SILVA - a comprehensive online resource for high-quality ribosomal RNA sequence data

REFERENCE DATABASES - SERVICES - TOOLS

Christian Quast1, Jan Gerken2, Alan Beccati3, Amandine Nunes-Jorge1, Maksym Pyatygorskyi1, Markus Klimmek1, Pablo Yarza2, Ralph Florenti2, Jörg Peplies1, Frank Oliver Glöckner1,3,4
1. Department of Life Sciences and Chemistry, Jacobs University gGmbH, Bremen
2. Microbial Genomics and Bioinformatics Research Group, Max Planck Institute for Marine Microbiology, Bremen
3. Computing and Data Center, Alfred Wegener Institute - Helmholtz Center for Polar- and Marine Research, Bremerhaven
4. MARUM - Center for Marine Environmental Sciences, University of Bremen, Bremen

SILVA rRNA Databases

SILVA is a comprehensive web resource for up-to-date, quality-controlled databases of aligned ribosomal RNA (rRNA) gene sequences from the Bacteria, Archaea and Eukaryota domains and supplementary online services. All sequences are checked for anomalies, carry a rich set of sequence associated contextual information, multiple taxonomic classifications and the latest validly described nomenclature.

SILVA provides: a) curated guide trees with the latest taxonomy and nomenclature, b) consistent naming of clades of uncultivated (environmental) sequences, c) a complete eukaryotic taxonomy, ranging from insects to ciliates.

de.NBI Services

SILVA Parc:
Comprehensive quality checked SSU & LSU datasets
- SSU Parc (138): 9,469,656 +56%
- LSU Parc (132): 910,134 +24%

SILVA Reference:
High-quality SSU & LSU datasets
- SSU Ref (138): 2,225,272 +6%
- LSU Ref (132): 201,588 +32%

SILVA Ref NR 99:
Non-redundant SSU Ref dataset
- SSU Ref NR (138): 510,984 -27%
  (new clustering)

Online Services:
- Sequence Alignment,
- Classification & Phylogenetics,
- Probe and Primer evaluation,
- Custom-tailored Datasets,
- SILVAngs: rDNA amplicons analysis.

Progress Report

SILVA Taxonomy:
- Member of Bergey's Manual Trust,
- Member of the UniEuk (technology provider),
- Manually curated taxonomy and nomenclature,
- Adaptated the Genome Taxonomy,
- Adaptated the UniEuk Taxonomy.

SILVA (Web) Services / Processing Pipeline:
- Ported SILVA(ngs) to the de.NBI cloud,
- Virtualised SILVA (web) services,
- Updated imports from/experts to many 3rd party resources.

Ongoing:
- Redesign of the website.

General information on the project (funding)

- de.NBI (BMBF):
  3 full-time developers,
  1 full-time ELIXIR liaison / Communication Officer,
- MPG: 1 full-time and 1 part-time developer,
- Moore Foundation: 1 full-time developer,
- RiboCon GmbH: 1 part-time curator.

Publications


https://www.denbi.de
https://www.arb-silva.de