# ARB_genome

## A software environment for functional genomics

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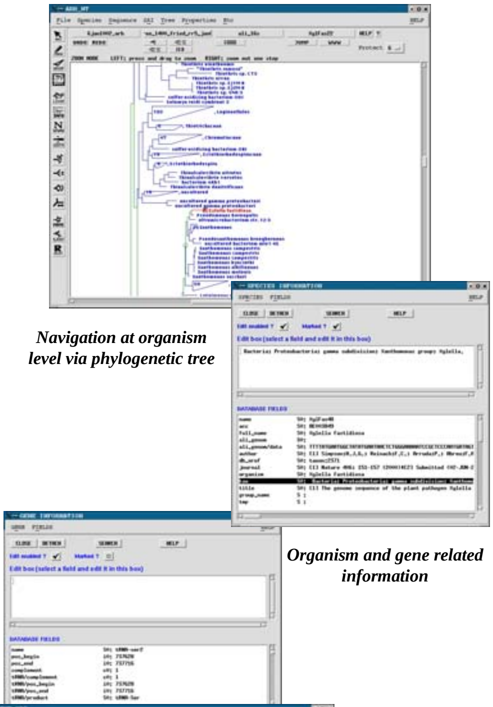


*Navigation at organism level via phylogenetic tree*

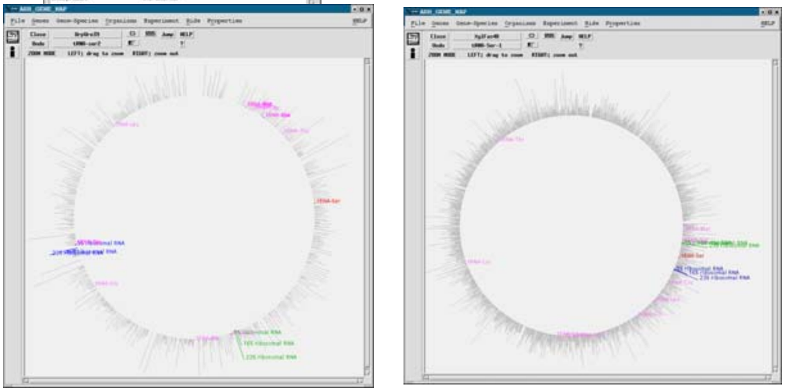
*Organism and gene related information*

### ARB_genome

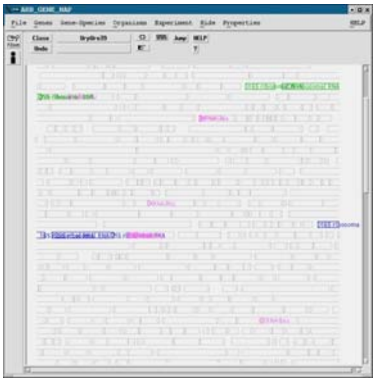
As genome DNA sequence data are emerging at an ever-increasing rate, the incoming amount of data requires more and more sophisticated software tools to handle the huge rush of genome data in a user-friendly way. One such software tool is "**ARB_genome**", a computational tool mainly designed and developed as a working bench for the comparison of annotated genomes allowing the integration and comparison of experimental data from functional genomics.

The fundamental strategy in a Functional Genomics approach is to expand the scope of biological investigation from studying single genes or proteins to studying all genes or proteins at once in a systematic fashion. And the functional genomics is characterised by mining data sets for particular valuable information and promises to rapidly narrow the gap between sequence and function and yield new insights into the behaviour of biological system. The main feature of **ARB_genome** tool is the possibility of genome analysis with respective organism or group and analysis of the same at gene level and experiment level. The former gives access to the descriptive data and sequences of the individual genes, the latter allows to assign experimental conditions and raw and processed data (proteomics, transcriptomics) to the organisms and genes. Interacting search tools for the different levels were also included in a more user-friendly way. Genome maps can be interactively visualized in different formats, edited and printed for publication purposes as well. In addition, any information stored in ARB databases fields can be visualized along with the gene positions and selected genes can be highlighted according to user defined criteria for eg., gene expression under certain conditions. The primary structures of selected genes can be exported to ARB gene databases and processed using the integrated tools such as sequence editors (primary and secondary), tree building tools, probe design, probe match, etc.,.

The **ARB_genome** project is supported by the bmb+f as part of the regx program ( http://www.regx.de ). It is integrated into the ARB package and can be freely downloaded from our home page (see below) along with the classical ARB phylogeny program.



*Direct comparison of genome maps of different organisms*



*Genome view in block format*

### The ARB project

The ARB (arbor, latin: tree) project was started nine years ago at the Technical University of Munich as an interdisciplinary initiative of the Lehrstuhl für Mikrobiologie and the Lehrstuhl für Rechnertechnik und Rechnerorganisation. Initially, the ARB software package was primarily designed for establishing, analyzing and maintaining rRNA gene sequence data bases. Later it was adopted for handling other gene and protein primary structures.

The basic idea which was followed from the beginning of the ARB project is i) *an integrated database which contains along with processed primary structure data any additional information assignable to the individual sequence entries in specific data base fields or via internet links* and ii) *a set of directly cooperating and interacting software tools for data management and analysis.* The sequence and additional data may be retrieved from different databases or provided by the user. The database is structured according to the organisms phylogeny or other (user provided) criteria and highly compressed. Any type of information can can be visualized and accessed via phylogenetic trees or genome maps and by versatile search tools. Primary and secondary structure editors, tools for user guided or automated alignment, programs for establishing profiles and filters, different treeing facilities as well as import and export tools are among the major software components of the ARB package. Furthermore, rapid *taxon or gene specific probe/primer design* as well as in silico evaluation against the full background of all available sequences of interest is possible with the aid of an ARB integrated positional tree server.

**http://www.arb-home.de/**