

# On an Application of Relative Entropy

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We show that in problems of authorship attribution and other linguistic applications, a Markov Chains approach is a more attractive technique than Lempel-Ziv based compression.

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We wish to point out a number of inaccurate and misleading statements that Benedetto *et al.* make in their paper titled “Language Trees and Zipping” [1]. First, they claim the technique they used for construction of a language tree does not make use of any a-priori information about the alphabet, but it does, both in the alphabet chosen (Unicode) and in the set of languages they chose to experiment with; second, they propound Lempel-Ziv (LZ, *gzip*) compression as being applicable to DNA analysis, where the usefulness of LZ is quite doubtful; third, in practice their definition of relative entropy and distance can yield negative values; fourth, the classification performance of the method they use is significantly worse than other entropy-based methods as has been noted in prior work; and fifth, the classification speed is significantly worse as well, which shows that its “potentiality” is questionable. We elaborate on each of these points in more detail in the subsequent paragraphs.

Notice that the “Language Tree” (LT) diagram [1] does not include the Russian language (Slavic family of Indo-European family of languages; 288 million speakers). Our computations show that once Russian is included, it does not cluster with the other members of the Slavic group. Obviously, certain Cyrillic alphabet based languages were left out of the study [1], which “improves” results significantly and shows that a-priori information about the alphabet is being taken advantage of to achieve the results outlined in paper [1].

The LZ compressor makes few assumptions about the input string, but in practice, we do have a-priori information that we can take advantage of. Biologists widely use an amino acid *substitution matrix* (PAM250 or BLOSUM62) in search for *similar* biological sequences [2]. It is not at all clear how a substitution matrix could be implemented with the LZ algorithm. That is why compression is not widely used for DNA analysis, although first trials for its application go back to 1990 [2].

The quantity  $S_{AB}$  [1] defined as “relative entropy” in (1) and redefined as “distance” in (2) can take negative values. Negative values indeed appeared in our study which showed that the “LT” [1] reflects significantly the structure of Unicode or vice versa, and its relevance to language classification should be supported additionally.

A traditional definition and estimates for (relative) entropy via  $n$ th order Markov Chain *on letters* [3–5] always lead to a proper positive number. Markov Chains are also traditional in text entropy analysis [3, 4], compression [6], authorship and subject attribution [7, 8]. In [5], the classification performance of compression programs was compared with the Markov Chain approach [8]. 82 authors of large enough texts ( $\geq 10^5$  characters) were chosen. Afterwards 82 one-per-author texts were held out and used for control purposes. The classification algorithm [5] had to determine the author of each control text among 82 alternatives. The corresponding numbers of exact guesses for 15 compression programs and Markov Chains are presented in the following list [5]:

Program(number of guesses): 7zip(39), arj(46), bsa(44), compress(12), dmc(36), gzip(50), ha(47), huff(10), lzari(17), ppmd5(46), rar(58), rarw(71), rk(52); Markov Chain approach (see [8]) 69 guesses.

Clearly, *gzip* is significantly outperformed by other compression algorithms and the first order Markov chain model [8]. Notice also that in practical implementations, the *gzip*-based approach [1] is significantly slower than the first order Markov chains method [8].

To sum up, in natural language processing (and, perhaps, in other fields) the  $n$ th order Markov chain models [7, 8] are more appropriate than an LZ-approach [1].

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