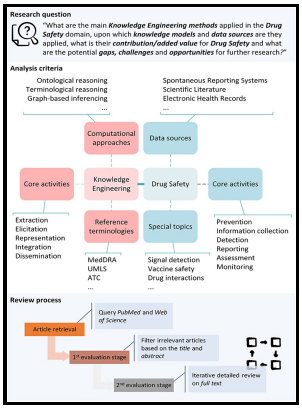
Pathway analysis for drug discovery - computational infrastructure and applications

John Wiley & Sons - Pathway Analysis for Drug Discovery: Computational Infrastructure and Applications by Anton Yuryev



Description: -
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Microarray Analysis -- methods
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Dramabook
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The most frequent mutation is the deletion of phenylalanine 508 DF508. Contact: Supplementary information: are available at Bioinformatics online.

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To this end, we defined a golden standard for each drug-set as follows: we selected the known target gene for each drug-set see.

Drug

Acknowledgement The authors would like to thank Ramanath Hegde for providing the referenced list of CFTR correctors.

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Rather than search for and pore through scores of articles published in disparate sources, readers can turn to Pathway Analysis for Drug Discovery. It covers traditional computational methods and software for pathway analysis microarray, proteomics, and metabolomics. After converting FC values to ranks, we built Prototype Ranked Lists PRLs by merging all the samples corresponding to the same drug, as described in , thus obtaining a 12 012 genes × 1309 drugs matrix of PRLs see b.

Pathway Analysis for Drug Discovery: Computational Infrastructure and Applications

For drugs with more than one known target, we chose the first member alphabetical order of the target protein family. Even social networks that

mirror interactions within the scientific community are helping to foster collaborations and novel research. In order to exclude that the results obtained in were due to a hidden bias in the golden standard pathways, we generated for each of the 5 drug-sets, 1000 random drug-sets with the same size as the corresponding original drug-set.

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We thus obtained, for each database, one Enrichment Score matrix ES whose rows correspond to pathways and whose columns correspond to drugs see c.

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DSEA aims at identifying these mechanisms by looking for recurrent pathways modulated by most of drugs in the set.

Drug

The acetylation-deacetylation balance is known as acetylation homeostasis and the existence of a HAT-HDAC coupling through a common signal has been suggested. The horizontal line indicates the 0.

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