG specification (Minimum Information about a Biosynthetic Gene cluster) these standards are expected to support marine microbial biotechnology for industrial applications in the near future.

Biodiversity research in Micro B3 has led to many novel published results, based on new tools like annotation pipelines, network and statistical analysis in microbial ecology, including interactive guidance for a community-led and -curated service.

Several bioinformatics tools were developed and tested for biotechnological applications: the 3DM database systems further developed by an SME-academia collaboration, uses a workflow for computational predictions of substrate selectivity of homologues to genes with known activities. Another novel tool is using co-occurrence networks for determining hypothetical functions of unknown genes found in marine microbes. Lately, this was combined with the popular open access software AntiSMASH to form a new tool, the ultra-fast Biosynthetic Gene Cluster recruiter, which is currently used to generate enzyme targets for wet-lab testing.

On the legal side, an Access and Benefit Sharing model agreement (ABS-MA) and a data policy were developed, tested during training courses and utilised during the two OSDs. Promotion included two multi-stakeholder workshops discussing the ABS-MA, as well as tracking and tracing of ABS-relevant material and data, and lectures at end-user meetings on EU- and UN level.

Further cross-cutting activities include the completed training pipeline (five Micro B3 courses) enhancing interdisciplinary oceanographic, biodiversity and bioinformatics knowledge. The courses and industry expert workshops integrated many partners, also of related projects, for knowledge exchange and technology transfer with academic and industrial stakeholders.

Data from the Tara Oceans Expedition were archived at PANGAEA and EMBL-EBI/ENA and are available for integrated analysis in comparison with OSDs datasets. Diverse results from genome mining for anti-tumour compounds, enzyme toolboxes, libraries and new expression systems for experimental screening are becoming available.

### **Micro B3's European Added Value**

The Science Academies' have recently advised the G7 countries to 'enhance international scientific cooperation to better predict, manage and mitigate future changes in the ocean'. By furthering understanding of the diverse roles of microbes in our changing oceans, designing and implementing the global Ocean Sampling Days and the citizen science campaign MyOSD, Micro B3 has set landmarks in this respect. It created a new kind of communication culture in marine science by enabling free exchange of data and skills within the community at large.

### **Micro B3 particularly fosters:**

Research on 'environmental intelligence' of European open ocean and coastal marine ecosystems for better understanding of their diversity and the functions they contain.

Community interaction, technology transfer and data sharing between science and the bio-economy to overcome fragmentation in European marine research as well as promote product and service developments.

Public awareness on the importance of marine research and the fundamental role of marine microbes in ecosystem functioning.

## Micro B3 Final Conference Agenda

2-5 November 2015

Royal Flemish Academy of Belgium for Science and the Arts

Hertogsstraat 1 - 1000 Brussels

<http://microb3.eu/events/meetings/microb3-final-conference-brussels>

### Monday 2 November (afternoon only)

<i>Time</i>	<i>Issue</i>	<i>Room</i>
14:00 – 15:00	<b>Registration</b>	<b>Main entrance</b>
15:00 – 15:30	Welcome coffee	<b>Main entrance</b>
15:30 – 16:00	<b>Welcome and Introduction</b> (chair Frank Oliver Glöckner)	<b>Auditorium</b>
16:00 – 18:00	<b>Session: OSD (WP2) and MyOSD</b> (chair Mesude Bicak)	<b>Auditorium</b>
16:00 – 16:20	<i>WP2: Ocean Sampling Day, A Global Mega-Sequencing Campaign</i> , <u>Mesude Bicak</u> (University of Oxford)	
16:20 – 16:30	<i>MyOSD: OSD meets Citizen Science</i> , <u>Julia Schnetzer</u> (Jacobs University)	
16:30 – 17:00	<i>A Decade of Censusing the Microbial Ocean: Lessons Learned and Future Prospects</i> , invited talk by <u>Linda Amaral Zettler</u> (Josephine Bay Paul Center/Brown University Department of Earth) AB member	
17:00 – 17:30	<i>Development of innovative tools for understanding marine biodiversity and assessing good environmental status: monitoring the oceans across multiple ecosystem components</i> , invited talk by <u>Angel Borja</u> (AZTI-Tecnalia), DEVOTES project Coordinator	
17:30 – 18:00	<i>Optimizing and Enhancing the Integrated Atlantic Ocean Observing System: the AtlantOS project</i> , invited talk by <u>Simon Claus</u> (VLIZ), AtlantOS project partner	
18:00 – 18:30	<b>OSD Movie Showcase</b> (chairs Frank Oliver Glöckner, Mesude Bicak)	<b>Auditorium</b>
18:30 - 20:30	Dinner	<b>Marble Room</b>

## Tuesday 3 November (morning)

<i>Time</i>	<i>Issue</i>	<i>Room</i>
<b>9:00 – 12:30</b>	<b><i>WP3, WP4 and WP5 Session: Interoperability across scientific domains and communities</i></b>	<b>Auditorium</b>
9:00 – 9:10	<i>WP3-5 Continuum, introduction by WP leaders/chairs <u>Dick Schaap</u>, <u>Guy Cochrane</u>, <u>Renzo Kottmann</u></i>	
9:10 – 9:25	<i>SeaDataNet as building block for marine environmental data, <u>Dick M.A. Schaap</u> (MARIS)</i>	
9:25 – 9:40	<i>EurOBIS as building block for biodiversity data, <u>Simon Claus</u> (VLIZ)</i>	
9:40 – 9:55	<i>ENA as building block for genomic data, <u>Guy Cochrane</u> (EMBL-EBI)</i>	
9:55 – 10:10	<i>The M2B3 standards and their legacy, <u>Petra ten Hoopen</u> (EMBL-EBI)</i>	
10:10 – 10:25	<i>Horizontal interoperability between the 3 building blocks + vertical towards MB3-IS, <u>Dick Schaap</u> (MARIS)</i>	
10:25 – 10:40	<i>Tara Oceans Data, <u>Stephane Pesant</u> (University of Bremen)</i>	
10:40 – 10:55	<i>Ocean Sampling Day Data, <u>Julia Schnetzer</u> (Jacobs University)</i>	
10:55 – 11:00	<i>Completion of work programme - closing statement by <u>Guy Cochrane</u></i>	
<b>11:00 – 11:30</b>	Coffee break	<b>Marble Room</b>
11:30 – 11:45	<i>The Micro B3 Information System: Interoperable Bioinformatics and Data Integration for Marine Microbiology, <u>Renzo Kottmann</u> (Max Planck Institute for Marine Microbiology)</i>	
11:45 – 12:00	<i>A brief history of marine metagenomics, <u>Rob Finn</u> (EMBL-EBI)</i>	
12:50 – 12:15	<i>Exploring the functional side of the Ocean Sampling Day metagenomes, <u>Antonio Fernandez-Guerra</u> (University of Oxford)</i>	
12:15 – 12:30	<i>Innovative sampling infrastructure for improved temporal and spatial resolution of microbial biogeochemistry, <u>Ian Salter</u> (AWI)</i>	
<b>12.30 – 13.00</b>	<i>ERA-NET MarineBiotech – future potentials and collaboration between academia and industry, invited talk by <u>Torger Børresen</u> (Innovation Fund Denmark)</i>	<b>Auditorium</b>
<b>13:00 - 14:30</b>	Lunch	<b>Marble Room</b>

Tuesday 3 November (afternoon)



**“Collaboration across Academia, SMEs, and Industry –  
Transforming Inventions into Innovations”**  
**3<sup>rd</sup> Micro B3 Industry Expert Workshop**

**Chair:** Jörg Peplies CEO at Ribocon GmbH (Bremen, Germany) - Partner of the MicroB3 project

<b>Time</b>	<b>Talk</b>	
14:30 – 14:40	<i>Welcome and Introduction, <u>Jörg Peplies</u> (Ribocon)</i>	
14:40 – 14:55	<i>An Academic Perspective on Collaborating with a Software SME on Bioinformatics Solutions, <u>Renzo Kottmann</u> (Max Planck Institute for Marine Microbiology)</i>	
14:55 – 15:10	<i>IT business and Micro B3 - We did it very good. Can we do it even better?, <u>Aleksandar Pop Ristov</u> (InterWorks):</i>	
15:10 – 15:35	<i>Mobilization of public rRNA gene sequence data: the dbblast system for microbial quality control at Roche, <u>Wolfgang Eder</u> (Roche Diagnostics GmbH)</i>	
15:35 – 16:00	<i>From mind to market: How to develop competitive products by using EU projects enabled collaborations, <u>Jiri Snajdr</u> (Vermicon AG)</i>	
<b>16:00 – 16:30</b>	Coffee break	<b>Marble room</b>
<b>16:30 – 16:55</b>	<i>Sustainably using the ocean's services- tapping the potential of marine living resources by Marine Biotechnology, <u>Levent Piker</u> (oceanBASIS GmbH)</i>	
<b>16:55 – 17:20</b>	<i>The OTARI project "Ostreococcus tauri from Research to Industry": a joint laboratory between academics and a SME, <u>Francois-Yves Bouget</u> (CNRS)</i>	
<b>17:20 – 18:00</b>	<b>Panel discussion</b>	
<b>18:00 – 18:30</b>	<b>Micro B3 Movie Showcase</b> (chair Johanna Wesnigk)	
<b>18:30 – 20:30</b>	Dinner	<b>Marble room</b>

## Wednesday 4 November (morning)

<i>Time</i>	<i>Issue</i>	<i>Room</i>
<b>9:00 – 11:00</b>	<b>Session: Biodiversity and community dynamics of marine microbial life (WP6)</b> (chair Frédéric Partensky)	<b>Auditorium</b>
9:00 – 9:20	<i>WP6: Exploring ecosystems biology, Frédéric Partensky</i> (CNRS Roscoff)	
9:20 – 9:50	<i>Assessing global plankton biodiversity patterns with high-throughput sequencing and imaging technologies</i> , invited talk by <b>Colomban de Vargas</b> (Station Biologique de Roscoff), TARA Oceans project	
9:50 – 10:20	<i>OSD metagenome data to model small-scale processes with large-scale implications: carbon-phosphorus cycle</i> , invited talk by <b>Francesca Malfatti</b> (OGS - National Institute of Oceanography and Experimental Geophysics)	
10:20 – 10:40	<i>Mapping the ocean microbiome, Carlos Pedrós-Alió</i> (CSIC)	
10:40 – 11:00	<i>A holistic view of the plankton response to environmental perturbations, Daniele Iudicone</i> (Stazione Zoologica di Napoli)	
<b>11:00 – 11:30</b>	Coffee break	<b>Marble Room</b>
<b>11:30 – 13:00</b>	<b>Session: Training pipeline and stakeholder engagement (WP9)</b> (chair Johanna Wesnigk)	<b>Auditorium</b>
11:30 – 11:50	<i>Capacity building through training and knowledge transfer in environmental bioinformatics, marine biodiversity and biotechnology – an overview for the Micro B3 Project, Johanna Wesnigk</i> (EMPA-Bremen)	
11:50 – 12:05	<i>Micro B3 summer school: from sampling to analyzing microbial diversity &amp; function, Anastasis Oulas</i> (HCMR)	
12:05 – 12:20	<i>Priorities and strategies for marine biocatalyst discovery - training and dissemination, Dick Janssen</i> (University of Gröningen)	
12:20 – 12:45	<i>JPI Oceans: Pilot Actions, Capacity Building and Future Actions</i> , invited talk by <b>Tom Redd</b> (JPI Oceans)	
12:45 – 13:00	<i>Innovative IP models: open research collaboration partnerships in marine biotechnology, Tom Dedeurwaerdere</i> (University of Louvain)	
<b>13:00 - 14:30</b>	Lunch	<b>Marble Room</b>

### Wednesday 4 November (afternoon)

<i>Time</i>	<i>Issue</i>	<i>Room</i>
14:30 – 16:00	<b>Session: Bioinformatics tools for the discovery, description, and exploitation of new gene functions (WP7)</b> (chair Dick Janssen)	<b>Auditorium</b>
14:30 – 15:00	<i>Exploring marine genomes for biocatalysts and bioactives, <u>Dick Janssen</u></i> (University of Groningen)	
15:00 – 15:15	<i>Exploiting Systems Biology Platforms to develop innovative Bioactives for Therapeutic and Industrial applications, <u>Fergal O’Gara</u></i> (BIOMERIT)	
15:15 – 15:30	<i>Microbial diversity and enzyme discovery in cultivated and non-cultivated microbiomes from marine environments in Iceland, <u>Viggó Marteinson</u></i> (MATIS)	
15:30 – 16:00	Coffee break	<b>Marble Room</b>
16:00 – 17:00	<b>Session: Importance of data sharing and open access in environmental research – Micro B3 legal tools, CIESM charter (WP8)</b> (chairs Tom Dedeurwaerdere and Michèle Barbier)	<b>Auditorium</b>
16:00 – 16:20	<i>Global scientific research commons under the Nagoya Protocol: Towards a collaborative economy model for the sharing of basic research assets, <u>Tom Dedeurwaerdere</u></i> (University of Louvain)	
16:20 – 16:30	<i>The CIESM Charter, for access to knowledge and to prevent the abuses of the ocean global commons, <u>Michèle Barbier</u></i> (CIESM)	
16:30 – 17:00	<i>The Nagoya Protocol and its implications for environmental research in the EU, invited talk by <u>Chris Lyal</u></i> (Natural History Museum of London)	
17:00 – 18:00	<b>Take home message – Recommendations and future research needs, <u>Frank Oliver Glöckner</u></b> (Jacobs University)	<b>Auditorium</b>
18:00 - 20:30	Dinner	<b>Marble Room</b>

### Thursday 5 November (morning only)

<i>Time</i>	<i>Issue</i>	<i>Participants</i>
09:00 – 11:00	<b>General Assembly Meeting and debriefing</b> (chair Frank Oliver Glöckner)	GA representatives

## Keynote Speakers

### Linda Amaral Zettler

Marine Biological Laboratory, Woods Hole, MA

<http://www.mbl.edu>



Dr. Linda Amaral-Zettler is an Associate Scientist at the Josephine Bay Paul Center for Comparative Molecular Biology and Evolution at the Marine Biological Laboratory in Woods Hole, MA. She is also an Associate Professor in the Department of Earth, Environmental and Planetary Sciences at Brown University in Providence, Rhode Island. She obtained her Ph.D. in Biological Oceanography at the Massachusetts Institute of Technology/Woods Hole Oceanographic Institution Joint Program after receiving a Bachelor of Science in Aquatic Biology at Brown University. Amaral-Zettler's research investigates the relationships between microbes and the mechanisms that determine their diversity, distribution, survival and impact on local and global processes. From 2004-2010 she served as the Program Manager and Education and Outreach Lead for the International Census of Marine Microbes (<http://icomm.mbl.edu>), a global effort to census the microbial ocean as part of the Census of Marine Life Program. She led the NSF-funded MIRADA-LTERS project that carried out microbial biodiversity inventories and is exploring large-scale patterns in microbial biogeography across the 13 aquatic US Long Term Ecological Research Sites. As part of the Woods Hole Center for Oceans and Human Health, her research employs next generation sequencing techniques to understand the presence and persistence of pathogens and harmful algal blooming species in the natural and man-made environment. Her current research investigates microbes on Plastic Marine Debris and the "Plastisphere".

### Àngel Borja

AZTI-Tecnalia, Marine Research Division, Pasaia, Spain

<http://www.azti.es>



Àngel Borja (San Sebastian, Spain) is PhD in Marine Ecology (University of the Basque Country, 1984) and DSc (honoris causa), by the University of Hull (2015). He works at AZTI, a private research foundation in Spain, where he has been Head of the Department of Oceanography, Head of the Marine Environment Area, and now is Principal Investigator. His main work is making marine ecology research useful for policy-makers and managers, studying the effects of human activities on marine ecosystems, monitoring of marine waters and recovery after impact, and developing methodologies to assess the marine status under European directives, which are used worldwide.

He is member of the Scientific Committee of the European Environment Agency (2012). He is author of more than 170 peer-reviewed papers, Editor and member of the Editorial Board of seven international journals. Referee in near 70 international journals and project evaluation agencies, is member of different scientific associations (ASLO, CERF, ECSA), serving as chair in numerous international conferences. He has participated in more than 100 European and international projects, being now the coordinator of the EU 7th FP project DEVOTES (DEvelopment Of innovative Tools for understanding marine biodiversity and assessing good Environmental Status, [www.devotes-project.eu](http://www.devotes-project.eu)).

### Simon Claus

Flanders Marine Institute, Oostende, Belgium

<http://www.vliz.be/en/>



Simon Claus is coordinator of EMODnet Biology. He has a MSc in Ecology and a MSc in Oceanography. As a scientific staff member of the marine data and information centre of the Flanders Marine Institute (VLIZ) he is involved in the data management activities of several European Research projects. His main interest is coastal and marine data and information management; including processes and systems to archive, document, integrate and redistribute coastal and marine data and information focusing on biological, taxonomic and ecological data, spatial data and marine environmental metadata in general.

### Colomban de Vargas

CNRS – Station Biologique de Roscoff, France

<http://www.sb-roscoff.fr>



Research Director at the CNRS France, and leader of the EPEP - Evolution of Pelagic Ecosystems & Protists - team at the Station Biologique de Roscoff, Colomban de Vargas has co-authored >80 scientific publications around his main research interest: How rich and diverse is plankton life, and how has plankton life evolved, and transformed/stabilized the Earth system? Along his 20-years long scientific career from Tahiti (MSc, 1995) to Switzerland (PhD, 2000), USA (PostDoc at Harvard and Assistant Professorship at Rutgers), and France, Colomban has supervised >15 PhD students and postdocs, and coordinated major research programs on marine plankton (paleo)ecology (e.g. BioMarkS, 2009-2012, [www.biomarks.eu/](http://www.biomarks.eu/)). He pioneered the use of combined genetic, morphological, and geological data to assess rates and modes of biodiversity change in planktonic unicellular eukaryotes or protists on various ecological to geological time scales. Since 2008, he coordinated the 'biodiversity' and 'protist' components of the Tara Oceans expeditions (<http://oceans.taraexpeditions.org/>), exploring the interaction networks and dynamics of modern plankton eco-systems using high-throughput DNA sequencing and imaging technologies. Until 2020, Colomban will coordinate the program OCEANOMICS (wOrld oCEANs biOressources, biotechnologies, and Earth-system servICeS, <http://www.oceanomics.eu/>), aiming at analyzing and transferring to the society the complex eco-morpho-genetic datasets collected during Tara Oceans. His new dream is to create a long-lasting fleet of volunteer sailing boats -the planktonauts-, that will collect plankton samples on relevant spatial and temporal scales. This innovative citizen sailing oceanography will take the pulse of our global oceans health, while preserving a memory of fast-changing oceans biodiversity for future generations (<http://planktonplanet.org>).

### Francesca Malfatti

OGS - National Institute of Oceanography and Experimental Geophysics, Trieste, Italy

<http://www.ogs.trieste.it>



Dr. Francesca Malfatti received her PhD degree at the Scripps Institution of Oceanography (UCSD) in 2009 under the guidance of Dr. Farooq Azam. She is currently Marie Curie Fellow researcher at OGS - National Institute of Oceanography and Experimental Geophysics in Trieste (Italy). Dr. Malfatti is a marine microbial ecologist and biogeochemist, and her research focuses on the role of marine microbes in oceanic carbon cycle. In 2010, she was awarded with the IRPE (International Recognition of Professional Excellence) Prize in Marine Ecology, for her innovative and important contributions to the emerging field of microscale biogeochemistry of the surface ocean. She is involved in several research projects, funded by EU and NSF.

### Torger Børresen

Innovation Fund Denmark, Østergade, Denmark

<http://innovationsfonden.dk/en>



Dr. Torger Børresen holds a position as Senior Executive Officer at the Technical University of Denmark, and is presently working for the Innovation Fund Denmark. He graduated at Department of Biotechnology, Norwegian University of Science and Technology, and has held various research and leadership positions in USA, Norway and Denmark concerning food biochemistry and biotechnology. Among his leadership positions shall be mentioned the management of a marine biotechnology research centre and coordination of a major EU supported project consisting of 70 partners in 17 different countries. He was responsible for drafting the plan for a Danish research programme on marine biotechnology and he served as a member of the Collaborative Working Group on Marine Biotechnology appointed by the KBBE-NET. Further, he participated in the CSA-MarineBiotech. In parallel to this work he was a member of the Marine Board-ESF ad hoc group for drafting Position Paper 15 'Marine Biotechnology: A new vision and strategy for Europe'. He has participated in Nordic collaboration on Marine Biotechnology, and in a think-tank for developing marine biotechnology collaboration between the Baltic and Mediterranean areas. He is presently the president of European Society of Marine Biotechnology.

### Tom Redd

JPI Oceans, Brussels, Belgium

<http://www.jpi-oceans.eu/>



Tom Redd is currently employed by the Flanders Marine Institute and seconded full time as an Advisor to the secretariat of JPI Oceans. Within the secretariat, he is contact point for activities in biotechnology, food security and capacity building. He previously worked at the United Kingdoms' National Oceanography Centre where he helped develop recommendations for how JPI Oceans can improve science-policy mechanisms at a European level. Tom graduated from Bangor University with a degree in Ocean Science and he holds a Masters degree in Marine Science, Policy and Law from the University of Southampton.

### Chris Lyal

Natural History Museum, London, United Kingdom

<http://www.nhm.ac.uk/>



Taxonomist of more than 40 year's experience working on a variety of insect groups, currently focussing on the hyperdiverse beetle group 'weevils'. My key interests here are the higher classification and nomenclature, and the evolution and host specificity of seed-feeding groups. Much of my non-taxonomic work is directed at global biodiversity policy, in particular the Nagoya Protocol on Access and benefit-sharing, the Global Taxonomy Initiative (GTI), and Invasive Alien Species. I am UK national Focal Point for the GTI, and a member of the SCBD's GTI Coordination Mechanism. As Parties prepare to implement the Nagoya Protocol non-commercial biodiversity research bodies, particularly the large collection-holding taxonomic institutions, have to find ways of managing relevant activities. My work in this area has been focussed on institutional compliance through revision of policies and processes and staff training, development of sectoral codes of conduct, best practices and tools in collaboration with the GTI Coordination mechanism, the Global Genome Biodiversity Network, the Consortium of European Taxonomic Facilities and the World federation of Culture Collections, support of the UK Government and EU in policy development and international meetings, and support for the CBD through Co-Chairing the 2011 "Expert Meeting on the Modalities of Operation of the Access and Benefit-sharing Clearing-House" in Montreal and as Chair of the Informal Advisory Committee to the Pilot Phase of the ABS Clearing House.



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## Final Conference

### WP2: Ocean Sampling Day, A Global Mega-Sequencing Campaign

Bicak, M.

University of Oxford, 7 Keble Road, Oxford, Oxfordshire, OX1 3QG, United Kingdom.

Ocean Sampling Day (OSD) achieved global success in becoming a simultaneous, collaborative, global mega-sequencing campaign to obtain a snapshot of the marine microbial biodiversity and function of the world's oceans. With four pilot studies in 2012 and 2013 solstices and two global events in 2014 and 2015, OSD ramped up to more than 155 teams of scientists from all continents around the world per event collecting surface marine water samples, generating the largest standardized data set on marine microbes taken on a single day. Coupled with MyOSD Hubs with citizen scientists also sampling marine microbes and collecting environmental parameters like salinity and water temperature via MyOSD kits and OSD App, OSD grew stronger on its path to global success. Data from all events are currently being organized and analysed across a group of 140 experts; the OSD Analysis Consortium.

### MyOSD: OSD meets Citizen Science

Schnetzler J.<sup>1,2</sup>, Kottmann R.<sup>2</sup>, Kopf A.<sup>1,2</sup>, Mea M.<sup>2</sup>, Pop Ristov A.<sup>3</sup>, Glöckner F.O.<sup>1,2</sup>

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<sup>3</sup>Interworks Karpos bb, 7000, Bitola, Macedonia

Ocean Sampling Day (OSD) achieved global success in becoming a simultaneous, collaborative, global mega-sequencing campaign to obtain a snapshot of the marine microbial biodiversity and function of the world's oceans. With four pilot studies in 2012 and 2013 solstices and two global events in 2014 and 2015, OSD ramped up to more than 155 teams of scientists from all continents around the world per event collecting surface marine water samples, generating the largest standardized data set on marine microbes taken on a single day. Coupled with MyOSD Hubs with citizen scientists also sampling marine microbes and collecting environmental parameters like salinity and water temperature via MyOSD kits and OSD App, OSD grew stronger on its path to global success. Data from all events are currently being organized and analysed across a group of 140 experts; the OSD Analysis Consortium.



## **A Decade of Censusing the Microbial Ocean: Lessons Learned and Future Prospects**

Amaral-Zettler, L. A.<sup>1,2</sup>

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<sup>2</sup> Department of Earth, Environmental and Planetary Sciences, Brown University, Providence, RI 02912, USA

The International Census of Marine Microbes ICoMM (2004-2010) enabled the first census of marine microbial life and advanced our knowledge of marine microbial diversity and biogeography. Despite estimating that Bacteria alone exceed 450,000 kinds and, when considered in a microbiome setting, likely approach a billion different kinds, the census is far from complete. The few temporal studies performed highlighted the importance of considering seasonality in sampling. The Ocean Sampling Day effort has simultaneously sampled the world's ocean on the summer solstice in 2014/2015 with an eye towards repeated sampling every year. Unlike the samples collected from ICoMM, the OSD approach involves coordinated timing, standardized sampling methods, a common DNA extraction protocol and has extended the inventory of microbial diversity to a one that includes functional potential. Leveraging existing marine biodiversity observatories and erecting new ones will further our abilities to better understand the importance of microbes in a changing ocean.

## **Development of innovative tools for understanding marine biodiversity and assessing good environmental status: monitoring the oceans across multiple ecosystem components**

Borja A.

AZTI, Marine Research Division, Pasaia (Spain)

The FP7 project DEVOTES is developing innovative tools to monitor and assess the environmental status of marine waters, within the Marine Strategy Framework Directive (MSFD). This talk will show the main outputs from the project related to: (i) development of matrices of pressure-impact to understand the response of ecosystems to human activities, and their interactions with climate change; (ii) development of indicators (DEVOTool software) and selection of the most suitable, including criteria for selection, for different descriptors within the MSFD; (iv) development of monitoring tools (participation in the Ocean Sampling Day, genomic tools for different ecosystem components, remote sensing,...); and (v) development of an assessment tool to integrate indicators and evaluate the environmental status of the oceans, following the criteria of the MSFD.



## **Optimizing and Enhancing the Integrated Atlantic Ocean Observing System: the AtlantOS project**

Claus S.<sup>1</sup>, Visbeck M.<sup>2</sup>

<sup>1</sup> Flanders Marine Institute

<sup>2</sup> GEOMAR Helmholtz Zentrum für Ozeanforschung Kiel

The overarching objective of AtlantOS is to promote transition from a loosely-coordinated set of existing ocean observing activities to a more integrated, more efficient, more sustainable and fit-for-purpose Atlantic Ocean Observing System. This will be done by advancing requirements and systems design, improving the readiness of observing networks and data systems, and engaging stakeholders around the Atlantic. AtlantOS's will bring Atlantic nations together to strengthen their complementary contributions to and benefits from the Global Ocean Observing System (GOOS) and the Blue Planet Initiative of the Global Earth Observation System of Systems (GEOSS).

AtlantOS will fill gaps of the in-situ observing system networks and will ensure that their data are readily accessible and useable. AtlantOS will demonstrate the utility of integrating in-situ and remotely sensed Earth observations to produce information products supporting a wide range of sectors. AtlantOS will benefit from the Copernicus Marine Monitoring Services and the European Marine Observation and Data Network and connect them with similar activities around the Atlantic. AtlantOS will promote network integration and optimization, deployment of new technologies, and help to increase the competitiveness of European industries, including small and medium enterprises of the marine sector. Finally, AtlantOS will establish a structured dialogue with funding bodies, including the European Commission, European nations, USA, Canada, Brazil, South Africa and other countries to ensure sustainability and adequate growth of the Integrated Atlantic Ocean Observing System.

## **SeaDataNet as building block for marine environmental data**

Schaap, D.M.A.

Mariene Informatie Service 'MARIS' BV, The Netherlands

SeaDataNet is an operational pan-European infrastructure for managing, indexing and providing access to ocean and marine data sets and data products, acquired from research cruises and other observational activities in European marine waters and global oceans. It is undertaken by National Oceanographic Data Centres, and marine information services of major institutes, from 35 coastal states bordering European seas. SeaDataNet works closely with European RTD projects and initiatives such as EMODnet (European Marine Observation and Data Network), Copernicus Marine Service, and EuroGOOS, providing standards, services, data centres and infrastructure for managing data, and experience and expertise for joint development of new standards and services. The SeaDataNet CDI Data Discovery and Access service connects and gives access to marine data sets from more than 100 data centres from 34 countries, riparian to European seas, and nearly 1.8 million data sets for physical oceanography, chemistry, geology, geophysics, bathymetry and biology, originating from more than 550 organisations.

## **EurOBIS as building block for biodiversity data**

Claus S.<sup>1</sup>, Deneudt K.<sup>1</sup>, Hernandez F.<sup>1</sup>

<sup>1</sup> Flanders Marine Institute, Belgium

The European Ocean Biogeographic Information System—EurOBIS—is an integrated data system developed by the Flanders Marine Institute (VLIZ) in 2004. Its principle aims are to centralise the largely scattered biogeographical data on marine species collected by European institutions and to make these quality-controlled data freely available and easily accessible. It is in essence a distributed system in which individual datasets go through a series of quality control procedures before they are integrated into one large consolidated database. EurOBIS is freely available online at [www.eurobis.org](http://www.eurobis.org), where marine biogeographical data—with a focus on taxonomy, temporal and spatial distribution—can be consulted and downloaded for analyses. Over the last 10 years, EurOBIS has collected more than 600 datasets contributed by more than 150 institutes, representing over 20 million distribution records. It is now the largest online searchable public source of European marine biological data, holding biogeographical information on 24,588 species, mapped against the World Register of Marine Species (WoRMS). EurOBIS acts as the European node of OBIS, the Ocean Biogeographic Information System which in its turn shares its content with the Global Biodiversity Information Facility (GBIF) and is used as the data engine behind the biology node of the European Marine Observation and Data Network (EMODnet).



## ENA as a building block for genomic data

Cochrane G.

European Molecular Biology Laboratory, European Bioinformatics Institute, Wellcome Genome Campus, Hinxton, Cambridge. CB10 1SD. United Kingdom.

The European Nucleotide Archive is a platform for the management, sharing, integration and dissemination of sequence data. ENA includes, on the technical side, core databasing infrastructure for the rapid archiving of petabytes of sequence data, the Webin data application used by several thousands of data providers, and sophisticated data access tools used by many times this number. On the content side, ENA offers extensive public domain data from over a million species. ENA provides a foundation for global bioinformatics, supporting such resources as Ensembl, EMBL-EBI Metagenomics, UniProtKB and – now – MicroB3 IS. Under MicroB3, we have extended ENA better to suit marine applications. The legacy of this work includes richer and more tailored submissions services, new services for content delivery and, through OSD and Tara Oceans, a high-profile, well-structured and richly described body of marine content to serve henceforth as an exemplar for those in the marine domain and beyond.

## The M2B3 standards and their legacy

ten Hoopen P.

European Nucleotide Archive, European Molecular Biology Laboratory, European Bioinformatics Institute, Wellcome Genome Campus, Hinxton, Cambridge. CB10 1SD. United Kingdom.

The multi-disciplinary Micro B3 platform facilitated dialogues of experts across oceanographic, biodiversity and genomic domain, which resulted in development of the trans-disciplinary M2B3 data reporting and service standards (<http://www.standardsingenomics.com/content/10/1/20>). This contextual data reporting and service guidelines: (1) enable coherent and unified description of marine microbial sample provenance, (2) enhance interoperability between established pan-European data resources and (3) allow comparisons of datasets originating from independent high profile investigations of marine ecosystems, such as the Ocean Sampling Day campaign and Tara Oceans expedition. The core of the M2B3 data reporting standard was for the first time formulated as the Micro B3 checklist in the Ocean Sampling Day Handbook ([https://www.microb3.eu/sites/default/files/osd/OSD\\_Handbook\\_June\\_2015.pdf](https://www.microb3.eu/sites/default/files/osd/OSD_Handbook_June_2015.pdf)), a best practice guide on policies, procedures, logistics and bioinformatics associated with marine microbial sampling in the frame of the Ocean Sampling Day enterprise.

The M2B3 harmonisation effort focused mostly on microbial sampling and its legacy will be used to further develop a marine metagenomics infrastructure but also to improve integration of data in a cluster of European marine research infrastructures, where aquacultures, shellfish, finfish and biochemical entities will have to be taken into the consideration.



## Horizontal interoperability between the 3 building blocks + vertical towards MB3-IS

Schaap D.M.A.

Mariene Informatie Service 'MARIS' BV, The Netherlands

Micro B3 aims for a better understanding of the complexity of marine microbial communities and their role in climate change. This requires that the data sets and information on marine organisms and genes are complemented with their environmental context. For that purpose Micro B3 has worked on establishing horizontal interoperability between the 3 leading European infrastructures, SeaDataNet for marine environmental data, EurOBIS for biodiversity data, and EMBL-EBI's ENA for genomic data, using OGC WMS – WFS and OpenSearch protocols, in order to provide better service and a more complete data provision to their internal and external users. Moreover, vertical interoperability has been established from each of the 3 infrastructures towards the Micro B3 Information System (MB3-IS). In particular for SeaDataNet as a distributed system this has been achieved by developing an automatic buffer harvesting service for discovery and retrieval of Micro B3 relevant data and an API for machine-to-machine interaction with MB3-IS.

## Tara Oceans Data

Pesant S.<sup>1</sup>, Tara Oceans Consortium

<sup>1</sup> PANGAEA, University of Bremen

The Tara Oceans expedition (2009–2013) sampled contrasting ecosystems of the world oceans, collecting environmental data and plankton, from viruses to metazoans, for later analysis using modern sequencing and state-of-the-art imaging technologies. It surveyed 210 ecosystems in 20 biogeographic provinces, collecting over 35,000 samples of seawater and plankton. The interpretation of such an extensive collection of samples in their ecological context requires means to explore, assess and access raw and validated data sets. To address this challenge, the Tara Oceans Consortium offers open science resources, including the use of open access archives for nucleotides (ENA) and for environmental, biogeochemical, taxonomic and morphological data (PANGAEA, SeaDataNet, EurOBIS). Here, we present an overview of Tara Oceans Data workflow, including the collection, storage and curation of metadata and samples, and the publication, interoperability and dissemination of metadata and data.



## Ocean Sampling Day Data

Schnetzer J.<sup>1,2</sup>

<sup>1</sup>Jacobs University Bremen gGmbH, Campus Ring 1, Bremen, D-28759, Germany

<sup>2</sup>Max Planck Institute for Marine Microbiology, Celsiusstrasse 1, Bremen, D-28359, Germany

For gathering and managing the Ocean Sampling Day (OSD) data several tools and procedures were developed. Smartphone apps and tailored web forms as well as log-sheets were used to gather the metadata of each OSD sample. The OSD Registry, part of the Micro B3 Information system, holds all information about all OSD sampling sites and samples. To ensure compliance with the trans-disciplinary M2B3 data reporting standard several procedures were used to curate all OSD metadata. After curation the data was submitted to several archives for dissemination and long-term storage.

## The Micro B3 Information System: Interoperable Bioinformatics and Data Integration for Marine Microbiology

Kottmann R.

Max Planck Institute for Marine Microbiology

Micro B3 developed several software components with the aims to provide an integrated view of microbial diversity and function in the marine environment and to support users in effectively gathering, managing, analysing, and sharing genomic and metagenomic data. The presentation will give an overview and highlight the different software tools which together constitute the Micro B3 Information System.



## A brief history of marine metagenomics

Finn R.

European Bioinformatics Institute (EMBL-EBI)

The EBI metagenomics portal is a generic platform for the archiving and analysis of metagenomics. The Ocean Sampling Day (OSD) 2014 dataset provides a large-scale study of global ocean surface waters, with rich contextual data. Using the EBI metagenomics portal, we can now not only provide a consistent analysis of the data and thereby allow different sites to be compared, but can also provide OSD in context of other marine metagenomics projects.

## Exploring the functional side of the Ocean Sampling Day metagenomes

Fernandez-Guerra A.<sup>1,2</sup>, Kottmann R.<sup>2</sup>, Wallom D.<sup>1</sup>, Glöckner F.O.<sup>2,3</sup>

<sup>1</sup>Oxford e-Research Centre, University of Oxford, Oxford, United Kingdom

<sup>2</sup>Microbial Genomics and Bioinformatics Research Group, Max Planck Institute for Marine Microbiology, Bremen, Germany

<sup>3</sup>Jacobs University Bremen gGmbH, Bremen, Germany

Unlike other ocean mega-surveys such as Global Ocean Sampling (GOS) or the TARA expedition that mostly sampled open ocean waters most of the Micro B3's Ocean Sampling Day (OSD) samples are from coastal sampling sites, an area not previously well studied in this regard. The result is that OSD adds more than three million new genes to the recently published Ocean Microbial-Reference Gene Catalog (Sunawaga et al., 2015). This allows us to significantly increase our knowledge of the ocean microbiome, identify hot-spots of novelty in terms of function and investigate the impact of human activities on oceans coastal areas where there is the largest interaction between dense human populations and the marine world. Additionally, these cumulative samples, related in time, space and environmental parameters, are providing insights into fundamental rules describing microbial diversity and function and contribute to the blue economy through the identification of novel ocean-derived biotechnologies.



## **Innovative sampling infrastructure for improved temporal and spatial resolution of microbial biogeochemistry**

Salter I<sup>1</sup>, Metfies K<sup>1</sup>, Boetius, A<sup>1,2</sup>.

<sup>1</sup>Alfred-Wegener-Institute for Polar and Marine Science

<sup>2</sup>Max Planck Institute for Marine Microbiology

To improve our understanding of microbial function in the ocean, the spatial and temporal resolution of genomic observations should be closely aligned to biogeochemical measurements. Future monitoring platforms should therefore provide a novel and innovative sampling infrastructure that can be directly interfaced with standardized and functional bioinformatic workflows. The presentation will give an overview of a burgeoning microbial observatory in the Arctic (FRAM) and collaborative efforts on a European Scale (AtlantOs) to use fixed-point observatories as a launch platform for integrated genomics.

## **ERA-NET MarineBiotech – future potentials and collaboration between academia and industry**

Børresen, T.

Innovation Fund Denmark

The Marine Biotechnology ERA-NET (ERA-MBT) is a consortium of 19 partners in 14 countries seeking complementarities between national activities by pooling resources to undertake joint funding of transnational projects. The ERA-MBT vision is to support Europe's marine biotechnology community to participate in a lasting enterprise-driven network that adds value to marine biological resources in ways that nurtures and sustain the lives of European citizens. The aim of the first thematic call was to develop efficient and sustainable biorefinery processes for marine bioresources. Six projects spending a total of about eight M € will be funded. A second thematic call to be launched will target 'Bioactive molecules from the marine environment – Biodiscovery'. Further future potentials will be outlined in a Strategic Roadmap, to be published in November 2015. Inputs to this roadmap are a foresight study, a stakeholder consultation, and a survey focusing on the collaboration between academia and industry.



## **WP6: Exploring ecosystems biology**

Bowler C.<sup>1</sup> & Partensky F.<sup>2</sup>

<sup>1</sup> Ecology and Evolutionary Biology Section, Institut de Biologie de l'École Normale Supérieure (IBENS), CNRS UMR 8197/INSERM U1024, Paris, France

<sup>2</sup> Dept of Adaptation and Diversity in the Marine Environment, Station Biologique, UMR 7144 CNRS & UPMC, Roscoff, France

The ocean is the largest ecosystem on Earth yet we know very little about it, in particular about the plankton (bacteria, viruses, and protists) that drift within. Although at least as important for the Earth system as the forests on land, many marine microbes are largely uncharacterized. The genomics revolution is transforming our understanding of microbial ecosystems, and major developments in environmental bioinformatics are helping support our ecological and evolutionary understanding of them. WP6 of MicroB3 brings together many resources, most notably from the Malaspina and Tara Oceans expeditions, that captured biodiversity of a wide range of organisms rarely studied together, exploring interactions between them and integrating them with environmental conditions to further our understanding of life in the ocean and beyond in the context of ongoing climate changes. The work also provides a valuable foundation for global initiatives such as Ocean Sampling Day.

## Assessing global plankton biodiversity patterns with high-throughput sequencing and imaging technologies

De Vargas C.<sup>1,2</sup>, Audic S.<sup>1,2</sup>, Colin S.<sup>1,2</sup>, the EPEP team<sup>1,2</sup> & Tara-Oceans consortium.

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Automated, high-throughput DNA sequencing and imaging technologies are revolutionizing ecology, allowing to dramatically increase spatio-temporal sampling granularity while erasing the boundaries between organismal size fractions and taxonomic divisions. In *Tara Oceans*, we used massive DNA metabarcoding to assess the entire diversity of eukaryotic organisms from the smallest unicell (or protist) to small animals across a planetary biome. The sequencing of ~800 million metabarcodes from >300 size-fractionated plankton communities allowed biodiversity assessment close to saturation, both locally and globally. We estimated that sunlit marine plankton contain ~150 000 genetic types of eukaryotes, which is much greater than the ~11 000 described species of eukaryotic plankton. The large majority of this biodiversity belongs to protists, and most of it comes from unknown and uncultured organisms. This eukaryotic biodiversity is significantly greater than the bacterial one, and ~2/3 of it belongs to poorly known groups of heterotrophic protists, including a huge variety of parasites and species known to live in symbiosis. We assigned broad ecological functions to the metabarcodes and used OTUs abundance profiles to better understand the ecological behavior of this unveiled majority of plankton life, and reconstruct a global photic plankton interactome including viruses, prokaryotes, eukaryotes, and environmental parameters. Eucaryotes appear to play a fundamental role in structuring the plankton network, and, overall, biotic and positive interactions -in particular through parasites- are significantly more prevalent than abiotic and/or negative interactions. We finally developed a new automated confocal fluorescent imaging process (eHCFM) to validate network-generated hypotheses, unveil and quantify the complexity of novel plankton symbioses, and provide the needed tool to link genetic and morpho-functional diversity for future holistic studies of plankton systems.

## **OSD metagenome data to analyse small-scale processes with large-scale implications: the carbon-phosphorus cycle**

Malfatti F.<sup>1</sup>, Kahlke T.<sup>2</sup> and OSD consortium

<sup>1</sup> OGS, Istituto Nazionale di Oceanografia e di Geofisica Sperimentale (OGS), Trieste, Italy

<sup>2</sup> CSIRO, Marine and Atmospheric Research, Hobart, Australia

Pelagic bacteria (and Archaea) play major roles in the marine biogeochemical cycles. They are an essential part of the oceanic food web and they interact with organic matter and other organisms on a nanometer and micrometer scale. The strength and variability of the coupling between bacteria-primary production determines the fate of the fixed carbon in the environment (respiration/nutrient regeneration; biomass for higher trophic levels; downward particle fluxes). Bacteria utilise organic matter through an array of cell-surface hydrolases and membrane transporters. Based on the annotation of the OSD2014 dataset we investigate the taxonomy and distribution of InterPro domains that are specific to bacterial hydrolysis-uptake systems within the carbon and phosphorus cycles. We will discuss the results in the light of importance of connecting large-scale exploration (OSD) to small-scale features of marine microbial machineries.

## **Mapping the ocean microbiome**

Pedrós-Alió, Carlos<sup>1</sup>, Cornejo-Castillo, F.<sup>1</sup>, Ferrera, I.<sup>1</sup>, Giner, C. R.<sup>1</sup>, Pernice, M.<sup>1</sup>, Rodríguez, C.<sup>1</sup>, Salazar, G.<sup>1</sup>, Sánchez, P.<sup>1</sup>, Sebastián, M.<sup>1</sup>, Gasol, J.M.<sup>1</sup>, Logares, R.<sup>1</sup>, Massana, R.<sup>1</sup>, Acinas, S.G.<sup>1</sup>

<sup>1</sup> Institut de Ciències del Mar, CSIC, Barcelona, Spain.

High Throughput Sequencing is addressing the challenge of understanding marine microbial communities. Circumnavigation cruises TARAOceans and Malaspina2010 have collected samples from the sunlit to the dark (4000 m) ocean, generating about 14 Tb of sequence data. Richness estimates indicate a minimum of 35000 and 5000 prokaryotic OTUs for photic and bathypelagic zones respectively. Roughly similar figures apply to microeukaryotes. Taxonomic composition is similar in contrasting regions, but with changing relative abundances. Metagenomes have revealed functional traits specific of photic and aphotic zones. Thus, cyanobacteria have many organic matter transporters, suggesting they are actually mixotrophic. Chemotaxis, flagella assembly and contaminant processing genes are enriched in the deep oceans. Unlike in surface waters, some of the most abundant taxa in the deep ocean match cultured bacteria. Metagenomic analysis also indicates the importance of fungal metabolism in the deep. Metatranscriptomes will help build a 3D map of the activities of the ocean microbiome.



## **A holistic view of the plankton response to environmental perturbations**

Iudicone D.<sup>1</sup>, the Tara Oceans Consortium

<sup>1</sup>Stazione Zoologica Anton Dohrn, Naples, Italy.

The biological and ecological processes that regulate the planktonic life are largely unknown. In fact, the analysis of only a small percent of the Tara Oceans database (Science, 2015) has shown that an end-to-end approach, from genes to communities, to understand the responses to environmental changes, is at reach.

As an example of the power of this holistic approach, the analysis of the open-ocean ecosystem response to a natural fertilization in the Equatorial Pacific High-Nutrient Low-Chlorophyll region will be presented. The bloom wax and waning was characterised by shifts in population composition and network structure. The metabolic response was also investigated using metatranscriptomic data from a large range of organism sizes, i.e., the first ever marine eukaryote reference gene catalogue including 9M of non-redundant sequences. Finally, we will discuss how Tara Oceans metagenomics can enrich the laboratory derived information and also orient laboratory and numerical studies, thus revolutionizing our views.



## **Capacity Building through Training and Knowledge Transfer in Environmental Bioinformatics, Marine Biodiversity and Biotechnology – an Overview for the Micro B3 Project**

Wesnigk, J. B.

EMPA Bremen, Westerdeich 11, D-28197 Bremen, Germany

The presentation will provide an overview on the development and implementation of a training pipeline for marine ecologists to enlarge their capacities in using bioinformatics concepts and tools as well as getting state-of-the-art knowledge on

- (i) the legal base of accessing marine genetic resources and
- (ii) using genomics for biotechnological applications.

A training and information needs analysis and the resulting training concepts will be explained, all done under the European-funded Micro B3 project (FP7). Concepts for dissemination and outreach activities to enhance multi-disciplinary and cross-sectorial thinking will be presented which covered industry expert workshops for knowledge and technology transfer as well as stakeholder workshops. These aimed to reach a broader audience and discussed legal aspects of sampling as well as of genomic, environmental and biodiversity data management.

More information can be found under [www.microb3.eu/work-packages/wp9](http://www.microb3.eu/work-packages/wp9) and [www.microb3.eu/events/workshops](http://www.microb3.eu/events/workshops)



## **Micro B3 summer school: from sampling to analyzing microbial diversity & function**

Oulas A.

Institute of Marine Biology, Biotechnology and Aquaculture (IMBBC), Hellenic Centre for Marine Research (HCMR), P.O. Box 2214, 710 03 Heraklion, Greece

This summer school was organized as a two-week interactive training from Monday 26 May to Friday 6 June 2014 at HCMR (Institute of Marine Biology, Biotechnology and Aquaculture, Hellenic Centre for Marine Research) in Crete, Greece. Experts from a wide array of topics and fields shared valuable information with students/participants, focusing on standards & methods. Morning sessions provided theory and interactive practical work was undertaken in the afternoon sessions.

The summer school focused on preparing and planning integrated sampling work and data flows, with a focus on bioinformatics and oceanographic tools. Participants performed data and sample management during the course, using existing (OSD) data sets and the OSD handbook. Trainees explored how to decide on methods and standards to address their research questions in the fields of plankton diversity, ecology and function, including biotechnological applications.



## **Priorities and strategies for marine biocatalyst discovery - training and dissemination**

Janssen D.B.<sup>1</sup>, Masman M.<sup>1</sup>, Wijma H.<sup>1</sup>

<sup>1</sup>Groningen Biomolecular Sciences and Biotechnology Institute, University of Groningen, The Netherlands

Microorganisms are a vast source of novel enzymes that offer a range of useful applications in the conversion of food and feed, the production of biofuels and platform chemicals, the valorisation of biomass, and in the synthesis of fine chemicals and pharmaceutical compounds. In all fields of applied biocatalysis, the discovery of new or better enzymes and the tailoring of enzyme properties for a specific process are of key importance for industrial implementation. One of the goals of MicroB3 is to explore marine systems for new microbial activities needed for such biotechnological applications. Therefore, outreach and dissemination activities in MicroB3's WP7 focused on interacting with the industrial and educational sectors, both for establishing an environment that helps to define important trends and targets, and for creating awareness of the possibilities of innovative tools developed within MicroB3.

For the discovery of novel enzyme variants with specific catalytic properties, the use of modern bioinformatics helps to efficiently mine genomic information. Prediction algorithms employing statistical function-sequence relations and/or knowledge from structural biology may reduce the amount of laboratory work, such as high-throughput screening. Enzyme discovery and engineering of enzymes towards improved properties are partly based on the same algorithms, originating from computational enzyme design. Training young researchers with little background in computational methods in this area is a key aim of the Groningen masterclasses on Enzyme Engineering, which were established in collaboration with other EU projects and national initiatives.



## **JPI Oceans: Pilot Actions, Capacity Building and Future Actions**

Redd T.

JPI Oceans Secretariat, Brussels, Belgium

JPI Oceans can be seen as an organisation which is constantly learning. In the beginning, several Pilot Actions were initiated to test new tools and look at how JPI Oceans could operate after it published its Strategic Research and Innovation Agenda (SRIA). Now that this has been published, JPI Oceans will initiate new actions to achieve its goals. This talk will present how the Pilot Action: *Ecological Impacts of Microplastics* developed to demonstrate how JPI Oceans could act in the future. It will also present the process by which JPI Oceans selects and develops new actions.

Within the SRIA, JPI Oceans commits to address three cross cutting issues: Science-Policy Interfaces, Human Capacity Building, and Shared Use of Infrastructures. This talk will look at how JPI Oceans, as a long term initiative, can address the capacity building within marine and maritime sciences. Finally, it is important to consider how JPI Oceans can work with existing organisations and initiatives to add value and address the grand societal challenges it was established to address.

## **Innovative IP models: open research collaboration partnerships in marine biotechnology**

Dedeurwaerdere T.

Universite' Catholique de Louvain, Belgium

In a world of widely distributed knowledge, companies cannot afford to rely entirely on their own research, but instead buy and license processes or inventions from other companies. In addition, inventions not being used in a firm's business can be licensed for use outside of the company (e.g. through direct licensing, joint ventures or spin-offs). Open innovation does not require giving away patents for free: it actually heavily depends on patents. The idea is for companies to engage in open innovation organizing licensing activities and strategic alliances for proactive intellectual property strategies that aims at sharing technologies rather than hoarding IP as a defence mechanism.



## Exploring Marine Microorganisms for Novel Enzymes and Bioactive Compounds

Janssen D.B.<sup>1</sup>, Heberling M.<sup>1</sup>, Masman M.<sup>1</sup>

Groningen Biomolecular Sciences and Biotechnology Institute, University of Groningen, The Netherlands

Microorganisms are an extremely rich and diverse source of tools and products for the development of biotechnological applications. Within the MicroB3 project, efforts focused on the discovery of microbial enzymes with application potential in the production of fine-chemicals, the conversion of food and feed ingredients, and as building blocks for synthetic biology. These discovery studies make use of high-throughput laboratory screening but also increasingly employ bioinformatics and computational tools that allow prediction of function and activity from sequence. Enzyme panels for important conversions were established. The work in MicroB3 also pursued the discovery of new bioactive compounds, including antimicrobials, cytotoxic agents, surfactants and quorum quenching agents. Again, analysis of (meta)genome sequences by bioinformatics as well as discovery based on micro-cultures and metagenome expression libraries were used. The diversity of marine sampling sites that were explored, including hot pools on the Icelandic coast, hypersaline brine lakes at the bottom of the Mediterranean Sea, and sponge ecosystems on the Atlantic coast, is reflected in the broad range of activities that were characterized.

## Exploiting Systems Biology Platforms to develop innovative Bioactives for Therapeutic and Industrial applications.

O'Gara F.

Biomerit Research Centre . National University of Ireland Cork, Ireland

The main emphasis of the marine biodiscovery programme in the BIOMERIT Research Centre in Cork is the utilisation of culture dependent and independent genomic and metagenomic approaches to mine microbial communities associated with marine sponges for novel bioactive compounds with the potential to be exploited for innovative medical / industrial biotechnological applications.

The search for new / next generation antimicrobials has become a global issue due to the exponential rise in antimicrobial resistance. Against this the genomes of several marine bacteria have been sequenced and potential bioactive gene clusters identified. A number of 'classical' antimicrobial compounds, particularly from sponge associated *Streptomyces*, *Bacillus* and *Pseudovibrio* species have been successfully characterized, while bioactive compounds targeting microbial signaling systems essential for biofilm formation of clinically relevant pathogens have also been identified.

In parallel, functional metagenomic analysis of marine sponges has successfully identified several enzymatic compounds including, lipases, proteases and transaminases, with improved properties for industrial applications.

## **Microbial diversity and enzyme discovery in cultivated and non-cultivated microbiomes from marine environments in Iceland**

Marteinsson V. Þ.

Matis, Food safety, Environment and Genetics, Vínlandsleid 12, 113, Reykjavik, Iceland

Various samples were collected from open ocean waters around Iceland and from marine extreme sites or coastal hydrothermal vents in the Westfjords of Iceland and used for DNA extraction and strain cultivation. Geothermal springs are ideally suited for the investigation of extremophiles and adaptive mechanisms to extreme environments. Some geothermal springs are located at the intertidal zone and submerged in sea water at high tide but exposed at low tide, creating a unique environment where microorganisms are subjected to a wide range of environmental conditions on a tidal rhythm. Molecular taxonomic analyses of environmental and *in situ* enrichments samples revealed extensive microbial diversity. Bioinformatic analysis of metagenomes, fosmid libraries and whole genomes was screened for genes of biotechnological interest. *In silico* screening of bacterial genomes was the most effective method among our enzyme discovery approaches and various enzymes were successfully cloned, expressed and characterized with wide optimum temperature (5-65°C) and pH (5-8) ranges.

## **Global scientific research commons under the Nagoya Protocol: Towards a collaborative economy model for the sharing of basic research assets**

Dedeurwaerdere T.

Universite' Catholique de Louvain, Belgium

This paper aims to get a better understanding of the motivational and transaction cost features of building global scientific research commons, with a view to contributing to the debate on the design of appropriate policy measures under the recently adopted Nagoya Protocol. For this purpose, the paper analyses the results of a world-wide survey of managers and users of microbial culture collections, which focused on the role of social and internalized motivations, organizational networks and external incentives in promoting the public availability of upstream research assets. Overall, the study confirms the hypotheses of the social production model of information and shareable goods, but it also shows the need to complete this model. For the sharing of materials, the underlying collaborative economy in excess capacity plays a key role in addition to the social production, while for data, competitive pressures amongst scientists tend to play a bigger role.

## **The CIESM Charter, for access to knowledge and to prevent the abuses of the ocean global commons**

Barbier M.

CIESM, the Mediterranean Science Commission

Marine Genetic Resources have the potential to sustainably deliver wealth and business opportunities to local economies through the development of a wide array of applications in food, pharmaceuticals, cosmetics. In this context, the access and fair sharing of benefits (ABS) arising from their exploitation still remain an issue.

To help bridge some of the divergences and to facilitate dialogue among the relevant stakeholders, CIESM has drafted a Charter on ABS that apply to parties engaging in the collection and exploitation of MGRs. The Charter, built upon nine clear fundamental Principles, aims at favor marine research and development, while preventing abuses of the ocean global commons. It emphasizes essential core values, such as fair and equitable sharing of benefits, transparency, reciprocal relations. It is applicable to large scientific initiatives such as oceanographic campaigns and the Charter has been endorsed by hundred of scientists participating to the Ocean Sampling Day (50 countries).

## **The Nagoya Protocol and its implications for environmental research in the EU**

Lyal, C.H.C.

Department of Life Sciences, Natural History Museum, Cromwell Road, London SW7 5BD, UK

Research access genetic (and consequently biological) resources has increasingly been regulated. Most recently, the Nagoya Protocol on Access and Benefit Sharing came into force on 12 October 2014, at the same time as an EU Regulation to implement it. A further European Implementing Act is in force from 12 October 2015, and Member States are independently ratifying to Protocol and enacting national legislation. Many countries within and outside the EU are revising Access legislation. These novel legal frameworks will require researchers utilising genetic resources in the EU to develop appropriate data and sample management processes and policies, may demand reports to national authorities. The potential impact on research is unclear but potentially great. Current priorities are to raise awareness among researchers, and to develop tools to facilitate adoption of any necessary changes in procedures while minimising additional administrative requirements.



## Workshop

### An Academic Perspective on Collaborating with a Software SME on Bioinformatics Solutions

Kottmann R.

Microbial Genomics and Bioinformatics Research Group, Max Planck Institute for Marine Microbiology (Bremen, Germany)

Micro B3 exercised an unusual way of collaborating with a software company in order to achieve the goals of the “Bioinformatics and Data Integration” part of the project. The collaboration was established on a simple and clear open source strategy and implemented using a very agile and dynamic communication and working model. Overall, this resulted in numerous new software components for integrated marine metagenomics and many of which are vital part of the success of the Ocean Sampling Day. Would this extend and quality of software development have been possible otherwise? And might this way of collaboration inspire future collaborations? These questions will be discussed from an academic work perspective.

**Dr. Renzo Kottman, Max Planck Institute for Marine Microbiology (Bremen, Germany) - Lead of Micro B3 Work Package 5 (Bioinformatics & Data Integration)**

*Dr. Kottmann is scientist at the Max Planck Institute for Marine Microbiology (Bremen, Germany). He combines his expertise in computer science and marine microbiology to investigate optimal solutions in data integration, analysis, and visualization in the field of microbial environmental genomics. He gained experience in integration and analysis of (meta) genome and environmental data. Currently, he is leading the megx.net project (<http://www.megx.net>) as well as the workpackage “Bioinformatics and Data Integration” of the Micro B3 project ([www.microb3.eu](http://www.microb3.eu)), and he is a member of the Genomic Standards Consortium (GSC).*



## **IT business and Micro B3 - We did it very good. Can we do it even better?**

Pop Ristov A.

InterWorks (Bitola, Macedonia)

As a service oriented (subcontracting) IT Company, InterWorks has grown up on the US market entirely. As it is expected for an IT outsourcing company, InterWorks delivers solutions in many industry domains with different technical requirements. Still, these achievements were not enough for establishing itself more seriously on the EU market. In its quest towards being more present on this market, the management of the company embraced the invitation to become a partner on the Micro B3 project. By virtue of the more experienced partners on Micro B3, in a short while, InterWorks became a valuable member of the project consortium, providing its unambiguous contribution to the overall project's success. In addition to the opportunity to increase its EU market presence, among the other positive outcomes of the Micro B3 project, today, InterWorks can highlight the development of two products, focused on the education process and annotation of video footage for scientific purposes.

### **Aleksandar Pop Ristov - Managing Partner at InterWorks (Bitola, Macedonia) - Partner of Micro B3**

*Entrepreneur with over 35 years presence in the software industry, and more than 25 years proven experience in management, leadership, sales, consultancy and recruitment. Visioning to create innovative software solutions that will influence the world.*

*Founder and Managing partner of InterWorks, IT outsourcing company delivering a full spectrum of software development and support services. InterWorks' focus is on understanding Client's needs and delivering solutions that will exceed their expectations as well as providing sustainable professional environment for its employees. InterWorks' industry domain is focused on the Telecom, Healthcare, Banking, Agriculture and Energy sectors, in addition to the collaborative EU scientific projects and several GA high-tech projects and software solutions.*

*Managing InterWorks involves making strategic decisions, negotiating with clients, representing the company on conferences/events, making decisions regarding Sales & Marketing, Finance & Legal, nurture client relationships etc. It also includes the responsibility to make sure company's goals are being achieved, monitor employees and their everyday activities, work on improving the internal business processes and monitor they are in line with the Company Vision, Mission and Policy and the Quality standards embedded in the everyday work of the Company.*



## **Mobilization of public rRNA gene sequence data: the dbblast system for microbial quality control at Roche**

Eder W.

Roche Diagnostics GmbH (Penzberg, Germany)

A database named dbblast was implemented at microbial quality control labs at Roche for routine identification of bacteria and fungi. The dbblast database contains public available rRNA gene sequence data which are selected by applying specific quality criteria. dbblast created by Ribocon (Bremen, Germany) combines state-of-the-art ID analysis with up-to-date nomenclature. After comprehensive IT and microbiological validation, the web-based dbblast database is used as a cloud application (Software-as-a-Service) in a GxP environment for the entire Roche network to identify microorganisms. dbblast is a perfect example of combining modern science with industrial needs.

### **Dr. Wolfgang Eder - Manager Quality Control at Roche Diagnostics GmbH (Penzberg, Germany)**

*Dr. Wolfgang Eder holds a PhD in microbiology from the University of Regensburg (Germany). After working at Diversa Corporation (USA), profos AG (Germany) and the University of Regensburg (Germany) he joined Roche in 2006. Currently he is Senior Manager Quality Control for Environmental Monitoring and Cleaning in the Pharma Division at Roche Diagnostics GmbH (Germany) and involved in several microbial identification and RMM projects.*



## **From mind to market: How to develop competitive products by using EU projects enabled collaborations**

Snaidr J.

Vermicon AG (München, Germany)

The participation in multi-national projects funded by the European Commission is a powerful tool for SMEs to support the development of innovative products. The multi-cultural environment as well as the involvement of academia, industry and end-users allows a profound analysis of pros and cons regarding the development therefore reducing the risk and time-to-market of the product.

Examples are shown how the involvement in different EU projects resulted in the successful development and marketing of new and target-oriented products. Strategies will be explained how to profit best from the unique opportunity of an EU collaboration which lead to a better understanding of the market segments and its environment and finally to the successful market launch of the innovations.

### **Jiri Snaidr - Managing Board at Vermicon AG (München, Germany)**

*Dr. Jiri Snaidr is an entrepreneur and microbiologist who got his Ph.D. at the Technical University in Munich, Department of Microbiology. After subsequent management education in England he founded the Vermicon AG in 1997 where he is the Chief Executive Officer and President until today. He built up the company to an international provider of solutions for microbiology. The platform technology VIT® provides fast and highly specific identification and quantification of microorganisms. Products and services of Vermicon are used worldwide in all segments of industrial microbiology. Customers range from multi-international companies to local producers, authorities and laboratories. Dr. Snaidr is furthermore active as an author and international speaker for microbiological and entrepreneurial topics and member in entrepreneurial and funds giving committees.*

## **Sustainably using the ocean's services - tapping the potential of marine living resources by Marine Biotechnology**

Piker L.<sup>1,2</sup>, Krost, P.<sup>1,2</sup>, Linke, I.<sup>2</sup>, Koch, C.<sup>1,2</sup>

<sup>1</sup> CRM – Coastal Research & Management

<sup>2</sup> oceanBASIS GmbH

This presentation gives an interim balance of two decades of R&D in Marine Biotechnology (MB) and of marketing products originating from marine living resources by the sister companies CRM and oceanBASIS (Kiel, Germany).

Whereas stakeholders pave ways for MB into research and policy, there is still no evidence that it will evolve to a relevant economic sector. It will be discussed, what the future could hold for MB from an entrepreneurial and societal perspective and how (bio-)diversity might play a key role for exploiting the potential of Marine Biotechnology on an entrepreneurial as well as on broader economic scale.

We will give examples of own research and economic activities in the fields of tissue engineering, wound-healing, screening of antitumoral and anti-infectious properties, development, production and marketing of seaweed and shellfish from an Integrated Multitrophic Aquaculture (IMTA) facility, bioactives for the cosmetic industry, as well as the natural cosmetics brand “Oceanwell”.

### **Levent Piker - Managing Board at oceanBASIS GmbH (Kiel, Germany)**

*Levent Piker, Marine Biologist with focus in Sediment Microbiology, founded CRM-Coastal Research & Management in 1994 together with colleagues and works there on various aspects of anthropogenic impacts on marine ecosystems and ICZM. He has directed his research focus on anti-infectious and anti-cancer effects of seaweed compounds over the last ten years. Levent Piker co-founded another company, oceanBASIS GmbH, in 2001 developing and marketing marine natural products, e.g. extracts from algae as active ingredients for the cosmetic industry. At oceanBASIS he is shareholder, head of R&D and also responsible for innovation management and internet marketing. Several studies and publications on pollution, ecotoxicity, impact of aquaculture, and health effects of marine natural substances. Member of the Society of Marine Sciences (DGM), and “Sea Future” group in Schleswig-Holstein, and the “Maritime Consulting Group – MCG”. Co-founder and member of “Transmare e.V.”, an NGO, which informs and educates on marine issues with respect to AGENDA 21 (Chapter 17). Levent Piker is actively involved in developing a strategy of marine biotechnology on enterprise, national and European level. He has participated in numerous working groups, conferences and seminars in the national and international context for this topic since the late 90s. Vision: Intelligent and sustainable use of living marine resources by adding value in order to make them available for human health.*

## **The OTARI project, “*Ostreococcus tauri* from Research to Industry”: a joint laboratory between academics and a SME.**

Bouget F.Y.<sup>2</sup>, Pradelle R.<sup>2</sup>

<sup>1</sup> Laboratory of Microbial Oceanography, University Paris 06, Banyuls sur Mer (France).

<sup>2</sup> Microphyt SA, Route de Mudaison, Baillargues, France.

Microalgae provides an importance source of compounds of interest for blue biotech, such as exopolysaccharides, pigments or polyunsaturated fatty acids. These molecules have a wide range of applications in the fields of nutraceutical, dermo-cosmetics or health. The economic valorisation of these compounds however, requires to lift two major constraints: (1) the selection of lines overexpressing molecules of interest, (2) the standardized high scale production of microalgae under controlled conditions in industrial photobioreactors.

The OTARI Lab, supported by the French national agency of research, associates two partners with complementary expertise. The Laboratory of microbial oceanography (Banyuls sur Mer, France) has developed and patented techniques for genetic engineering of the picoalga *Ostreococcus tauri*, while the SME Microphyt (Baillargues, France) has developed a unique photobioreactor and technologies for producing algal biomass and purifying compounds of interest. The objective of OTARI is to implement a platform for the production of high added value compounds from *Ostreococcus tauri*.

**François-Yves Bouget - CNRS Research Director at Laboratory of Microbial Oceanography, University Paris 06 (Banyuls sur Mer, France)**

*Dr. Bouget is currently CNRS Research Director at Laboratory of Microbial Oceanography and responsible of the team “Regulation of microbial functions by light and nutrients at Laboratory of microbial oceanography, Banyuls sur Mer. His current research focuses on the use of functional genomics approaches in model organisms to understand how marine phytoplankton optimises the use of environmental factors and the impact of global warming, his research interest is also to promote microalgal model organisms in oceanography and biotechnology. Dr. Bouget is currently involved in several national and international projects.*



# Tara Oceans studies plankton at PLANETARY SCALE

By P. Bork,<sup>1</sup> C. Bowler,<sup>2</sup> C. de Vargas,<sup>3,4</sup> G. Gorsky,<sup>5,6</sup> E. Karsenti,<sup>2,7</sup> P. Wincker<sup>8</sup>

**T**he ocean is the largest ecosystem on Earth, and yet we know very little about it. This is particularly true for the plankton that inhabit the ocean. Although these organisms are at least as important for the Earth system as the rainforests and form the base of marine food webs, most plankton are invisible to the naked eye and thus are largely uncharacterized. To study this invisible world, the multinational Tara Oceans consortium, with use of the 110-foot research schooner *Tara*, sampled microscopic plankton at 210 sites and depths up to 2000 m in all the major oceanic regions during expeditions from 2009 through 2013 (1).

Success depended on collaboration between scientists and the *Tara* Expeditions logistics team. The journey involved not only science but also outreach and education as well as negotiation through the shoals of legal and political regulations, funding uncertainties, threats from pirates, and unpredictable weather (2). At various times, journalists, artists, and teachers were also on board. Visitors included Ban Ki-moon (Secretary-General of the United Nations) and numerous youngsters, including schoolchildren from the favelas in Rio de Janeiro.

Sampling, usually 60 hours per site, followed standardized protocols (3) to capture the morphological and genetic diversity of the entire plankton community from viruses to small zooplankton, covering a size range from 0.02  $\mu\text{m}$  to a few millimeters, in context with physical and chemical information. Besides the sampling, a lab on board contained a range of online instruments and microscopes to monitor the content of the samples as they were being collected. The main focus was on the organism-rich sunlit upper layer of the ocean (down to 200 m), but the twilight zone below was also sampled. Guided by satellite and in situ data, scientists sampled features such as mesoscale eddies, upwellings, acidic waters, and anaerobic zones, frequently in the open ocean. In addition to being used for genomics and oceanography, many samples were collected for other analyses, such as high-throughput microscopy imaging and flow cytometry. The samples and data collected on board were archived in a highly structured

way to enable extensive data processing and integration on land (4). The five Research Articles in this issue of *Science* describe the samples, data, and analysis from *Tara* Oceans (based on a data freeze from 579 samples at 75 stations as of November 2013).

De Vargas *et al.* used ribosomal RNA gene sequences to profile eukaryotic diversity in the photic zone. This taxonomic census shows that most biodiversity belongs to poorly known lineages of uncultured heterotrophic single-celled protists. Sunagawa *et al.* used metagenomics to study viruses, prokaryotes, and picoeukaryotes. They established a catalog with >40 million genes and identified temperature as the driver of photic microbial community composition. Brum *et al.*, by sequencing and electron microscopy, found that viruses are diverse on a regional basis but less so on a global basis. The viral communities are passively transported by oceanic currents and structured by local environments. Lima-Mendez *et al.* modeled interactions between viruses, prokaryotes, and eukaryotes. Regional and global parameters refine resulting networks. Villar *et al.* studied the dispersal of plankton as oceanic currents swirl around the southern tip of Africa, where the Agulhas rings are generated. Vertical mixing in the rings drives nitrogen cycling and selects for specific organisms.

*Tara* Oceans combined ecology, systems biology, and oceanography to study plankton in their environmental context. The project has generated resources such as an ocean microbial reference gene catalog; a census of plankton diversity covering viruses, prokaryotes, and eukaryotes; and methodologies to explore interactions between them and their integration with environmental conditions. Although many more such analyses will follow, life in the ocean is already a little less murky than it was before.

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## Eukaryotic plankton diversity in the sunlit ocean

C. de Vargas,\* S. Audic, N. Henry, J. Decelle, F. Mahé, R. Logares, E. Lara, C. Berney, N. Le Bescot, I. Probert, M. Carmichael, J. Poulain, S. Romac, S. Colin, J.-M. Aury, L. Bittner, S. Chaffron, M. Dunthorn, S. Engelen, O. Flegontova, L. Guidi, A. Horák, O. Jaillon, G. Lima-Mendez, J. Lukeš, S. Malviya, R. Morard, M. Mulot, E. Scalco, R. Siano, F. Vincent, A. Zingone, C. Dimier, M. Picheral, S. Searson, S. Kandels-Lewis, *Tara Oceans Coordinators*, S. G. Acinas, P. Bork, C. Bowler, G. Gorsky, N. Grimsley, P. Hingamp, D. Iudicone, F. Not, H. Ogata, S. Pesant, J. Raes, M. E. Sieracki, S. Speich, L. Stemmann, S. Sunagawa, J. Weissenbach, P. Wincker,\* E. Karsenti\*

Marine plankton support global biological and geochemical processes. Surveys of their biodiversity have hitherto been geographically restricted and have not accounted for the full range of plankton size. We assessed eukaryotic diversity from 334 size-fractionated photic-zone plankton communities collected across tropical and temperate oceans during the circumglobal *Tara Oceans* expedition. We analyzed 18S ribosomal DNA sequences across the intermediate plankton-size spectrum from the smallest unicellular eukaryotes (protists, >0.8 micrometers) to small animals of a few millimeters. Eukaryotic ribosomal diversity saturated at ~150,000 operational taxonomic units, about one-third of which could not be assigned to known eukaryotic groups. Diversity emerged at all taxonomic levels, both within the groups comprising the ~11,200 cataloged morphospecies of eukaryotic plankton and among twice as many other deep-branching lineages of unappreciated importance in plankton ecology studies. Most eukaryotic plankton biodiversity belonged to heterotrophic protistan groups, particularly those known to be parasites or symbiotic hosts.

The list of author affiliations is available in the full article online. \*Corresponding author. E-mail: vargas@sb-roscoff.fr (C.d.V.); pwincker@genoscope.cns.fr (P.W.); karsenti@embl.de (E.K.) Cite as C. de Vargas *et al.*, *Science* 348, 1261605 (2015).

Read the full article at <http://dx.doi.org/10.1126/science.1261605>

## Structure and function of the global ocean microbiome

S. Sunagawa,\* L. P. Coelho, S. Chaffron, J. R. Kultima, K. Labadie, G. Salazar, B. Djahanschiri, G. Zeller, D. R. Mende, A. Alberti, F. M. Cornejo-Castillo, P. I. Costea, C. Cruaud, F. d'Ovidio, S. Engelen, I. Ferrera, J. M. Gasol, L. Guidi, F. Hildebrand, F. Kokoszka, C. Lepoivre, G. Lima-Mendez, J. Poulain, B. T. Poulos, M. Royo-Llonch, H. Sarmiento, S. Vieira-Silva, C. Dimier, M. Picheral, S. Searson, S. Kandels-Lewis, *Tara Oceans Coordinators*, C. Bowler, C. de Vargas, G. Gorsky, N. Grimsley, P. Hingamp, D. Iudicone, O. Jaillon, F. Not, H. Ogata, S. Pesant, S. Speich, L. Stemmann, M. B. Sullivan, J. Weissenbach, P. Wincker, E. Karsenti,\* J. Raes,\* S. G. Acinas,\* P. Bork\*

Microbes are dominant drivers of biogeochemical processes, yet drawing a global picture of functional diversity, microbial community structure, and their ecological determinants remains a grand challenge. We analyzed 7.2 terabases of metagenomic data from 243 *Tara Oceans* samples from 68 locations in epipelagic and mesopelagic waters across the globe to

generate an ocean microbial reference gene catalog with >40 million nonredundant, mostly novel sequences from viruses, prokaryotes, and picoeukaryotes. Using 139 prokaryote-enriched samples, containing >35,000 species, we show vertical stratification with epipelagic community composition mostly driven by temperature rather than other environmental factors or geography. We identify ocean microbial core functionality and reveal that >73% of its abundance is shared with the human gut microbiome despite the physicochemical differences between these two ecosystems.

The list of author affiliations is available in the full article online. \*Corresponding author. E-mail: sunagawa@embl.de (S.S.); karsenti@embl.de (E.K.); jeroen.raes@vib-kuleuven.be (J.R.); sacinas@icm.csic.es (S.G.A.); bork@embl.de (P.B.) Cite as S. Sunagawa *et al.*, *Science* 348, 1261359 (2015).

Read the full article at <http://dx.doi.org/10.1126/science.1261359>

## Patterns and ecological drivers of ocean viral communities

J. R. Brum, J. C. Ignacio-Espinoza, S. Roux, G. Doucier, S. G. Acinas, A. Alberti, S. Chaffron, C. Cruaud, C. de Vargas, J. M. Gasol, G. Gorsky, A. C. Gregory, L. Guidi, P. Hingamp, D. Iudicone, F. Not, H. Ogata, S. Pesant, B. T. Poulos, S. M. Schwenck, S. Speich, C. Dimier, S. Kandels-Lewis, M. Picheral, S. Searson, *Tara Oceans Coordinators*, P. Bork, C. Bowler, S. Sunagawa, P. Wincker, E. Karsenti,\* M. B. Sullivan\*

Viruses influence ecosystems by modulating microbial population size, diversity, metabolic outputs, and gene flow. Here, we use quantitative double-stranded DNA (dsDNA) viral-fraction metagenomes (viromes) and whole viral community morphological data sets from 43 *Tara Oceans* expedition samples to assess viral community patterns and structure in the upper ocean. Protein cluster cataloging defined pelagic upper-ocean viral community pan and core gene sets and suggested that this sequence space is well-sampled. Analyses of viral protein clusters, populations, and morphology revealed biogeographic patterns whereby viral communities were passively transported on oceanic currents and locally structured by environmental conditions that affect host community structure. Together, these investigations establish a global ocean dsDNA viromic data set with analyses supporting the seed-bank hypothesis to explain how oceanic viral communities maintain high local diversity.

The list of author affiliations is available in the full article online. \*Corresponding author. E-mail: mbsulli@gmail.com (M.B.S.); karsenti@embl.de (E.K.) Cite as Brum *et al.*, *Science* 348, 1261498 (2015).

Read the full article at <http://dx.doi.org/10.1126/science.1261498>

## Determinants of community structure in the global plankton interactome

G. Lima-Mendez, K. Faust, N. Henry, J. Decelle, S. Colin, F. Carcillo, S. Chaffron, J. C. Ignacio-Espinoza, S. Roux, F. Vincent, L. Bittner, Y. Darzi, J. Wang, S. Audic, L. Berline, G. Bontempi, A. M. Cabello, L. Coppola, F. M. Cornejo-Castillo, F. d'Ovidio, L. De Meester, I. Ferrera, M.-J. Garet-Delmas, L. Guidi, E. Lara, S. Pesant, M. Royo-Llonch, G. Salazar, P. Sánchez, M. Sebastian, C. Souffreau, C. Dimier, M. Picheral, S. Searson, S. Kandels-Lewis,

## Plankton diversity

*Tara* Oceans sampled the smallest in the planktonic world, including viruses, bacteria, protists, and zooplankton. These spectacular and plentiful organisms form the microscopic basis of marine food webs. Analysis of their genes and genomes provides the basis for research insights into identities and interactions.

Podovirus



50 nm

Siphovirus



100 nm

Coccolithophore,  
*Rhabdosphaera* sp.



5 μm

Eubacteria,  
*Bacteroidetes* sp.



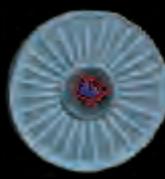
10 μm

Dinoflagellate,  
*Ceratium* sp.



20 μm

Diatom,  
*Planktoniella* sp.



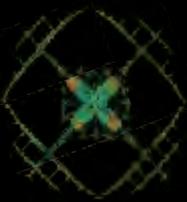
20 μm

Foraminiferan,  
*Globigerinoides* sp.



50 μm

Acantharian,  
*Lithoptera* sp.



60 μm

Copepod,  
*Centropages* sp.



500 μm

Polychaete annelid,  
*Myrianida* sp.



500 μm

Colonial radiolarian,  
*Sphaerozoum* sp.



1000 μm

Siphonophore,  
*Leusia* sp.



2000 μm

**Tara Oceans Coordinators, G. Gorsky, F. Not, H. Ogata, S. Speich, L. Stemmann, J. Weissenbach, P. Wincker, S. G. Acinas, S. Sunagawa, P. Bork, M. B. Sullivan, E. Karsenti,\* C. Bowler,\* C. de Vargas,\* J. Raes\***

Species interaction networks are shaped by abiotic and biotic factors. Here, as part of the *Tara* Oceans project, we studied the photic zone interactome using environmental factors and organismal abundance profiles and found that environmental factors are incomplete predictors of community structure. We found associations across plankton functional types and phylogenetic groups to be nonrandomly distributed on the network and driven by both local and global patterns. We identified interactions among grazers, primary producers, viruses, and (mainly parasitic) symbionts and validated network-generated hypotheses using microscopy to confirm symbiotic relationships. We have thus provided a resource to support further research on ocean food webs and integrating biological components into ocean models.

The list of author affiliations is available in the full article online. \*Corresponding author. E-mail: jeroen.raes@vib-kuleuven.be (J.R.); vargas@sb-roscoff.fr (C.d.V.); cbowler@biologie.ens.fr (C.B.); karsenti@embl.de (E.K.) Cite as G. Lima-Mendez *et al.*, *Science* 348, 1262073 (2015).

Read the full article at <http://dx.doi.org/10.1126/science.1262073>

## Environmental characteristics of Agulhas rings affect interocean plankton transport

**E. Villar,\* G. K. Farrant, M. Follows, L. Garczarek, S. Speich, S. Audic, L. Bittner, B. Blanke, J. R. Brum, C. Brunet, R. Casotti, A. Chase, J. R. Dolan, F. d'Ortenzio, J.-P. Gattuso, N. Grima, L. Guidi, C. N. Hill, O. Jahn, J.-L. Jamet, H. Le Goff, C. Lepoivre, S. Malviya, E. Pelletier, J.-B. Romagnan, S. Roux, S. Santini, E. Scalco, S. M. Schwenck, A. Tanaka, P. Testor, T. Vannier, F. Vincent, A. Zingone, C. Dimier, M. Picheral, S. Searson, S. Kandels-Lewis, Tara Oceans Coordinators, S. G. Acinas, P. Bork, E. Boss, C. de Vargas, G. Gorsky, H. Ogata, S. Pesant, M. B. Sullivan, S. Sunagawa, P. Wincker, E. Karsenti,\* C. Bowler,\* F. Not,\* P. Hingamp,\* D. Iudicone\***

Agulhas rings provide the principal route for ocean waters to circulate from the Indo-Pacific to the Atlantic basin. Their influence on global ocean circulation is well known, but their role in plankton transport is largely unexplored. We show that, although the coarse taxonomic structure of plankton communities is continuous across the Agulhas choke point, South Atlantic plankton diversity is altered compared with Indian Ocean source populations. Modeling and in situ sampling of a young Agulhas ring indicate that strong vertical mixing drives complex nitrogen cycling, shaping community metabolism and biogeochemical signatures as the ring and associated plankton transit westward. The peculiar local environment inside Agulhas rings may provide a selective mechanism contributing to the limited dispersal of Indian Ocean plankton populations into the Atlantic.

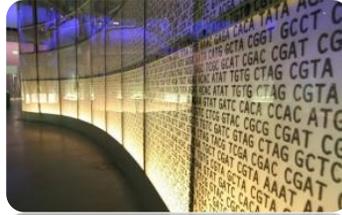
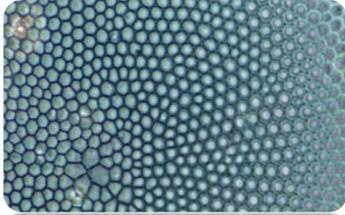
The list of author affiliations is available in the full article online. \*Corresponding author. E-mail: villar@igs.cnrs-mrs.fr (E.V.); not@sb-roscoff.fr (F.N.); hingamp@igs.cnrs-mrs.fr (P.H.); iudicone@szn.it (D.I.); karsenti@embl.de (E.K.); cbowler@biologie.ens.fr (C.B.) Cite as E. Villar *et al.*, *Science* 348, 1261447 (2015).

Read the full article at <http://dx.doi.org/10.1126/science.1261447>





# Biodiversity, Bioinformatics, Biotechnology



## Overview

In Micro B3 32 partners from 14 countries work together in nine interdisciplinary teams of experts in bioinformatics, computer science, biology, ecology, oceanography, biotechnology, ethics and law for a better understanding of the marine ecosystem and to pave the way for novel biotechnological applications. Micro B3's primary objective is to integrate biodiversity, genomic, and oceanographic data into one Information System (IS), the Micro B3-IS, which is based on global standards for sampling and data processing.

## Key Products and Results

1. Best-practice guidelines and standards for collecting marine water samples, environmental data, logistics and bioinformatics for long-term ecological research sites and cruises
2. Integrated biodiversity, genomic, and oceanographic data via the Micro B3-IS
3. An annotation pipeline to identify viral, bacterial, archaeal and eukaryotic sequences in metagenomic reads
4. Computational workflows for predicting substrate selectivity of genes with known activities
5. Co-occurrence networks for "unknown" genes using known data to improve functional predictions
6. Innovative model agreements on Access to marine microorganisms and Benefit Sharing (ABS) distinguishing between research and development for the public domain and for proprietary purposes
7. Propagation of standards and data flows to facilitate free and open sharing of data and metadata
8. Dissemination of the project outputs:
  - 80 peer-reviewed publications to date
  - Three workshops and five training courses
  - Participation in more than 70 international workshops, conferences, business meetings, and EU-wide events
  - OSD movie and Micro B3 documentary
  - Organisation of global Ocean Sampling Days (OSD): a world wide community network of scientists and citizens for orchestrated sampling

# OSD

Ocean Sampling Day

**Title:** Marine Microbial Biodiversity, Bioinformatics and Biotechnology (Micro B3)

**Funding Scheme:** FP7-OCEAN

**Total Budget:** € 11,507,843 **EU Financial Contribution:** € 8,987,491

**Duration:** January 2012 – December 2015

**Coordinator:** Jacobs University Bremen gGmbH, Bremen (Germany)

[www.microb3.eu](http://www.microb3.eu)



Micro B3 has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration (Joint Call OCEAN.2011-2: Marine microbial diversity – new insights into marine ecosystems functioning and its biotechnological potential) under grant agreement no 287589.

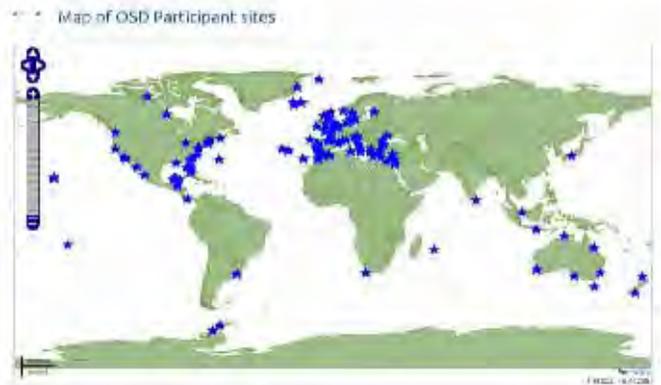
# Ocean Sampling Day a Global Event for Sequencing the Oceans



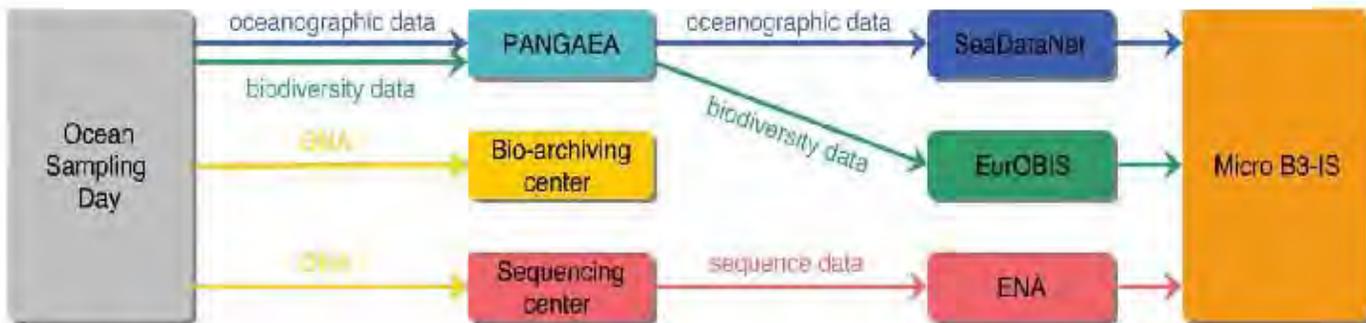
The Micro B3 Consortium initiated the idea of an orchestrated Ocean Sampling Day (OSD) with the ambitious aim to turn this into long-term time series (Genomic Observatories). The main goal of OSD is to analyse marine microbial biodiversity and function of the World's ocean.



*The first Ocean Sampling Day took place on **June 21<sup>st</sup> 2014**. This OSD event involved 191 sampling sites from all continents ranging from tropical waters around Hawaii to extremely cold environments such as the Fram Strait in the Arctic Ocean.*



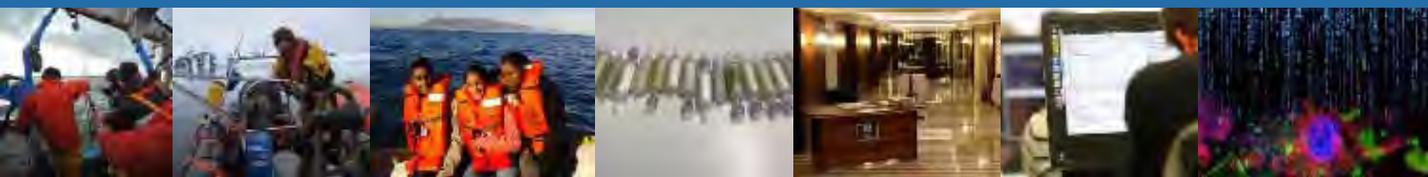
Standardized procedures, including the OSD handbook and a centralized hub for laboratory work and data processing assure a high level of consistency and data interoperability. The required bioinformatics capacity for data management, processing and analysis are combined in the Micro B3 Information System (Micro B3-IS). The Micro B3 Reporting- and Service Standards (M2B3) ensure consistent data storage across domains in the data archives shown below.



The OSD on June 21<sup>st</sup> 2014 has shown that more than 190 marine stations can be mobilized, organized and trained to work closely together to create a snapshot of the microbes in the World's ocean.

The next OSD is planned for **June 21<sup>st</sup> 2015**

For more information please visit: [www.oceansamplingday.org](http://www.oceansamplingday.org)





**Thanks to all Micro B3, OSD and MyOSD  
participants for their valuable contribution to  
this successful project**



**Annex 5: Press release published on Cordis**



## Micro B3 Final Conference in Brussels

Contributed by: Jacobs University Bremen gGmbH

From 2015-11-02 to 2015-11-04, Belgium

**The Micro B3 Final Conference will take place at the Royal Flemish Academy of Belgium for Science and the Arts (Brussels) from 2nd to 4th November 2015. The objective of this high-level marine conference is to bring together policy and biodiversity stakeholders from Europe and overseas. It will present fascinating results of genomic-driven marine research, discuss emerging new knowledge and provide key recommendations to European Commission and further policy and industry stakeholders.**

The conference is led by the EU Micro B3 Project (Marine Microbial Biodiversity, Bioinformatics, Biotechnology, [www.microb3.eu](http://www.microb3.eu)), coordinated by Dr. Frank Oliver Glöckner, Professor of Bioinformatics at Jacobs University gGmbH in Bremen.

From 2012 until end of 2015 Micro B3 is implementing its primary objective by providing integrated access to biodiversity, genomic, oceanographic and earth-observation databases. Micro B3 is developing an innovative, transparent and user-friendly Information System for seamless integration, and visualisation of huge amount of marine data from past and on-going biodiversity sampling campaigns (i.e., Global Ocean Sampling, Tara Oceans and Malaspina expeditions, long-term ecological research stations, and from Micro B3's novel Ocean Sampling Days).

The agenda covers the three main pillars of Micro B3: biodiversity, bioinformatics and biotechnology. It outlines the scientific and policy outcomes of Micro B3, including showcasing two movies produced during the project. The first day of the Conference, 2nd November, is dedicated to the Ocean Sampling Days, which performed global snapshots of marine microbial diversity and function. Innovations on marine monitoring techniques will be highlighted. Invited talks will be given by Linda Amaral Zettler (Josephine Bay Paul Center/Brown University, USA, Micro B3 Advisory Board Member), Ángel Borja (EU FP7 DEVOTES project Coordinator), and Simon Claus (EU H2020 AtlantOS project partner).

3rd November starts with a multidisciplinary session on interoperability across scientific domains and communities and is closed by an invited talk by Torger Børresen (Innovation Fund Denmark) on behalf of the Marine Biotechnology ERA-NET. After lunch the third Industry Expert Workshop takes place, titled "Collaboration across Academia, SMEs, and Industry - Transforming Inventions into Innovations", to which industry stakeholders are especially invited. It is organized by Ribocon GmbH Bremen and takes place in the Auditorium of the Academy. The last day will present the fascinating scientific outcomes of the TARA Ocean Expedition as recently published in Science, with invited talks by Colomban de Vargas (Station Biologique de Roscoff) and on Ocean Sampling Day metagenome data by Francesca Malfatti (OGS-National Institute of Oceanography and Experimental Geophysics). It will continue with sessions on transfer of knowledge through training and will highlight legal and policy outcomes of Micro B3, like the CIESM Charter and a Model Agreement to implement the Nagoya Protocol on Access and Benefit Sharing. The day will be rounded up by a talk of the invited speaker Chris Lyal from the Natural History Museum of London about the Nagoya Protocol and its implications for environmental research in the EU.

The full programme is available at [www.microb3.eu/events/meetings/finalconference/programme](http://www.microb3.eu/events/meetings/finalconference/programme)

Participation is free of charge and registration should be done online best until 02 Oct 2015 at [www.microb3.eu/events/meetings/final-conference/registration](http://www.microb3.eu/events/meetings/final-conference/registration)

More information can be found here: [www.microb3.eu/events/meetings/final-conference](http://www.microb3.eu/events/meetings/final-conference)

### Venue:

Royal Flemish Academy of Belgium for Science and the Arts  
Hertogsstraat, 1  
1000 - Bruxelles (Belgium)

For press enquiries please contact:

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[See more events from this contributor](#)

## Related information

### Projects

- [MICRO B3 - "Marine Microbial Biodiversity, Bioinformatics and Biotechnology"](#)

### Events

- [Third Micro B3 Industry Expert Workshop](#)

### Countries

- [Belgium](#)

## Subjects

[Biotechnology](#) - [Industrial biotech](#) - [Innovation and Technology Transfer](#) - [Scientific Research](#)

**Last updated on** 2015-09-25

Category: Event

Provider: WIRE

Revision: 0

**Retrieved on** 2015-10-06

**Permalink:** [http://cordis.europa.eu/event/rcn/143655\\_en.html](http://cordis.europa.eu/event/rcn/143655_en.html)

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**Annex 6: German and English press release prepared by EMPA**



## **Invitation to the Micro B3 Final Conference**

2 to 4 November 2015, Royal Flemish Academy for Science and the Arts  
Hertogsstraat/Rue Ducale 1, B-1000 Brussels (Belgium)

# **Tracking and Tracing the Smallest Marine Life Forms**

Micro B3 is a large integrative European Project, which is processing large amounts of data from worldwide marine research campaigns with modern bioinformatic methods. This instigated a new understanding of the diversity of marine plankton. In cooperation with biotechnologists novel opportunities are explored, how to utilize these small organism while safeguarding marine resources. Furthermore, Micro B3 developed international standards to enable the trans-disciplinary use of a range of different existing databases. These standards were mainly tested during the 'Ocean Sampling Days' (OSD), a Micro B3-initiated activity joining scientists and interested citizens worldwide.

The final conference is dedicated to put to wider use bioinformatics and genomic technologies for ocean observation and monitoring. Already, greater public interest in marine research has been achieved with the citizen science component of the Ocean Sampling Days. Now, documentary films will show exceptional footage, highlighting Micro B3's key topics. Furthermore, project partners and invited speakers will present the following scientific results:

1. Use of bioinformatics tools for discovery, description and visualisation for the utilisation of novel gene functions;
2. Development of integrated trans-disciplinary access to existing international databases (marine biodiversity, genomics, oceanography and earth observation)
3. Model Agreement on implementing the Nagoya Protocol on Access and Benefit Sharing of (marine) genetic resources to the Convention on Biological Diversity.

Please find the detailed programme at

[www.microb3.eu/events/meetings/final-conference/programme](http://www.microb3.eu/events/meetings/final-conference/programme)

Embedded into the programme is the third Micro B3 Industry Expert Workshop on knowledge exchange between academia and industry titled: 'Collaboration across Academia, SMEs, and Industry: Transforming Inventions into Innovations'.

Please find the workshop programme at

<https://www.microb3.eu/events/workshops/Industry-Workshop>

### **Registration:**

<https://www.microb3.eu/events/meetings/final-conference/registration>

RSVP. We would like to support you to identify sessions or interview partners of interest for you. Please register and/or contact us.

## **More Information and Contacts:**

The Micro B3 project includes 32 Partner from 14 European countries, including the international organisations EMBL-EBI, ICES, IUCN and CIESM.

For more see [www.microb3.eu](http://www.microb3.eu)

Prof. Dr. Frank Oliver Glöckner (Professor for Bioinformatics at Jacobs University gGmbH Bremen, coordinator of the conference and the Micro B3 project)

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Mobile +49-170-755 7826

## **Einladung zur Micro B3 Final Conference (in englischer Sprache)**

2. bis 4. November 2015, Royal Flemish Academy for Science and the Arts  
Hertogsstraat/Rue Ducale 1, B-1000 Brüssel (Belgien)

# **Auf den Spuren kleinster Meereslebewesen**

Micro B3 ist ein integratives EU-Projekt mit 32 Partnern aus 14 europäischen Ländern, das unzählige Daten aus weltweiten Meeresforschungs-Kampagnen mit modernsten Methoden der Bioinformatik verarbeitet. Die Arbeit des Projektes hat ein neues Verständnis für die Vielfalt des Meeresplanktons geschaffen. In Zusammenarbeit mit Biotechnologen werden neue Möglichkeiten zur Nutzung dieser Kleinstlebewesen entwickelt. Außerdem hat Micro B3 weltweite Standards festgelegt, um den fachübergreifenden Zugang zu verschiedensten Datenbanken zu ermöglichen. Diese Standards wurden vor allem während der „Ocean Sampling Days“ (OSD) getestet, einer von Micro B3 initiierten weltweiten Aktion von Wissenschaftlerinnen, Wissenschaftlern und interessierten Laien.

Die Konferenz ist der breiten Nutzung bioinformatischer und genomischer Techniken zur Meeresbeobachtung gewidmet. Mit den Ocean Sampling Days gelang es bereits, ein größeres öffentliches Interesse an der Meeresforschung zu wecken. Eindrucksvolle Bilder zu diesen Themen zeigen zwei Filmvorführungen während der Konferenz.

Partner und Gastredner stellen unter anderem Forschungsergebnisse zu diesen Themen vor:

- 1) Nutzung bioinformatischer Werkzeuge für die Entdeckung, Beschreibung und Visualisierung neuer Genfunktionen
- 2) Entwicklung eines fachübergreifenden integrierten Zugangs zu existierenden Datenbanken (marine Biodiversität, Genomik, Ozeanographie und Erdbeobachtung)
- 3) Modellabkommen zur Umsetzung des Nagoya-Protokolls für den Zugang und Vorteilsausgleich zu marinen genetischen Ressourcen (Access and Benefit Sharing, ABS) zur Biodiversitäts-Konvention (Convention on Biological Diversity, CBD)

Das detaillierte Programm finden Sie unter

[www.microb3.eu/events/meetings/final-conference/programme](http://www.microb3.eu/events/meetings/final-conference/programme)

Eingebettet in das Konferenzprogramm ist zudem der 3. Micro B3 Industry Expert Workshop. Es handelt sich um ein Wissensaustauschforum zwischen Akademikern und Industrievertretern, dieses Mal zum Thema „Collaboration across Academia, SMEs, and Industry: Transforming Inventions into Innovations“.

Das Workshop-Programm finden Sie unter

<https://www.microb3.eu/events/workshops/Industry-Workshop>

**Teilnahme:**

Die Teilnahme an der englischsprachigen Konferenz ist kostenlos. Bitte nutzen Sie diesen Link für Ihre Anmeldung:

<https://www.microb3.eu/events/meetings/final-conference/registration>

Wir unterstützen Sie gerne bei der Auswahl von Veranstaltungen.

**Weitere Informationen und Ansprechpartner:**

[www.microb3.eu](http://www.microb3.eu)

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**Wir freuen uns auf Ihren Besuch!**

**Annex 7: Press release reporting the Conference published on Cordis**



## Micro B3 Final Conference: Ocean Sampling Day in the spotlight of the International Microbiome Initiative

Contributed by: **Jacobs University Bremen gGmbH**

**Micro B3 Final Conference was held at Royal Flemish Academy of Belgium for Science and the Arts in Brussels from 2nd to 5th November 2015**

The final Micro B3 conference was a big success. It brought together 46 institutions from 16 countries including high-level guests and invited speakers.

The coordinator, Prof. Frank Oliver Glöckner from Jacobs University highlighted the worldwide attention the project has already received. The 80 plus peer-reviewed publications from the project reflect its significant contribution to the advancement of science. Furthermore, the Micro B3/OSD aligns nicely with the ongoing discussions on creating the Unified Microbiome Initiative (UMI) or an International Microbiome Initiative (IMI), with both proposals just published in the journals *Science* and *Nature* (October 29/30 2015).

Especially Micro B3's two world-wide Ocean Sampling Days (OSD) and its citizen science campaign MyOSD can be considered a proof of concept for the main issues denoted, like standardisation for comparative data analysis and data sharing, internationality, interdisciplinary, training, as well as a solid legal framework with respect to the recently ratified Nagoya Protocol to the Convention on Biological Diversity.

This Protocol is an important cornerstone to provide a solid legal framework on Access to and Benefit Sharing (ABS) of marine genetic resources as outlined and emphasized by an illustrative talk by Chris Lyal from the Natural History Museum, London.

Building on all the enthusiasm generated through the OSD and MyOSD campaigns, Frank Oliver Glöckner emphasizes: 'Micro B3 with its OSD 2014 and 2015 sampling campaigns has just marked the beginning of a global endeavour to better understand the role microorganisms play in providing essential ecological, social and economic services.'

As invited speaker and Advisory Board Member Linda Amaral Zettler (Woods Hole, USA) highlighted promising US-American initiatives dealing with the high diversity of marine microorganisms - some finished, and some running in parallel - but all fuelling world-wide microbiome data comparisons for better understanding biodiversity and functions. This was complemented by a fascinating talk of Colomban de Vargas (CNRS, Roscoff) on results of the TARA Oceans circumnavigations which brought to our attention the incredible biodiversity within the marine micro-, phyto- and zooplankton.

Tom Redd from the European Joint Programming Initiative JPI Oceans presented their wide-ranging pilot actions, into which future OSDs might fit well. Simon Claus and Angel Borja outlined how Micro B3 integrates well with the ongoing DEVOTES project and the recently started infrastructure project AtlantOS.

Kicked off by Torger Børresen from the ERA-NET Marine Biotech the conference continued with presenting many biotechnological results relevant for blue growth. Two patents are planned to result from Micro B3-funded research, many new methods and software tools were tested, expanded and are now widely available. Some stem from extreme environments - and as such are of high interest to enzyme-developers in environmental, cosmetics, pharmaceutical food and feed markets. The embedded third industrial expert workshop of Micro B3 with invited speakers from several successful SME's and industry paved the way how to collaborate to better exploit diverse value chains with marine inputs.

Presentations and pictures from the event are available at: <https://owncloud.mpi-bremen.de/index.php/s/p9i8lr5NU7GPgv5>

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- [MICRO B3 - "Marine Microbial Biodiversity, Bioinformatics and Biotechnology"](#)

**Events**

- [Micro B3 Final Conference in Brussels](#)

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**Last updated on** 2015-11-19

Category: news

Provider: WIRE

Revision: 0

**Retrieved on** 2015-12-15

**Permalink:** [http://cordis.europa.eu/news/rcn/129194\\_en.html](http://cordis.europa.eu/news/rcn/129194_en.html)

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