Battelle CRITERIOME™

BIO-SEQUENCE CHARACTERIZATION SOFTWARE



BATTELLE CRITERIOME RAPIDLY REPORTS ON DRUG RESISTANCE ENABLED BY GENETIC ELEMENTS

CHALLENGE

Identifying drug resistance of microbial pathogens is critical to productive analysis of infectious disease in biosurveillance applications. Current diagnostic methods rely on culturing microbes, antibodybased assays and other methods, which can be time-consuming and inaccurate due to assay limitations.

SOLUTION

Biomedical

Literature

Battelle's proprietary software, Criteriome, analyzes genomic sequence data to rapidly and accurately identify

Natural language processing / semantic calculus microbes and to predict potential drug susceptibility/resistance profiles. Our approach uses characteristics of the entire genome to ascertain bacterial identity along with a proprietary database to determine the spectrum of antibiotic resistance harbored within bacterial genomes. Battelle's database includes more than 250,000 genetic elements from more than 200 genera of bacteria which includes most major types of clinicallyrelevant drug resistance. Our assertions regarding antibiotic resistance elements are backed by over 1000 citations from the professional literature in our proprietary knowledgebase. Systematic interrogation of these resources with custom software allows identification of the complement of antibiotic resistance genes.

Key benefits

- BATTELLE **CRITERIOME** is flexible with data input
 - Imports data from FastA or FastQ files
 - Easily adapted to any sequence data format and analysis workflow
- BATTELLE CRITERIOME provides drug resistance data
 - Rapidly reports on drug resistance enabled by genetic elements
 - Extensive knowledge base with >200,000 microbial sequences linked to scientific publications; edited by in-house SMEs.
- BATTELLE CRITERIOME speeds end results
 - ONE DAY vs. 2-3 weeks with traditional analysis

Battelle's process melds automatic extraction of terms and relationships from the professional literature with expert-guided editing and selection to produce a high quality dataset used to recognize antibiotic resistance elements from genomic data. (Sematrix is Battelle's proprietary tool which leverages natural language processing to rapidly process published literature.)

Battelle Antibiotic stance (AbR) Onto

Battelle Criteriome. See reverse side for full screen image.





Battelle Criteriome rapidly reports on drug resistance, enabled by genetic elements.

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Details:	 Drugs resist to: Cloxacillin, Novobiocin, Nalidixic_acid, Erythromycin, Tetracycline, Norfloxacin, Oxacillin, AcrA from Escherichia coli(NP_309890: multidrug-efflux transport protein [Escherichia coli O157:H7 str. Sakai]) AcrB from Escherichia coli(NP_309891: multidrug-efflux transport protein [Escherichia coli O157:H7 str. Sakai]) TolC from Escherichia coli(CAA24914: unnamed protein product [Escherichia coli K-12]) References: <u>21513882</u>; 			
Sin	gle component factors:			
	 Tet38 from Staphylococcus aureus(AAV804 Drugs resisted to: Tetracycline, References: <u>15774883</u>; 	64: tetracycline resistant protein Tet38 [Staphylococcus aure	sus])	
Summary Drug	Report			

Every day, the people of Battelle apply science and technology to solving what matters most. At major technology centers and national laboratories around the world, Battelle conducts research and development, designs and manufactures products, and delivers critical services for government and commercial customers. Headquartered in Columbus, Ohio since its founding in 1929, Battelle serves the national security, health and life sciences, and energy and environmental industries. For more information, visit www.battelle.org.



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