

# A grammar compressor for string collections with applications to the construction of the BWT

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**Abstract.** The analysis of massive and repetitive strings collections in succinct space is an active field of research. In this regard, self-indexes that rely on *context-free grammars (CFG)* or Lempel-Ziv factorization achieve high compression ratios. Nevertheless, the string queries they can efficiently answer are still limited. On the other hand, classical self-indexes based on the *Burrows-Wheeler Transform (BWT)* answer different types of queries efficiently. However, they rely mostly on statistical entropy for compacting the data, which is not a good approach for capturing the long blocks of identical or highly similar patterns in repetitive text. Motivated by these limitations is that we propose a new grammar compression framework that facilitates the processing of repetitive data. We produce a *CFG* that only generates the input text, and that can be quickly transformed into the *BWT* of the collection. Thus, if the input is not used, then we maintain it in its *CFG* form to reduce space usage. However, if we need to retrieve information about the strings (maximal repeats, suffix-prefix overlaps, or something similar), then we quickly transform the *CFG* into a *BWT*-based self-index. Our framework consists of three algorithms, called *LMSg*, *SuffPair* and *infBWT*. The first one produces a preliminary *CFG* whose nonterminal symbols are used as building blocks for inferring the *BWT*; the second one reduces the size of the *CFG* while maintaining its properties, and the third algorithm computes the *BWT* from the final *CFG*. Preliminary experimental results show that the compression ratio achieved by the combination of *LMSg* and *SuffPair* is competitive with the classical *LZMA* and *Deflate* techniques. However, our approach compacts the data much faster. Also, further preliminary experiments show that the space usage of *infBWT* is not greater than the size of the uncompressed text. The primary application for our work is the processing of DNA sequencing reads, massive but highly-compressible string collections whose most relevant operation is the computation of suffix-prefix overlaps.