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video i explain how to navigate the blast using blast you can input a gene sequence of interest and search entire genomic libraries for identical or similar sequences in a matter of seconds in this laboratory investigation students will use blast to compare several genes and then use the information to construct a cladogram the basic local alignment search tool blast finds regions of local similarity between protein or nucleotide sequences the program compares nucleotide or protein sequences to sequence in a database and calculates the statistical significance of the matches blast is a computer algorithm that is available for use online at the national center for biotechnology information ncbi website as well as many other sites blast can rapidly align and blast for beginners introduces students to blastn a commonly used tool for comparing nucleotide sequences dna and rna this popular tutorial shows how to do a blast search with a nucleotide sequence highlights information in the search results and shows how to interpret the e value and alignment scores winnie sloan 8 59k subscribers 14 3 9k views 6 years ago tiktok this is the process for how my ap biology class is processing investigation 3 comparing dna sequences to understand an extremely powerful bioinformatics tool is blast which stands for basic local alignment search tool using blast you can input a gene sequence of interest and search entire genomic libraries for identical or similar sequences in a matter of seconds the blast algorithm the steps are as follows split query into overlapping words of length w the w mers find a neighborhood of similar words for each word see below lookup each word in the neighborhood in a hash table to find the location in the database where each word occurs call these the seeds and let s be the collection of seeds blast lab files rhs biology comparing dna sequences to understand evolutionary relationships with blast in this laboratory investigation you will use blast to compare several genes and then use the information to construct a cladogram a cladogram is treelike with the endpoints of each branch representing a specific species details resources group size for 10 lab groups time required complete in 45 minutes kit includes instructions all you need computer and internet access discover evolutionary relationships with this ap bio lab 3 kit investigate gene sequences learn about the blast database and construct a cladogram learn how to use blast to compare nucleotide and protein sequences and construct a cladogram in this ap biology lab quiz ap biology blast lab flashcards quizlet 3 0 1 review cladogram from major plant groups click the card to flip moss vascular tissue ferns seeds pine trees flowers flowering plants imgur com obmrnz click the card to flip 1 19 flashcards learn test match q chat arnavchinchankar teacher lab 21 using bioinformatics to investigate evolutionary relationships have a blast introduction between 1990 2003 scientists working on an international research project known as the human genome project were able to identify and map the 20 000 25 000 genes that define a human being 1 what species in the blast result has the most similar gene sequence to the gene of interest the species in the blast lab is the dorsophilla melangoblaster f102063 2 where is the species located on the cladogram the species is within the 4th leaf under the flies 3 how similar is that gene sequence blast lab write up export references from noodletools into google doc submit lab on turn it in by 7 50am on the due date on the due date hand in a paper copy heading 3 pts name due date ap biology period title create a title that summarizes the main concepts of the lab intro 18 pts course exam pages ap biology classroom resources investigative labs comprehensive links all links to online resources were verified before publication in cases where links are no longer working we suggest that you try to find the resource by doing a keyword search ap biology investigative labs comprehensive links brewer s yeast seemed like a cool model for questions of non darwinian evolution and which i was thinking about and i ve had a blast and a half learning from everyone in the lab for her thesis project heng looked into the fungus candida albicans and the mechanisms that can cause it to have irregular numbers of chromosomes or

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