Solving the Perfect Reversal Median Problem with PQ-trees

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Perfect Sorting by Reversals
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Perfect RMP
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Overview

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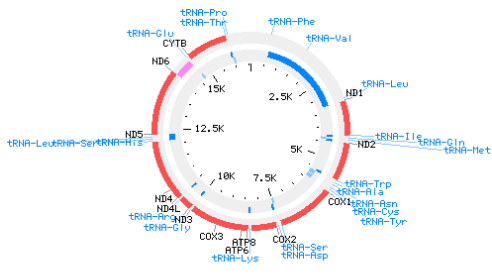
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Gene Order Data
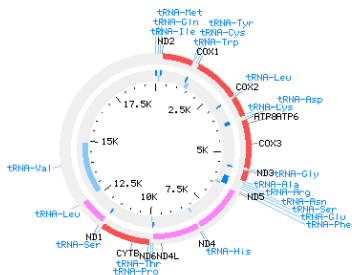
Homo Sapiens: *cox1, -Ser2, Asp, cox2, Lys, atp8, atp6, cox3, Gly, nd3, Arg, nd4l, nd4, His, Ser1, Leu1, nd5, -nd6, -Glu, cytb, Thr, -Pro, Phe, rrnS, Val, rrnL, Leu2, nd1, Ile, -Gln, Met, nd2, Trp, -Ala, -Asn, -Cys, -Tyr*

Drosophila Melanogaster: *cox1, Leu2, cox2, Lys, Asp, atp8, atp6, cox3, Gly, nd3, Ala, Arg, Asn, Ser1, Glu, -Phe, -nd5, -His, -nd4, -nd4l, Thr, -Pro, nd6, cytb, Ser2, -nd1, -Leu1, -rrnL, -Val, -rrnS, Ile, -Gln, Met, nd2, Trp, -Cys, -Tyr*

Signed Permutations and Reversals

- Genomes are modeled as signed permutations $\pi = (\pi_1, \ldots, \pi_n)$ over $\{1, \ldots, n\}$ (genes) Sign marks orientation (strand) of a gene
- Often considered rearrangements: **reversals**

$$
\begin{array}{ccccccc}
1 & 2 & 3 & 4 & 5 & 6 & 7 \\
1 & -6 & -5 & -4 & -3 & -2 & 7 \\
1 & -6 & -5 & 3 & 4 & -2 & 7 \\
\end{array}
$$
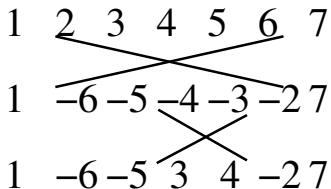
- Reversal distance $d(\pi, \sigma)$:
  - Minimal number of reversals needed to transform π into σ
  - Can be computed in O(n) [Hannenhalli, Pevzner 95]
- Sorting szenario in $O(n\sqrt{n \ log(n)})$ [Tannier et al. 05]

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A Sorting Scenario

B E E M P E R O R W E F U N

One optimal reversal scenario

Step	Description														
0	(Source)	1	7	9	3	4	11	12	2	14	10	13	5	6	8
1	Reversal	1	-7	9	3	4	11	12	2	14	10	13	5	6	8
2	Reversal	1	-7	9	3	4	11	12	2	14	10	13	5	6	-8
3	Reversal	1	-7	-6	-5	-13	-10	-14	-2	-12	-11	-4	-3	-9	-8
4	Reversal	1	-7	-6	-5	-13	-10	-14	-2	-12	-11	-4	-3	8	9
5	Reversal	1	5	6	7	-13	-10	-14	-2	-12	-11	-4	-3	8	9
6	Reversal	1	13	-7	-6	-5	-10	-14	-2	-12	-11	-4	-3	8	9
7	Reversal	1	13	14	10	5	6	7	-2	-12	-11	-4	-3	8	9
8	Reversal	1	2	-7	-6	-5	-10	-14	-13	-12	-11	-4	-3	8	9
9	Reversal	1	2	-7	-6	-5	-10	-9	-8	3	4	11	12	13	14
10	Reversal	1	2	-7	-6	-5	-4	-3	8	9	10	11	12	13	14
11	Reversal (Destination)	1	2	3	4	5	6	7	8	9	10	11	12	13	14

A Sorting Scenario

Be emperor!
We fun!

The Multiple Genome Rearrangement Problem (MGRP)

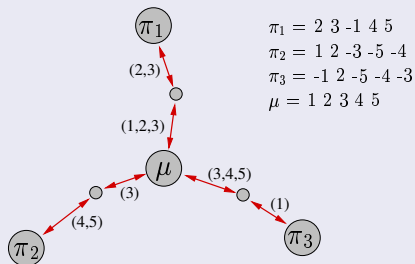### Definition

<u>Given</u>: a set of permutations Π,

<u>Find</u>: a tree T with leaf set Π, and
permutations for the inner nodes,
such that $\sum_{(\pi,\sigma) \in E(T)} d(\pi, \sigma)$ is minimal.

A Special Case: The Reversal Median Problem

Definition

Given three signed permutations π_1, π_2, π_3: find a permutation μ with a minimal score $\sum_i d(\mu, \pi_i)$

$\pi_1 = 2\ 3\ \text{-}1\ 4\ 5$
$\pi_2 = 1\ 2\ \text{-}3\ \text{-}5\ \text{-}4$
$\pi_3 = \text{-}1\ 2\ \text{-}5\ \text{-}4\ \text{-}3$
$\mu = 1\ 2\ 3\ 4\ 5$

- NP-hard [Caprara 03]
- Starting point for phylogeny reconstruction algorithms

Common Intervals

Definitions

Interval of a permutation π: set of consecutive elements of the permutation π.

Common Interval: a subset of elements that is an interval in a set Π of signed permutations.
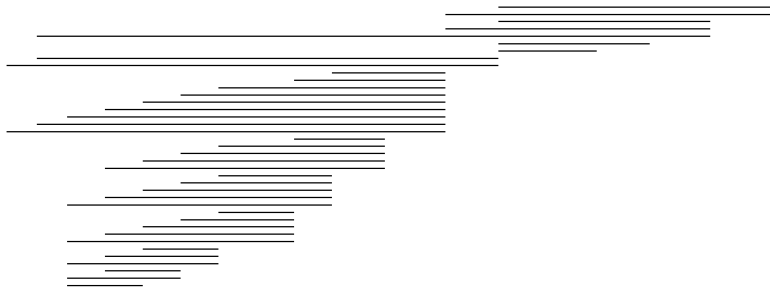
Example:

- Similarities: Common control, functionally coupled genes
- Highly similar condensed mitochondrial gene orders of three Arthropods (M: Mosquito, S: Silkworm, C: Centipede)

M	1	2	3	4	5	6	8	7	9	10	11	12	13	14	15	16	17
S	1	2	3	4	5	6	7	8	9	10	11	12	14	13	15	16	17
C	1	3	4	5	6	7	8	9	10	11	2	12	16	13	14	15	17
μ	1	2	3	4	14	13	12	11	10	9	8	7	6	5	15	16	17

Example

M	1	2	3	4	5	6	8	7	9	<u>10</u>	11	12	13	14	15	16	17
S	1	2	3	4	5	6	7	8	9	10	11	12	14	13	15	16	17
C	1	3	4	5	6	7	8	9	10	11	<u>2</u>	12	16	13	14	15	17

M: 1 2 3 4 5 6 8 7 9 <u>10</u> 11 12 13 14 15 16 17

Example

M	1	2	3	4	5	6	8	7	9	<u>10</u>	11	12	13	14	15	16	17
S	1	2	3	4	5	6	7	8	9	10	11	12	14	13	15	16	17
C	1	3	4	5	6	7	8	9	10	11	<u>2</u>	12	16	13	14	15	17
μ	1	2	3	4	<u>14</u>	<u>13</u>	<u>12</u>	<u>11</u>	<u>10</u>	<u>9</u>	<u>8</u>	<u>7</u>	<u>6</u>	<u>5</u>	15	16	17

M: 1 2 3 4 5 6 8 7 9 <u>10</u> 11 12 13 14 15 16 17

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Perfect Sorting with Strong Interval / PQ-Trees

Definitions:

Preserving Reversal: does not destroy any common interval

Perfect Reversal Distance: minimal number of preserving reversals needed to transform one sequence into another. (Bad news: NP-complete [Figeac and Varre 04])
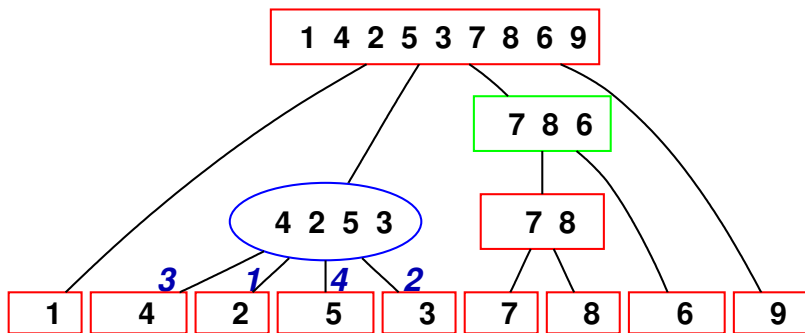
Strong Common Intervals

A common interval c of Π is a strong common interval if no other common interval overlaps with c, formally:
for any other common interval c' of Π: $c \subset c'$, $c \supset c'$, or $c \cap c' = \emptyset$.

- Can be computed in $O(kn)$
- Efficient representation of the common intervals
- Inclusion order defines a tree

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Strong Interval Trees / PQ-trees

1 4 2 5 3 7 8 6 9 ⟶ 1 2 3 4 5 6 7 8 9

Computing Perfect Scenarios [Bérard et al 07]
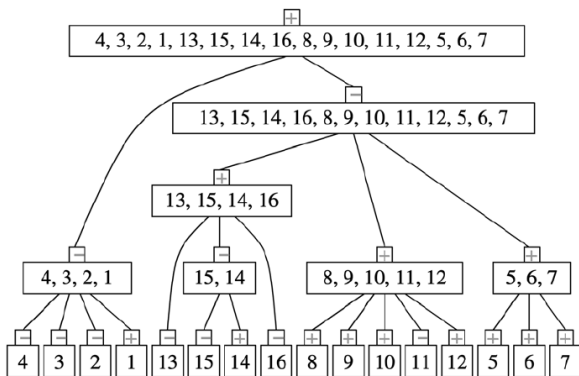
Proposition

A scenario S is perfect iff each of the reversals of S is either a vertex of the PQ-tree or the union of children of a prime vertex.

Parity Lemma

Let I be a vertex of the PQ-tree. If I has a linear parent and a sign different from the sign of its parent, then I belongs to any perfect scenario.

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Definite Trees

Mouse =	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
Rat =	$\bar{4}$	$\bar{3}$	$\bar{2}$	1	$\bar{13}$	$\bar{15}$	14	$\bar{16}$	8	9	10	$\bar{11}$	12	5	6	7

Unambigous Trees

Human =	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
Rat =	$\bar{13}$	$\bar{4}$	5	$\bar{6}$	$\bar{12}$	$\bar{8}$	$\bar{7}$	2	1	$\bar{3}$	9	10	11	14	$\bar{15}$	16

Ambigous Trees

$$\text{Identity} = \quad 1 \quad 2 \quad 3 \quad 4 \quad 5 \quad 6 \quad 7$$
$$\mathbf{P} = \quad 2 \quad \bar{5} \quad 7 \quad 4 \quad \bar{6} \quad 1 \quad 3$$

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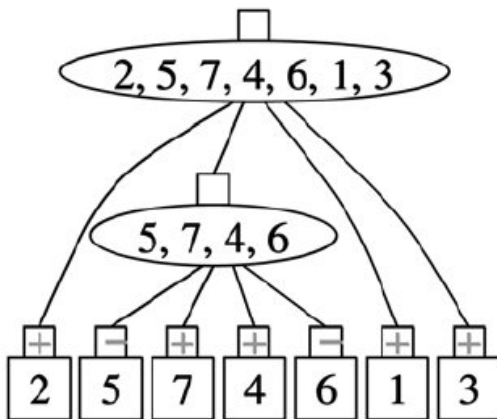
Overview

The remaining slides will (finally) explain this:
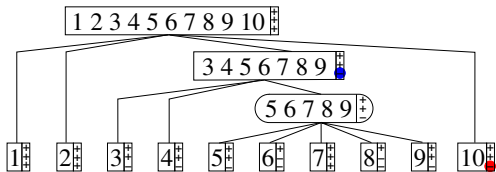
Extension: k-signed Strong Intervals Trees

- Wlog. π_1 is the identity

k-sign

A tuple $s = (s^1, \ldots, s^k)$, where $s^i \in \{+, -\}$, is called a k-**sign**.
$\bar{s}$ denotes the inverted tuple.

$\pi^1 = \iota$, $\pi^2 = (1\ 2\ 3\ 4\ \bar{6}\ 9\ 7\ 5\ \bar{8}\ 10)$, $\pi^3 = (1\ 2\ \bar{9}\ \bar{8}\ 7\ \bar{6}\ \bar{5}\ \bar{4}\ \bar{3}\ \bar{10})$

- Leaf ← signs of the element
- Linear ← inc. / dec.
- Prime ← inherit from lin. parent

Propositions

Proposition: "What is the goal"

1. Children of a prime node are reordered, such that they are all in the same order

2. Reversals change the k-signs of linear and prime nodes, such that for each node l either $\forall i : s^i(l) = +$ or $\forall i : s^i(l) = -$

Proposition: "Consequences of a reversal"

A reversal ρ:

a) with $\rho \cap l = \emptyset$ or $\rho \subset l$ do not change $s^i(l)$

b) with $l \subseteq \rho$ inverts $s^i(l)$

Median Parity Theorem

Median Parity Theorem

If node I has a linear parent J, with $s(I) \neq s(J)$ and $s(I) \neq \overline{s}(J) \Rightarrow$ there exists a reversal of I on one of the traces, which leads to either $s(I) = s(J)$ or $s(I) = \overline{s}(J)$. This reversal belongs to any perfect median scenario of Π.

Sketch: If the reversal is not applied then

1. $s(I) \neq s(J)$ and $s(I) \neq \overline{s}(J)$ still holds after applying other preserving reversals

2. $\rightarrow s^i(I)$ can not be equal if the $s^i(J)$ are equal (and the other way round)

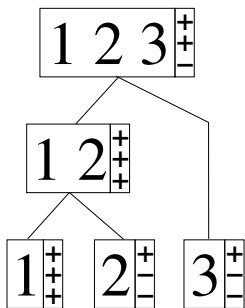3. $\Rightarrow I$ has to be included in any perfect median scenario

Solving Linear Nodes with Linear Parent

- A linear node with $s = (s^1, s^2, s^3)$ and its linear parent with $s_p = (s_p^1, s_p^2, s_p^3)$
  1. 1 sign different ($s^2 \neq s_p^2$ **or** $s^3 \neq s_p^3$)
     $\rightarrow$ reverse l in the corresponding trace $\rightarrow$ $s = s_p$
  2. 2 signs different ($s^2 \neq s_p^2$ **and** $s^3 \neq s_p^3$)
     $\rightarrow$ reverse l in the 1st trace $\rightarrow$ $s = \overline{s_p}$
- Note: 3 sign differences can not occur ($\pi_1 = \iota$)

Example: Unambiguous Trees without Prime Nodes

Example: $\pi^1 = (1\ 2\ 3)$, $\pi^2 = (1\ \overline{2}\ \overline{3})$, and $\pi^3 = (\overline{3}\ 1\ \overline{2})$

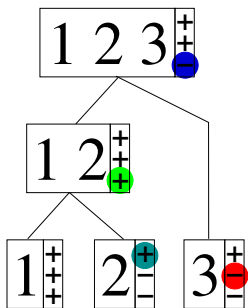non-trivial strong common interval: $\{1, 2\}$

Example: Unambiguous Trees without Prime Nodes

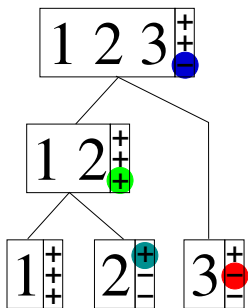Example: $\pi^1 = (1\ 2\ 3)$, $\pi^2 = (1\ \overline{2}\ \overline{3})$, and $\pi^3 = (\overline{3}\ 1\ \overline{2})$

non-trivial strong common interval: $\{1,2\}$

Example: Unambiguous Trees without Prime Nodes

Example: $\pi^1 = (1\ 2\ 3)$, $\pi^2 = (1\ \overline{2}\ \overline{3})$, and $\pi^3 = (\overline{3}\ 1\ \overline{2})$

non-trivial strong common interval: $\{1, 2\}$

$$\pi^1 = (1\ 2\ 3) \quad \pi^2 = (1\ \overline{2}\ \overline{3}) \quad \pi^3 = (\overline{3}\ 1\ \overline{2})$$
$$\Rightarrow (1\ \overline{2}\ 3) \quad \Rightarrow (1\ \overline{2}\ 3) \quad \Rightarrow (\overline{3}\ 2\ \overline{1})$$
$$\Rightarrow (1\ \overline{2}\ 3)$$

Example: Unambiguous Trees without Prime Nodes

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non-trivial strong common interval: $\{1,2\}$

$$\pi^1 = (1\ 2\ 3) \quad \pi^2 = (1\ \overline{2}\ \overline{3}) \quad \pi^3 = (\overline{3}\ 1\ \overline{2})$$
$$\Rightarrow (1\ \overline{2}\ 3) \quad\quad \Rightarrow (1\ \overline{2}\ 3) \quad\quad \Rightarrow (\overline{3}\ 2\ \overline{1})$$
$$\Rightarrow (1\ \overline{2}\ 3)$$

One median $\mu = (1\ \overline{2}\ 3)$ with score 4.

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Example: Unambiguous Trees without Prime Nodes

Another Example
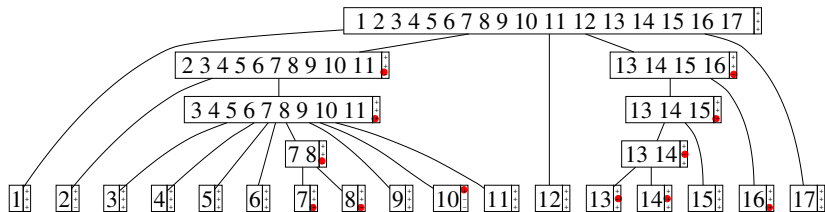
Can be sorted with 12 Reversals.

Properties: Unambiguous Trees without Prime Nodes

- Instances can be solved in $O(n)$
- There is exactly one median.

Medians for Prime Nodes

- Prime nodes may have sign information

oriented RMP (oRMP)

Find a median such that for a given tuple of signs $(s^1, s^2, ..., s^k)$
the value $\sum_{i=1}^{k} d(\pi^i, s^i \circ \mu)$ has to be minimal.

- $d(\pi, s \circ \sigma) = d(s \circ \pi, \sigma)$
- $\rightarrow$ Standard median solver can be used

Example: Unambiguous Tree with Prime Node

$\pi^1 = \iota$, $\pi^2 = (1\ 2\ 3\ 4\ \overline{6}\ 9\ 7\ 5\ \overline{8}\ 10)$, $\pi^3 = (1\ 2\ \overline{9}\ \overline{8}\ 7\ \overline{6}\ \overline{5}\ \overline{4}\ \overline{3}\ \overline{10})$

non-trivial strong common intervals $\{3,4,5,6,7,8,9\}, \{5,6,7,8,9\}$
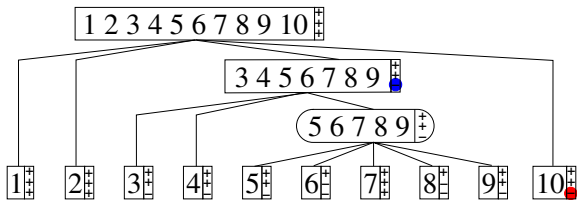
Example: Unambiguous Tree with Prime Node

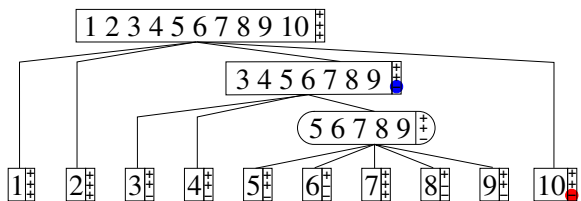$\pi^1 = \iota$, $\pi^2 = (1\ 2\ 3\ 4\ \overline{6}\ 9\ 7\ 5\ \overline{8}\ 10)$, $\pi^3 = (1\ 2\ \overline{9}\ \overline{8}\ 7\ \overline{6}\ \overline{5}\ \overline{4}\ \overline{3}\ \overline{10})$

non-trivial strong common intervals $\{3,4,5,6,7,8,9\}, \{5,6,7,8,9\}$

$\Gamma^1 = (1\ 2\ 3\ 4\ 5)$
$\Gamma^2 = (\overline{2}\ 5\ 3\ 1\ \overline{4})$
$\Gamma^3 = (\overline{5}\ \overline{4}\ 3\ \overline{2}\ \overline{1})$

$\mu_p^{++-} = (1\ 2\ \overline{3}\ 4\ 5)$
score 4

$\Gamma^1 \overset{3}{\curvearrowright} \mu_p^{++-}$

$\Gamma^2 \overset{531}{\curvearrowright} (\overline{2}\ \overline{1}\ \overline{3}\ \overline{5}\ \overline{4}) \overset{\overline{21}}{\curvearrowright} (1\ 2\ \overline{3}\ \overline{5}\ \overline{4}) \overset{\overline{54}}{\curvearrowright} \mu_p^{++-}$

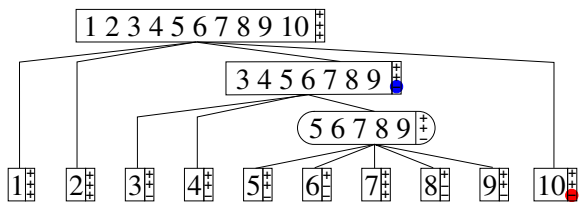$\Gamma^3 = -\mu_p^{++-}$

$\Rightarrow$ Score 6

Example: Unambiguous Tree with Prime Node

$\pi^1 = \iota$, $\pi^2 = (1\ 2\ 3\ 4\ \overline{6}\ 9\ 7\ 5\ \overline{8}\ 10)$, $\pi^3 = (1\ 2\ \overline{9}\ \overline{8}\ 7\ \overline{6}\ \overline{5}\ \overline{4}\ \overline{3}\ \overline{10})$

non-trivial strong common intervals $\{3,4,5,6,7,8,9\},\{5,6,7,8,9\}$

$$\Gamma^1 = (1\ 2\ 3\ 4\ 5)$$
$$\Gamma^2 = (\overline{2}\ 5\ 3\ 1\ \overline{4})$$
$$\Gamma^3 = (\overline{5}\ \overline{4}\ 3\ \overline{2}\ \overline{1})$$

$$\mu_p^{++-} = (1\ 2\ \overline{3}\ 4\ 5)$$
score 4

$\pi^3 = (1\ 2\ \overline{9}\ \overline{8}\ 7\ \overline{6}\ \overline{5}\ \overline{4}\ \overline{3}\ \overline{10})$
   $\Rightarrow (1\ 2\ \overline{9}\ \overline{8}\ 7\ \overline{6}\ \overline{5}\ \overline{4}\ \overline{3}\ 10)$
   $\Rightarrow (1\ 2\ \overline{9}\ \overline{8}\ 7\ \overline{6}\ \overline{5}\ \overline{4}\ \overline{3}\ 10)$
   $\Rightarrow (1\ 2\ 3\ 4\ 5\ 6\ \overline{7}\ 8\ 9\ 10)$
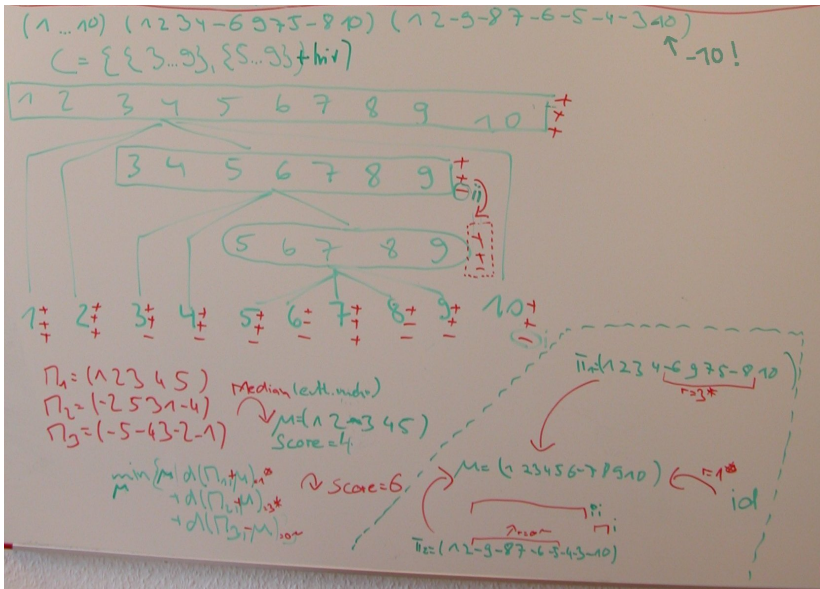$\Rightarrow$ Score 6

$\Gamma^1 \overset{3}{\curvearrowright} \mu_p^{++-}$

$\Gamma^2 \overset{531}{\curvearrowright} (\overline{2}\ \overline{1}\ \overline{3}\ \overline{5}\ \overline{4}) \overset{\overline{21}}{\curvearrowright} (1\ 2\ \overline{3}\ \overline{5}\ \overline{4}) \overset{\overline{54}}{\curvearrowright} \mu_p^{++-}$

$\Gamma^3 = -\mu_p^{++-}$

Example: Unambiguous Tree with Prime Node

Ambigous Trees

- Problem: The signs of some prime nodes is unknown
- Brute Force: Test every possible 3-sign assignment
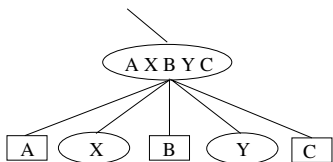
- Sign of the Prime node unknown $\rightarrow 8$ possibilities
- Signs of X and Y unknown $\rightarrow 8^2$ possibilities
- Generaly 8^e oRMP instances (e: number of edges to prime nodes)

- Choose the best out of 8^{v-1} combinations. (v: number of prime nodes)

Ambigous Trees

Observations:

- Components induced by the prime nodes can be solved separately
- Solving the oRMP with 3 inverted permutations leads to the inverted median.
- Ambigous prime childs can renamed
- 4^e oRMP instances per prime node and 4^{v-1} combinations to test

Example: Ambiguous Trees

$\pi^1 = \iota$, $\pi^2 = (2\ 1\ \overline{10}\ \overline{9}\ \overline{6}\ 4\ 5\ \overline{3}\ 8\ 7)$, $\pi^3 = (1\ \overline{10}\ \overline{9}\ \overline{2}\ \overline{5}\ \overline{4}\ \overline{3}\ 8\ 7\ 6)$

Example: Ambiguous Trees

$$\pi^1 = \iota, \ \pi^2 = (2 \ 1 \ \overline{10} \ \overline{9} \ \overline{6} \ 4 \ 5 \ \overline{3} \ 8 \ 7), \ \pi^3 = (1 \ \overline{10} \ \overline{9} \ \overline{2} \ \overline{5} \ \overline{4} \ \overline{3} \ 8 \ 7 \ 6)$$
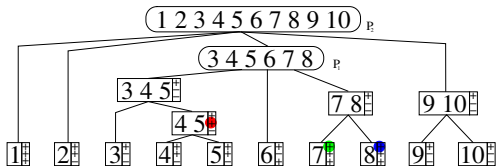

$P_1 : (1 \ 2 \ 3), (-2 \ -1 \ -3), (-1 \ -3 \ -2); \ P_2 : (1 \ 2 \ \pm 3 \ 4), (2 \ 1 \ -4 \ \pm 3), (1 \ -4 \ -2 \ \pm 3)$

3-sign	s	medians (P_1)	s	medians (P_2)	Σ
(+,+,+)	4	$\{(\overline{2} \ \overline{1} \ \overline{3})\}$	5	$\{(1 \ \overline{4} \ \overline{2} \ 3)\}$	9
(+,+,−)	3	$\{(\overline{2} \ \overline{1} \ \overline{3})\}$	6	$\{(1 \ \overline{4} \ \overline{2} \ 3), (1 \ \overline{4} \ \overline{2} \ 3), (1 \ \overline{4} \ 3 \ \overline{2}), (2 \ 1 \ \overline{4} \ \overline{3})\}$	9
(+,−,+)	4	$\{(\overline{1} \ \overline{3} \ 2), (3 \ 1 \ 2)\}$	5	$\{(1 \ \overline{4} \ \overline{3} \ \overline{2})\}$	9
(+,−,−)	4	$\{(\overline{2} \ \overline{1} \ \overline{3})\}$	5	$\{(1 \ \overline{4} \ \overline{2} \ \overline{3}), (2 \ 1 \ \overline{4} \ \overline{3})\}$	9

Example: Ambiguous Trees

$$\pi^1 = \iota,\ \pi^2 = (2\ 1\ \overline{10}\ \overline{9}\ \overline{6}\ 4\ 5\ \overline{3}\ 8\ 7),\ \pi^3 = (1\ \overline{10}\ \overline{9}\ \overline{2}\ \overline{5}\ \overline{4}\ \overline{3}\ 8\ 7\ 6)$$

$P_1 : (1\ 2\ 3), (-2\ -1\ -3), (-1\ -3\ -2);\ P_2 : (1\ 2\ \pm3\ 4), (2\ 1\ -4\ \pm3), (1\ -4\ -2\ \pm3)$

3-sign	s	medians (P_1)	s	medians (P_2)	Σ
$(+,+,+)$	4	$\{(\overline{2}\ \overline{1}\ \overline{3})\}$	5	$\{(1\ \overline{4}\ \overline{2}\ 3)\}$	9
$(+,+,-)$	3	$\{(\overline{2}\ \overline{1}\ \overline{3})\}$	6	$\{(1\ \overline{4}\ \overline{2}\ 3),(1\ \overline{4}\ \overline{2}\ 3),(1\ \overline{4}\ 3\ \overline{2}),(2\ 1\ \overline{4}\ \overline{3})\}$	9
$(+,-,+)$	4	$\{(\overline{1}\ \overline{3}\ 2),(3\ 1\ 2)\}$	5	$\{(1\ \overline{4}\ \overline{3}\ \overline{2})\}$	9
$(+,-,-)$	4	$\{(\overline{2}\ \overline{1}\ \overline{3})\}$	5	$\{(1\ \overline{4}\ \overline{2}\ \overline{3}),(2\ 1\ \overline{4}\ \overline{3})\}$	9

$\Rightarrow$ Score $= 12$

Example: Ambiguous Trees

Circular Permutations

Data sets

Simulated Data Sets:

- Generated 3 permutations by applying d reversals on the identity permutation

Mitochondrial Data Sets:

- All triples from all complete mitochondrial genomes, grouped into:

- Deuterostomia: The Chordata (Cho) (Actinopterygii (Act), and Sarcopterygii (Sar)), and Hyperotreti, Cephalochordata, Echinodermata, and Hemichordata (HCEH)

- Protostomia: Arthropoda (Art) (Crustacea (Cru), Hexapoda (Hex)), and Annelida, Pogonophora, Brachiopoda, and Mollusca (APBM).

Properties of the Strong Interval Trees: Simulated Data Sets

$n = 100$

d	p	q	c	r	t	l
1	0.67	1.00 (1)	1.00 (1)	1.00 (1)	1.00 (1)	3.76 (5)
2	0.98	1.10 (3)	1.09 (3)	1.18 (8)	1.13 (4)	7.53 (11)
5	1.00	1.05 (3)	1.04 (3)	1.14 (24)	1.09 (16)	22.63 (29)
10	1.00	1.01 (2)	1.01 (2)	1.03 (8)	1.02 (4)	42.96 (51)
25	1.00	1.00 (2)	1.00 (2)	1.03 (8)	1.01 (4)	76.44 (88)

d: number of reversals applied for generating data set
p: percentage of triple instances for which the tree has at least one prime node
q: number of prime nodes
c: number of prime node subtrees
r: number of oRMPs to be solved
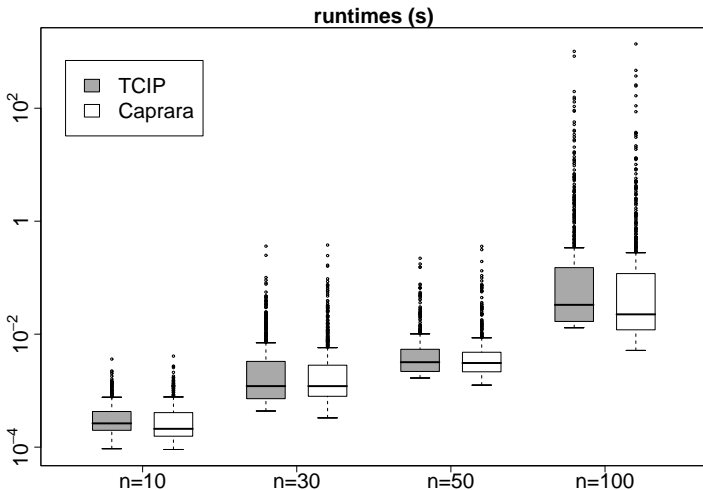t: number of 3-sign combinations to be tested
l: maximal number of children of the prime nodes

Properties of the Strong Interval Trees: mtDNA Data Sets

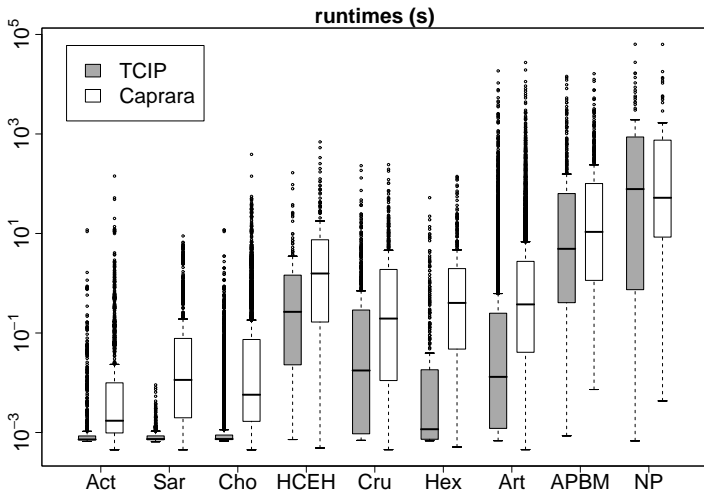|	#	p	q	c	r	t	l
Act	27	0.26	1.00 (1)	1.00 (1)	1.00 (1)	1.00 (1)	11.93 (22)
Sar	28	0.41	1.06 (2)	1.06 (2)	1.06 (8)	1.06 (4)	4.43 (10)
Cho	47	0.40	1.03 (2)	1.03 (2)	1.03 (8)	1.03 (4)	7.44 (23)
HCEH	11	0.99	1.10 (2)	1.07 (2)	1.33 (8)	1.18 (4)	23.87 (30)
Cru	18	0.91	1.09 (2)	1.02 (2)	1.51 (8)	1.23 (4)	20.26 (35)
Hex	15	0.71	1.08 (3)	1.07 (3)	1.10 (8)	1.08 (4)	15.88 (32)
Art	42	0.92	1.12 (4)	1.09 (3)	1.28 (24)	1.17 (16)	19.14 (35)
APBM	16	1.00	1.01 (2)	1.01 (2)	1.02 (8)	1.01 (4)	32.35 (36)
NP	9	0.99	1.05 (3)	1.05 (3)	1.05 (3)	1.05 (3)	32.65 (35)
All	115	0.95	1.04 (4)	1.03 (3)	1.07 (24)	1.05 (16)	26.73 (36)

Properties of strong common interval trees for the mtDNA data set;

Runtimes: simulated Data Sets

$(n,d) \in \{(10,1),\ldots,(10,5),(30,1),\ldots,(30,10),(50,2),(50,4),\ldots,(50,12),(100,5),(100,10),\ldots,(100,30)\}$

Introduction
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Perfect Sorting by Reversals
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Perfect RMP
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Results
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Runtimes: mtDNA Data Sets

runtimes (s)

Conclusion

- The pRMP is not always difficult
- TCIP: A fast and exact algorithm for the pRMP
- Trick: usage of PQ-trees

Future Work:

- Use the median solver for reconstructing phylogenies?
- Incorporate other operations like transpositions and TDLs

Introduction
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Perfect Sorting by Reversals
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Perfect RMP
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Results
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Thank you!

Introduction
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Perfect Sorting by Reversals
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Perfect RMP
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Results
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 Berufenem Power
Werbe neuem Prof
Wem bereuen Prof
Perfume Beer One
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