

# Identifying Hierarchical Structure in Sequences: A linear time algorithm

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follow the presentation



<https://mangoiv.github.io/sequi-slides> - follow my presentation (at home)

# structure

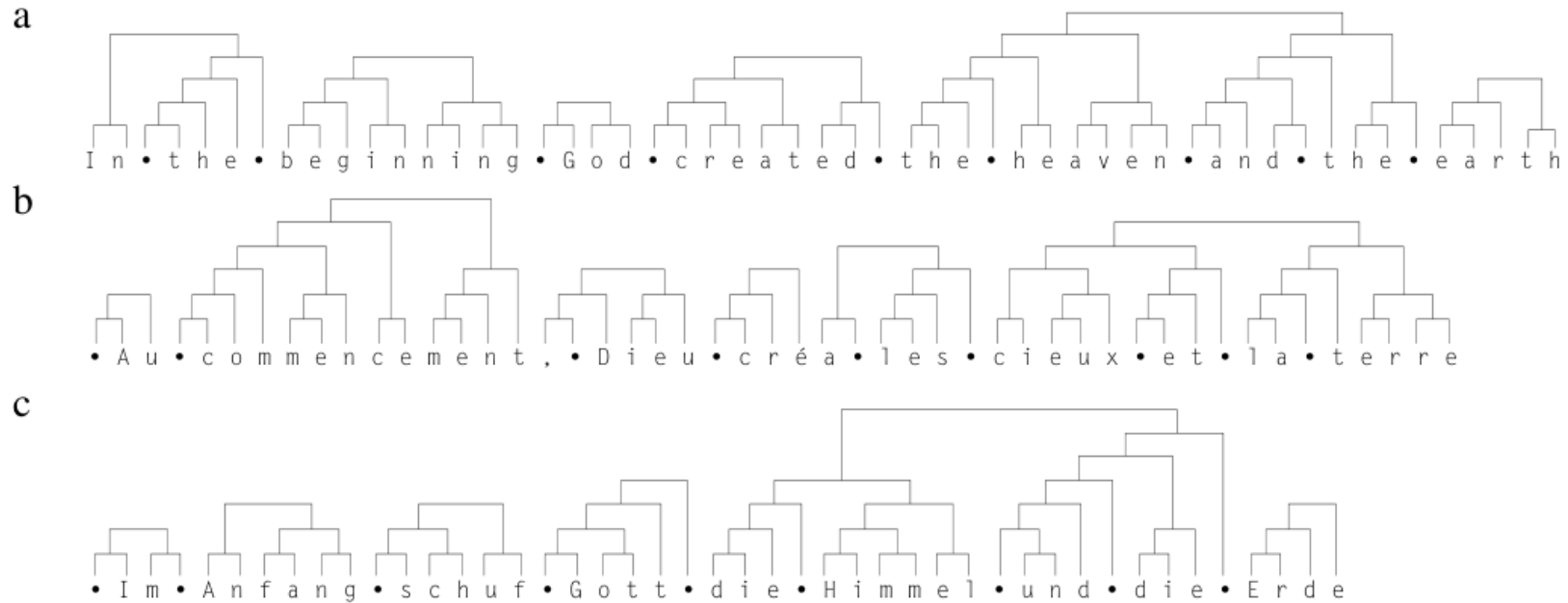
- 0. structure
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# motivation

what goal does `sequitur` pursue?

- infer structure from a *stream* of symbols
- use this structure to compress the stream in a continuous/incremental manner
- do it *fast* and *lossless*

# motivation - bible



inferred structure for the same sentences in the (a) English, (b) French and (c) German bible

# motivation - corpus, chorales

d

Most Labour sentiment would still favour the abolition of the House of Lords

e

imperfect perfect

inferred structure for (d) a sentence in the oslo-bergen corpus (e) chorales by J.S. Bach

# algorithm

the `sequitur` algorithm

# algorithm - concept: digram uniqueness

each digram appears at most once in the grammar

*observed:* `abcdbc` (`a[bc]d[bc]`)

```
1  S → abcdbc  -- `bc` appears twice
2
3  S → aAdA    -- ensure digram uniqueness
4  A → bc
```

*observed:* `abcdbcabcdbc` (`[[a[bc]][d[bc]][a[bc]][d[bc]][bc]`)

```
1  S → AAbc    -- `bc` appears in `S` and `B`
2  A → aBdB
3  B → bc
4
5  S → AAB      -- ensure digram uniqueness
6  A → aBdB
7  B → bc
```



# algorithm - concept: rule utility

if a rule is only used once, we resubstitute to save space and extend the length of the rule

observed: ``abcabc` (`[abc][abc]`)`

```

1  S → AcAc    -- `Ac` appears twice
2  A → ab
3
4  S → BB      -- digram uniqueness
5  A → ab      -- `A` only appears once
6  B → Ac      -- namely here
7
8  S → BB
9  B → abc     -- resubstitute

```

observed: ``abcbcbcabcd` (`[a[bc]d][bc][a[bc]d]`)`

```

1  S → CAC
2  A → bc
3  B → aA      -- `B` is used only once
4  C → Bd      -- namely here
5
6  S → CAC
7  A → bc
8  C → aAd     -- resubstitute `aA` for `B`

```

look back over operation for (4) - can only be performed if a sequence (5) is used for the single operation

# algorithm - full example

observed: `abcdbcabc` (`[a[bc]]d[bc][a[bc]]`)

- 1 S → BdAB
- 2 A → bc
- 3 B → aA

observe `d`

observed: `abcdbcabcd` (`[a[bc]d][bc][a[bc]d]`)

- 1 S → BdABd -- append `d`, `Bd` appears twice
- 2 A → bc
- 3 B → aA
- 4
- 5 A → CAC -- digram uniqueness
- 6 A → bc
- 7 B → aA -- `B` only appears once
- 8 C → Bd
- 9
- 10 S → CAC
- 11 A → bc
- 12 C → aAd -- rule utility

(3) - ..ab + A -> look at how operation for (4) can only be performed if A sequence (5) is added to the digram of the left

# implementation

running `sequitur` on a machine

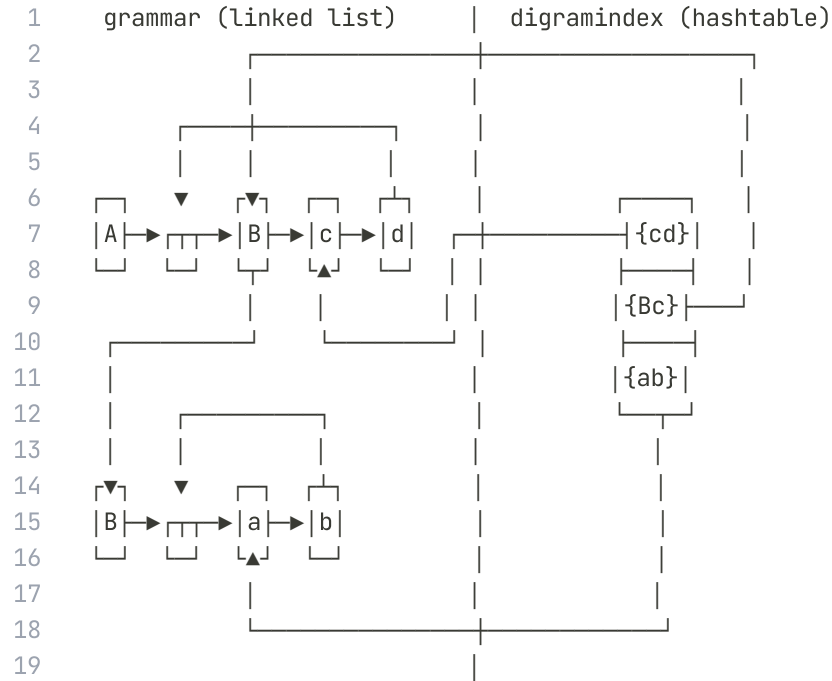
# implementation - constraints

- *append* to ``S``
  - we need fast ``snoc``<sup>1</sup>
- *use* a rule
  - substitute a non-terminal by any digram (this *shortens* the rule)
- *create* a rule
  - non-terminal on LHS
  - digram on RHS
- *delete* a rule
  - move RHS to replace a non-terminal
  - delete LHS

<sup>1</sup>(3) - ..ab + A -> look at how operations for (4) can only be performed on a sequence (5) instead of a single character

# implementation - datastructures

## grammar and digramindex



# implementation - example

observed: ``abcdbc` (`a[bc]d[bc]`)`

```

1  S → abcd bc { ab, bc, cd, db }
2
3  S → abcd bc { ab, bc, cd, db } -- create rule that produces `bc`
4  A → bc
5
6  S → aAd bc { bc, db, aA, Ad } -- update `ab`, `cd`; update `S` rule
7  A → bc
8
9  S → aAdA { bc, dA, aA, Ad } -- update `db`; update `S` rule
10 A → bc

```

# implementation - complexity

```

1  upon observation append symbol to `S` - Rule (1)
2
3  entry in grammar rule is made: (2)
4    if digram is repetition then
5      if other occurrence is rule then
6        replace digram by non-terminal of that rule (3)
7      else
8        form new rule (4)
9    else
10     insert digram into index
11
12  digram replaced by a non-terminal:
13    if either symbol is non-terminal that only occurs once then
14      remove rule substituting its LHS for observed non-terminal (5)

```

- `(1)` performed exactly  $n$  times
- `(2)` performed upon link creation
- `(3)`, `(4)`, `(5)` with savings 1, 0, 1<sup>1</sup> respectively

<sup>1</sup>(3) - ..ab + A -> look at how operation for (4) can only be performed if A sequence (5) is not for the single operation

# implementation - complexity

- $n$  - size of input
- $o$  - size of final grammar
- $r$  - number of rules in final grammar
- $a_1 - a_5$  actions ``(1)´` - ``(5)´` respectively
- $n - o = a_3 + a_5$
- $r = a_4 - a_5 \equiv a_4 = r + a_5$
- $r < o \equiv r - o < 0$
- $a_5 = n - o - a_3 < n$

- *savings are the amount of times  $a_3, a_5$  are performed*

- *formed- minus deleted rules,  $a_5$  bounded by 1.*

- *less rules than symbols (per rule  $\geq 2$  symbols)*

- *see first rule*

$$\sum_{i=1}^5 a_i = n + a_2 + (n - o) + (r + a_5) \quad (1)$$

$$= n + a_2 + n + (r - o) + a_5 \quad (2)$$

$$< 3n + a_2 \quad (3)$$

<sup>1</sup>(3) - ..ab + A -> look at how operation is performed. A sequence like (5) is not formed. For the single operation it



# implementation - complexity

- $a_2$ : check for duplicate digrams
- with occupancy  $< 80\%$  lookups are  $\mathcal{O}(1)$
- hashtable size smaller than grammar (which itself is linearly bounded by the input)
- $a_2$  can only be executed, when either of  $a_1, a_3 - a_5$  are run (bounded by  $\mathcal{O}(n)$ )

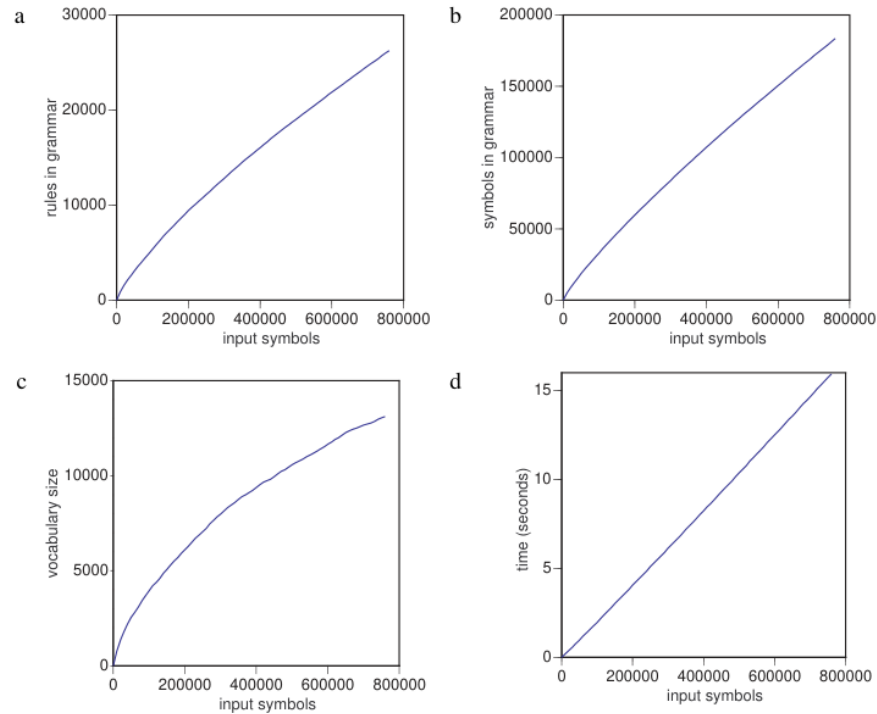
$$\implies a_2 \in \mathcal{O}(n)$$

$$\implies \texttt{`sequitur` runs in } \mathcal{O}(n)$$

*but*

- in theory the hashing and hence addressing will be  $\mathcal{O}(\log n)$ , remains stable up to  $10^{19}$  symbols on 64bit archs (10 Exabytes if 1 Byte per symbol is assumed)
- ``sequitur`` is also linear in memory

# implementation - complexity



behaviour on English text; rules-symbols (a); grammar-symbols (b); vocabulary-symbols (c); time-symbols (d)

# evaluation

how does `sequitur` perform?

# evaluation - showcase



<http://sequitur.info> - JS-implementation by C. Nevill-Manning

# evaluation - comparison

``sequitur`` [...] outperforms other schemes that achieve compression by factoring out repetition, and approaches performance of schemes that compress based on probabilistic predictions

- performance in compressing macromolecular sequences is better than ``PPM``
- generally (in most cases) performs better than other generic compression algorithms like ``gzip``
- compresses the bible (King James version) best
- *linear in time* (cf. ``MK10``,  $\mathcal{O}(n^2)$ , Wolff, 1975)

# evaluation - comparison

*but*

- linear in space
  - split input; merge grammars
  - $\mathcal{O}(\log n)$  memory
  - sacrifices digram uniqueness
- issues with hashtable
  - resizing (to maintain amortized<sup>1</sup>  $\mathcal{O}(1)$  ``lookup`` and ``insert``) is costly

<sup>1</sup>(3) - ..ab + A -> look at how operations for (4) can only be performed in a sequence (5) instead of a single operation

# evaluation - summary

Use two simple rules:

- digram uniqueness
- rule utility

to achieve algorithm that compresses...

- in  $\mathcal{O}(n)$  space and time
- losslessly

which can be implemented...

- by the use of doubly linked lists
- and hash tables

# Thank you for your attention

questions welcome