

Essential idea: Bioinformatics is the use of computers to analyse sequence data in biological research.

B.5 Bioinformatics	
<p>Nature of science:</p> <p>Cooperation and collaboration between groups of scientists—databases on the internet allow scientists free access to information. (4.3)</p>	
<p>Understandings:</p> <ul style="list-style-type: none"> Databases allow scientists easy access to information. The body of data stored in databases is increasing exponentially. BLAST searches can identify similar sequences in different organisms. Gene function can be studied using model organisms with similar sequences. Sequence alignment software allows comparison of sequences from different organisms. BLASTn allows nucleotide sequence alignment while BLASTp allows protein alignment. Databases can be searched to compare newly identified sequences with sequences of known function in other organisms. Multiple sequence alignment is used in the study of phylogenetics. EST is an expressed sequence tag that can be used to identify potential genes. <p>Applications and skills:</p> <ul style="list-style-type: none"> Application: Use of knockout technology in mice to determine gene function. Application: Discovery of genes by EST data mining. Skill: Explore chromosome 21 in databases (for example in Ensembl). Skill: Use of software to align two proteins. Skill: Use of software to construct simple cladograms and phylograms of related organisms using DNA sequences. 	<p>Theory of knowledge:</p> <ul style="list-style-type: none"> Knowledge claims justified by reference to databases raise unique knowledge questions. How reliable are knowledge claims justified by reference to data sources developed for different purposes by different researchers using different methods? <p>Aims:</p> <ul style="list-style-type: none"> Aim 6: Sequence alignment of related proteins such as hemoglobin and myoglobin could be investigated.