



Marine Biodiversity and Ecosystem Functioning



Network of Excellence under the 6th Framework
Program of the European Union

Report on the ARB training course at the Max-Planck Institute for Marine Microbiology (4.-8. October 2004)

Participants:

Laura Alonso, female, PhD student, CSIC, Spain, marbef partner 20 Andrea Malits, female, postdoc, OBS-VLFR, France, marbef partner 44d Antoniou Aglaia, female, PhD student, IMBC, Greece, marbef partner 42 Matina T salavouta, female, PhD student, IMBC, Greece, marbef partner 42 Matthias Labrenz, male, scientist, IOW, Germany, marbef partner 19 Michael Hannig, male, PhD student, IOW, Germany, marbef partner 19 Pedro Martinez Arbizu, male, Prof., Senckenberg, Germany, marbef partner 10 Maria Valens Vadell, female, PhD student, CSIC, Spain, marbef partner 20 Bente Edvarden, female, Prof., UOslo, Norway, partner 33 Kjetil Roberg, male, PhD student, UOslo, Norway, partner 33 Ingvild Riisber, female, PhD student, UOslo, Norway, partner 33

Access:

The homepage of the software ARB is www.arb-home.de. The softwarepackage used in the course can be downloaded via file transfer protocol at ftp://ftp.mpi-bremen.de/molecol_p/arb/Marbef_Oct04/

Content:

Topics of the course were trained in lectures, demonstrations and computer work by the participants: Linux and installation of Linux – public sequence data bases – phylogeny – the concept of ARB – installation of ARB – data retrieval from public databases – data handling in ARB – formation of alignments – models of evolution – construction and use of filters - methods of tree construction – confidence tests for trees – bootstrapping - phylogenetic marker – probes and probe design with ARB - Bayesian inference of phylogeny – evolution revisited – alternative treeing methods – concatenated proteins – work with data provided by the participant The detailed program of the course is enclosed. The participants used intensively the opportunity to continue with the computer work after 17.00 into the late evening hours.

The participation in the course is valued two credit points according to the European Credit Transfer System

Evaluation:

The training course was the first course that was evaluated by the participants with the marbef training evaluation questionnaire (the questionnaire is enclosed). The participants evaluated the course (on average) as excellent: the general view, content, length, organization, instructors, presentations, presentation style and handouts were with a majority evaluated as excellent (6 to 10 of 11 ratings were excellent, the rest very good, only content and length received once a good). 93 % of the expectations of the participants were covered in the course. In comparison with other courses the course was rated excellent (4/8 participants) and very good (4/8 participants). Additional comments on the course were very individual, including arguments for more and for less theory.

October 29, 2004
Frank-Oliver Glöckner
Jens Harder

Max-Planck Institute for Marine Microbiology



	04.10.04	05.10.04	06.10.04	07.10.04	08.10.04
9.15-10.45 Lecture	Introduction Linux Sequence databases Phylogenetic programs The concept of ARB	Phylogeny, Part I Alignment Models of evolution Methods for tree reconstruction	Phylogeny, Part II Methods for tree reconstruction Confidence tests Filters Phylogenetic markers	Phylogeny, Part III Probe design Multiple probes Bayesian analysis	Phylogeny, Part IV Evolution Alternative treeing methods Concatenated proteins Whole genome trees
	Break	Break	Break	Break	Break
11.15-13.00 Demo	Demonstration Installation of Linux Installation of ARB	Demonstration Import of sequences Aligner + Alignment Fast addition of new sequences to a phylogenetic tree	Demonstration Phylogenetic tree reconstruction Bootstrapping Construction and use of filters	Demonstration Probe design Import/export of data and trees	Demonstration Bayesian analysis (MrBayes) Repetition Discussion
13.00 – 14.00	Lunch break	Lunch break	Lunch break	Lunch break	Lunch break
14.00 – 17.00 Course Break 15.30-15.45	Computer work Accounts Basic commands Linux/KDE Data retrieval from public databases	Computer work Import of sequences Alignment Phylogenetic addition of sequences	Social Event 13.30 to ~ 23.00 River cruise Dinner	Computer work Phylogenetic tree reconstruction Probe Design	Computer work MrBayes Finish own work

Report on Participation in

ARB- A Comprehensive Software Package for Phylogenetic Analysis Training Course

Participation of Matina Tsalavouta (MSc), currently Ph.D. student in IMBG, and of Aglaia Antoniou (MSc), currently Ph.D. student at University of Crete, Hellenic Centre of Marine Research, Crete Greece.

The ARB Training course was organized within the MarBEF activities and took place in Max Planck Institute for Marine Microbiology in Bremen, Germany. The duration of the course was 5 days, 4/10-8/10/2004. The course was organized by Dr. Jens Harder and the series of lectures and practicals during the five days were presented by Prof. Frank Oliver Gloeckner. On the last day, Dr. Hanno Teeling also a member of MPI Bremen, presented an interesting lecture.

The purpose of the course was to give participants an insight in phylogeny and the methods for tree reconstruction on a theoretical basis, as well as demonstrating how ARB can be used for phylogenetic analysis.

More specifically, there were daily morning lectures on phylogenetic markers, public sequence data bases and data retrieval, alignment of sequences, models of evolution, methods of tree reconstruction and the pros and cons of each of these methods. Finally, there was a lecture given for alternative treeing methods and how the whole genome information that is presently available could be used for constructing whole genome trees. The theoretical background presented during the lectures was most thorough and very well presented (including illustrations), giving enough information and scope for understanding, especially for individuals for whom the topic is not his/her field, as well as providing considerable insights for specialists in the field.

During the late morning and afternoon sessions, a comprehensive demonstration of the ARB software was presented (concept of ARB, installation, data handling, probe design), followed by an opportunity to practice and gain experience in using the software. This was given with very helpful guidance by the organizers/presenters of the course. The computer lab was equipped with the necessary PC workstations for the participants to work efficiently and comfortably. The guidance, instructions and discussions with Prof. Frank Oliver Gloeckner and Jens Harder were most informative and beneficial, contributing to a good understanding of the philosophy, the function, the capabilities and applications of the ARB software.

The course material provided a) a Quick Reference Guide for ARB and b) a handout of the content of each lecture presented during the course, along with a demo CD for ARB. All the course material was most useful both during the course and later, at home, in installing and using ARB.

Matina Tsalavouta was particularly interested in learning how to use ARB since she has been working with bacterial sequences for some time. The requirement to learn how to use a complete, single software, where alignment, editing of the alignment, tree reconstruction and tree presentation can be achieved was evident. Combining the presentation and practical experience in using ARB with some theoretical background made the course even more beneficial for her.

There was a lot of guidance in how to properly install and use ARB at home. Naturally, with practice and further use of the software, valuable experience and real insight would be achieved, but it would not have been as immediate or comprehensive without having participated in the course.

Training courses like the one that we have participated are helping young researchers gaining knowledge, experience and of course are giving them the opportunity to meet researchers that can help them on their request of knowledge.