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A Software Tool for Whole Genome Synteny Comparisons \\ \title{
A Software Tool for Whole Genome Synteny Comparisons Olivier Gingras ${ }^{(1)}$, Yannick Gingras ${ }^{(1,2)}$, André Levasseur ${ }^{(1)}$, Anne Bergeron ${ }^{(1)}$, Cedric Chauve ${ }^{(1,2)}$
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## Introduction

Genomes can be compared at many different levels of details: sequences, signals, domains, genes, or large synteny blocks such as those computed in [?]. When each marker has one and only one - occurrence in each of the compared genomes, common intervals [?, ?] can be used to identify clusters [?], detect assembly inconsistencies [?], or propose evolution scenarios [?]. In this poster, we present Sequoia, a software tool that computes and displays the $P Q$-trees of the strong common intervals of two or more genomes. Sequoia implements the algorithms described in [?].

## Definitions

A signed permutation on $n$ elements is a permutation on the set of integers $\{1,2, \ldots, n\}$ in which each element has a sign, positive or negative. An interval of a signed permutation is a segment of consecutive elements of the permutation. Two distinct intervals $I$ and $J$ are said to commute if either $I \subset J$, or $J \subset I$, or $I \cap J=\emptyset$. If intervals $I$ and $J$ do not commute, they are said to overlap.
A common interval of permutations $P$ and $Q$ is a set of one or more integers that is an interval in both $P$ and $Q$. The singletons and the set $\{1,2, \ldots, n\}$ are always common intervals, and called trivial common intervals.
A common interval $I$ of permutation $P$ and $Q$ is a strong if it commutes with every common interval of $P$ and $Q$. Strong intervals are partially ordered by the inclusion relation. The inclusion order defines a tree whose ordered leaves spell out $P$ or $Q$, and whose root is the whole permutation. A node of the strong intervals tree is:
linear if consecutive pairs of its children are common intervals,
prime, otherwise.

## Strong intervals tree

Example of strong intervals tree obtained by comparing the identity permutation and permutation $P=$ (142537869). Prime and linear nodes are distinguished by their shape. There are two non-trivial linear nodes, the rectangular nodes: $(7,8)$ is increasing and $(7,8,6)$ is decreasing. There is only one prime node, the round node $(4,2,3,5)$.

## Examples

Comparing the Human and Rat Chromosomes X.


Human $=1 \begin{array}{llllllllllllll}1 & 2 & 3 & 4 & 5 & 6 & 7 & 8 & 9 & 10 & 11 & 1213 & 14 & 15\end{array} 16$

$$
\mathrm{Rat}=\begin{array}{llllllllllllllll}
\overline{13} & \overline{4} & 5 & \overline{6} & \overline{12} & \overline{8} & \overline{7} & 2 & 1 & \overline{3} & 9 & 10 & 11 & 14 & 15 & 16
\end{array}
$$

## Comparing the Mouse and Rat Chromosomes X.



Mouse $=\begin{array}{lllllllllllllll}1 & 2 & 3 & 4 & 5 & 6 & 7 & 8 & 9 & 10 & 11 & 12 & 13 & 14 & 15\end{array} 16$ $\boldsymbol{R a t}=\begin{array}{llllllllllllll}\overline{4} & \overline{3} & \overline{2} & 1 & \overline{13} & \overline{15} & 14 & \overline{16} & 8 & 9 & 10 & \overline{11} & 12 & 5\end{array} \quad 6 \quad 7$

## Sequoia

Sequoia accepts FASTA-like inputs. Multiple sequences are supplied with a comment line followed by a list of identifiers. The identifiers can be strings, numbers, or a combination of both. Positive signs are optional. Duplicate identifiers within a sequence, and identifiers that are missing in some sequences, are ignored.

## Examples of input sequences

```
Homo sapiens Chromosome X
2 3 4 5 6 7 8 9 10 11 12 13 14 15 16
Rattus norvegicus Chromosome X
-13 -4 5 -6 -12 -8 -7 2 1 -3 9 10 11 14 -15 16
Any set of identifiers can be used, such as pairs of orthologs in the following example.
E. coli Genome, paired with S. typhimurium orthologs
yaaJ-yaaJ talB-talB dnaK-dnaK dnaJ-dnaJ nhaR-STMO014 ribF-fruR fkpB-slpA rihC-rihC
caiE-caiE caid-caiD caic-caic caiA-caiA cait-cait fixA-fixA fixB-fixB fixC-fixC
fixX-fixX yaaU-yaaU yabF-yabF kefC-kefC pdxA-pdxA rluA-rluA araD-araD araC-araC
yabI-yabI yabJ-yabJ tbpA-phnS yabN-yabN setA-STMO212 leuD-leuD leuC-leuc leuB-leuB leuO-leuO ilvi-ilvI fruR-STMO257 ftsI-ftsI murE-mure murF-murF murD-murD ftsW-ftsw murC-murC ddlB-ddlB mutT-STM0030 hofC-hofC .
```


## Examples of output trees

The following tree is a sub-tree of the strong intervals tree obtained by comparing 391 synteny blocks [?] obtained by the whole comparison of the human, mouse and rat genomes. Each block identifier is followed by its chromosomal location in each of the three species. It reveals interesting rearrangments of human chromosome 17, mouse chromosome 11, and rat chromosome 10.
Human Chr. 17, Mouse Chr. 11, Rat Chr. 10


The following tree is a sub-tree of the strong intervals tree obtained by comparing 3000 pairs of orthologs E. coli and S. typhimurium. Sequoia can easily handle thousands of identifiers over dozens of species.
Comparing E. coli and S. typhimurium


## URL : cgl.bioinfo.uqam.ca

## References

[1] Bérard, S., Bergeron, A., Chauve, C., Paul, C., Perfect sorting by reversals is not always difficult. To appear in WABI 2005 Proceedings, LNCS.
[2] S. Bérard, A. Bergeron and C. Chauve. Conserved structures in evolution scenarios. In Comparative Genomics, RECOMB 2004 International Workshop, RCG2004, volume 3388 of Lecture Notes in Bioinformatics, pages 1-15, Springer-Verlag, 2005.
[3] Bergeron, A., Chauve, C., De Montgolfier, F., Raffinot, M., Computing common intervals of $K$ permutations, with applications to modular decomposition of graphs. To appear in ESA 2005 Proceedings, LNCS.

4] G. Bourque, P. A. Pevzner and G. Tesler. Reconstructing the genomic architecture of ancestral mammals: Lessons from human, mouse, and rat genomes. Genome Res., 14(4):507-516, 2004.
[5] S. Heber and J. Stoye. Finding all common intervals of $k$ permutations. In Combinatorial Pattern Matching, 12th Annual Symposium, CPM 2001, volume 2089 of Lecture Notes in Comput. Sci., pages 207-218, Springer-Verlag, 2001.
[6] G.M. Landau, L. Parida and O. Weimann. Using PQ trees for comparative genomics. To appear in Combinatorial Pattern Matching, 16th Annual Symposium, CPM 2005, 2005.
[7] T. Uno and M. Yagiura. Fast algorithms to enumerate all common intervals of two permutations. Algorithmica, 26(2):290-309, 2000

