

Pantograph: Scalable Interactive Graph Genome Visualization

Intro

- Pangenome graphs provide extensive benefits over reference based approaches but so far lack scalable visualization solutions.

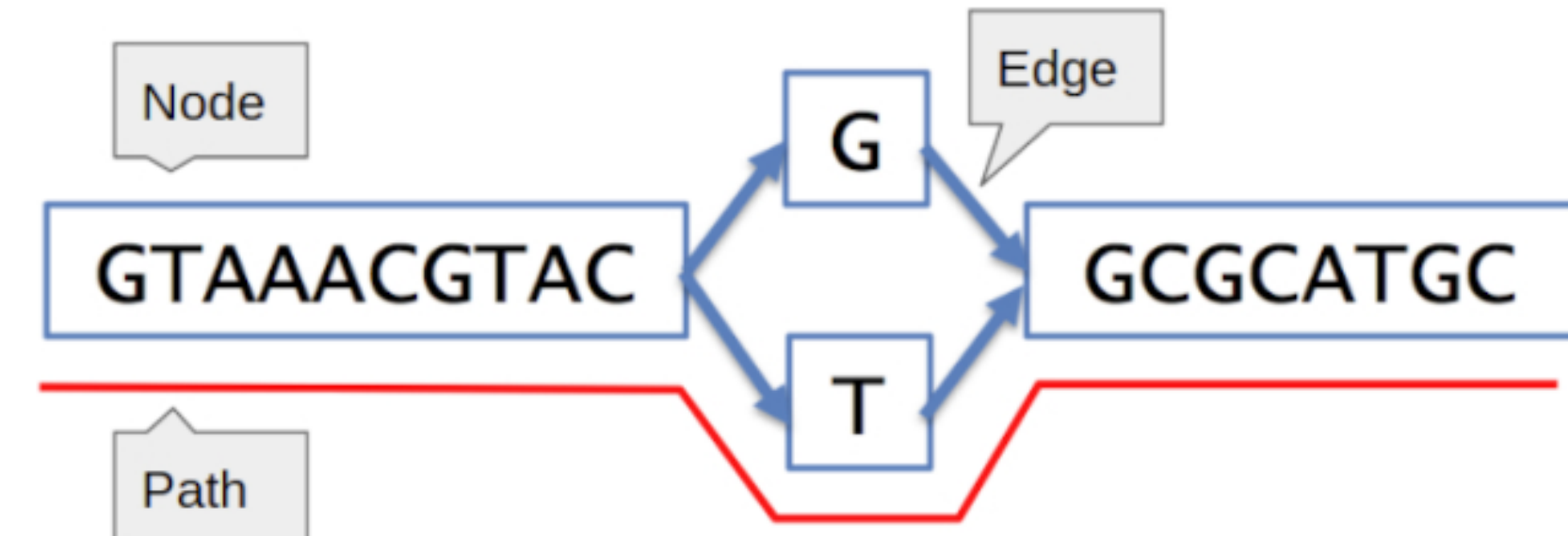
- A pangenome can be encoded in the form of a variation graph.

GTAAACGTACGCGCATGC

+

GTAAACGTACTGCGCATGC

||



Courtesy of Prof. Kasahara

<https://bit.ly/PangenomeGraph>

Methods

- vgteam's odgi sorts a graph genome's nodes into a roughly linear ordering to allow easy browsing.
- Pantograph identifies co-linear syntenic regions, exposing the presence of structural variants.

Results

- A public server provides an instance of Pantograph, giving access to a live updating view of a SARS-CoV-2 pangenome.

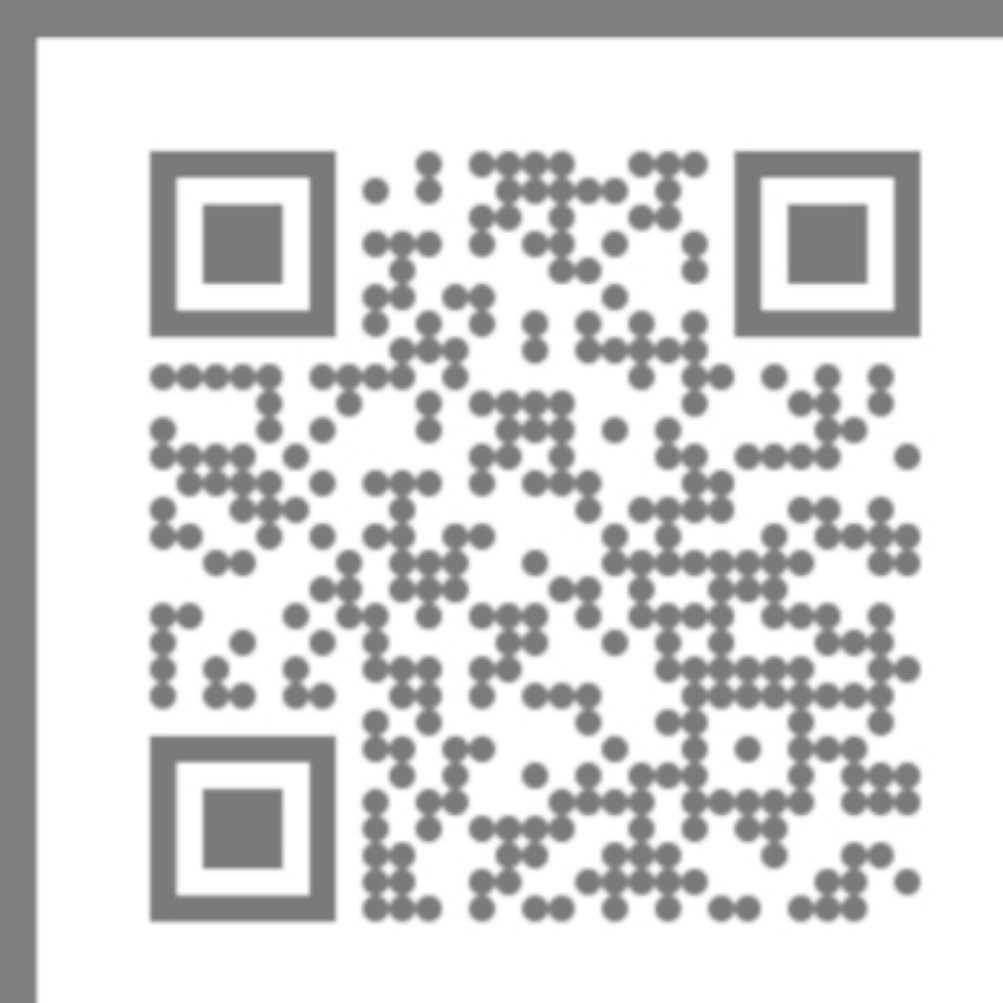
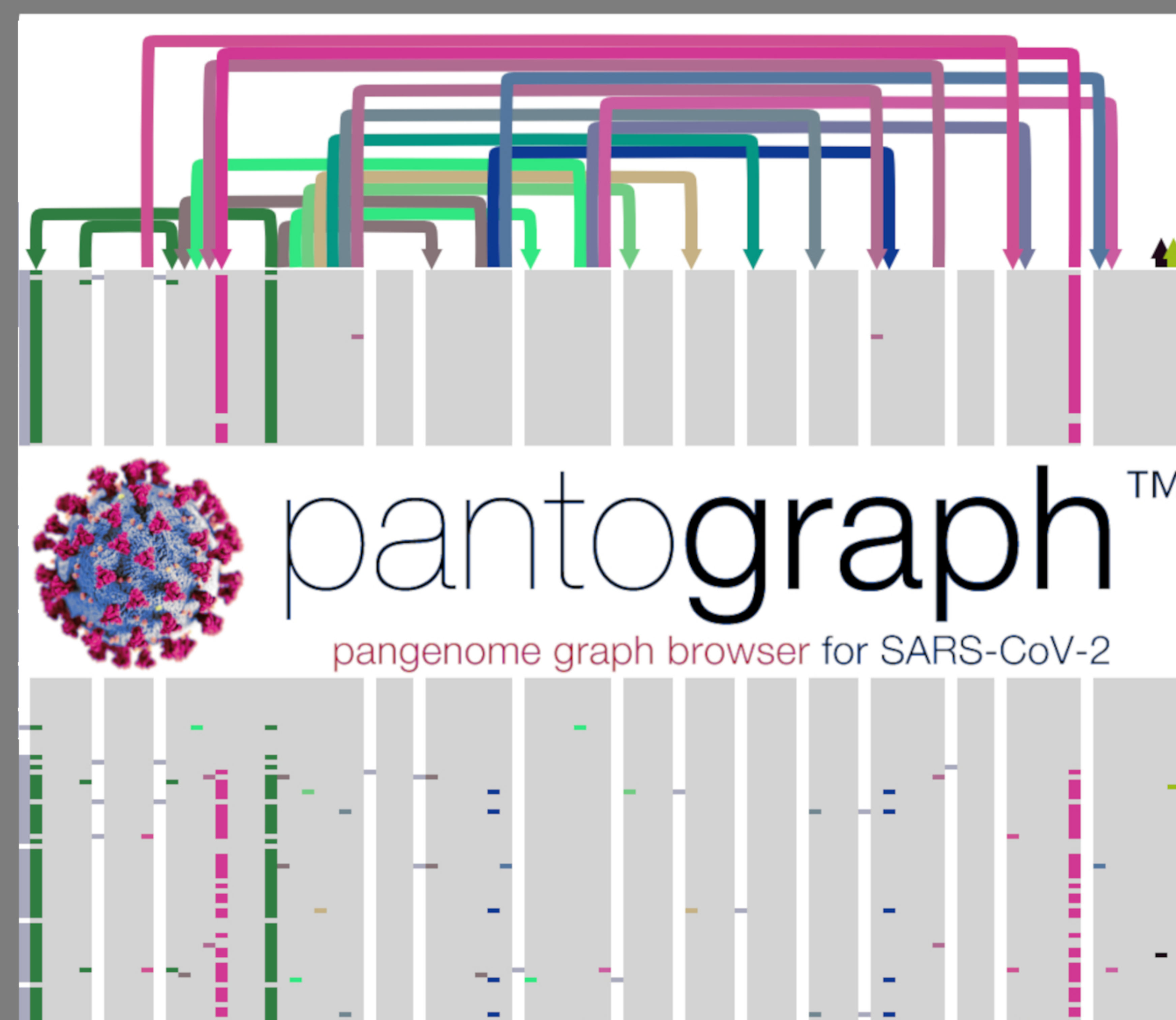
<https://graph-genome.github.io/Schematize>

- The entire pipeline is available to create your own pangenome.

<https://github.com/graph-genome/pipeline>

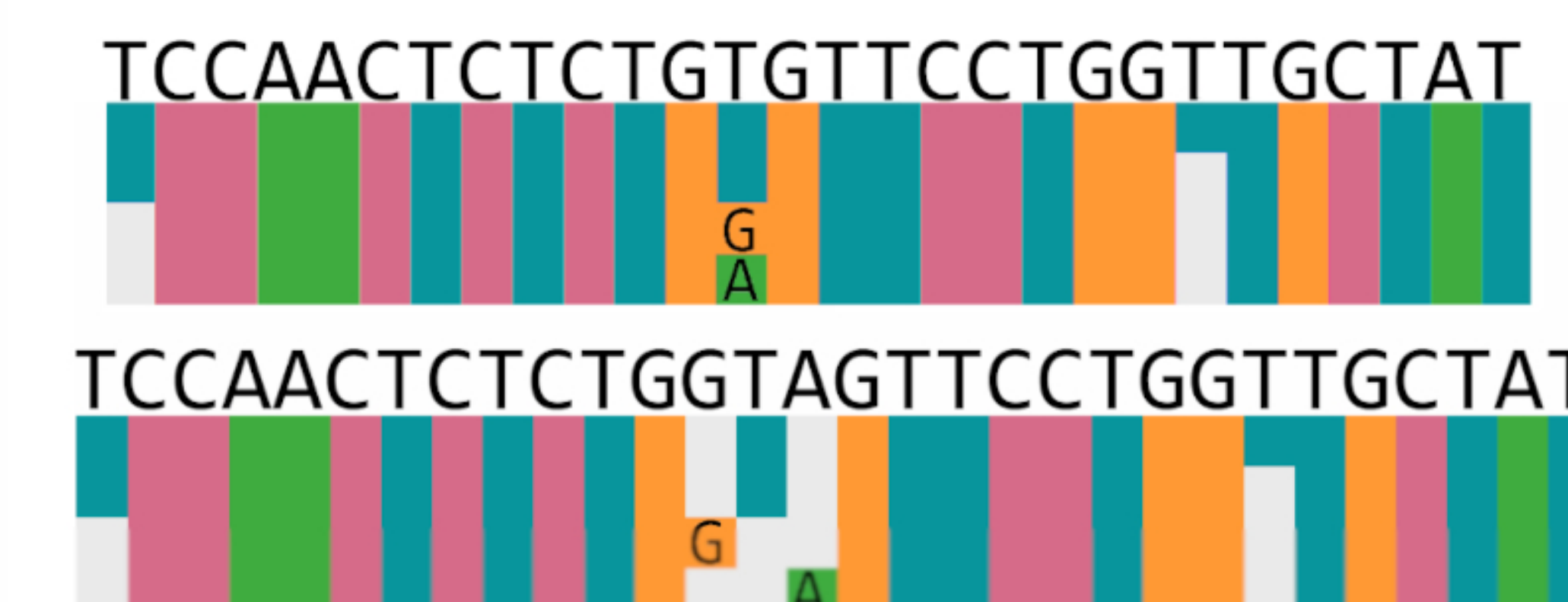


Pantograph can avoid reference bias pervading comparative genomics, allowing researchers to study SARS-CoV-2 **structural variants** that would otherwise go unnoticed



GraphGenome.org

Multiple Sequence Alignment vs Pangenome Columns



Navigating Rearrangements

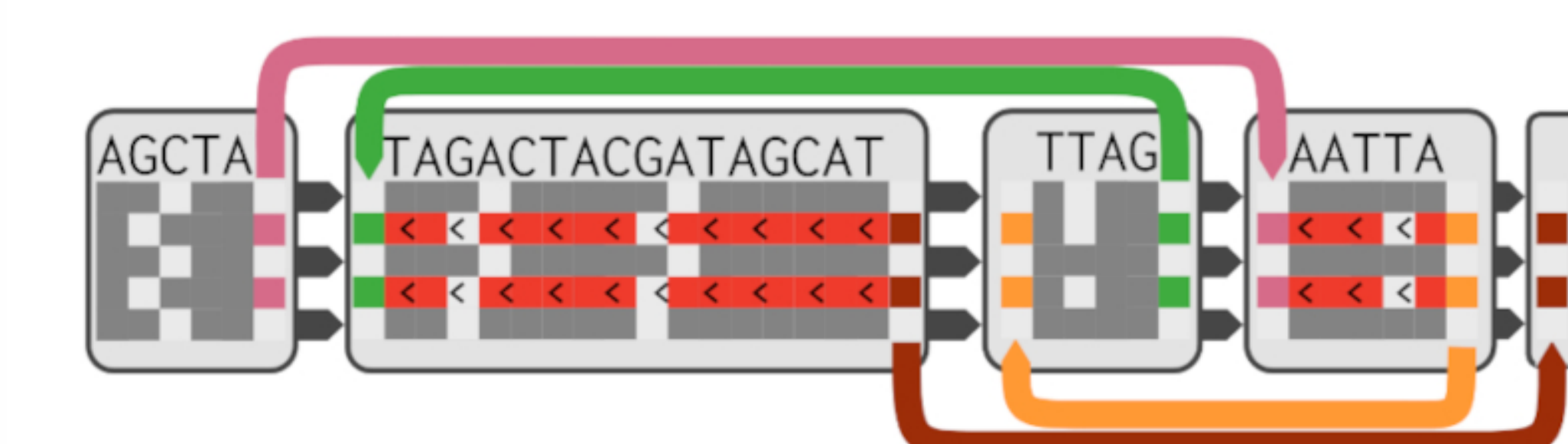
TCCAA---CTCTCTGTGGTTCCGGTTGCTAT*
TCC-AGGTCCTCTCTGTGGTTCC---GCTATGGT*
TCCAA---CTCTCTGGGGTTCCGG-TGTATGGT*
TCC-AGGTCCTCTCTGAGGTTCC---GTAT*
TCC-AGGTCCTCTGTGGTTCCGG-TGTAT*



Every row is an individual
Only follow each link once

Nested Inversions

AGTA -----TAG-CTACG-TAGCAT T-AG AATTA*
ACTA T-ATT T-AG ATGCTA-CGTAG-CTA*
AGTA -----TAG-CTACG-TAGCAT TTAG AATTA*
ACTA T-ATT T-AG ATGCTA-CGTAG-CTA*
AGTA -----TA-ACTAC-ATAGCAT TTAG AATTA*



Complex rearrangements can still
be displayed in Pantograph

Contributors

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