

## ISOS Course

# ARB

## A Software Environment for Sequence Data

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ARB ([www.arb-home.de](http://www.arb-home.de)) is a fully-integrated package of cooperating software tools for the management and analysis of DNA marker sequences with a focus on the ribosomal RNA gene.

It represents the gold standard for identification/classification and phylogenetic analysis of microbial organisms.

ARB is supplemented by the SILVA ribosomal RNA gene database project ([www.arb-silva.de](http://www.arb-silva.de)).

### Contents:

- | Public sequence databases
- | Quality issues - concepts and limitations of phylogenetic sequence analysis
- | How to build and present an adequate tree
- | Concept of (rDNA) sequence alignments and their impact on phylogenetic analysis
- | Relevance of filtering alignments
- | How to work with ARB (sequence import, database management, sequence analysis from alignment to treeing, export of data and trees, post processing of trees)
- | How to integrate ARB and the tools of the SILVA web portal

**Dr. Jörg Peplies (Ribocon; [www.ribocon.com](http://www.ribocon.com))** is a trained molecular microbiologist with a strong background in ribosomal RNA gene sequence analysis, including phylogeny, probe design and evaluation (in situ hybridization techniques), database management, and recent solutions for high-throughput microbial community analysis.

In the last 8 years, he has taught more than 500 ARB/SILVA workshop participants from all over the world.

*Registered ISOS PhDs have priority in our courses.*

**Venue:** to be announced

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[www.futureocean.org/isos](http://www.futureocean.org/isos)