

SUMMARY

Nucleotide sequence alignment is a useful comparison technique that detects existing mutations in the DNA sequences. While some mutations are silent mutations that pose no harm to an individual, others that occur in the coding regions of the DNA could very well predispose humans to diseases. In Dr. Robert Hegele's Blackburn Cardiovascular Genetics Laboratory at Robarts Research Institute (RRI), nucleotide sequence alignment is carried out to detect single nucleotide polymorphisms (SNPs) and insertion or deletion mutations in the coding regions of patients' DNA, in hope to discover the genetic basis of the diseases.

The purpose of this report is to compare and analyze three different sequence alignment softwares – SeqScape, Lasergene, and Sequencher – that are available to the laboratory for mutation detection. Scientists working in the laboratory are currently looking for a sequence alignment program that facilitates the mutation detection process. The software that is most suitable for the purposes of RRI is determined based on parameters such as the algorithm used for mutation detection, the amount of sequences that the software can handle, time efficiency, cost and ease of use. In particular, the same set of sequences with known mutations is imported to all three softwares to test for their efficacy to accurately pinpoint the location of the mutation.

Based on the alignment results generated from the three softwares, SeqScape software has demonstrated to be the most effective alignment program to detect mutations that exist in the nucleotide sequences. SeqScape software is integrated with the Smith-Waterman local alignment algorithm that is able to match the sample gene sequences at

the correct position along the reference sequence during the alignment. The algorithm is also a successive pairwise method where multiple sequences can be aligned simultaneously to improve time efficiency in the laboratory. New and improved alignment features are also integrated in the software at the convenience of first-time users.

Although results showed that the SeqScape software is best suited for the purposes of the laboratory, it is recommended that sample sequences be aligned in all three softwares to ensure the reproducibility of the alignment result. Furthermore, users should avoid aligning too many sequences simultaneously to improve time efficiency of the process.

1.0 INTRODUCTION

Dr. Robert Hegele is the Director of the Blackburn Cardiovascular Genetics Laboratory at Robarts Research Institute (RRI). His research interest is focused on the genetic basis of cardiovascular diseases such as diabetes, atherosclerosis, and dyslipidemia. He and his team of dedicated scientists work together in the lab to study gene mutations in the human genome that could very well predispose humans to such diseases.

As a part of the research, tremendous effort is put forth to the finding of single nucleotide polymorphisms (SNPs). SNPs are single base mutations that occur when a single nucleotide in the DNA sequence is substituted with one of the three other nucleotides (Karp, 2005). While some SNPs are silent mutations that will not cause any harm to an individual, others could induce detrimental effects and be associated with pathology (Karp, 2005).

The study of SNPs is a promising field of research as it helps identify genes that are potentially linked to certain diseases. For a variation to be considered as a SNP that predispose humans to disease, the mutation must occur in at least 1% of the population (Dale and von Schantz, 2002). In Dr. Hegele's lab, population studies and related experiments are conducted to discover SNPs. First, blood samples are collected from patients who are affected by cardiovascular disease. The DNA from the samples will be extracted, purified and amplified. After isolating the gene of interest from the processed samples with the design of specific primers, the genes will be sequenced for further analysis. The set of sequences obtained will be compared and examined for the presence of SNPs or other changes such as insertions or deletions.

With many sequences to compare and analyze, it would be more efficient if the sequences could be examined simultaneously with the help of an alignment program. An alignment program which performs sequence alignments quickly and accurately to pick out sequence variations can facilitate the SNP identification process, as well as minimize possible human errors. The purpose of this report is to assess and discuss the advantages and disadvantages of three sequence alignment softwares over the currently in-use software Sequence Navigator available in RRI. The three softwares are ABI Prism[®] SeqScape[®] Software Version 2.0, Lasergene[®] Version 7.0, and Sequencher[®] Version 4.7.

This report will thoroughly describe the features and functions of each sequence alignment software. The softwares will be assessed individually for their accuracy and efficiency in performing sequence alignments. In particular, the alignment algorithm and the speed of performance will be looked at in detail. Other assessment parameters such as the ease of use as well as the cost of the softwares will also be considered in the evaluation. At the end of the report, a recommendation will be made as to the software that is most supportive to the ongoing SNP detection project in RRI.

2.0 INTRODUCTON TO SEQUENCE ALIGNMENT

Sequence alignment is the most direct method to measure sequence similarity between two or more nucleotide or amino acid sequences. It is the process of comparing individual nucleotides or residues at the position corresponding to how the sequences are superimposed (Lesk, 2002). Given a set of sequences with different lengths and context, there are numerous ways that the sequences can be aligned; the goal is to seek the one that exhibits the best alignment. While gaps can be inserted within the sequences to achieve more matching pairs in the alignment, the order of the nucleotides or residues must be conserved as the original sequence (Lesk, 2002). How is it determined that a particular arrangement of the sequences be the best alignment? The topic will be addressed in Section 3.3 of the report.

2.1 Purpose of Performing Sequence Alignment

Sequence alignment is a useful comparison technique with many applications in evolutionary and molecular studies. In both protein and nucleotide sequence alignments, the goal is to identify regions of similarity between aligned sequences, known as the consensus sequence (Pearson and Wood, 2002). With protein alignments, the degree of resemblance noted from a set of amino acid sequences demonstrates the homology or the relative closeness of the aligned species (Applied Biosystems, 2002). A phylogenetic tree deduced from the aligned sequences can also track down the common ancestor of the species. Furthermore, the identification of conserved or unchanged regions of the protein sequence in one species leads to the prediction of the structure and the function of the particular protein in another (Applied Biosystems, 2002).

Alternatively, aligning nucleotide or DNA sequences identifies any variant or mutation that might be present in the sequences (Altschul, 1997). Some well known mutations within the nucleotide sequence are substitution mutations such as single base changes, or frameshift mutations such as an insertion, deletion or duplication of several nucleotides. For the purposes in Dr. Hegele's laboratory, DNA sequence alignment is mostly performed to detect the presence of SNPs or any major frameshift mutations in patients' DNA. The comparative study is conducted to verify the hypothesis about the genetic basis of certain cardiovascular diseases. Hence, topics covered in the remaining parts of the report will mainly focus on methods and applications of nucleotide sequence alignment.

3.0 HOW ARE NUCLEOTIDE SEQUENCES ALIGNED?

In general, two components are involved in a nucleotide sequence alignment: the reference and the query. The reference sequence is a known sequence with the order of nucleotides predetermined from a valid source that is suitable to be compared against. Query sequences, on the other hand, could be DNA fragments or bacterial genomes with an unknown sequence yet to be decoded (Dale and von Schantz, 2002). The nucleotide sequence of the query can be verified with the reference for any existing mutations. Once the components for alignment have been gathered, similarity searches within the sequences can proceed with a program containing the appropriate alignment algorithm that performs the desired method of alignment.

3.1 Obtaining the Reference Sequence

Several electronic databases containing a collection of known nucleotide sequences are available to the general public as reference. For example, reference sequences can be retrieved online from NCBI's GenBank at <http://www.ncbi.nlm.nih.gov>, or from Ensembl at <http://www.ensembl.org>. Many of these sequences are submitted by reliable sources such as scientific publications and genome projects which accounts for the validity of the entries (Lesk, 2002). Useful annotations such as restriction enzyme cleavage sites and the coding and non-coding regions of the nucleotide sequence are also provided for investigators' own interest. Details regarding the retrieval of the desired reference sequence are outlined in Appendix A.

3.2 Obtaining the Query Sequence

In Dr. Hegele's lab, 99% of the DNA sequences to be analyzed are obtained from patient's blood samples. Specific genes that are thought to be related to a particular cardiovascular disease are isolated from the DNA. The exons or the coding regions of the genes are studied one by one to check for the presence of SNPs or other existing mutations. Briefly, the DNA that is extracted from the carefully treated blood samples is subjected to PCR amplification. Two custom designed primers have been added prior to the PCR reaction so that only the gene of interest is multiplied. The end products of the PCR reaction will go through a thorough purification process to rid excess nucleotides or enzymes that remained in solution (Wang, 2006). The clean DNA templates containing the gene of interest along with the appropriate primer will be sent for automated sequencing with Applied Biosystem's 3730 DNA Analyzer (Applied Biosystems, Foster City, CA). Once DNA sequencing is completed, the raw data will be basecalled to decode the sequence. Refer to Appendix B for the protocols on DNA extraction, DNA amplification and DNA purification during sample preparation.

3.3 Measuring Sequence Similarity

Once the reference and the query sequences are acquired, sequence alignment can be done with the use of an alignment software. Given all possible ways of aligning the sequences, how is the best alignment determined? Most alignment softwares are integrated with an algorithm that searches for the optimal alignment. Briefly, the algorithm assigns to each possible way of arrangement a *score*, which is defined as the standard measure of sequence similarity within a set of aligned sequences (Lesk, 2002). Depending on the algorithm that is used to perform the calculations, the best alignment

either reflects the maximum score or the minimum score from a set of aligned sequences (Altschul, 1997). In the case where the maximum score is sought, a match in the aligned sequence is granted a point, while a mismatch, a gap initiation, a gap extension, or any deviation within the sequences will result in a penalty that contributes negatively to the final score (Lesk, 2002). The summation of score bits finalizes the overall score of the set of aligned sequences.

The scoring function that the algorithm refers to for score computation takes into account various evolutionary factors. In the case of mutation detection, some substitutions occur at a higher frequency than others. For example, in nucleotide sequence alignments, the likelihood of a transition mutation is greater than that of a transversion mutation; that is, substitution mutation of a purine to purine, or a pyridine to a pyridine are more commonly observed than replacing a purine with a pyridine, or vice versa (Lesk, 2002). Therefore, scores should be weighted accordingly to account for the frequency of certain mutations; that is, a transition mutation should get a higher score than a transversion mutation. The following example illustrates the principle of scoring behind a simple sequence alignment:

Consider 2 short oligonucleotides
Reference: AATCTA
Query: AAGAT

The 2 sequences can be aligned in several ways:

AATCTA AAGAT--	AATCTA A--AGAT	AATCTA AA--GAT	AATCTA AAG--AT	AATCTA AAGA--T	AATCTA --A AGAT
0	-15	-8	-8	-8	-15

Score	Match: +3	Gap: -2	Mismatch: 0	Transition: -3	Transversion: -4
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Figure 1: The basic principle of sequence alignment is demonstrated in the above illustration. For simplicity, two short fragments are aligned with one superimposed on the other. Some of the possible ways of aligning the reference and the query are shown. The score of each pair of sequences is calculated based on the scoring scheme provided for this alignment. It appears that the first alignment achieved the highest final score of 0 with 3 matches, 2 mismatches, 1 gap, and 2 transversion mutations (Lesk, 2002).

Most nucleotide sequence alignment algorithms refer to a scoring matrix to score a particular alignment of sequences (Lesk, 2002). The matrix is filled based on the scoring parameters that were set for the algorithm. The algorithm will then proceed with the search for the best alignment by tracking a path along the matrix that produces the highest score. Figure 2 below shows a scoring matrix that outlines a random scoring scheme for simple substitution mutations. Here, the diagonal path exhibits the highest score, meaning that aligning ATCG on top of ATCG will be the best alignment.

	A	T	C	G
A	20	10	5	5
T	10	20	5	5
C	5	5	20	10
G	5	5	10	20

Figure 2. A substitution scoring matrix (Lesk, 2002).

The scoring scheme of different algorithms may be modified depending on the type of alignment that the algorithm is designed to compute. Users are recommended to get familiarized with the algorithms so they can select the most appropriate algorithm to carry out the type of alignment that they want, generating the most ideal results suitable for their purposes.

4.0 DIFFERENT TYPES OF SEQUEENCE ALIGNMENT

Different methods of alignments are available for different types of sequence alignment. Many custom designed algorithms have been developed to suit different demands. For example, different softwares are available to users who want to explore homology between sequences, or say, study genetic variations within the sequences (Applied Biosystems, 2002). Depending on the type of alignment that the algorithm is designed to measure, the same set of sequences that is aligned in one will not necessarily give the same alignment result in another. The key is to find out which type of alignment is to be performed. Consider the following types of alignment: local vs. global, heuristic vs. optimal, pairwise vs. multiple alignment. With an understanding of different alignment methods, users can narrow down from a selection of softwares to the one that performs the desired alignment.

4.1 Global vs. Local Alignment

In general terms, algorithms that are designed to perform global alignment attempt to align every nucleotide in a set of aligned sequences. Given a set of sequences that are different in length, gaps will be inserted into the shorter sequences in effort to span the entire length of the longer sequence (Pearson and Wood, 2003). With global alignment, it is most useful when the sequences to be aligned are approximately the same length.

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...AATTCGATGGCAT TTGCATGAGA...  
  |  | | | | | | | | | | | | | |  
...CA--TCGGTGGCAC----GC--T...
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Figure 3. Aligning two sequences globally

The method is effective for identifying frameshift mutations such as insertion or deletion in one allele; gaps will be inserted into the positions where the insertion or the deletion has occurred in the mutated allele (Pearson and Wood, 2003). One of the first algorithms that was used to measure global optimal alignments is called Dynamic Programming. While this method is guaranteed to find the global optimum, there are some disadvantages to the technique (Lesk, 2002). First and foremost, the method inserts excessive gaps into the sequences due to the nature of the algorithm. The region of interest to be aligned will be stretched over the entire length of the longer sequences, resulting in some biologically insignificant alignments that are not suitable for comparison (Lesk, 2002). For the purpose of aligning sequences that only share a specific region of similarity, local alignment would be the method of choice. The algorithm uses a modified version of Dynamic Programming to search for the most similar region between two or more sequences that might be dissimilar in context or length (Lesk, 2002).

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...AATTCGGTGGCATTGATGAGA...
      | | | | |
.....GCGGTGGCACGC...

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Figure 4. *Aligning two sequences with the local alignment method.*

Local alignment produces a more biologically meaningful comparison that is useful for investigating structural and functional aspects of the protein, or the similarity between two or more nucleotide sequences (Altschul, 1997). Nevertheless, with sufficient similarity displayed in the reference and the query, either the local or global alignment method is able to accurately generate the most desirable alignment.

4.2 Pairwise vs. Multiple Alignment

The procedure of aligning two sequences is termed pairwise alignment. The method only looks at two sequences at a time. On the other hand, multiple alignment is the process of aligning more than two sequences simultaneously as the term implies (Dale and von Schantz, 2002). Older algorithms perform pairwise alignment, using simple statistical methods to compute sequence similarity. More sophisticated algorithms have been developed to perform multiple alignment. For example, the progressive pairwise method is a type of multiple alignment that first performs pairwise alignment and then progressively compare the sets of aligned pairs to carry out multiple alignment (Altschul, 1997).

4.3 Optimal vs. Heuristic Alignment

Some famous alignment programs that utilize heuristic algorithms are BLAST and FASTA. The theory behind heuristic methods is that the algorithm uses matching words to perform sequence alignments (NCBI, 2006). The pairwise method first identifies a short consensus common to the two sequences to be aligned. Based on the locally identified consensus known as the *word*, the algorithm will continue to search for matching pairs in both directions outwards from the word until a mismatch is encountered, where the extension of the consensus will cease (NCBI, 2006). The longest consensus common to both sequences will be displayed. This method of alignment is good at identifying specific regions of similarity quickly in two unrelated sequences; it will not miss the strong regions of similarity that might appear at different positions in the aligned sequences (Pearson and Wood, 2003). However, heuristic alignment is an approximation method which does not guarantee the search of the optimal alignment,

because the nature of the algorithm does not allow the introduction of gaps (Altschul, 1997). A better approach to generate biologically meaningful alignments is to align the sequences optimally. Optimal alignment is a method to align sequences systemically with the use of scoring matrices and gaps (Skiena, 2002). Both local and global alignment algorithms use the optimal approach that allows the introduction of gaps to align sequences (Skiena, 2002). Comparatively, the optimal approach is able to generate a more desirable alignment between related sequences with a higher confidence than the heuristic approach.

4.4 Choosing the Methods of Alignment

As mentioned previously, one of the tasks carried out in Dr. Hegele's laboratory is to identify SNPs and other genetic mutations such as insertions or deletions in patients' DNA. Related exons of the gene of interest in the DNA sequences are examined individually. Since the exons of interest are isolated and amplified in PCR using the same pair of primers, the lengths of the query sequences are more or less the same in size (Dale and von Schantz, 2002). With a reference sequence that displays similar length as the query sequences, it is most preferred to align the sequences globally. However, with an alignment software that is not able to truncate the reference to show a similar length as the query sequences, local alignment would be the method of choice. The method will match the query sequences to the most similar region in the reference without inserting unnecessary gaps into the sequences.

Furthermore, it would be more time efficient if the software we use is able to perform multiple alignment. Considering the large number of sample sequences to be analyzed, the most convenient method is to compare more than two sequences simultaneously.

With multiple alignment, SNPs that are present in the samples can be picked out all at once. The convenience that multiple sequence alignment provides is invaluable to the busy laboratory setting.

Lastly, since the sequences that we analyze show sufficient similarity with one another, the best approach is to use optimal alignment that is most effective when comparing related sequences. The heuristic approach should not be used since the method cannot identify major insertion or deletion mutations.

4.5 The Currently In-use Software in RRI

In the laboratory, the alignment software that is currently in use for sequence alignment analysis is the Sequence Navigator software v1.1 from Applied Biosystems. The software has limited alignment features, and is only capable of doing pairwise analysis. The software is discontinued in the market because more updated versions of the software have been developed for enhanced usage (Applied Biosystems Technical Support).

It would be beneficial to the laboratory to gain access to a sequence alignment software that can perform multiple alignments to save time. More importantly, having a software that performs the desired type of alignment ensures accuracy of mutation detection. The convenience and quality alignments that such a software offers are invaluable to the busy, research-intensive laboratory.

5.0 THE THREE ALIGNMENT SOFTWARES AVAILABLE IN RRI

Fortunately, we have licenses to three additional alignment softwares integrated with new and improved alignment functions and features suitable for complicated sequence alignments. The three softwares that are available for use are Applied Biosystems's SeqScape® Version 2.0, DNASTar's Lasergene® Version 7.0, and Gene Code's Sequencher™ Version 4.7. This section of the report will briefly describe the softwares' features related to nucleotide sequence alignment.

5.1 ABI SeqScape® Version 2.0

Applied Biosystems' SeqScape software is a sequence analysis program that processes electropherogram traces or the raw data generated by an automated sequencing system. Although the software is mainly used for sequence editing, users have the option to align their sequences once they have been base called. The software uses the famous Smith-Waterman local alignment algorithm to align the base called sequences with a user-defined reference (Applied Biosystems, 2002). Although the algorithm is technically a pairwise method, the software is designed in such a way that it is capable of displaying more than two sequences simultaneously in the same window, all of which have been analyzed and aligned with the reference sequence. This technique is known as the progressive pairwise alignment method (Applied Biosystems Technical Support, 2006). The software is ideal for investigators who are conducting in-depth studies of various gene segments along the same reference sequence.

5.1.1 Aligning Sequences with SeqScape

Users are recommended to follow the software's set up procedures before performing sequence analysis (Applied Biosystems, 2002). Briefly, the protocol is outlined as follows:

1. Create Analysis Defaults

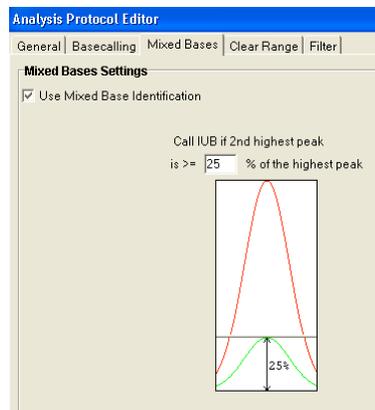


Figure 5. The analysis protocol editor.

- a) In the *Basecalling* tab, users select from the drop-down menus the automated sequencer as well as the Dye set they use for sequencing. Users can also tell the software when to stop the basecalling, whether it is at a PCR stop or at a position where a specific number of ambiguities (N) has been displayed.
- b) In the *Mixed Bases* Tab, the *Mixed Base Identification* option can be used in case of encountering a heterozygous allele. The option takes into effect if the second peak height is of a certain percentage (user-defined) of the main peak height (Figure 5).
- c) The parameters listed in the *Clear Range* tab enable users to define the quality of their sequences. For example, the software can be instructed to display the sequence in between a certain range where all other ambiguous bases outside of the range are trimmed.
- d) In the *Filter* tab, users can reject sequences that are of poor quality by defining the parameters of a good quality sequence.

2. Define Analysis Settings

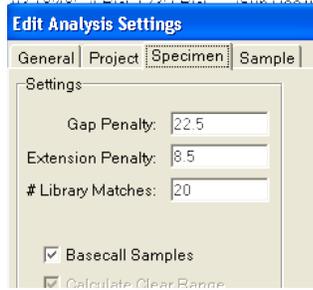


Figure 6. Analysis settings.

- a) The software's alignment algorithm uses the numeric values entered in the *Gap* and *Extension Penalties* fields in the *Project* and *Specimen* tabs respectively to score an alignment with gaps (Figure 6).

3. Define Display Settings

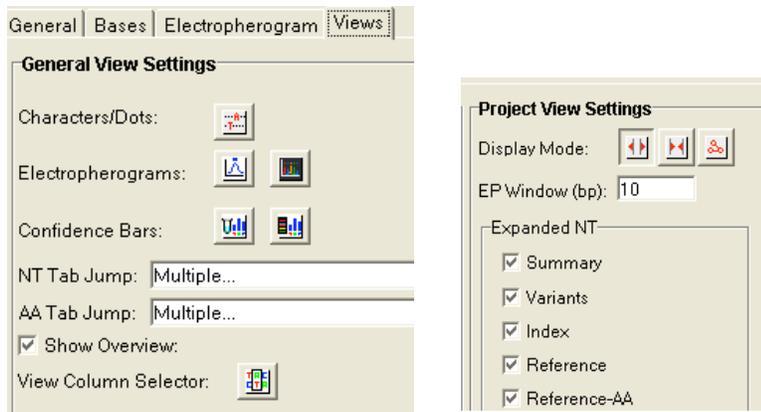


Figure 7. Options in Display Settings.

- a) Users can customize the appearance of the screen layout by choosing the colours and text styles according to their preference. The software also allows users to choose which icons or features are to be shown and which ones to be removed (Figure 7). For example, it can show or hide electropherogram(s), the reference sequence, the corresponding amino acid sequence, the consensus, and variants, etc.

4. Create Reference Data Group

ROI Name	Segment	Seg. Start	Seg. End	ROI Start	ROI Length	Translation	Color	on Layer 1
1 NC_000019	NC_000019	1	3576	1	3576	<input checked="" type="checkbox"/>		<input checked="" type="checkbox"/>
2 APOC2_gene	NC_000019	1	3576	1	3576	<input checked="" type="checkbox"/>		<input type="checkbox"/>
3 STS_1	NC_000019	134	284	1	151	<input type="checkbox"/>		<input type="checkbox"/>
4 STS_2	NC_000019	139	434	1	296	<input type="checkbox"/>		<input type="checkbox"/>
5 STS_3	NC_000019	186	286	1	101	<input type="checkbox"/>		<input type="checkbox"/>

Reference Sequence	NC_000019
1	gttgtggctg
41	atcctctctg
81	ccadagctctg
121	gggggctca
161	gaattttaag
201	catgactgtg
241	tgtgtgtgtg
281	tatgtagccc
321	atcctctctg
361	gttgtggctg
401	atcctctctg
441	ccadagctctg
481	gggggctca
521	gaattttaag
561	catgactgtg
601	tgtgtgtgtg
641	tatgtagccc
681	atcctctctg
721	gttgtggctg
761	atcctctctg
801	ccadagctctg
841	gggggctca
881	gaattttaag
921	catgactgtg
961	tgtgtgtgtg
1001	tatgtagccc
1041	atcctctctg
1081	gttgtggctg
1121	atcctctctg
1161	ccadagctctg
1201	gggggctca
1241	gaattttaag
1281	catgactgtg
1321	tgtgtgtgtg
1361	tatgtagccc
1401	atcctctctg
1441	gttgtggctg
1481	atcctctctg
1521	ccadagctctg
1561	gggggctca
1601	gaattttaag
1641	catgactgtg
1681	tgtgtgtgtg
1721	tatgtagccc
1761	atcctctctg
1801	gttgtggctg
1841	atcctctctg
1881	ccadagctctg
1921	gggggctca
1961	gaattttaag
2001	catgactgtg
2041	tgtgtgtgtg
2081	tatgtagccc
2121	atcctctctg
2161	gttgtggctg
2201	atcctctctg
2241	ccadagctctg
2281	gggggctca
2321	gaattttaag
2361	catgactgtg
2401	tgtgtgtgtg
2441	tatgtagccc
2481	atcctctctg
2521	gttgtggctg
2561	atcctctctg
2601	ccadagctctg
2641	gggggctca
2681	gaattttaag
2721	catgactgtg
2761	tgtgtgtgtg
2801	tatgtagccc
2841	atcctctctg
2881	gttgtggctg
2921	atcctctctg
2961	ccadagctctg
3001	gggggctca
3041	gaattttaag
3081	catgactgtg
3121	tgtgtgtgtg
3161	tatgtagccc
3201	atcctctctg
3241	gttgtggctg
3281	atcctctctg
3321	ccadagctctg
3361	gggggctca
3401	gaattttaag
3441	catgactgtg
3481	tgtgtgtgtg
3521	tatgtagccc
3561	atcctctctg
3601	gttgtggctg
3641	atcctctctg
3681	ccadagctctg
3721	gggggctca
3761	gaattttaag
3801	catgactgtg
3841	tgtgtgtgtg
3881	tatgtagccc
3921	atcctctctg
3961	gttgtggctg
4001	atcctctctg
4041	ccadagctctg
4081	gggggctca
4121	gaattttaag
4161	catgactgtg
4201	tgtgtgtgtg
4241	tatgtagccc
4281	atcctctctg
4321	gttgtggctg
4361	atcctctctg
4401	ccadagctctg
4441	gggggctca
4481	gaattttaag
4521	catgactgtg
4561	tgtgtgtgtg
4601	tatgtagccc
4641	atcctctctg
4681	gttgtggctg
4721	atcctctctg
4761	ccadagctctg
4801	gggggctca
4841	gaattttaag
4881	catgactgtg
4921	tgtgtgtgtg
4961	tatgtagccc
5001	atcctctctg
5041	gttgtggctg
5081	atcctctctg
5121	ccadagctctg
5161	gggggctca
5201	gaattttaag
5241	catgactgtg
5281	tgtgtgtgtg
5321	tatgtagccc
5361	atcctctctg
5401	gttgtggctg
5441	atcctctctg
5481	ccadagctctg
5521	gggggctca
5561	gaattttaag
5601	catgactgtg
5641	tgtgtgtgtg
5681	tatgtagccc
5721	atcctctctg
5761	gttgtggctg
5801	atcctctctg
5841	ccadagctctg
5881	gggggctca
5921	gaattttaag
5961	catgactgtg
6001	tgtgtgtgtg
6041	tatgtagccc
6081	atcctctctg
6121	gttgtggctg
6161	atcctctctg
6201	ccadagctctg
6241	gggggctca
6281	gaattttaag
6321	catgactgtg
6361	tgtgtgtgtg
6401	tatgtagccc
6441	atcctctctg
6481	gttgtggctg
6521	atcctctctg
6561	ccadagctctg
6601	gggggctca
6641	gaattttaag
6681	catgactgtg
6721	tgtgtgtgtg
6761	tatgtagccc
6801	atcctctctg
6841	gttgtggctg
6881	atcctctctg
6921	ccadagctctg
6961	gggggctca
7001	gaattttaag
7041	catgactgtg
7081	tgtgtgtgtg
7121	tatgtagccc
7161	atcctctctg
7201	gttgtggctg
7241	atcctctctg
7281	ccadagctctg
7321	gggggctca
7361	gaattttaag
7401	catgactgtg
7441	tgtgtgtgtg
7481	tatgtagccc
7521	atcctctctg
7561	gttgtggctg
7601	atcctctctg
7641	ccadagctctg
7681	gggggctca
7721	gaattttaag
7761	catgactgtg
7801	tgtgtgtgtg
7841	tatgtagccc
7881	atcctctctg
7921	gttgtggctg
7961	atcctctctg
8001	ccadagctctg
8041	gggggctca
8081	gaattttaag
8121	catgactgtg
8161	tgtgtgtgtg
8201	tatgtagccc
8241	atcctctctg
8281	gttgtggctg
8321	atcctctctg
8361	ccadagctctg
8401	gggggctca
8441	gaattttaag
8481	catgactgtg
8521	tgtgtgtgtg
8561	tatgtagccc
8601	atcctctctg
8641	gttgtggctg
8681	atcctctctg
8721	ccadagctctg
8761	gggggctca
8801	gaattttaag
8841	catgactgtg
8881	tgtgtgtgtg
8921	tatgtagccc
8961	atcctctctg
9001	gttgtggctg
9041	atcctctctg
9081	ccadagctctg
9121	gggggctca
9161	gaattttaag
9201	catgactgtg
9241	tgtgtgtgtg
9281	tatgtagccc
9321	atcctctctg
9361	gttgtggctg
9401	atcctctctg
9441	ccadagctctg
9481	gggggctca
9521	gaattttaag
9561	catgactgtg
9601	tgtgtgtgtg
9641	tatgtagccc
9681	atcctctctg
9721	gttgtggctg
9761	atcctctctg
9801	ccadagctctg
9841	gggggctca
9881	gaattttaag
9921	catgactgtg
9961	tgtgtgtgtg
10001	tatgtagccc

Figure 8. Reference Data Group settings.

- a) Users can either import a reference sequence from NCBI's *Entrez* database, or copy-and-paste a sequence from another source.
- b) Users can define as many regions of interest (ROIs) as they desire in separate layers so that the sequences, when imported, will only align with that particular segment of the reference.

- 5. Create Project Template
- 6. Import Sequence Samples
- 7. Perform Sequence Analysis

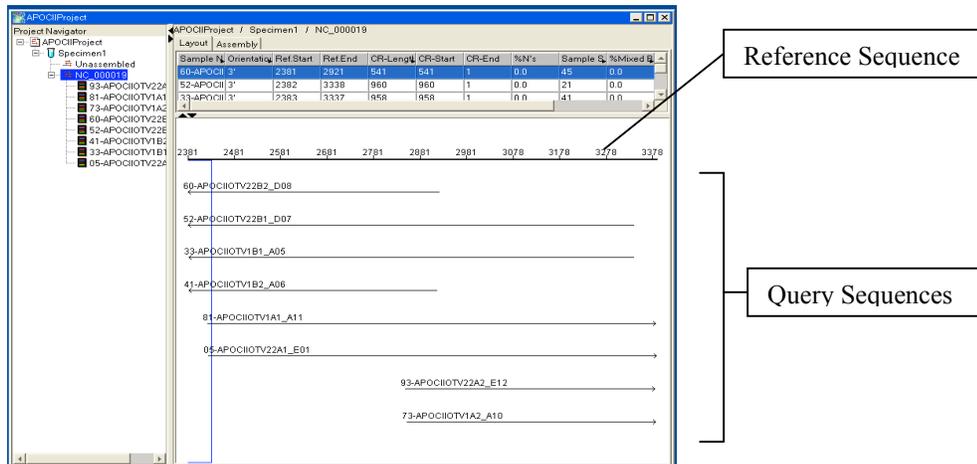


Figure 9. The Layout view.

- a) The software is able to display the sequences' relative positioning along the reference using the Smith-Waterman local alignment algorithm. The sequences, represented as arrows, are positioned at their alignment sites against the reference. Furthermore, the direction of the arrowheads is

indicative of the orientation of the sequences.

- b) One of the components of the alignment report is the *Mutation Report*. In the report, any variations observed that is different from the reference are listed in the table. It identifies the mutation (ie. Base change, Insertion, or Deletion), its position in the sequence, the type of mutation and its effect on the sequence (ie. Missense, Nonsense, or Silent).

5.2 Lasergene[®] Version 7.0

Lasergene is a sequence analysis software with five applications: SeqBuilder, GeneQuest, PrimerSelect, Protean, and MegAlign. The software features synchronous updating which allows users to work on the same file in any or all of the applications at the same time (DNASTAR, 2006). The applications that concern sequence alignment are SeqBuilder and MegAlign, which will be introduced as follows. Refer to the user guide - *GETTING STARTED with DNASTAR Lasergene 7: Software Suite for Sequence Analysis* for more information.

5.2.1 SeqBuilder

SeqBuilder is a powerful program that allows users to design their own DNA sequence by entering individual nucleotides (A, T, C, or G) into the program, or by just simply pasting any sequences that they have copied from another source. Users can also edit the copied sequence with the program to make modifications as they need. The program is also capable of identifying any open reading frames and enzyme restriction sites for cloning purposes. Other useful features include translating, back-translating, and selecting the reverse complement of the newly designed DNA.

5.3.2 *MegAlign*

MegAlign performs sequence comparison with either nucleotide or protein sequences, and is able to do both pairwise and multiple alignments. Based on the aligned sequences, the program can generate phylogenetic trees, alignment reports and tables to summarize the match results and variants identified within sequences. Four algorithms are available to perform pairwise sequence alignments. The users can choose to display a dot plot from each for a visual representation of the alignment. Furthermore, four additional algorithms are designed for multiple sequence alignments. The Jotun Hein algorithm is designed for multiple protein sequence alignments, while Clustal V and two Clustal W are suitable for multiple nucleotide sequence analyses (Gindullis *et al.*, 1999). The Clustal algorithms are the most commonly used statistical measures that exploit the progressive pairwise method to carry out multiple alignments. Clustal V is a global multiple alignment method, while Clustal W is a local multiple alignment method.

5.3.3 *Aligning Sequences with Lasergene*

Aligning nucleotide sequences in Lasergene is rather simple. For reference and query sequence comparisons, users can either import their reference from NCBI's *Entrez* database, or use a pre-existing reference file in MegAlign. Users can also take advantage of the synchronous updating feature in Lasergene to transfer their reference sequence designed in SeqBuilder. The following example shows the procedure of aligning a few LPL¹ exon 5 sequences with the appropriate reference obtained in NCBI database; additional features relating to the alignment are also described.

¹ LPL is the gene that encodes the protein Lipoprotein Lipase. The deficiency of the protein leads to the accumulation of triglyceride which leads to high blood pressure and potentially the development of atherosclerosis. The gene sequence is extracted in patients' DNA for mutation detection analysis (NCBI, 2006).

1. Edit the Reference Sequence in SeqBuilder

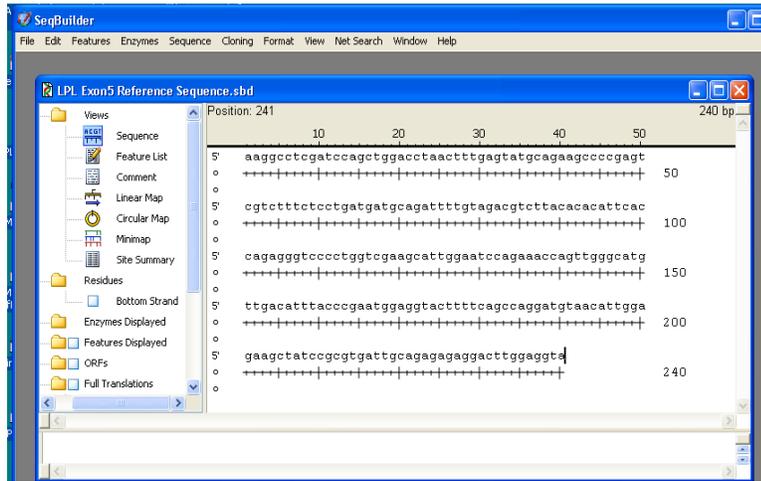


Figure 10. Editing the sequence in SeqBuilder.

- a) The reference sequence can be edited in SeqBuilder so that only the region of interest, or the segment that is relevant for alignment is displayed. At the top right corner, the sequence's length is displayed. The ruler beneath the sequence is included to indicate the base position.

2. Import the Reference Sequence to MegAlign



Figure 11. LPL Exon 5 is imported in MegAlign.

- a) The reference is sent to MegAlign as shown in the working panel above. The sequence is displayed in two separate panels. Users can scroll along the scroll bar to view a particular section of the sequence that they want to examine. The coloured bar at the top of the window is the consensus meter, which shows the consensus strength. The colour scheme shown at the left of the consensus meter is indicative of the relative strength of the consensus (Red indicates the strongest consensus, black indicates the weakest consensus). Two rows below the consensus meter is the position ruler. It helps identify the position of the bases in the sequence.

3. Import Sequence Samples into the Project

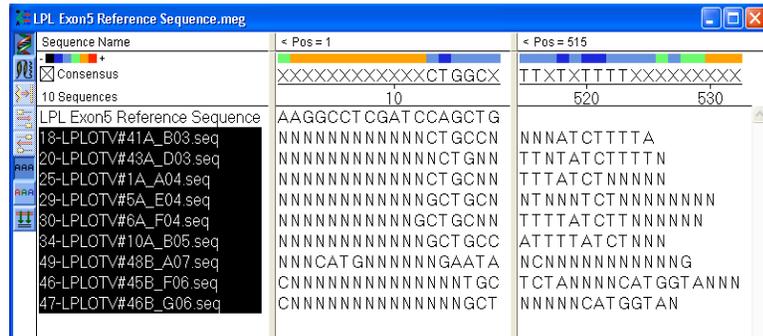


Figure 12. Imported sequences are listed below the reference sequence.

- a) Imported sequences are listed below the reference sequence. Note that the consensus meter is now displaying different colours due to the variations shown in the sequences. Because the software does not recognize a particular sequence as the reference sequence, the consensus sequence is reflective of all sequences listed in the panel.

4. Trim Sequence Samples

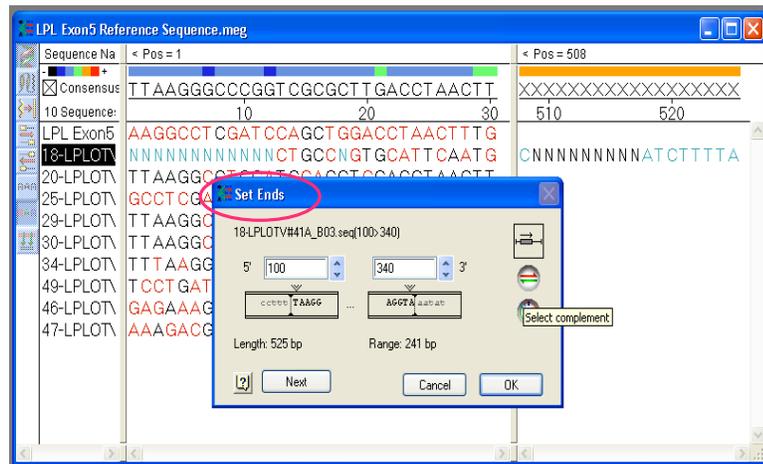


Figure 13. Setting the 5' and the 3' ends of the sequences.

- a) The “N” represents an ambiguity in the sequence. They are usually present at the beginning of the sequences as they are the priming regions. Clean sequences can be obtained by specifying the start and end positions for trimming. There is also the option to select the complementary strand of the sequence if it appears in the opposite orientation. The coloured bases represent variants that are different from the consensus.

5. Select an Alignment Method

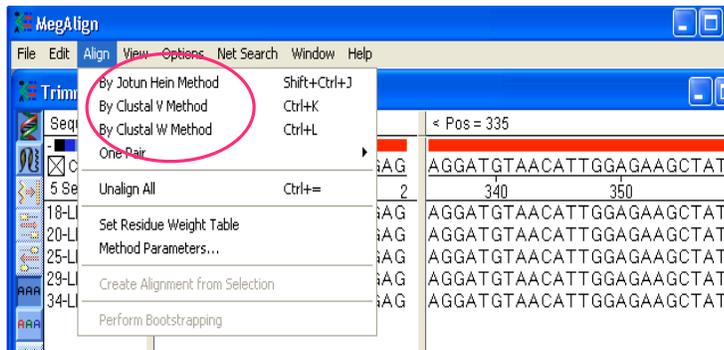


Figure 14. Three multiple alignment algorithms are available for selection.

- a) Sequences can be aligned by selecting the appropriate algorithm under the *Align* command. Clustal V and Clustal W algorithms are the methods suitable for aligning multiple sequences simultaneously.

Example:

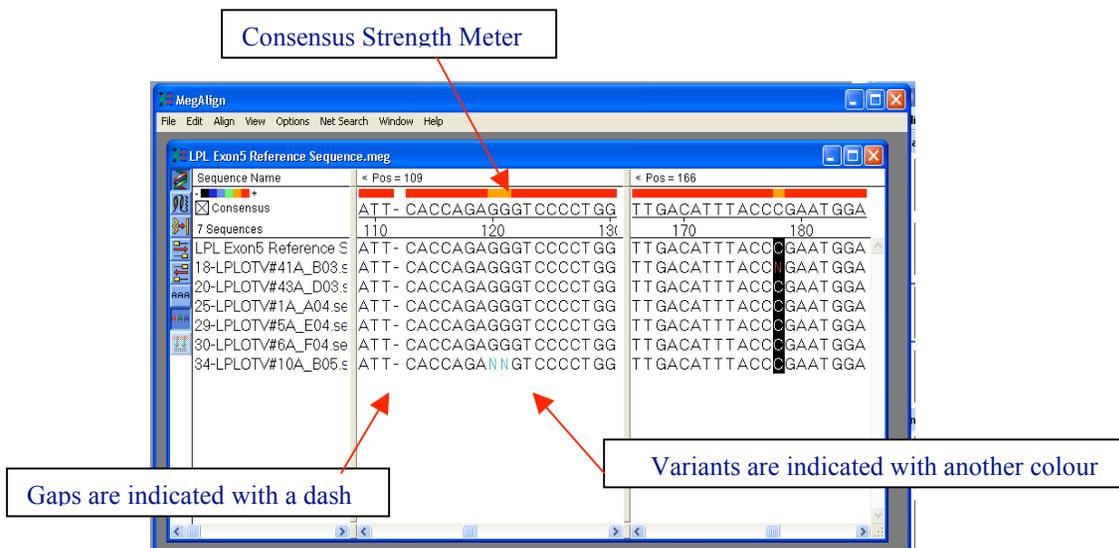


Figure 15. The sequences are aligned with Clustal V.

- b) In this example, Clustal V is chosen to perform the alignment. It is a global multiple alignment method where sequences are spanned in attempt to align nucleotides starting from the first nucleotide in the longest sequence until the end is reached.

6. Examine the Alignment Report

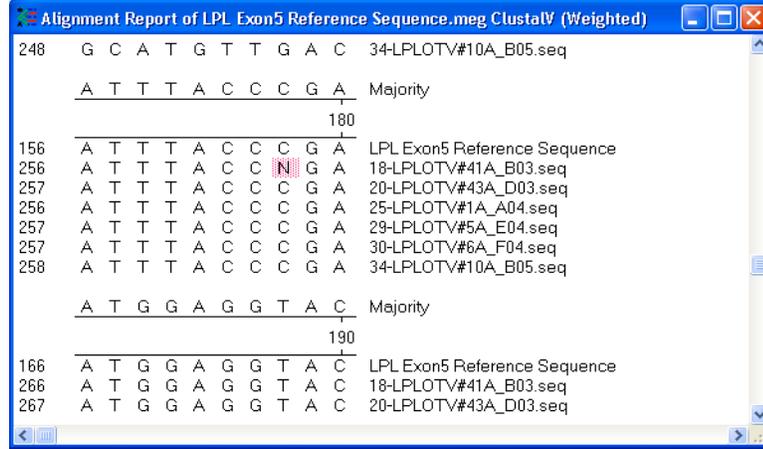


Figure 16. A SNP is identified in sample 18.

- a) The alignment report summarizes any mutations detected within the aligned set of sequences. In this case, a SNP is identified in sample 18-LPLOTV#41A_B03.seq.

Users can also choose another algorithm for alignment depending on the nature and characteristic of their nucleotide sequences.

5.3 Sequencher™ Version 4.7

Sequencher 4.7 is a sequence analysis software that specializes in contig assemblies. It aligns overlapping regions of short sequence fragments, which at the end, will put together a complete nucleotide sequence (Figure 17). Users can take advantage of the algorithms used for contig assembly to perform sequence alignment. The algorithms, *Dirty Data*, *Clean Data*, and *Large Gap*, are modified versions of the Smith-Waterman local sequence alignment algorithm (Tippmann, 2003). In particular, the Dirty Data algorithm can align sequences that are untrimmed at the 5' or the 3' end. Aligning sequences containing ambiguities (N) that are possibly caused by a substitution or a frameshift mutation with Dirty Data will not affect the alignment result. Clean Data

algorithm is designed to align sequences that are trimmed as the name suggests. The sequences that are to be aligned with this particular algorithm should not contain any ambiguities. It is recommended to exclude the use of poor quality data with this algorithm. Finally, the Large Gap algorithm is designed to align large DNA such as genomic or cDNA. It is able to accept gaps that are larger than two bases long in the overlapping regions between DNA fragments during contig assembly (Ginsburg, 2006).

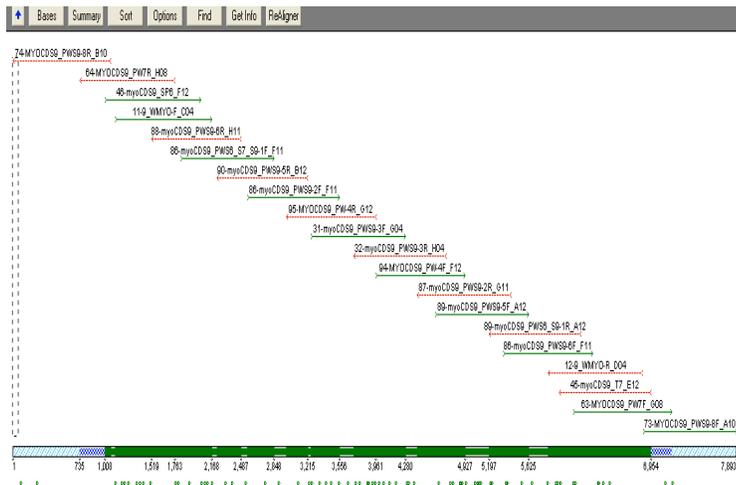


Figure 17. A map of overlapping contigs.

5.2.1 Aligning Sequences in Sequencher

Sequencher software is compatible with sample files that are in .ab1 format. Just like SeqScape, the software is able to accept and analyze traces of raw data for alignment purposes. The following provides an overview of aligning nucleotide sequences in Sequencher. More information can be found the Gene Codes Sequencher 4.7 website at www.genecodes.com

1. Import the Reference Sequence

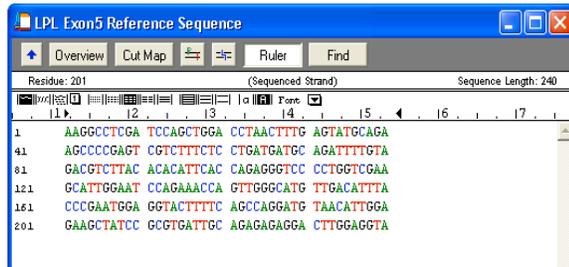


Figure 18. A reference sequence is pasted to the sequence editing panel.

- A reference sequence can be copied and pasted to *Create New DNA* window. This sequence should be set as the reference sequence under the *Sequence* command. Sequences in this panel can be trimmed by simply deleting all the bases that are not desirable.

2. Import Sequence Samples

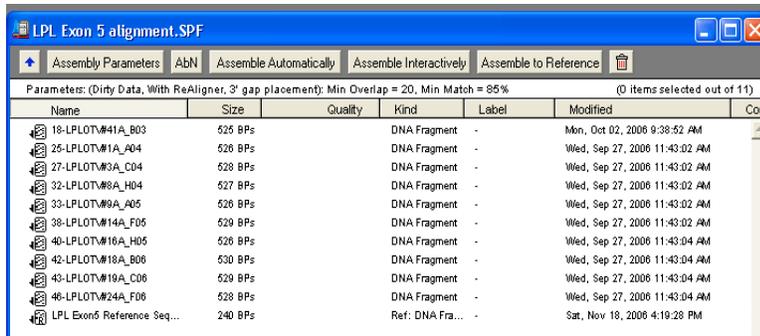


Figure 19. Samples are imported for analysis.

- All the samples to be aligned are listed in the panel along with the reference sequence.

3. Choose Assembly Parameters

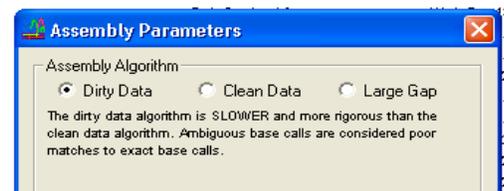


Figure 20. Three algorithms are available for alignment.

- a) Since the samples imported into the software are traces of raw data that have not been processed, the *Dirty Data* algorithm is chosen to perform the sequence alignment.

4. Align Sequences to Reference

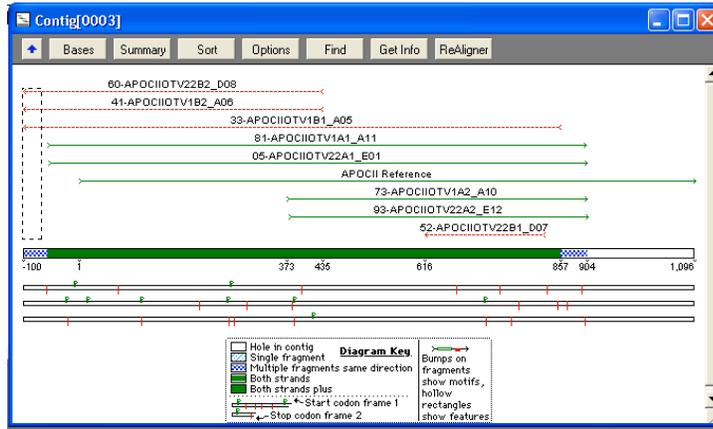


Figure 21. Sample sequences are aligned along the reference sequence.

- a) In the overview, all sequences are shown at their aligned position relative to the reference sequence. Each sequence is labeled with the corresponding sample name. Green arrows indicate the sequence is being read in the forward direction, while red arrows indicate that the sequences are in the reverse direction.

5. Analyze the Aligned Sequences

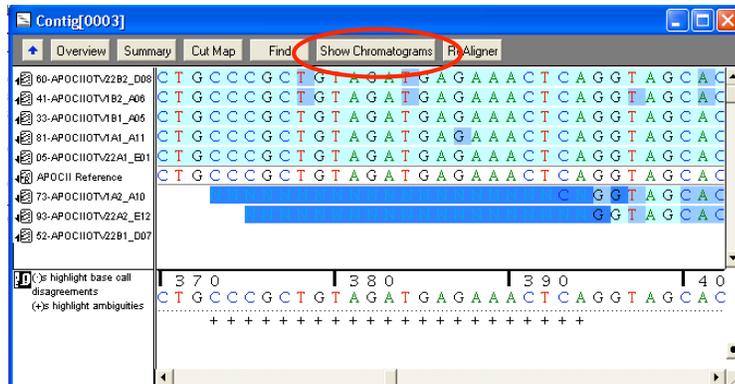


Figure 22. The samples are aligned with respect to the reference sequence.

- a) All the sequences are aligned against the reference sequence. The reference sequence is distinguished by a row selector. The different shades of blue represent the degree of ambiguity of the base at the particular position. The consensus sequence is easily identified at the bottom of the panel. The +

symbol represents an ambiguity and the ● symbol represents a base change at the corresponding position.

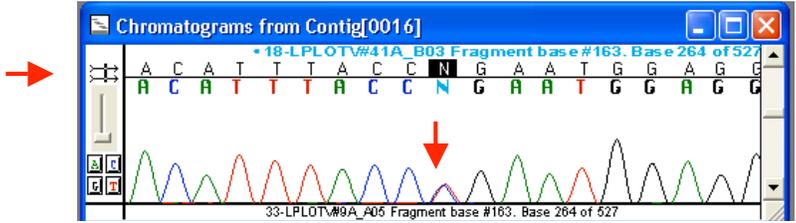


Figure 23. The double peak represents a heterozygous allele in the sample.

- a) The *Show Electropherogram* option allows traces of raw data to be displayed. The electropherogram can be used for the visual inspection of the heterozygous allele if a base change is encountered. One can also tell the orientation of the sequence by observing the arrow shown at the top left corner. In this case, the arrowhead points forward, meaning that this particular sequence in the forward direction.

6. View the Alignment Report

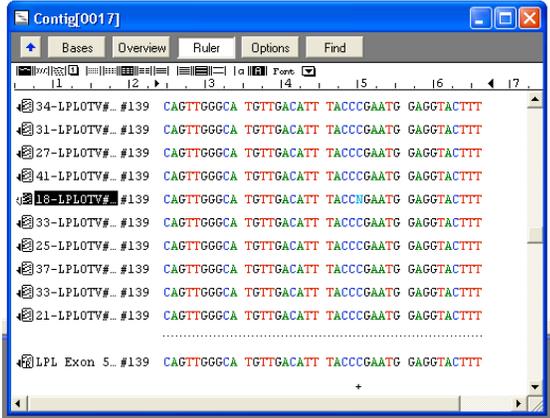


Figure 24. A variant is noted in sample 18 in the report.

- a) The alignment report summarizes the finding of all variants in the samples.

6.0 ASSESSMENT OF THE THREE ALIGNMENT SOFTWARES

Aligning DNA sequences with a software that produces quick and accurate alignment results will improve work and time efficiency in the laboratory. In order to decide which software is able to carry out sequence alignments most effectively, the same set of sequences will be aligned respectively in all three softwares (SeqScape, Sequencher, and Lasergene). The alignment results generated by the softwares will be used for comparison. The parameters of the assessment include the software's accuracy in determining the location of existing mutations, the amount of sequences that the software can handle vs. time efficiency, the ease of use and cost.

6.1 Accuracy of Sequence Alignment

6.1.1 SNP Detection

In this experiment, 10 LPL exon 5 sequences are chosen to align with the corresponding reference sequence to test the software's ability to detect the presence of SNPs at the accurate position. One of the sample sequences, 18-LPLOTV#41A, is known to carry a C/T SNP at position 15013 relative to the LPL gene reference, or at position 163 relative to the LPL exon 5 reference (Wang, 2006).

Results

i) Aligning the Sequences in Lasergene

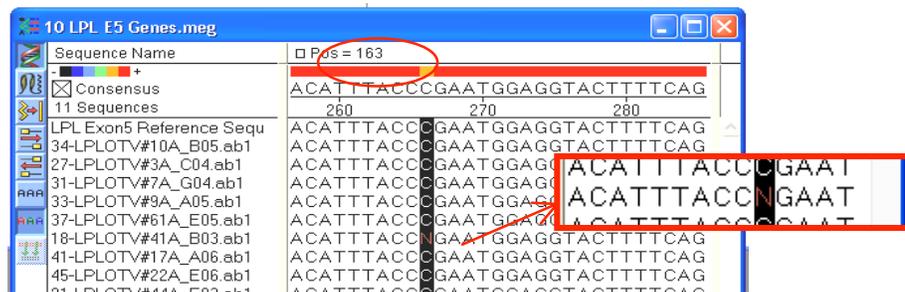


Figure 25. A SNP, represented as an N, is detected in sample 18 at position 163.

ii) Aligning the Sequences in Sequencher

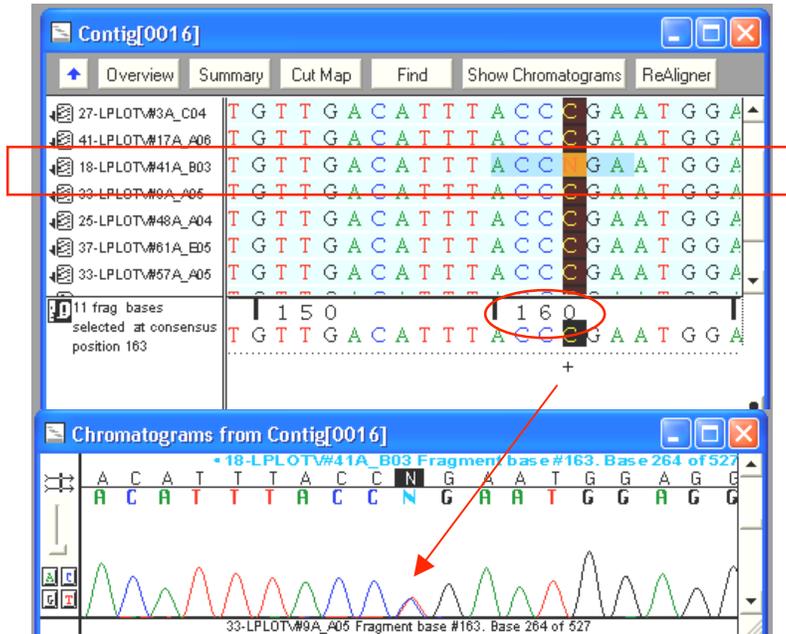


Figure 26. The double peak shown in the electropherogram confirms that the SNP detected in sample 18 is a C/T SNP.

i) Aligning Sequences in SeqScape

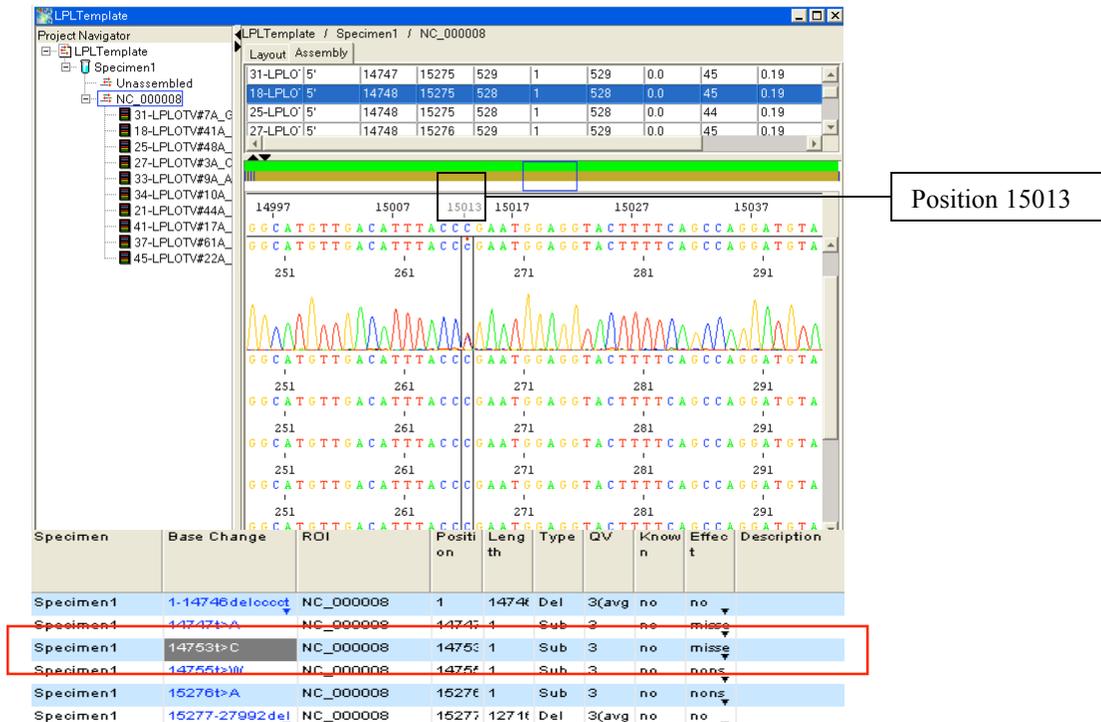


Figure 27. The mutation report in SeqScape identifies that the mutation found in sample 18 is a substitution mutation of a C to a T.

Analysis

All three softwares were able to correctly identify the position of the SNP in sample 18. The variation was either highlighted in a different colour (Lasergene and Sequencher) or marked with a dot (SeqScape) for easy recognition. The ruler feature in the software conveniently allows users to identify the position of the variation along the reference or the consensus sequence. In both SeqScape and Sequencher, the electropherograms that complemented the sequences provide a visual representation of the SNP. Both the electropherogram showed a blue red double peak at the SNP position, confirming C and T base substitution. In addition, the mutation report included in SeqScape verifies that the SNP is a substitution of the C allele. Other details about the mutation such as the type of mutation were also addressed in the report. Although MegAlign was also able to identify the presence of the SNP at the correct location, it cannot distinguish the substitution. Users will not be able to tell what the base change was because the SNP was base called as N, which represents an ambiguity in the sequence.

6.1.2 Heterozygous Insertion/Deletion Detection

Frameshift mutations occur when a mutation in gene sequence acquires an insertion or a deletion of nucleotides that interferes with the normal reading frame of the sequence. The mutation is heterozygous if the variation occurs only in one of the two alleles of the DNA (Wang, 2006). The mutation is characterized by overlapping peaks that usually start off in the mid-section of the electropherogram.

In the second part of the assessment, eight APOCII genes are chosen to test the software's ability to identify the bases that have been inserted or deleted within the set of

sequences. One of the sequences, 93-APOCIIOTV22A2, is known to carry a TCT insertion between position 3029 and 3030, just after the G/C SNP (Wang, 2006).

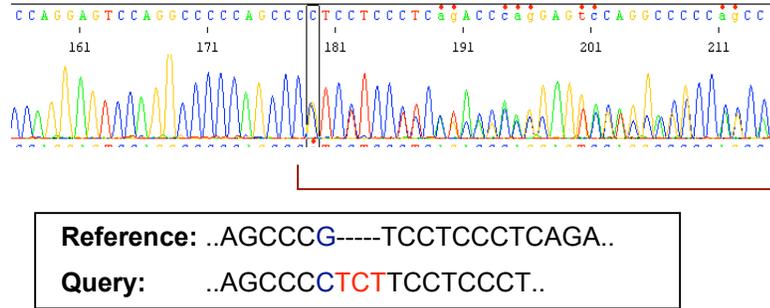


Figure 28. Three nucleotides TCT were inserted in sample 93.

Result

i) Aligning the Sequences in Lasergene

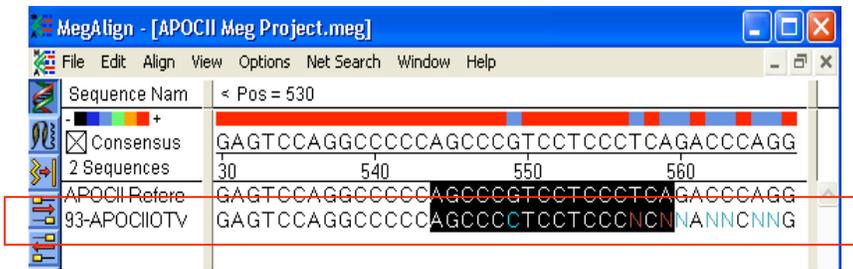


Figure 29. Sample sequences are aligned with Clustal W. The G/C SNP was identified; however, the insertion was not detected because the mutated heterozygous allele was not base called. The program only base calls for the higher peak.

ii) Aligning the Sequences in Sequencher

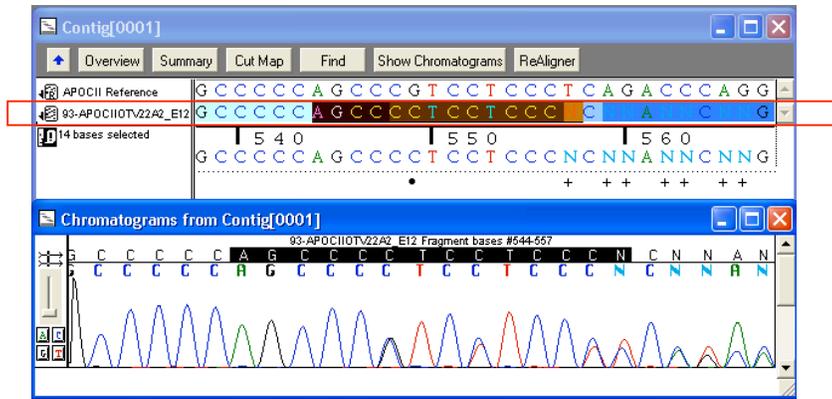
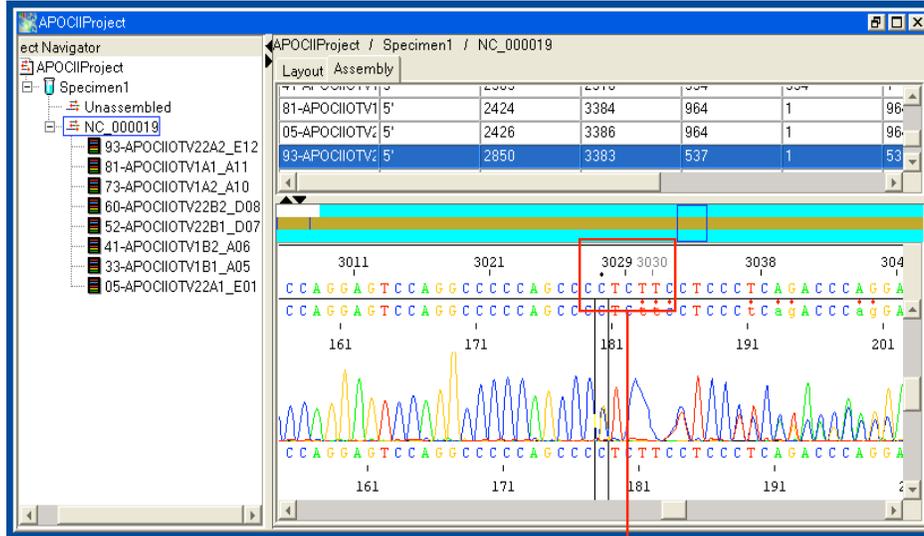


Figure 30. The G/C SNP was identified with Sequencher. The heterozygous allele was not base called however.

iii) Aligning Sequences in SeqScape



3 bases are inserted between position 3029 and 3030

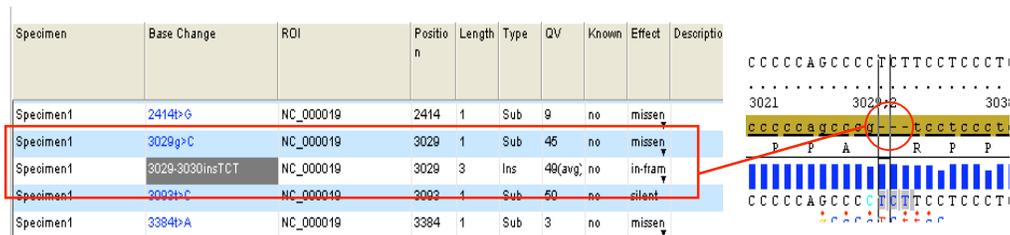


Figure 31. The software picked up both the SNP as well as the insertion mutation.

Analysis

As shown in Figures 29-31, all the softwares were able to pick up the G/C SNP. However, only SeqScape was able to identify the TCT insertion in the sample. In both MegAlign and Sequencher, the insertion was not detected because the program was not able to base call the heterozygous allele. It was set by default that the higher peak is to be base called in the case of encountering an overlapping peak on the trace data. Due to the nature of the reference and query sequences, the pair of sequences gave a false impression to align with the reference sequence perfectly even with an existing insertion. On the other hand, SeqScape was able to base call the

Result

i) Aligning Sequences in Lasergene

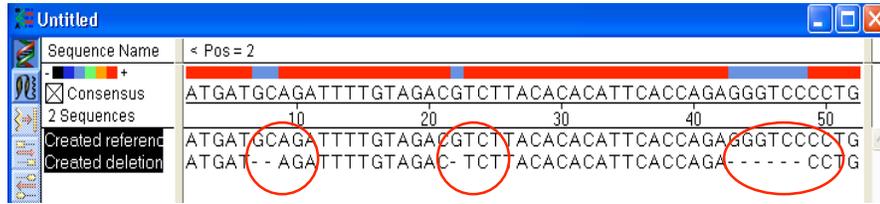


Figure 34. Sequences aligned with Clustal V, the global multiple alignment algorithm.

ii) Aligning Sequences in Sequencher

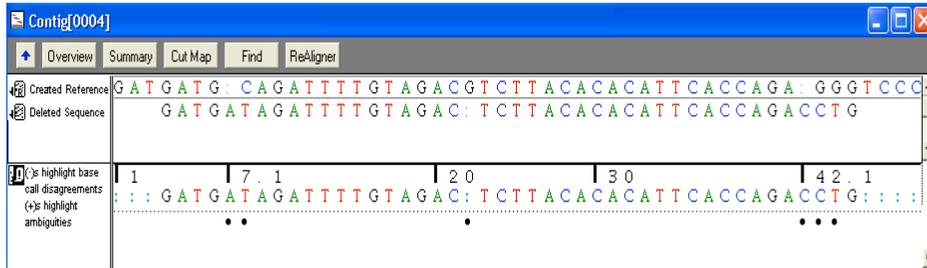
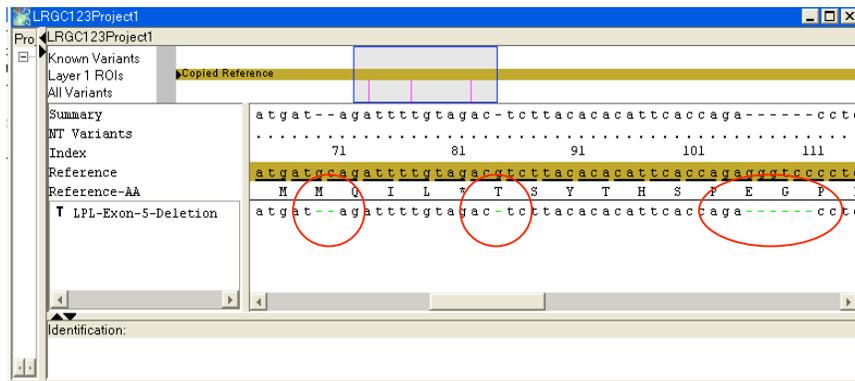


Figure 35. Clean Data algorithm was used to align the two sequences.

iii) Aligning Sequences with SeqScape



Specimen	Base Change	ROI	Position	Length	Type	QV	Known	E
LPL-Exon-5-Deletion	69-70delgc	Copied Reference	69	2	Del	0(avg)	no	
LPL-Exon-5-Deletion	84delg	Copied Reference	84	1	Del	0(avg)	no	
LPL-Exon-5-Deletion	105-110delgggtcc	Copied Reference	105	6	Del	0(avg)	no	

Figure 36. The software identified the three major deletions at the correct positions.

Analysis

Both the softwares Lasergene and SeqScape were able to pick up all three major deletions in the sequences. Clustal V was chosen to perform the alignment because the reference and query sequences have similar length. Since the algorithm applies the global alignment method, it made the detection of the three deletions possible. Similarly, the Smith-Waterman local alignment algorithm in SeqScape matches the test sequence to the region of the reference where highest similarity is observed. Gaps were inserted accordingly to the corresponding positions where the deletion was created. Furthermore, the software's mutation report indicated exactly where the deletion occurred, identifying the deleted bases accurately. Sequencher, however, was only able to identify the one base deletion. A possible explanation of the occurrence might have to do with the nature of the algorithm that was used to align the sequences. Since the custom-designed algorithm *Clean Data* employs a different scoring parameter intended for assembling contigs, it was not expecting gaps bigger than two bases as expected in result shown in Figure 33.

6.1.4 Summary

The assessment shows that all softwares – Lasergene, Sequencher, and SeqScape – were able to pinpoint the position of the SNP accurately. The *show electropherogram* feature in both Sequencher and SeqScape allows one to unravel the identity of the SNP.

SeqScape is also integrated with special base calling features with improved abilities to interpret traces. The software demonstrated its ability to recognize and identify the presence of SNPs, and insertion and deletion of bases in one or both alleles at the correct position. Since the software is intended to process the trace data generated by the

automated DNA sequencer we use in the laboratory, users can take advantage of the features that are compatible to the file type for quality alignment.

Lasergene's MegAlign is also integrated with the appropriate algorithms to carry out the detection. The software is effective in identifying homozygous insertion or deletion in both alleles, where the sequence is of good quality with confident base calls. However, the alignment is not effective with poor quality data. Although users have the option to select either Clustal V or Clustal W to align their sequences depending on the condition of the sequences, the software has a different base calling setting that neglects the presence of the heterozygous allele. Sometimes basecalling could not be made as the software reports any ambiguity in the sequence as an *N*.

Lastly, it was shown that Sequencher is not able to recognize any of the frameshift mutations. The algorithms designed for the software are intended for contig assembly that can only accommodate minor gaps. Furthermore, the default base calling settings in the software do not consider the heterozygous allele. The software is not suitable for frameshift mutation detection.

6.2 Time Effectiveness

All three softwares are capable of performing either multiple sequence alignment or progressive pairwise alignment, where numerous pairwise alignments are simultaneously carried out (Altschul, 1997). In the following assessment, sequences in multiples of ten (up to 60 sequences) will be entered into the softwares to examine time efficiency of each alignment software.

Result

i) Lasergene

Table 1. *Aligning sequences in MegAlign*

Number of Sequences	Time (s)
10	10
20	22
30	38
40	68
50	100
60	147

ii) Sequencher

Table 2. *Aligning sequences in Sequencher*

Number of Sequences	Time (s)
10	< 1
20	< 1
30	< 1
40	< 1
50	1
60	1

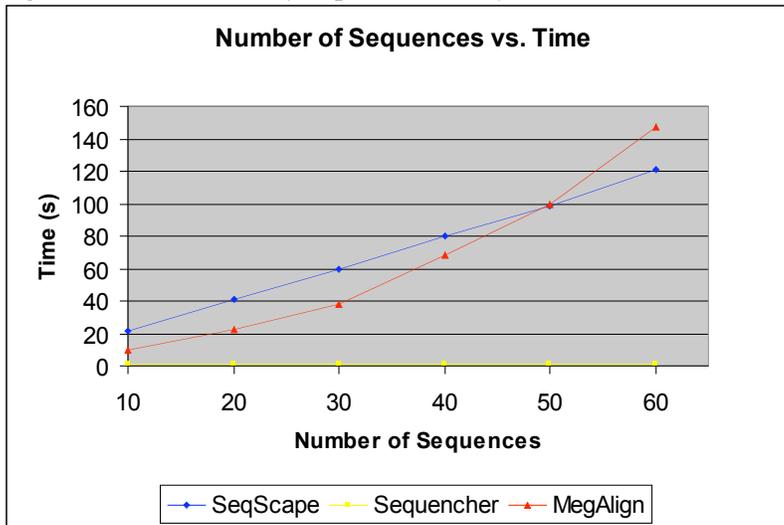
iii) SeqScape

Table 3. *Aligning sequences in SeqScape*

Number of Sequences	Time (s)
10	21
20	41
30	60
40	80
50	99
60	121

Tables 1, 2 and 3 show the time the softwares take to process the alignment as the number of sequences increase. With the exception of Sequencher, it is observed that the processing time is proportional to the number of sequences being analyzed with the other two softwares.

Figure 37. *The amount of sequences the softwares can handle with time.*



Analysis

In general, with the exception of aligning sequences in Sequencher, the time it requires to complete the alignment process is proportional to the number of sequences imported into the software. In SeqScape, a linear relationship is observed as the number of sequences increase with time; while in Lasergene, a power curve is observed between the number of sequences and time (Figure. 37). The more sophisticated algorithms such as Clustal V and Clustal W require much longer time to complete the alignment process (Altschul, 1997). Aligning sequences in Sequencher is most time efficient as the alignment process only takes an average of one second to complete (Table 2). Although the matching process slows down with the increasing number of sequences, all three softwares were able to generate the alignment result under 30 seconds when aligning 10 sequences at a time.

6.3 Ease of Use

6.3.1 SeqScape

The set-up procedures of the software are quite complicated for first time users. Once the user-specified settings are instructed to the software, later procedures are relatively simple. Although the trimming option is available, the software is still able to work with poor quality sequences and make corresponding matches to the reference. Ambiguities in the sequence will not affect the alignment result. In addition, the software can automatically convert the sequences to the correct orientation relative to the reference. Users do not have to worry about translating the sequences into their reverse complement if the sequences were amplified in the opposite orientation.

In terms of the software's design, the layout of the software can be customized according to personal preference. Some users might find the colours distracting as the reference sequence is not distinguished from the sample sequences. With the addition of coloured electropherograms, users might experience difficulties distinguishing one sample from the next. To improve the view, users can choose to display one electropherogram at a time.

6.3.2 Lasergene

Lasergene's simple software design allows for easy and quick identification of mutations. The procedure of aligning sequences with the software is simple and straight forward. The software works best with good quality sequences. The untrimmed 5' and 3' ends as well as the ambiguities within the sequences will affect the alignment result, since the software does not recognize a particular sequence as the reference. Raw data have to be

trimmed individually to obtain clean sequences. Furthermore, the software cannot automatically translate the sequences to the correct orientation if the samples were sequenced in the opposite orientation as the reference. It is very time-consuming to convert the sequences back to the right orientation because users have to repetitively select the *Select complementary* option one by one for all sequences that exhibit the opposite orientation.

6.3.3 Sequencher

Sequencher is a user-friendly, well-designed sequence analysis tool. Users simply import their reference and working sequences into the program. The sequences will be aligned automatically by clicking the *Assemble To Reference* button. There is the option to set the nucleotides to specific colours according to users' preference. Located at the bottom of the working panel, the consensus sequence is easily distinguishable. Symbols are used to mark any variation that is different than the consensus. The reference to which all the sample sequences are aligned against is also marked so it can be easily identified.

All aligned sequences are displayed in a contig map where users can observe the relative positioning of all sample sequences that are aligned to the reference. Each sequence fragment is labelled with its sample name for identification purposes. In addition, the orientation of each fragment is represented by the direction of the arrow. The software automatically converts the sequences into the correct orientation relative to the reference.

However, in order to produce ideal results, individual sequences have to be trimmed which requires a lot of base deleting work. With many sequences to align at once, the editing becomes repetitive.

6.4 Cost Analysis

Table 4. Quotes for the alignment softwares.

	SeqScape	Lasergene	Sequencher
Initial License Cost	\$8820 (CND)	\$4496 (USD)	\$3450 (USD)
Service Plan Renewal	-	\$780 (USD)	\$325 (USD)

Table 4 outlines the initial license cost of the three sequence alignment softwares. The initial license cost of SeqScape Software is \$8820 CND, which is about double the cost of Lasergene and Sequencher. Lasergene from DNASTAR costs \$4579 USD with a \$780 dollar annual service plan renewal, while Sequencher from Gene Codes cost \$3450 USD with an annual cost of \$325 USD. SeqScape is the most expensive alignment software; however, considering the multiple tasks that it can perform, the software is a worthwhile purchase.

6.5 Summary

The following tables summarize the features and functions of the three alignment softwares.

Table 5. The alignment algorithms of the three softwares.

	SeqScape	Lasergene	Sequencher
Local Alignment	√	√	√
Global Alignment		√	
Multiple Alignment	√	√	√
Optimal Alignment	√	√	√

Table 5 outlines the types of alignment that each of the softwares can perform.

Lasergene can carry out all four types of alignment – local, global, multiple and optimal.

SeqScape and Sequencher can only perform three types of the four.

Table 6. *The mutation detection efficacy of the softwares.*

	SeqScape	Lasergene	Sequencher
SNP	5	3	5
Homozygous Mutation	5	4	3
Heterozygous Mutation	5	3	2
Overall	15	10	10

The above evaluation ranks the software's ability to detect mutations in a scale of 5, with 5 representing the highest score. SeqScape scored the highest as it is capable of recognizing all three types of mutation. Lasergene and Sequencher both achieved equivalent scores. Lasergene is not the ideal software to detect the identity of the SNP as well as mutation in one allele. Sequencher is not the ideal tool to identify frameshift mutations in general.

Table 7. *The ease of use of the softwares.*

	SeqScape	Lasergene	Sequencher
Appearance	3	4	5
Setup Procedures	4	3	4
Alignment features - Select Reverse Complement - Work with Poor Quality Data - Trimming Options	5	2	3
Overall	12	9	12

The above evaluation looks at the ease of use of the softwares in a scale of 5, with 5 representing the highest score. Both SeqScape and Sequencher scored the highest overall score for its well-designed layout as well as the ease of use.

7.0 CONCLUSION

The SeqScape sequence analysis software from Applied Biosystems is thought to be the most effective sequence comparison tool that best suits the purposes of Dr. Hegele's research. As shown in Tables 5-7, the software obtained the highest overall score regarding the assessment of its alignment features, accuracy in mutation detection, and ease of use.

SeqScape is shown to produce the most accurate alignment results. The Smith-Waterman local alignment algorithm that the software uses can accurately position the exon sequences of interest to the corresponding region of the reference, allowing biologically meaningful comparison between sequences. SeqScape software's design for processing high quality sequences, as well as its ability to produce accurate alignment enhances the SNP and insertion and deletion detection process.

Furthermore, the software is capable of aligning more than two sequences simultaneously. The successive pairwise alignment method allows the software to perform multiple exon alignments all at once. The method greatly improves time efficiency which is invaluable to the busy lab setting.

Lastly, SeqScape's comprehensive user manual, its fine layout, and immediate response to queries from the company's technical support team generally accounts for the user-friendliness of the software. Customer services and technical support are freely available for novice users who want to get familiarized with the software.

8.0 RECOMMENDATION

It is the researchers' goal to obtain reliable experimental results before drawing a valid conclusion to support their research hypotheses, including scientists at RRI. In order to further improve the reliability of the sequence alignment results with Dr. Hegele's research, the following approaches are recommended for effective alignment performance.

1. Perform Alignment in All Three Sequence Alignment Softwares

Although the SeqScape Software has demonstrated to align sequences most effectively, sequences should be aligned in more than one alignment software to confirm the presence of any newly discovered mutations in the sample sequences. The position as well as the identity of the mutation should be double-checked to ensure the reproducibility of alignment the results.

2. Avoid Analyzing Large Quantity of Sequences Simultaneously

To improve the time efficiency of sequence alignment, it is recommended to align and analyze no more than 20 nucleotide sequences at a time. Although SeqScape is capable of analyzing and comparing as many sequences as the user desires, the time it requires to complete the alignment increases with the number of sequences. With less than 20 sequences to align per analysis, the alignment results are generated almost immediately.

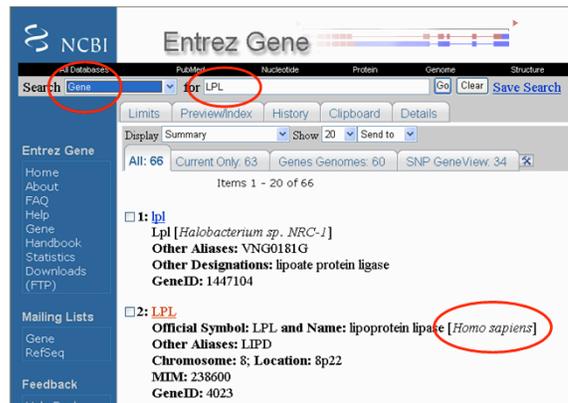
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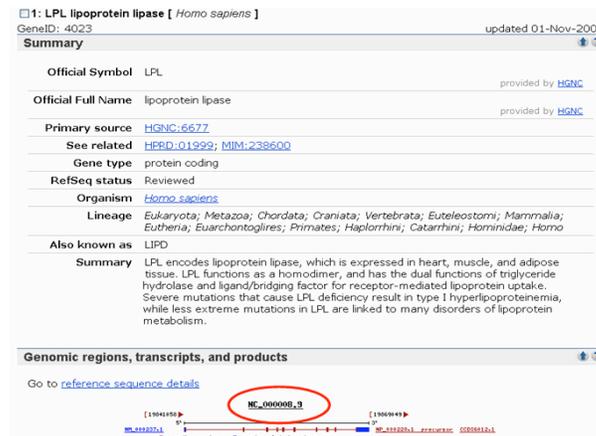
APPENDIX A: HOW TO OBTAIN A REFERENCE SEQUENCE?

I. Obtaining a Reference Sequence from NCBI

- i. In an internet browser, type in the web address: <http://www.ncbi.nlm.nih.gov>
- ii. Under the Search field, select *Gene*
- iii. Type in the name of the gene that is to be used as reference in the alignment (ie. LPL – Lipoprotein Lipase)



- iv. Select the corresponding species that the reference is extracted from (ie. *Homo sapiens*)
- v. Click on *Go to reference sequence details* to view the sequence



APPENDIX B: SAMPLE PREPARATION

I. DNA Extraction

In Dr. Hegele's lab, scientists use the PUREGENE[®] Kit to carry out DNA extraction. Below is a brief overview of the extraction process. Refer to *PUREGENE[®] DNA Purification Kit: DNA Purification Protocol For 10 ml Fresh Whole Blood* at the website <http://www.isisco.ie/isis/Main/Lifesciences%20Gentra.htm> for the complete protocol.

1. Obtain blood samples.
2. Add the appropriate amount of **RBC (Red Blood Cell) Lysis Solution** to the whole blood sample to remove red blood cells.
3. Mix the solution. Incubate the solution at room temperature for 5 minutes.
4. Centrifuge the solution for 5 minutes. Remove the supernatant and keep the white cell pellet and 200-400 µl residual liquid.
5. Mix the solution well. Resuspend the pellet in the residual liquid with **Cell Lysis Solution** to lyse the white blood cells in the sample. Incubate the cell lysate at 37°.
6. Add the appropriate amount of **Protein Precipitate Solution** to the cell lysate.
7. Mix the **Protein Precipitate Solution** uniformly with the cell lysate to obtain a homogeneous solution.
8. Centrifuge the solution for 5 minutes.
9. To the supernatant containing the DNA, add the appropriate amount of isopropanol to precipitate the DNA.
10. Centrifuge the mixture for 3 minutes. DNA will be in form of a white pellet.
11. Remove the supernatant. Add 70% ethanol to wash the pellet containing the DNA.
12. Dry the DNA pellet.
13. **DNA Hydration Solution** is added to preserve and hydrate the pellet. Store the DNA at 4°.

II. Isolate the Gene of Interest

In order to obtain the desired region in the DNA for sequence comparison, a pair of primers has to be designed to flank the gene of interest. During primer design, one has to ensure the same annealing temperature and GC content for both primers. Primers are usually designed so that they anneal to the template 50 base pairs away from the gene to be amplified. The gene of interest can then be amplified with the appropriate primers using the PCR (Polymerase Chain Reaction) machine (Wang, 2006).

III. DNA Purification

The laboratory currently uses Qiagen's QIAquick[®] PCR Purification Kit to purify the amplified gene of interest produced from the previous PCR reaction. The procedures are described as follows. Refer to the *QIAquick Spin Handbook* for the complete protocol on DNA purification.

1. Add the QIAquick's **Buffer PBI** to the PCR product in the ratio of 5:1.
2. Check to make sure that the colour of the mixture is yellow to ensure the correct pH range.
3. Place a QIAquick spin column in the collection tube provided.
4. Add the PCR product to the spin column to bind DNA. Centrifuge for 30-60s.
5. Discard the waste that passed through the spin column. Place the column back into the same tube.
6. Wash the DNA by adding a small amount of **Buffer PE** to the column and centrifuge for another 30-60s.
7. Discard the flow-through and place the column back to the tube.
8. Elute the DNA by adding the correct amount of **Buffer EB** or water to the QIAquick membrane to ensure the right concentration. Centrifuge for 1 minute.
9. The purified DNA can be collected after the DNA has passed through the membrane.