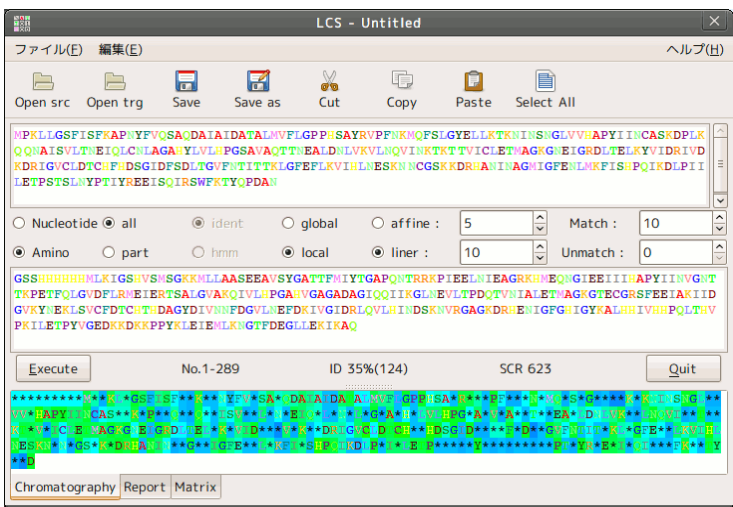


# LCS with GUI is a calculator of the Longest Common Subsequence



The LCS is software of calculate a Longest Common Subsequence by a dynamic programming. For Nucleotide and an Amino acid sequence. The LCS have GUI and CUI.

This software have a user interface of a standard GUI. The LCS can use a fasta format file and an only sequence file.

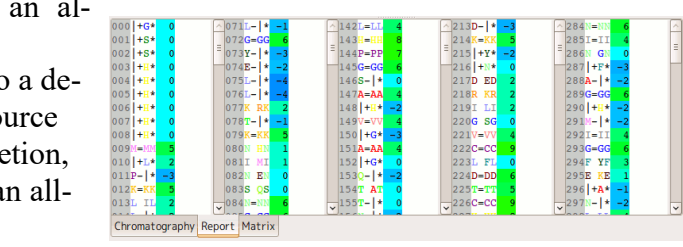
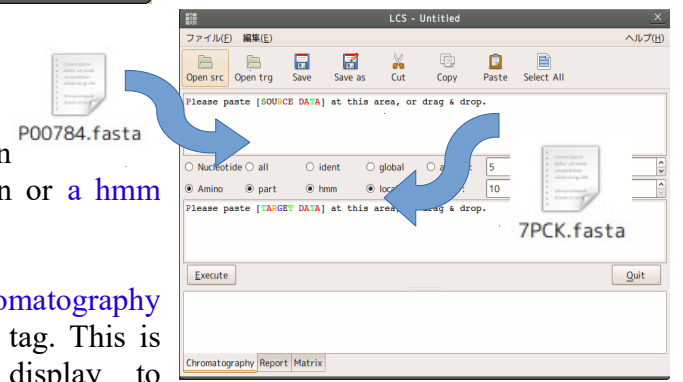
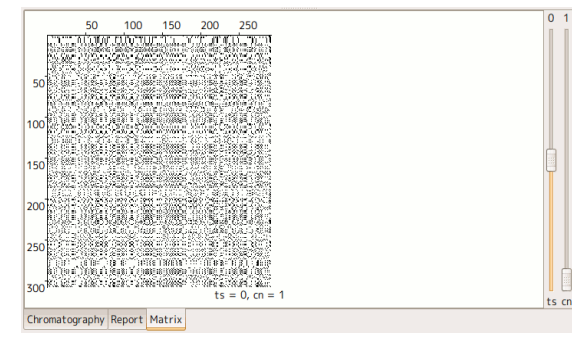
Example. GNOME GUI by Ubuntu 9  
Comparing sequence of Amino Acid and Amino Acid.  
And copy & paste from other window. I

designed for copy & paste. But you can use menu, toolbar and drag & drop.

This software use two method for search an alignment region. There are an identify scan or a hmm (Hidden Markov Model) scan.

The LCS have three output tag. One is a chromatography tag. This is display to an allocated sequence by a color separated graph.

And next one is a report tag. This is display to a detail of allocated sequence. that is number, a source sequence, gap, match, unmatched, insertion, deletion, a target sequence, an allocated sequence and an allocation parameter.



And last one is a matrix tag. This is display to an allocated sequence by a dot matrix plot(harr plot). It is displayed numbers of a Edit Graph. This tag has two scales. There are a threshold number and a continuity number. It can rise to the surface, to a

high matches and a continuity sequences.

And The LCS can output text data, there are a Edit Graph, a Similarly Score and a Back Tracking Pointer by CSV(Comma Separated Value).

Desined for Unix systems with Gtk+.  
Download from <http://sites.google.com/site/kashiwagiakihiro/>