
Bounds on the number of inference functions of a graphical model

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FPSAC 2006

- Background
 - Sequence alignment
 - Hidden Markov model
 - Graphical models
 - Inference functions
- Upper bound on the number of inference functions
 - Sketch of the proof:
 - From inference functions to vertices of a polytope
 - The number of vertices of a Minkowski sum of polytopes
- Lower bound on the number of inference functions
- Application to sequence alignment

Consider the sequences $S = \text{AGGAATTCG}$ and $T = \text{GGACGGTAT}$.

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Which of the following two alignments is better?

$S_1 = \text{AGGA-ATTCG}$

$T_1 = \text{-GGACGGTAT}$

$S_2 = \text{---A-GGAATTCG}$

$T_2 = \text{GGACGGTAT----}$

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4	←	$z = \#$ matches	→	5
4	←	$x = \#$ mismatches	→	1
1	←	$y = \#$ insertions	→	3

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$$\begin{array}{rcl} 4 & \longleftarrow & z = \# \text{matches} & \longrightarrow & 5 \\ 4 & \longleftarrow & x = \# \text{mismatches} & \longrightarrow & 1 \\ 1 & \longleftarrow & y = \# \text{insertions} & \longrightarrow & 3 \end{array}$$

One possible model: **matches** are rewarded by 1, **mismatches** are penalized by α , and **insertions** are penalized by β .

$$4 - 4\alpha - \beta \quad \longleftarrow \quad \text{score} := z - x\alpha - y\beta \quad \longrightarrow \quad 5 - \alpha - 3\beta$$

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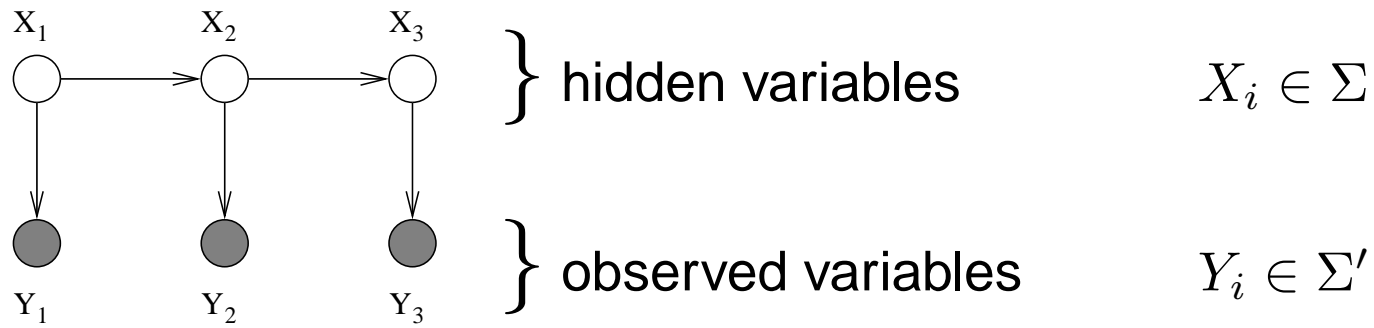
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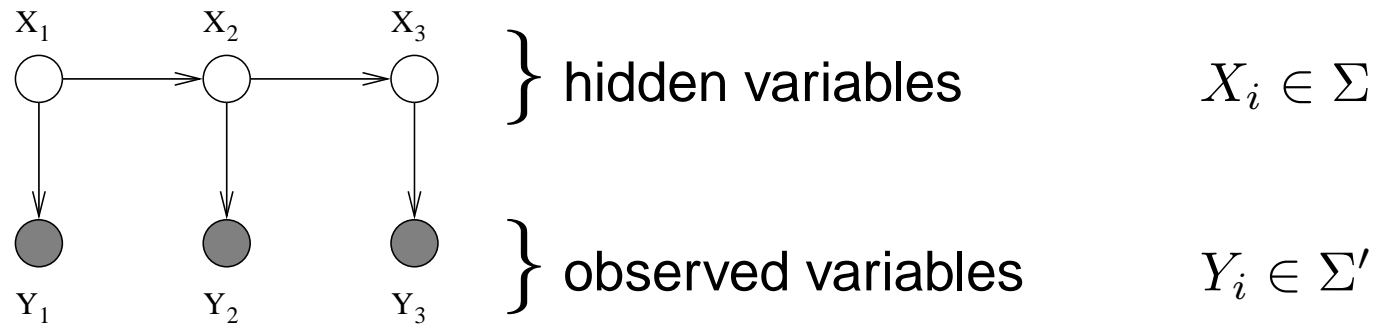
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Hidden Markov model



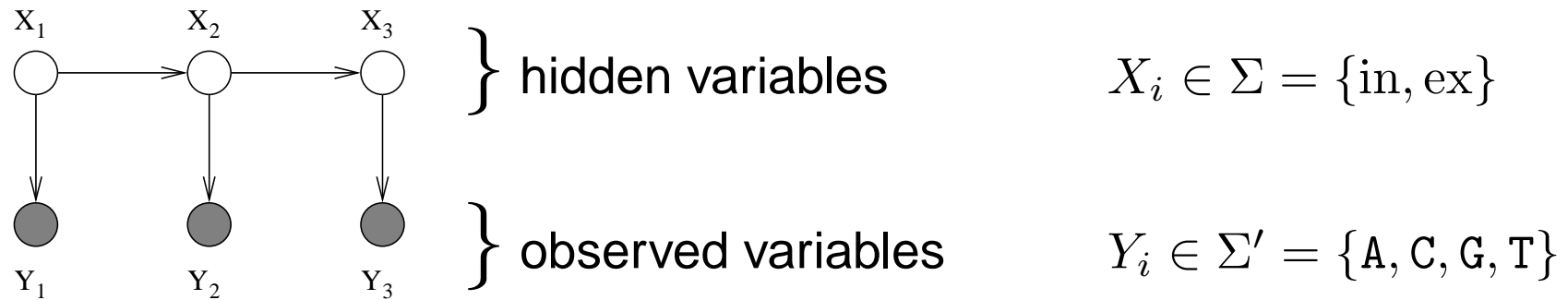


For $i, j \in \Sigma, \ell \in \Sigma'$,

$\theta_{i\ell}$ = transition probability from $X_k = i$ to $Y_k = \ell$

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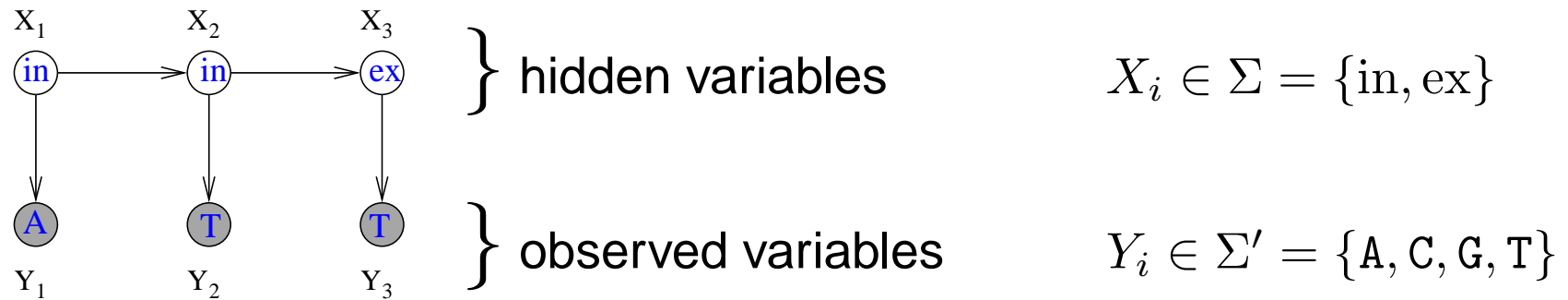


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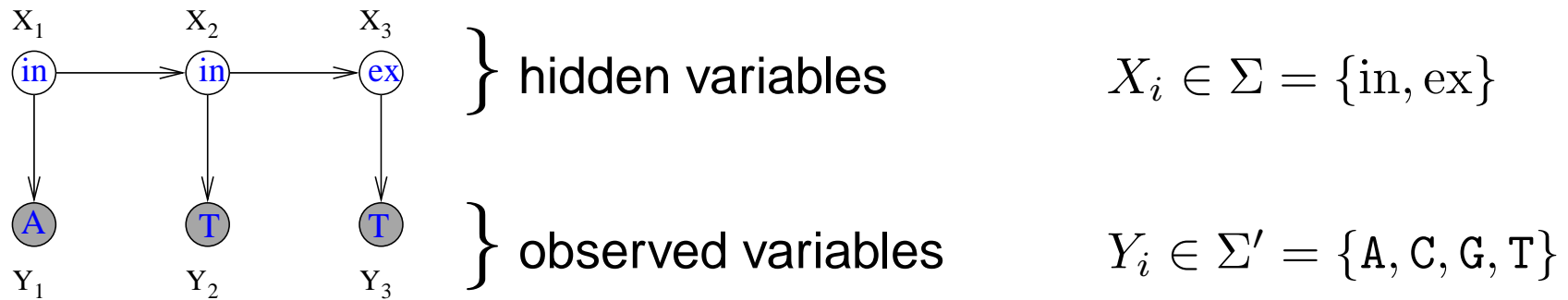
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This model can be used to determine what parts of the genome are introns and what parts are exons.



The model is represented by a polynomial map

$$\mathbf{f} : \begin{array}{c} \mathbb{R}^{12} \\ (\theta_{\text{in},\text{in}}, \theta_{\text{in},\text{ex}}, \theta_{\text{in},\text{A}}, \dots) \end{array} \longrightarrow \begin{array}{c} \mathbb{R}^{64} \\ (f_{\text{AAA}}, f_{\text{AAC}}, f_{\text{AAG}}, f_{\text{AAT}}, f_{\text{ACA}}, \dots) \end{array}$$

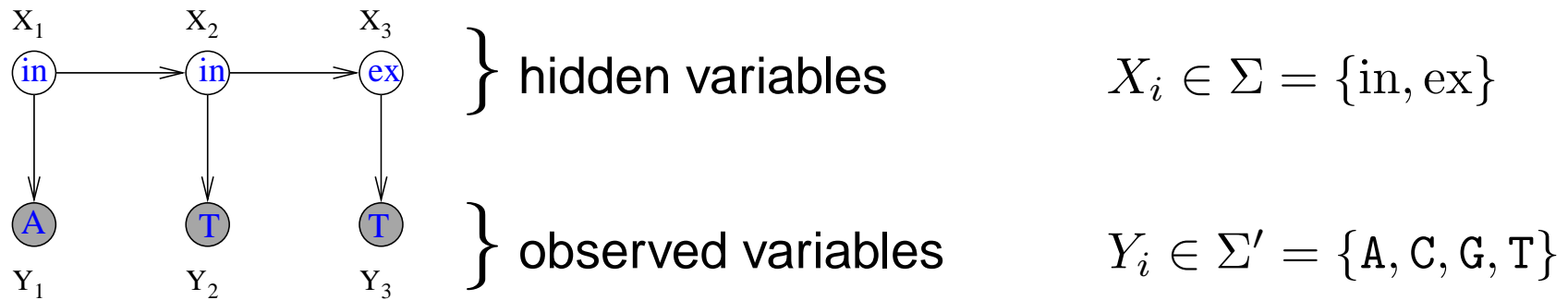


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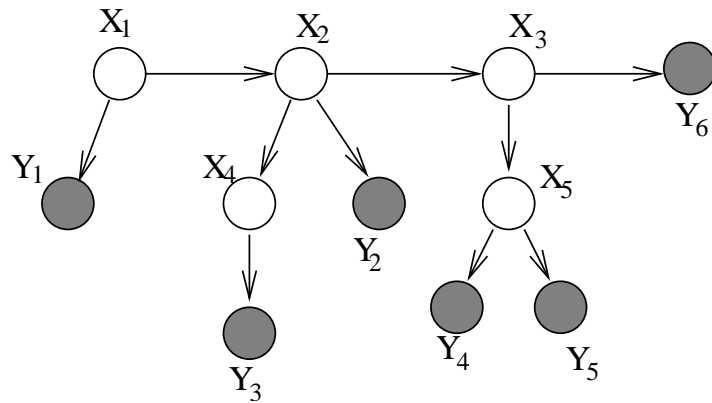
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Given an observation (e.g. ATT), one wants to find the most likely values of X_1, X_2, X_3 .

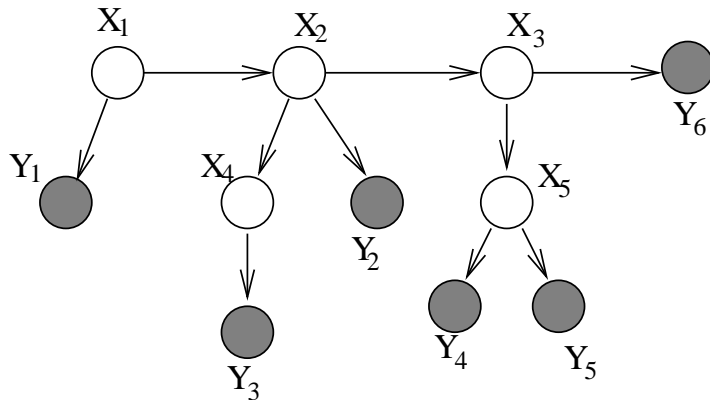
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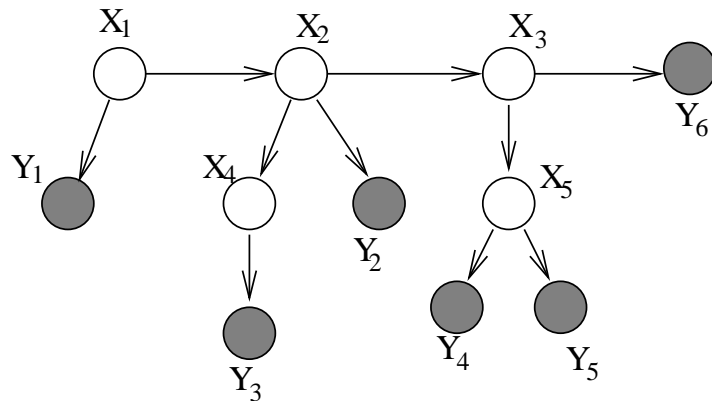


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For each observation $\tau \in (\Sigma')^n$,

$$f_{\tau} = \text{Prob}(\mathbf{Y} = \tau) = \sum_{\mathbf{h} \in \Sigma^q} \underbrace{\text{Prob}(\mathbf{X} = \mathbf{h}, \mathbf{Y} = \tau)}_{\text{monomial in } \theta_1, \theta_2, \dots, \theta_d}$$

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In the previous example, an inference function is a map

$\{\text{A, C, G, T}\}^n \longrightarrow \{\text{in, ex}\}^n$. These are called *gene finding functions*.

The number of inference functions

In general, if $l = |\Sigma|$, $l' = |\Sigma'|$, there are in total $l^q (l')^n$ functions

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Usually, E is a linear in n , so the number of inference functions is in fact $O(n^{d(d-1)})$.

Geometric interpretation of the inference problem

Definition. The *Newton polytope* of

$$f_{\tau}(\theta_1, \theta_2, \dots, \theta_d) = \sum_i \theta_1^{a_{1,i}} \theta_2^{a_{2,i}} \dots \theta_d^{a_{d,i}},$$

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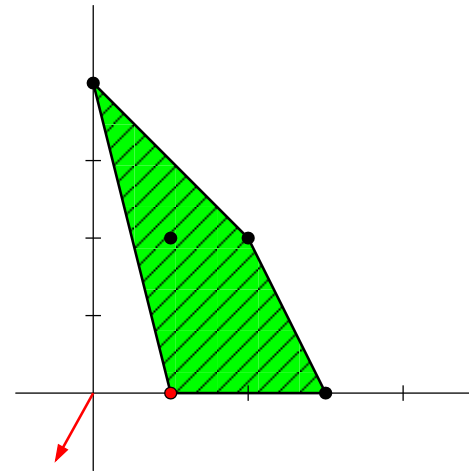
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$$f(\theta_1, \theta_2) = \theta_1^3 + \theta_1^2 \theta_2^2 + \theta_1 \theta_2^2 + \theta_1 + \theta_2^4$$



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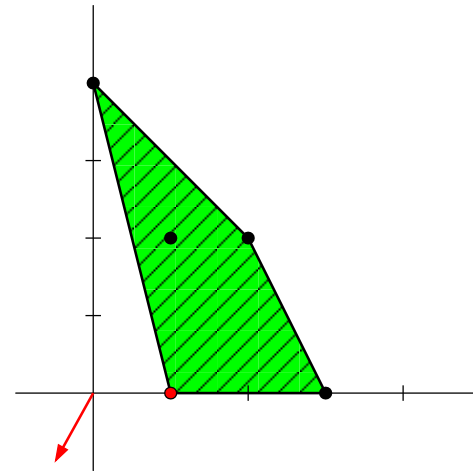
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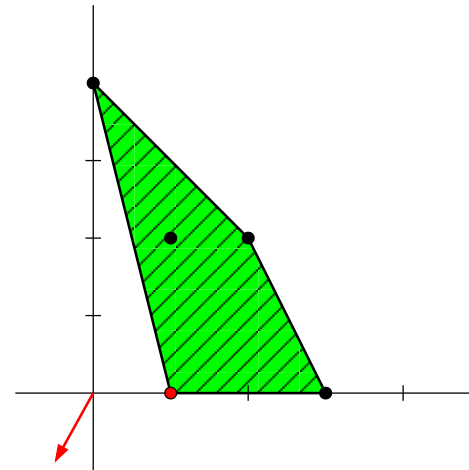
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$$\theta_1 = 0.6, \quad \theta_2 = 0.4,$$

$$\mathbf{v} = (\log \theta_1, \log \theta_2) = (-0.51, -0.92)$$



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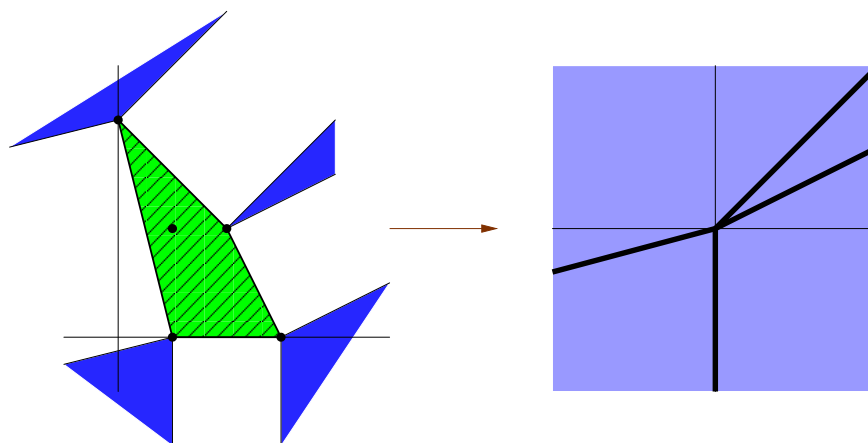
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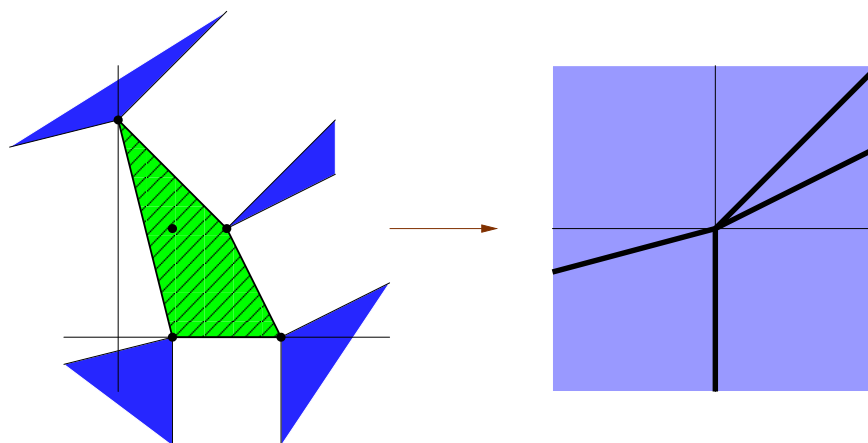
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The number of inference functions equals the **number of cones in the common refinement of fans.**

Minkowski sum of polytopes

The common refinement of the normal fans is the normal fan of the Minkowski sum of polytopes:

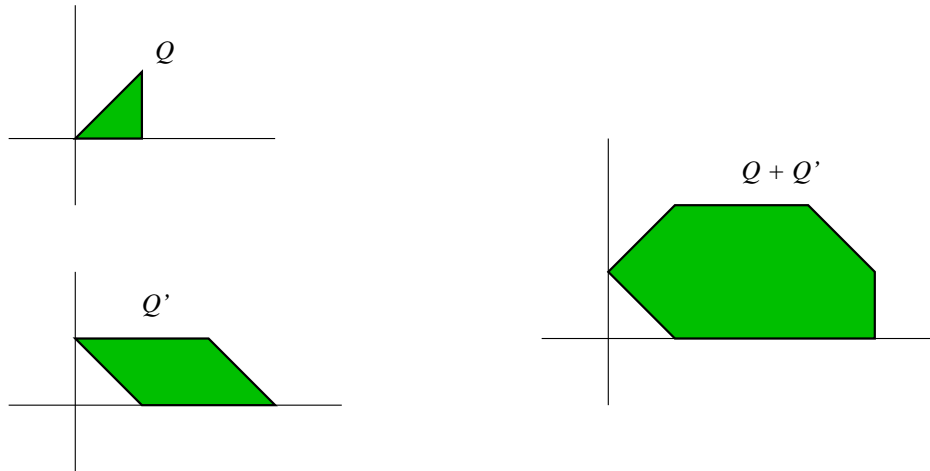
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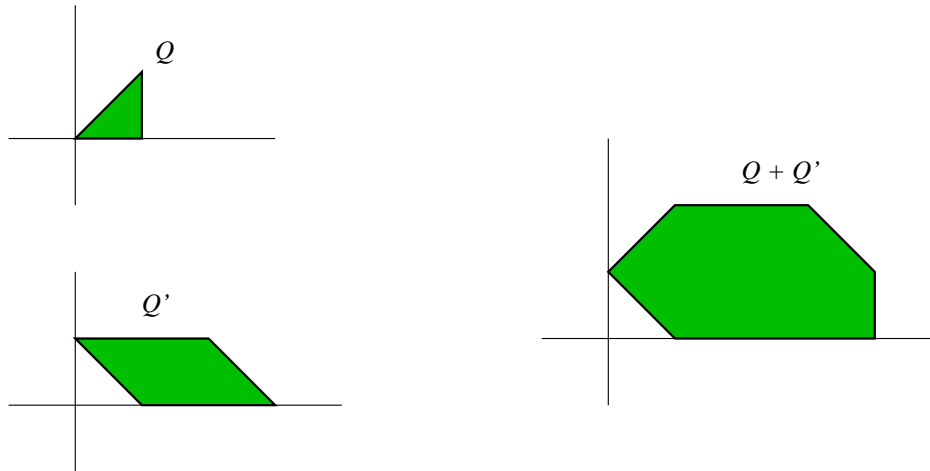


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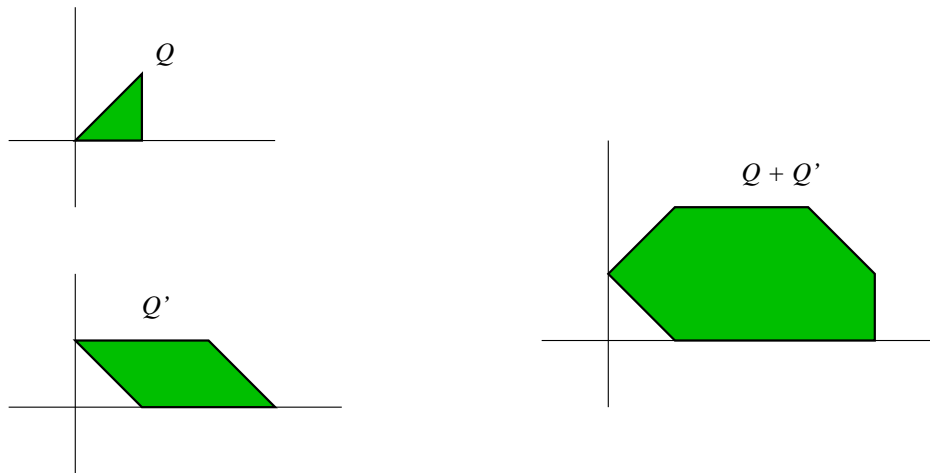
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The number of inference functions equals the number of vertices of P .

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As $E \rightarrow \infty$, the dominant term is $\frac{2^{d^2 - d + 1}}{(d-1)!} E^{d(d-1)}$.

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As $E \rightarrow \infty$, the dominant term is $\frac{2^{d^2-d+1}}{(d-1)!} E^{d(d-1)}$.

\Downarrow

The number of inference functions is $O(E^{d(d-1)})$. □

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- Construct an HMM \mathcal{M}_n of length n with d parameters s.t. for any $a = (a_1, \dots, a_d) \in \mathbb{Z}_+^d$ with $\sum_i a_i < n$, there is an observed sequence which has one explanation if $a_1 v_1 + \dots + a_d v_d > 0$ and another explanation if $a_1 v_1 + \dots + a_d v_d < 0$, where $v_i = \log(\theta_i)$.

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- Show that the hyperplane arrangement consisting of the hyperplanes of the form $\{x : \langle a, x \rangle = 0\}$ with $a \in \mathbb{Z}_+^d$ and $\sum_i a_i < n$ has at least $\Omega(n^{d(d-1)})$ chambers.
- So, \mathcal{M}_n has $\Omega(n^{d(d-1)}) = \Omega(E^{d(d-1)})$ distinct inference functions.

Application to sequence alignment

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explanation \hat{h}

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Sequence alignment

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optimal alignment

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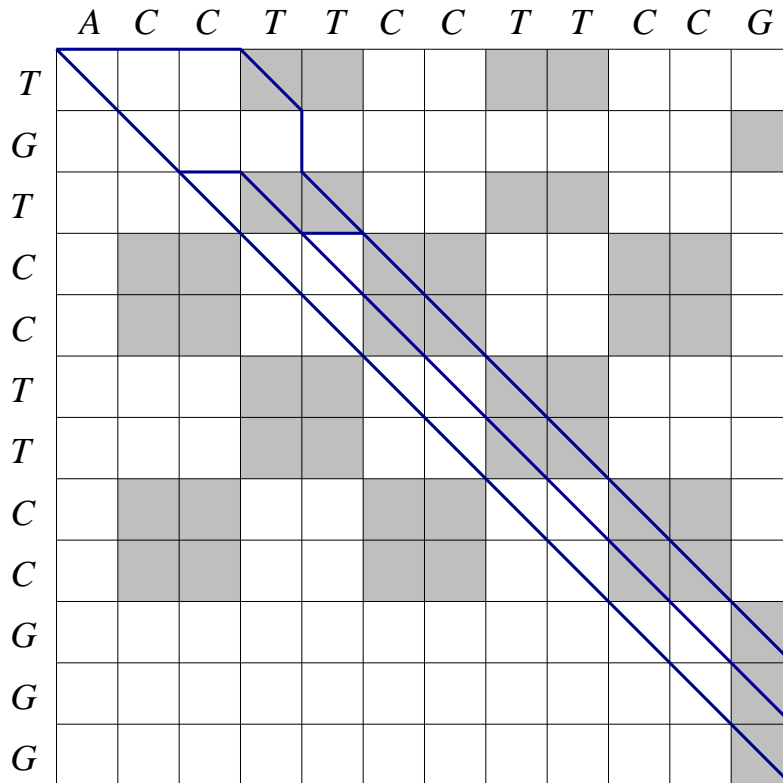
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By the Main Theorem, the number of inference functions of this model is

$$O(n^{d(d-1)}) = O(n^2).$$

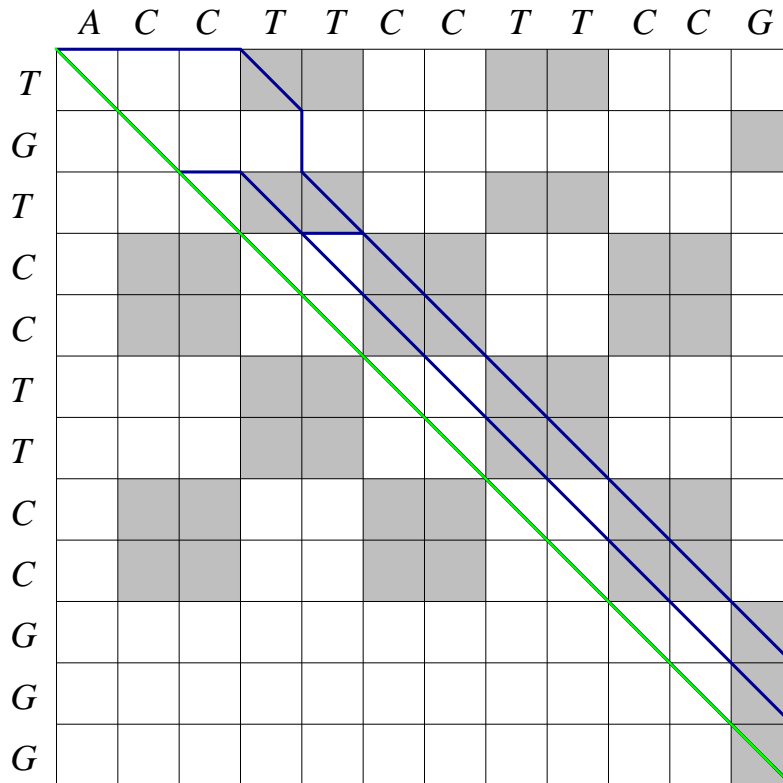
In fact, it is $\Theta(n^2)$.

- Alignments can be represented as paths from the upper-left to the lower-right corner in the alignment graph:



<i>x</i>	<i>y</i>	<i>z</i>

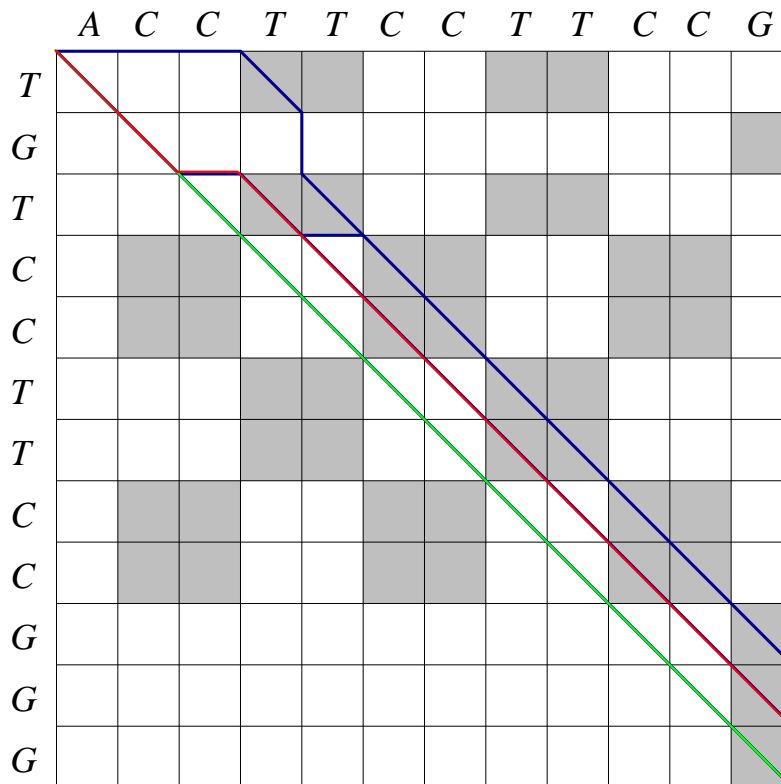
- Alignments can be represented as paths from the upper-left to the lower-right corner in the alignment graph:



x	y	z
11	0	1

TGTCCTTCCGGG
ACCTTCCTTCCG

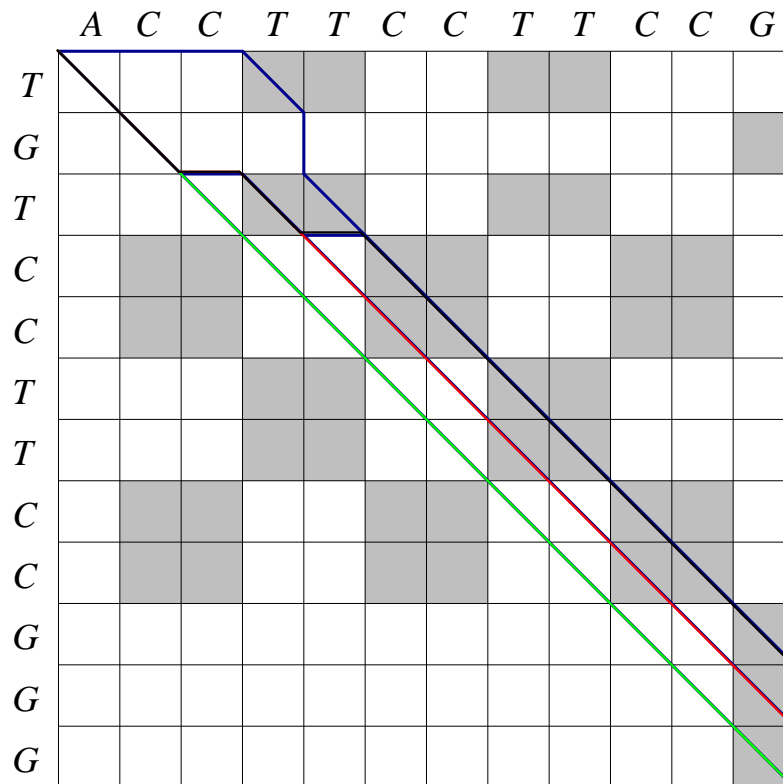
- Alignments can be represented as paths from the upper-left to the lower-right corner in the alignment graph:



x	y	z
11	0	1
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TGTCTTCCGGG TG-TCCTTCCGGG
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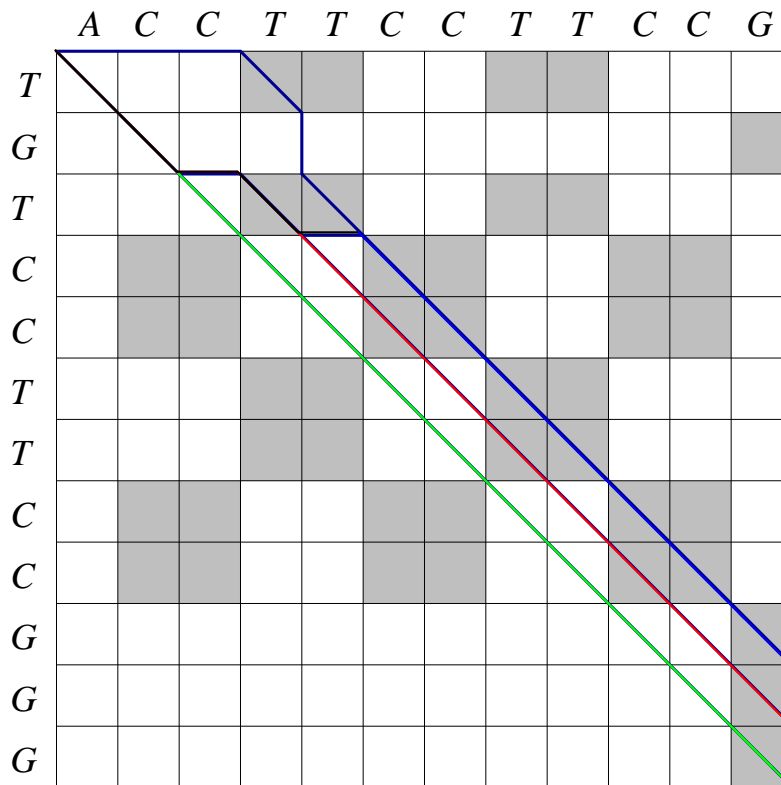
x	y	z
11	0	1
6	1	5
2	2	8

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x	y	z
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6	1	5
2	2	8
0	3	9
⋮	⋮	⋮

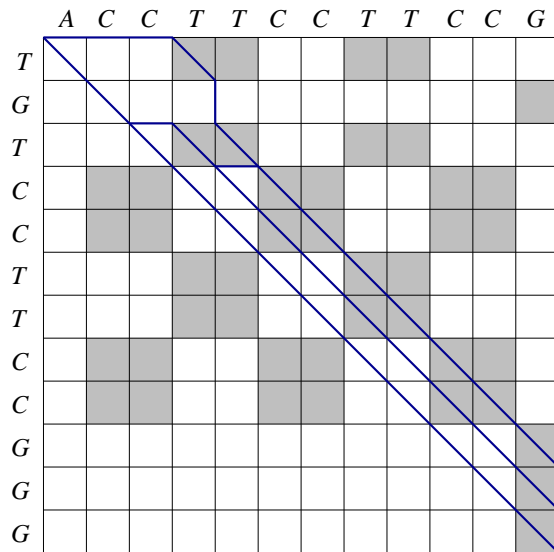
TGTCCTTCCGGG
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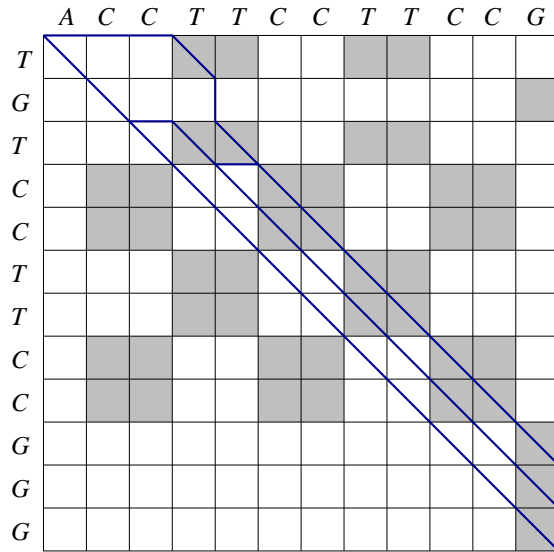
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The Newton polytope of a pair of sequences

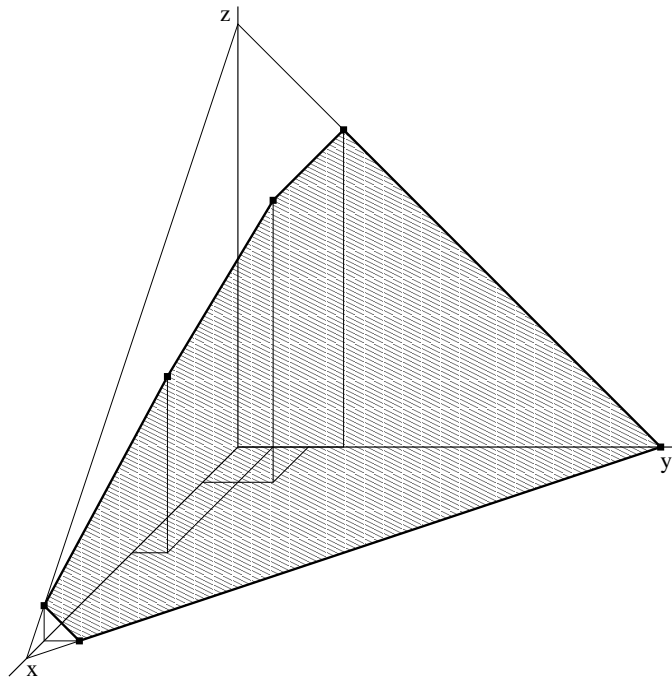


x	y	z
11	0	1
6	1	5
2	2	8
0	3	9
11	1	0
0	12	0

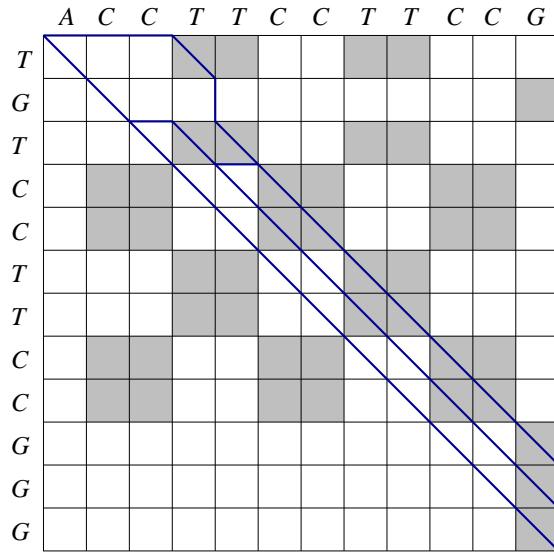
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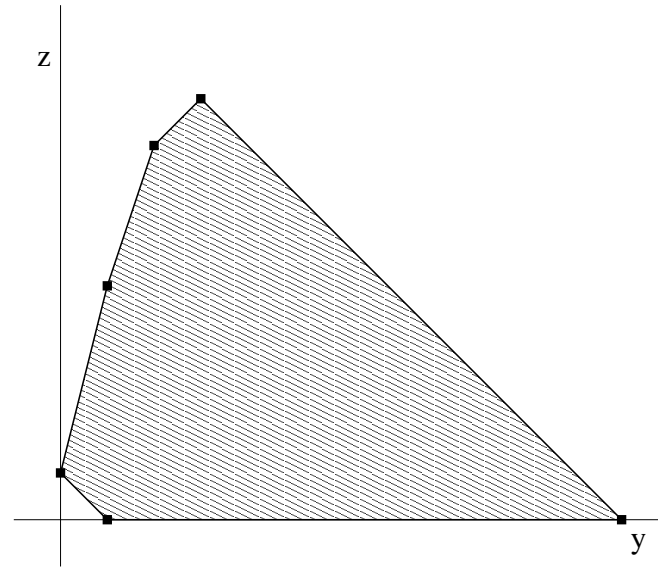
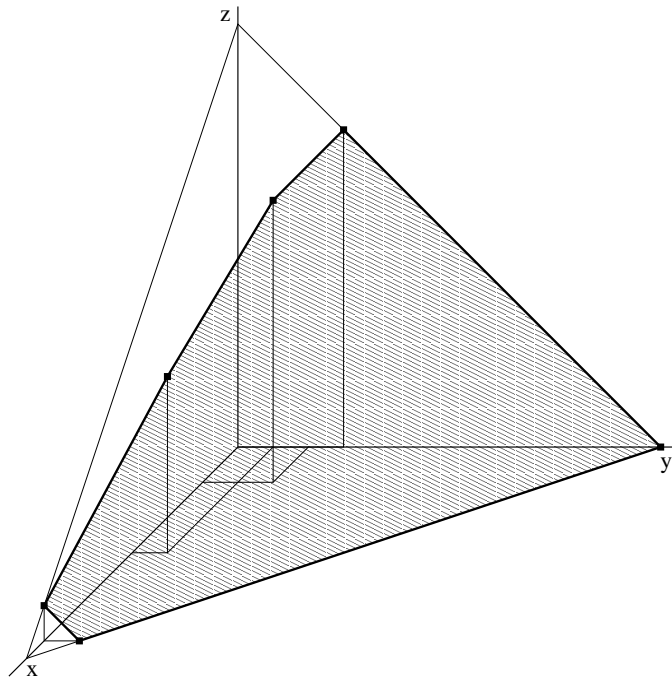
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Conjecture (?): It is $O(\sqrt{n})$ for sequences on any finite alphabet.