

# Indexable Elastic Founder Graphs of Minimum Height with Suffix Tree Maneuvers

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# Outline

- ① The Elastic Founder Graph for a MSA
- ② Preprocess: Computing the valid segments
- ③ Preprocess: Minimizing the maximum height

# The search for a pangenome data structure

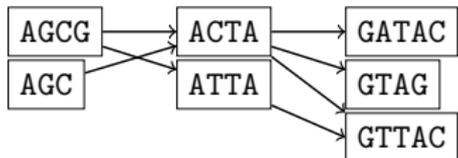
- **computational pangenomics**: find a data structure for a coherent collection of genomes supporting fast pattern matching
- graph-based candidates like Variation Graphs and Elastic Degenerate Strings usually represent a **multiple sequence alignment (MSA)**
- cannot support string matching in subquadratic time under the Orthogonal Vectors Hypothesis for simple classes of graphs

# The Elastic Founder Graph

## Definition (Mäkinen *et al* (2020))

A segmentation  $S$  of  $\text{MSA}[1..m, 1..n]$  induces an elastic block graph  $G(S) = (V, E, \ell)$  that we call **elastic founder graph** (EFG). EFGs respecting the **semi-repeat-free** property admit a poly-time index for linear-time pattern matching.

	1	2	3	4	5	6	7	8	9	10	11	12	13
1	A	G	C	G	A	C	T	A	G	A	T	A	C
2	A	G	C	-	A	C	T	A	G	-	T	A	G
3	A	G	C	G	A	T	T	A	G	T	T	A	C
4	A	G	C	-	A	C	T	A	G	T	T	A	C



## Example

Segmentation  $S = [1..4], [5..8], [9..13]$  induces this EFG  $G(S)$ .

- strings become **node labels**;
- **edges** are based on local occurrences  $\Rightarrow$  recombination;
- linear-time construction algorithms for the gapless setting, non-trivial to extend to the general setting

# The Elastic Founder Graph

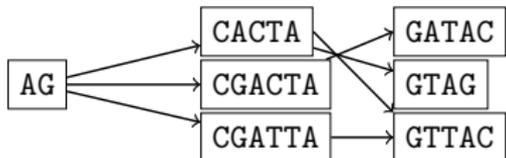
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# EFG construction algorithms

- we concentrate on constructing a semi-repeat-free EFG **minimizing the maximum block height**
- an optimal segmentation is found via **dynamic programming** (details in the paper) after two important preprocessing steps:
  - computing all valid semi-repeat-free segments
  - computing the height information of all valid segments

Our contributions:

- ① preprocessing in time  $O(mn\alpha \log|\Sigma|)$ , where  $\alpha$  is the length of longest aligned common substring
- ② we studied a **refined height definition** resulting in an  **$O(mn)$ -time** preprocessing and construction algorithm

# Representing the valid segments

The first step is computing the valid segments.

## Observation

If  $[x..y]$  is valid, then  $[x..y']$  is valid for all  $y' > y$ .

## Definition

Given  $x$ , the **minimal right extension**  $f(x)$  marks the first column so that  $[x..f(x)]$  is valid.

	1	2	3	4	5	6	7	8	9	10	11	12	13
1	A	G	C	G	A	C	T	A	G	A	T	A	C
2	A	G	C	—	A	C	T	A	G	—	T	A	G
3	A	G	C	G	A	T	T	A	G	T	T	A	C
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## Example

$[3..4]$  is not semi-repeat-free  
but  $[3..5]$  is, so  $f(3) = 5$ .

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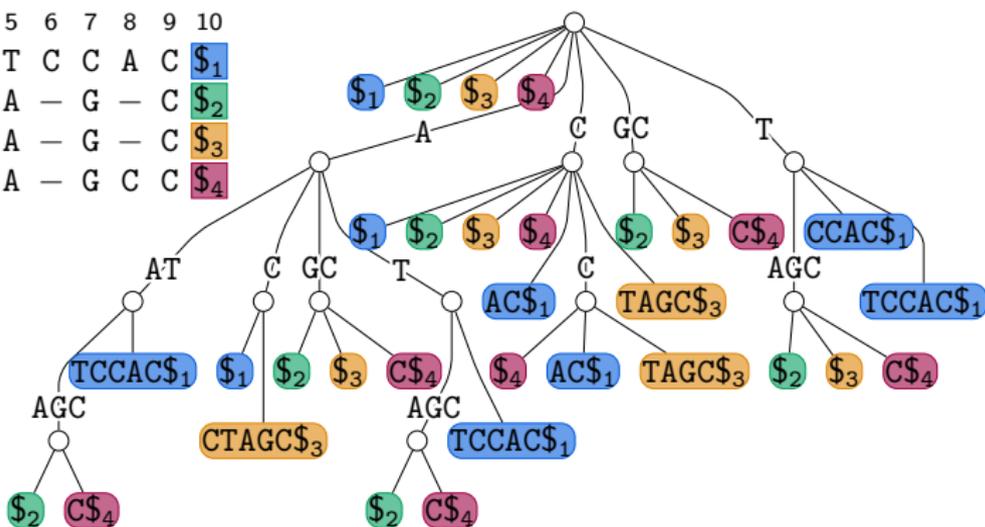
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# The generalized suffix tree

The main tool we use to compute  $[x..f(x)]$  is  $GST_{MSA}$ , the generalized suffix tree of strings  $spell(MSA[i, 1..n]) \cdot \$_i$ .

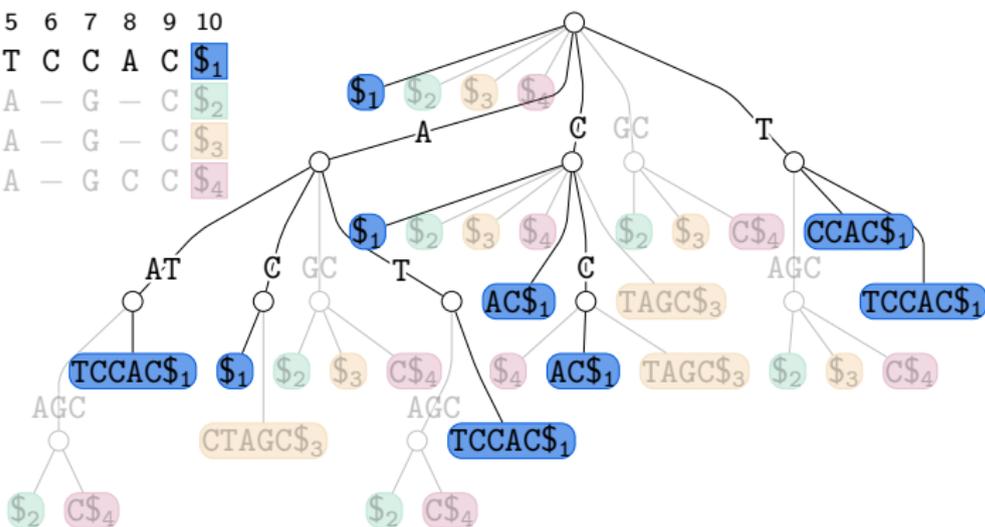
1	2	3	4	5	6	7	8	9	10
A	A	-	T	T	C	C	A	C	$\$_1$
A	A	-	T	A	-	G	-	C	$\$_2$
A	C	C	T	A	-	G	-	C	$\$_3$
A	A	-	T	A	-	G	C	C	$\$_4$



# The generalized suffix tree

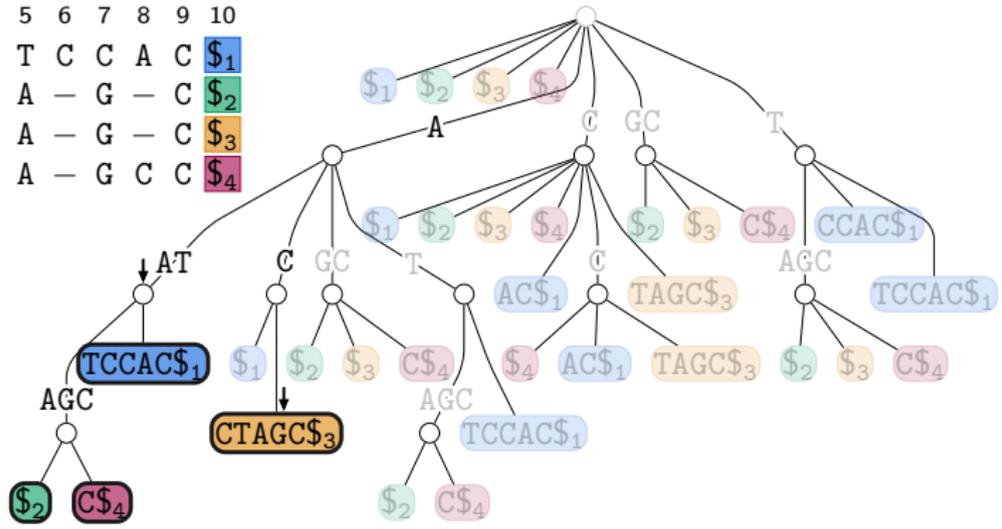
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A	C	C	T	A	-	G	-	C	$\$_3$
A	A	-	T	A	-	G	C	C	$\$_4$



# From the MSA to the suffix tree

1	2	3	4	5	6	7	8	9	10
A	A	-	T	T	C	C	A	C	\$ <sub>1</sub>
A	A	-	T	A	-	G	-	C	\$ <sub>2</sub>
A	C	C	T	A	-	G	-	C	\$ <sub>3</sub>
A	A	-	T	A	-	G	C	C	\$ <sub>4</sub>



- we can break down  $f(x)$  to single rows
- suffixes  $\Rightarrow$  leaves of  $GST_{MSA} \Rightarrow$  exclusive ancestors
- we navigate back to the MSA with rank and select queries
- $f(x)$  can be computed in time  $O(m) \Rightarrow$  global  $O(mn)$  time

# Min max height in the gapless setting

Now that we have the valid segments, we need to compute their height information.

## Observation

If  $\text{MSA}[1..m, 1..n]$  has no gaps, height  $H([x..y])$  is increasing with respect to  $y$ .

## Definition

We define the **meaningful right extensions**  $R_x$  as  $r_{x,1}, \dots, r_{x,c_x}$ , the positions  $y$  where height  $H([x..y])$  changes (increases).

	1	2	3	4	5	6	7	8
	T	T	C	C	C	G	G	\$ <sub>1</sub>
	T	T	A	C	C	G	A	\$ <sub>2</sub>
	T	T	A	C	A	C	A	\$ <sub>3</sub>
	T	T	A	C	A	C	G	\$ <sub>4</sub>
	T	T	A	C	A	A	G	\$ <sub>5</sub>
	G	T	C	A	A	G	G	\$ <sub>6</sub>
$H([1..y])$	2	2	3	3	4	5	6	6

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In the **gapless setting**,  $|R_x| \leq m$  so  $\sum_{x=1}^n |R_x| \in O(mn)$ :

- **Norri et al (2019)**  $O(mn)$ -time computation of all  $R_x$  w/ height values (in a different context from the semi-repeat-free one)
- **Mäkinen et al (2020)**  $O(mn)$ -time computation of  $f(x)$

Result:  **$O(mn)$ -time** segmentation algorithm for gapless MSAs.

# The more difficult setting with gaps

In the setting with gaps,  $R_x \in O(n)$ :

$$\begin{array}{cccccccccc}
 & 1 & 2 & 3 & 4 & 5 & 6 & 7 & \dots & n-2 & n \\
 1 & T & A & - & A & - & A & - & \dots & A & - & C \\
 2 & T & - & A & - & A & - & A & \dots & - & A & C \\
 H([1..y]) & 1 & 2 & 1 & 2 & 1 & 2 & 1 & \dots & 2 & 1 & 1
 \end{array}$$

Thus  $\sum_{x=1}^n |R_x| \in O(n^2)$ :

- computing  $R_x$  + height info naively (keyword tries) yields a  $O(mn\alpha \log|\Sigma|)$ -time algorithm, where  $\alpha$  is the length of the longest aligned substring between any two rows
- construction algorithm processes all  $R_x$  + height info as before

Solution is  $O(mn^2 \log|\Sigma|)$ : can we do better?

# Prefix-aware height

	1	2	3	4	5	6	7	8	9	10
T	C	-	C	-	-	C	G	-	\$	\$ <sub>1</sub>
T	-	A	C	-	-	C	-	-	\$	\$ <sub>2</sub>
T	-	A	C	-	A	C	-	A	\$	\$ <sub>3</sub>
T	-	A	C	-	A	C	G	-	\$	\$ <sub>4</sub>
T	-	A	C	A	A	-	G	-	\$	\$ <sub>5</sub>
G	C	A	-	-	A	-	G	-	\$	\$ <sub>6</sub>

$$\overline{H}([1..y]) \quad - \quad 2 \quad 3 \quad 3 \quad 3 \quad 3 \quad 5 \quad 5 \quad 6 \quad 6$$

## Definition

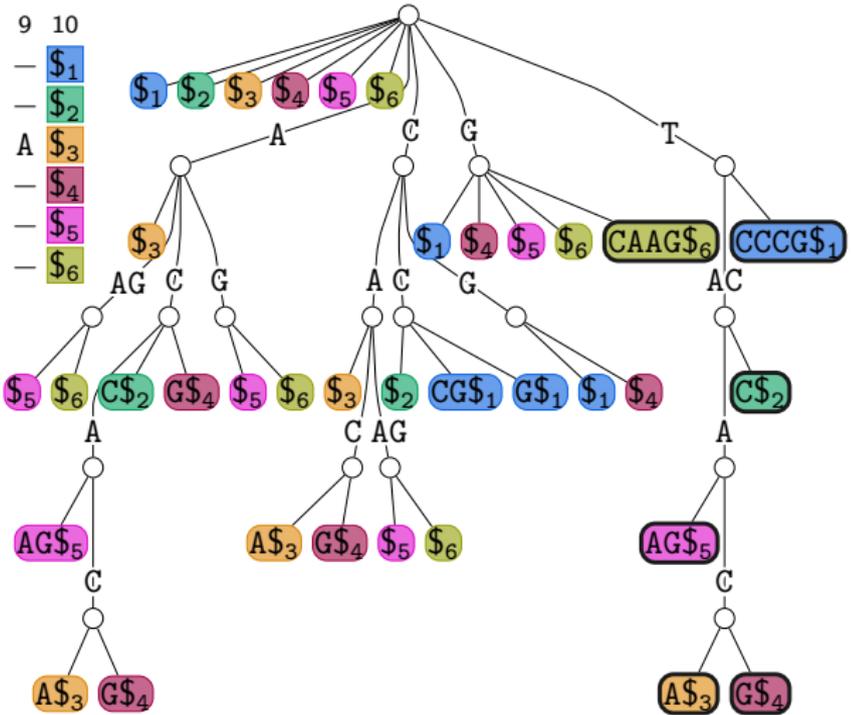
We define  $\overline{H}([x..y])$  as the number of distinct strings in  $[x..y]$  that are not proper prefixes of other strings in  $[x..y]$ .

- $\overline{H}([x..y]) \leq H([x..y])$  so it is a **lower bound**
- we can define the **meaningful prefix-aware extensions**  $\overline{R}_x$   
 $\Rightarrow \sum_{x=1}^n |\overline{R}_x| \in O(mn)$
- plug-and-play with the construction algorithm

# The suffix tree uncovers the prefix-aware height

Let's concentrate on the forest of  $GST_{MSA}$  for  $[x..n]$ , with  $x = 1$

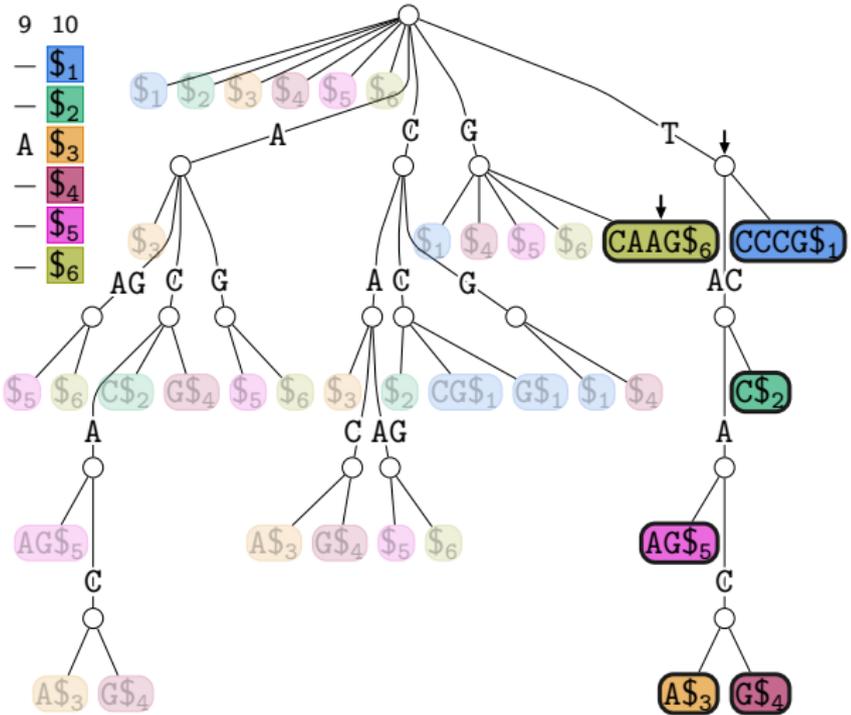
1	2	3	4	5	6	7	8	9	10
T	C	-	C	-	-	C	G	-	\$ <sub>1</sub>
T	-	A	C	-	-	C	-	-	\$ <sub>2</sub>
T	-	A	C	-	A	C	-	A	\$ <sub>3</sub>
T	-	A	C	-	A	C	G	-	\$ <sub>4</sub>
T	-	A	C	A	A	-	G	-	\$ <sub>5</sub>
G	C	A	-	-	A	-	G	-	\$ <sub>6</sub>



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	1	2	3	4	5	6	7	8	9	10
T	C	-	C	-	-	C	G	-	$\$1$	
T	-	A	C	-	-	C	-	-	$\$2$	
T	-	A	C	-	A	C	-	A	$\$3$	
T	-	A	C	-	A	C	G	-	$\$4$	
T	-	A	C	A	A	-	G	-	$\$5$	
G	C	A	-	-	A	-	G	-	$\$6$	

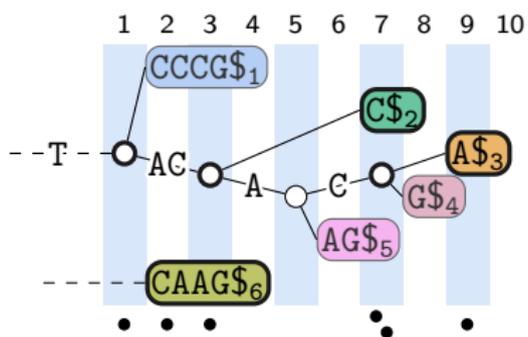
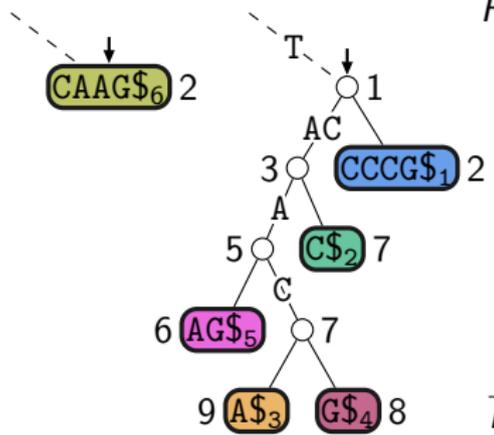


# The suffix tree uncovers the prefix-aware height

- for each node we find the **first ending column** of the relative MSA occurrence

	1	2	3	4	5	6	7	8	9	10
1	T	C	-	C	-	-	C	G	-	\$ <sub>1</sub>
2	T	-	A	C	-	-	C	-	-	\$ <sub>2</sub>
3	T	-	A	C	-	A	C	-	A	\$ <sub>3</sub>
4	T	-	A	C	-	A	C	G	-	\$ <sub>4</sub>
5	T	-	A	C	A	A	-	G	-	\$ <sub>5</sub>
6	G	C	A	-	-	A	-	G	-	\$ <sub>6</sub>

$$\bar{H}([1..y]) \quad - \quad 2 \quad 3 \quad 3 \quad 3 \quad 3 \quad 5 \quad 5 \quad 6 \quad 6$$



$$\bar{H}([1..y]) \quad - \quad 2 \quad 3 \quad 3 \quad 3 \quad 3 \quad 5 \quad 5 \quad 6 \quad 6$$

- most of these ending columns mark a +1 increase in  $\bar{H}$

# Final suffix tree maneuvers

Computing these values using just  $\text{GST}_{\text{MSA}}$  takes  $O(m^2n)$  time in total.

We obtain a linear-time solution with suffix tree maneuvers:

- we can compute the pos values in  $O(mn)$  time with  $\text{GPT}_{\text{MSA}}$ , the **generalized prefix tree** of the MSA rows
- $O(1)$ -time  $\text{GST}_{\text{MSA}}$ -to- $\text{GPT}_{\text{MSA}}$  navigation thanks to weighted ancestor queries/affix trees

# Conclusions

Summary of results for optimal EFG construction:

- $O(mn)$ -time solution for **min max height** in the gapless setting
- $O(mn\alpha \log|\Sigma|)$ -time solution for the setting with gaps
- $O(mn)$ -time solution for **min max prefix-aware height**

Future work:

- extending EFGs to allow **segments containing empty strings**

# Bibliography

-  Tuukka Norri, Bastien Cazaux, Dmitry Kosolobov and Veli Mäkinen. [Linear time minimum segmentation enables scalable founder reconstruction](#). Algorithms for Molecular Biology 14 (2019)
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-  Massimo Equi, Tuukka Norri, Jarno Alanko, Bastien Cazaux, Alexandru I. Tomescu, and Veli Mäkinen. [Algorithms and complexity on indexing elastic founder graphs](#). ISAAC 2021.