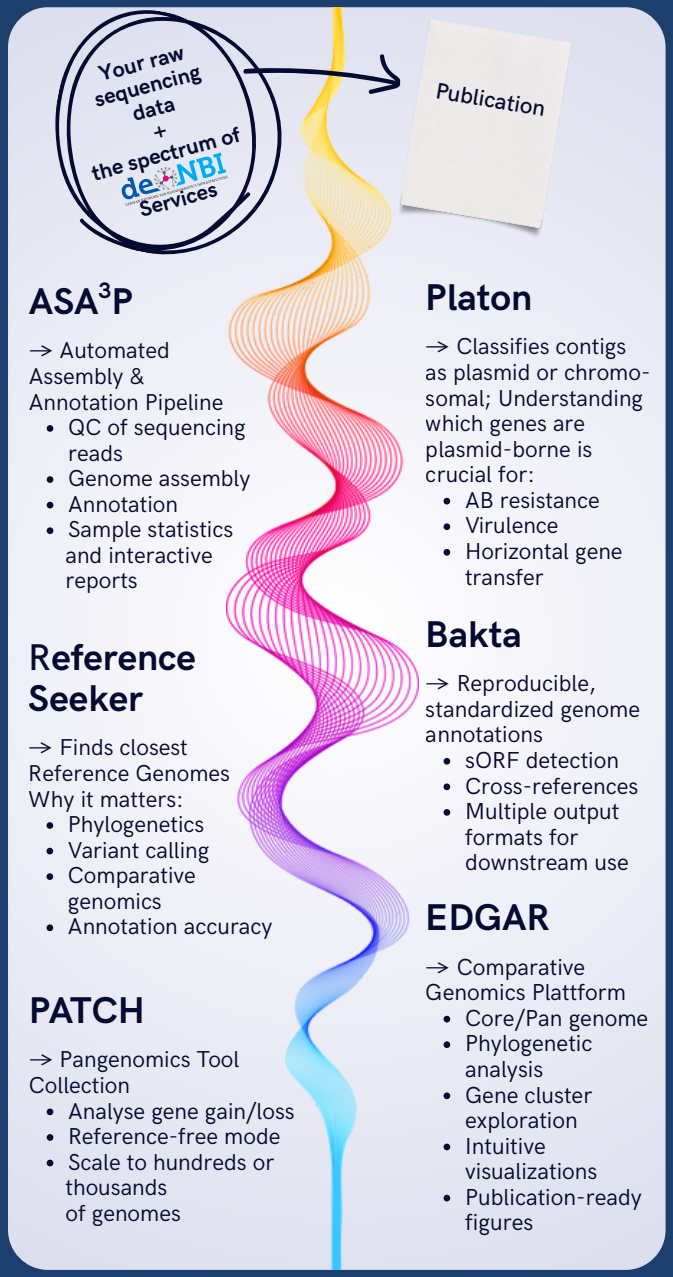
Sequenced Microbial Genomes?



ASA³P

→ Automated Assembly & Annotation Pipeline

- QC of sequencing reads
- Genome assembly
- Annotation
- Sample statistics and interactive reports

Reference Seeker

→ Finds closest Reference Genomes Why it matters:

- Phylogenetics
- Variant calling
- Comparative genomics
- Annotation accuracy

PATCH

→ Pangenomics Tool Collection

- Analyse gene gain/loss
- Reference-free mode
- Scale to hundreds or thousands of genomes

Platon

→ Classifies contigs as plasmid or chromosomal; Understanding which genes are plasmid-borne is crucial for:

- AB resistance
- Virulence
- Horizontal gene transfer

Bakta

→ Reproducible, standardized genome annotations

- sORF detection
- Cross-references
- Multiple output formats for downstream use

EDGAR

→ Comparative Genomics Plattform

- Core/Pan genome
- Phylogenetic analysis
- Gene cluster exploration
- Intuitive visualizations
- Publication-ready figures

de.NBI – Trusted Tools for Analysing Life Science Data

Get started:

Training | Services | E-Learning

What we Offer

- ✓ Curated tools for genomics, pangenomics, metagenomics, proteomics and more
- ✓ Training, documentation and expert support
- ✓ Access to the de.NBI Cloud
- ✓ Free of charge for academic users

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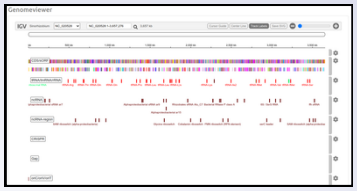
de.NBI – German Network for Bioinformatics Infrastructure
Coordination Office: Forschungszentrum Jülich (FZJ)

Analyse Microbial Sequence Data – with de.NBI Tools & Training

Free for academic life scientists

de.NBI
GERMAN NETWORK FOR BIOINFORMATICS INFRASTRUCTURE

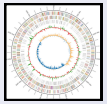
Bakta is a rapid and standardized annotation tool for bacterial genomes, MAGs and plasmids.



- Comprehensive, taxonomy-independent annotation database
- Alignment-free exact protein sequence identification
- Rich cross-references to many databases
- FAIR-compliant annotations
- Standard output formats (INSDC, GFF3)
- Usable via web interface or command line

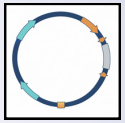
Bakta web application

Bakta is used worldwide!



Platon identifies plasmid-derived contigs in bacterial draft genomes.

- Fast and reliable plasmid detection
- Characterization of plasmid genes (replication, mobility, accessory genes)



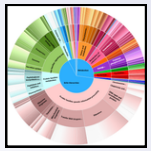
ReferenceSeeker identifies suitable reference genomes using fast ANI-based classification.

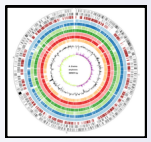
- Combines rapid k-mer screenings with ANI comparisons
- Ready-to-use databases for bacteria, archaea, fungi, viruses and plasmids

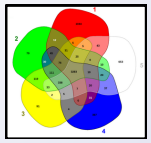
EDGAR is an online platform for comparative genomics and phylogenomics, enabling the identification of orthologs as well as phylogenetic/taxonomic analyses.

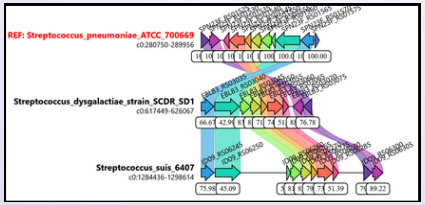
"One click" features for effortless comparative insights:

- KEGG/COG/GO classifications of all genes
- Syntenic gene cluster analyses
- Core genome based phylogeny, ANI, AAI
- High-quality figures: Krona plots, Venn diagrams, Circular plots





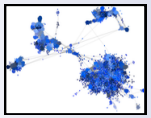




BakRep is a searchable bacterial genome repository

- Millions of QCed genomes
- Tax. classification & MLST subtypings
- Standardized genome annotations
- Rich submission metadata, e.g. sample date, location, source, …

sORFdb is a database for short open reading frames and small proteins in bacteria. Combines, filters, and enriches high-quality data sources, all accessible via a web interface.



PATCH is a collection of software tools for efficient and versatile pangenome analyses – whole-genome based, alignment- and reference-free.

One suite, many tasks:
Phylogenetic reconstruction, local alignments, core detection, and pangenome openness prediction.

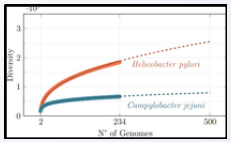
Highly scalable:
Allows comparison of thousands of genomes in parallel.

Included in the **Pangenome Analysis Toolbox:**

Corer identifies the core genome of a pangenome by detecting conserved sequence regions across all genomes – without relying on gene annotations or coding sequences.

PanBench is an online catalogue for k-mer-based pangenome tools. Browse, compare and test tools directly in the browser, supported by up-to-date benchmarks on runtime, memory usage and accuracy.

pangrowth quantifies pangenome openness, core-genome size and diversity. Supports genome and gene-level input and enables robust comparisons across datasets using diversity metrics.



PLAST searches graphical pangenomes for local sequence similarities, comparable to BLAST. Reports alignments across all pangenome members and allows focused searches within specific regions or subsets.

SANS enables rapid construction of phylogenies from genomes, reads or pangenome graphs. Supports large datasets, multiple filtering options and flexible visualization as trees or networks.