Expected Number of Distinct Subsequences in Randomly Generated Strings

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- This could be of biological relevance in the case of two DNA strings.
- Subadditivity arguments are easy to apply to prove that $L = \lim_{n \to \infty} \frac{E(L_n)}{n}$ exists.

► The value of the limit *L*, however, is still not known!

Yonah Biers-Ariel, Anant Godbole, Elizabeth Kelley Expected Number of Distinct Subsequences in Randomly Gene

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- But even here, calculation of the expected value was non-trivial.
- The combined results of Vershik and Kerov; Logan and Shepp from the 1970's gave

$$\lim \frac{EL_n}{\sqrt{n}} = 2.$$

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This was followed by concentration results—due to Bollobas and Janson; Kim; and Frieze among others—that revealed that the standard deviation of the size of the longest monotone subsequence (LMS) is of order $\Theta(n^{1/6})$, and culminated with the work of Baik, Deift and Johansson that exhibited the limiting law of a normalized version of the LMS. This is often cited as one of the crowning achievements of Probability/Analysis of the 20th Century. An AMS Notices article of Aldous and Diaconis gives a great summary.

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- The string 10110 contains the subsequences 0, 1, 01, 10, 11, 00, 100, 101, 110, 111, 011, 010, 1011, 1010, 1110, 0110, and 10110.

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- The string 10110 contains the subsequences 0, 1, 01, 10, 11, 00, 100, 101, 110, 111, 011, 010, 1011, 1010, 1110, 0110, and 10110.
- What is the average case behavior?

In our submitted paper, we proved

Theorem

Let s_1, s_2, \ldots be a sequence of independent and identically distributed random variables with $Pr(s_1 = j) = \alpha_j, j = 1, 2, \ldots, d, \sum_j \alpha_j = 1$. Set $\alpha = (\alpha_1, \ldots, \alpha_d)$. Let $\phi(S_n)$ be the number of distinct subsequences in $S_n = (s_1, \ldots, s_n)$. Let $\psi(n) = E(\phi(S_n))$. Then there exists $c = c_{d,\alpha} \ge 1$ such that

$$\psi(n)^{1/n} \to c; n \to \infty,$$

where c = 1 iff $d \ge 1$ and $\max_j \alpha_j = 1$.

Discussion

► The above theorem is hardly surprising, but raises other questions, namely as to whether the "true" numbers contain, additionally, polynomial factors as do several Stanley-Wilf limits in the theory of pattern avoidance (note that there are no polynomial factors in our next result with d = 2) Also, in general the existence of limits is not automatic, as seen by the following example:

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- ► Assume that *n* balls are independently thrown into an infinite array of boxes so that box *j* is hit with probability $1/2^j$ for j = 1, 2, ... Let π_n be the probability that the largest occupied box has a single ball in it. Then, as proved by several people in the 1990's, $\lim_{n\to\infty} \pi_n$ does not exist, and $\limsup_{n\to\infty} \pi_n$ and $\liminf_{n\to\infty} \pi_n$ differ in the fourth decimal place! Such behavior does not however occur in our context, as the theorem states.

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Theorem

Suppose $Pr[s_i = 1] = \alpha \in [0, 1]$ for all $1 \le i \le n$, and $Pr[s_i = 0] = 1 - \alpha$, $\alpha \ne 0, 1$. Then we have

$$\phi(S_n) = \frac{A+B}{2\sqrt{\alpha(1-\alpha)}}$$

where

.

$$\mathsf{A} = ig(1 - 2\sqrt{lpha(1 - lpha)}ig)ig(1 - ig(1 - \sqrt{lpha(1 - lpha)}ig)^nig)$$

and

$$B = \left(1 + 2\sqrt{lpha(1-lpha)}
ight) \left(\left(1 + \sqrt{lpha(1-lpha)}
ight)^n - 1
ight)$$

It was shown in a 2004 EJC paper of Flaxman et al.that when $\Pr[s_i = 1] = .5$ then $E[\phi(S_n)] \sim k(\frac{3}{2})^n$ for a constant k. Later, Collins improved this result by finding that $E[\phi(S_n)] = 2(\frac{3}{2})^n - 1$. We generalized this in the previous theorem to non-uniform letter generation. Moreover, our method for finding this formula is very different from that used by Collins. We defined a new property of a string - the number of new distinct subsequences - and then use these numbers as the entries in a binary tree. Our formula is then given as a weighted sum of the entries in this tree. This procedure is a modification of a 2008 method due to Elzinga, Rahmann, and Wang.

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Arbitrary d and Two-state Markov Chains

We are done with strings on a binary alphabet generated by a random process in which the probability that any given element was 1 was fixed at α . In the paper, we generalized this in two ways. First, we considered strings on the alphabet $\{1, 2, ..., d\} = [d]$ where each letter is independently *j* with probability α_i for all $i \in [d]$. After that, we returned to binary strings, but those generated according to a two-state Markov chain; in particular, if a letter follows a 1, then it is 1 with probability α , but if it follows a 0, then it is 1 with probability β . In both these cases, we found recurrences for the expected new weight contributed by the n^{th} letter, which led to explicit matrix equations for that expected new weight. Unfortunately, we have not yet been able able to find a closed-form formula for the total expected number of subsequences like we did for d = 2 (independent case). But we know that in the first of these two generalizations, the limit exists!

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Open Problem 1

One of the central questions in the Permutation Patterns community is that of packing patterns and words in larger ensembles; see, e.g., a paper by Burstein et al. In a similar vein, we have the question of superpatterns, i.e., strings that contain all the patterns or words of a smaller size; see, e.g., the same paper. A distinguished question in this area is the one posed by Alon, who conjectured that a random permutation on $[n] = \left\lceil \frac{k^2}{4}(1+o(1)) \right\rceil$ contains all the permutations of length k with probability asymptotic to 1 as $n \to \infty$. In the present context, a similar question might be: What is the largest k so that each element of $\{0,1\}^k$ appears as a subsequence of a binary random string with high probability?

Also, the basic question studied in this paper appears to not have been considered in the context of permutations; i.e., one might ask: What is the expected number of patterns present in a random permutation on [n]?

Open Question 2

In the baseline case of binary equiprobable letter generation, we have that $E(\phi(S_n)) \sim 2(1.5)^n$, which implies that the average number of occurrence of a subsequence is $\frac{1}{2}2^n/(1.5)^n = \frac{1}{2}(4/3)^n$. Now a subsequence such as 1 occurs "just" around n/2 times, and the sequence 11...1 with n/2 ones occurs an average of $\binom{n}{n/2} \cdot \frac{1}{2^{n/2}}$ times, which simplifies, via Stirling's formula, to around $\sqrt{2}^n$, ignoring constants and polynomial factors. The same is true of any sequence of length n/2; it is, on average, over-represented. We might ask, however, what length sequences occur more-or-less an average number $(1.33)^n$ of times. We can parametrize by setting k = xn and equating the expected number of occurrences of a k-long sequence to $(1.33)^n$. We seek, in other words, the solution to the equation

$$\binom{n}{xn}\frac{1}{2^{xn}}=(1.33)^n.$$

Ignoring non-exponential terms and employing Stirling's approximation, the above reduces to

$$2^{x}x^{x}(1-x)^{1-x}=0.75,$$

which, via Wolfram Alpha, yields the solutions x = .123... and x = .570...!

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