Overview of Information Organization in ARDB

A List of Analysis Tools Available in ARDB

1. Search antibiotic resistance information

Tool: (1) Search bar at the top of the webpage. (2) Choosing search words in advanced search (http://ardb.cbcb.umd.edu/search.shtml).

Usage:

(1)
Tool: browse the annotated antibiotic resistance genes of sequenced microbial genomes (http://ardb.cbcb.umd.edu/browsegenomes.shtml).

Result:

Annotation: ‘Best Hit’ is the best BLAST hit against the ARDB resistance genes. ‘Cutoff’ is the percent identity value in BLAST result used to define resistance types. If the ‘similarity’ is higher than ‘cutoff’ value, then this gene is very likely to be a real resistance gene. ‘Require’ means this resistance genes requires other cooperative genes to perform resistance function. For example, gene mdtp requires mdtn and mdto to form a multidrug resistance efflux pump.

3. Single query sequence search (annotation)

Tools: (1) Protein BLAST (Search against PROTEIN database). (2) Nucleotide BLAST (Search against NUCLEOTIDE database). (3) RPS BLAST (Search against PROTEIN CLUSTERS-Position Specific Score Matrix). Web address: http://ardb.cbcb.umd.edu/blast/index.shtml

Usage:
Annotation: Resistance genes are organized into types in the BLAST results. ‘Number of Hits’ is the number of resistance genes belonging to each type in the BLAST results. ‘Average Similarity’ is the average sequence similarity between the query sequence and all hits belonging to each type.

Clicking ‘View All BLAST Hits’ will show detailed BLAST information. Clicking the ‘Number of Hits’ shows detailed BLAST information for the genes belonging to a specific type.

4. Multiple query sequences (annotation)

Tool: The annotation database is a collection of protein sequences. Choose appropriate BLAST program. Upload your file containing multiple sequences (in FASTA format).
You can also select other pre-annotated genomes to compare. Web address: http://ardb.cbcb.umd.edu/blast/genome.shtml.

Usage:

Result:

5. Resistance profiles comparison of pre-annotated bacterial genomes
Tool: This tool allows the user to compare the resistance profiles of pre-annotated bacterial genomes. Web address: http://ardb.cbc.csb.umd.edu/genomecomp.shtml

Usage:

Result:

6. Mutational Resistance Identification

Tool: This tool allows the user to identify mutations that can confer antibiotic resistance in 12 genes: 16S rRNA, 23S rRNA, gyrA, gyrB, parC, parE, rpoB, katG, pncA, embB, folP, dfr.

Usage:
1. Select BLAST program. If 16S or 23S, select blastn, otherwise select blastp.

2. Select the name of your query gene.

3. Paste your query sequence.

4. Click 'Search'.

Result:

- Mutation Position in Query Sequence
- Mutation in Query Sequence
- Mutation Position in Reference Sequence
- Wild Type in Reference Sequence
- Literature Reference