

# Glossary

## Fitting alignment

A fitting alignment of a [string](#)  $s$  against another string  $t$  is defined as an [alignment](#) of  $s$  with a [substring](#)  $t'$  of  $t$ . As usual in alignment problems, we aim to find a minimum-score fitting alignment across all possible such substrings  $t'$  of  $t$ , where the particular [alignment score](#) used may vary.

Note that we are allowed to use a substring only of  $t$  in the alignment, not  $s$ . This makes the problem of finding a fitting alignment a hybrid of [global](#) and [local alignment](#). See the figure below for a comparison of global, local, and fitting alignments of the strings  $v = \text{GTAGGCTTAAGGTTA}$  and  $w = \text{TAGATA}$ , where  $w$  is aligned against a substring of  $v$  in the fitting alignment.

	global	local	fitting
<b>v</b>	<b>GTAGGCTTAAGGTTA</b>	<b>TAG</b>	<b>TAGGCTTA</b>
<b>w</b>	<b>-TAG----A---T-A</b>	<b>TAG</b>	<b>TAGA--TA</b>
<b>score</b>	<b>-3</b>	<b>3</b>	<b>2</b>

The most common biological application of fitting alignments arises when  $s$  represents a known [motif](#) that we are hoping to match against a larger [genetic string](#)  $t$  (with some errors due to small-scale [mutations](#)). For example,  $s$  may represent a known [gene](#) that we wish to locate with some changes within a [genome](#)  $t$ ; alternatively,  $s$  could encode a known [domain](#) that we are comparing against a newly discovered [protein](#).