## ON THE NUMBER OF MANY-TO-MANY ALIGNMENTS OF MULTIPLE SEQUENCES

## Steffen Eger

Computer Science Department, Goethe University Frankfurt am Main Robert-Mayer-Straße 10, Frankfurt, Germany e-mail: steeger@em.uni-frankfurt.de

## ABSTRACT

We count the number of alignments of  $N \geq 1$  sequences when match-up types are from a specified set  $S \subseteq \mathbb{N}^N$ . Equivalently, we count the number of non-negative integer matrices whose rows sum to a given fixed vector and each of whose columns lie in S. We provide a new asymptotic formula for the case  $S = \{(s_1, \ldots, s_N) \mid 1 \leq s_i \leq 2\}$ .

Keywords: alignment, composition, sum of discrete random variable, lattice path

## 1. Introduction

Alignments of sequences arise in computational biology and in computational linguistics. In computational biology, aligning DNA sequences is a standard task. In computational linguistics, aligning (historical) variants of linguistic forms is a field of study (see [8]). In addition, alignments of sequences arise in computational linguistics either in (machine) translation, where words from different languages are matched up, or in related string-to-string translation tasks such as letter-to-sound conversion, where the task is to translate a letter string into a phonetic representation, or in lemmatization, where the task is to translate a word form into a canonical lexicon representation. Traditionally, an alignment of N (for an integer  $N \geq 2$ ) sequences of various lengths is defined as a manner of inserting blanks into the N sequences such that all have equal length. For example, given  $\mathbf{x} = x_1$ ,  $\mathbf{y} = y_1 y_2$  and  $\mathbf{z} = z_1 z_2 z_3$ , three (out of 239 possible) alignments of  $\mathbf{x}$ ,  $\mathbf{y}$  and  $\mathbf{z}$  are:

$x_1$	-	-	x	1 -	-	-	-	-	$x_1$
$y_1$	$y_2$	-	y	1 -	$y_2$	-	$y_1$	$y_2$	-
$z_1$	$z_2$	$z_3$	z	$z_2$	_	$z_3$	$z_1$	$z_2$	$z_3$

In computational linguistics, alignments in which subsequences (of length  $\geq 1$ ) from the different sequences are matched up with each other ('many-to-many matches') are oftentimes more plausible and also more frequently made of use of (see [15, 19]). When we allow, for example, in addition to the above specification, matches-up of length up to 2, there are several further alignments of  $\mathbf{x}, \mathbf{y}$  and  $\mathbf{z}$ , including: