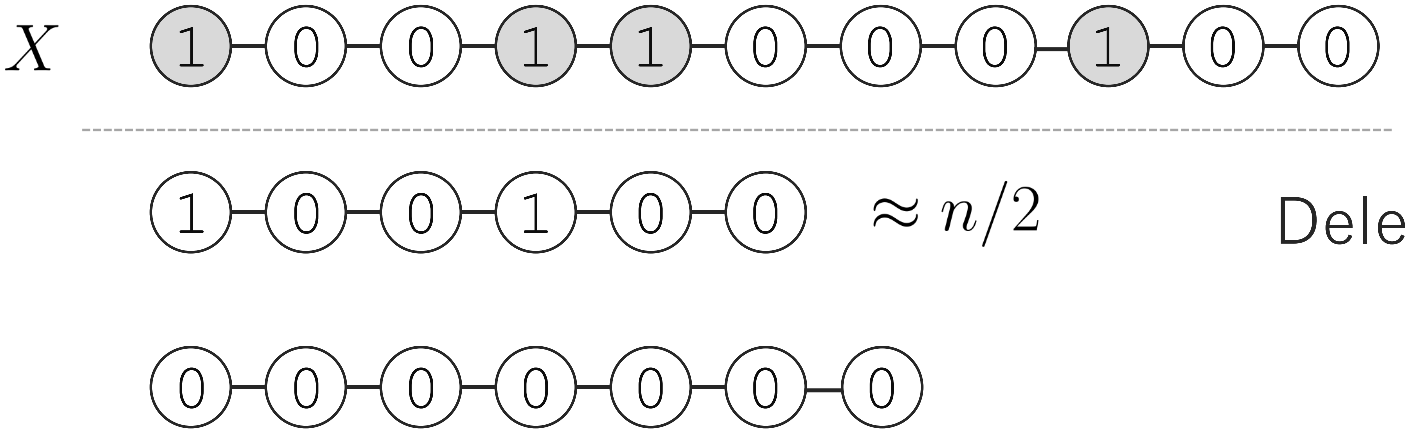
Trace Reconstruction

unknown worst-case string n bits



Deletion channel, probability *q=0.5*

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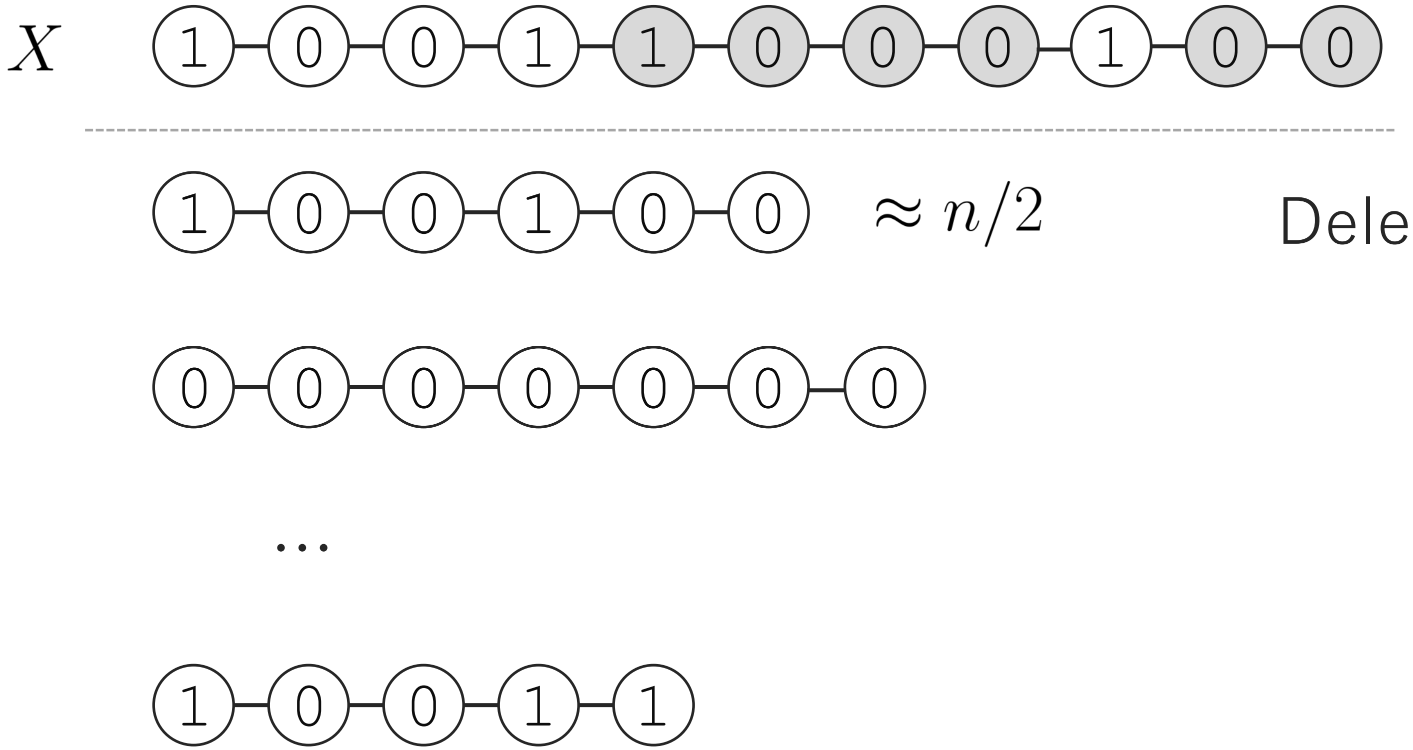

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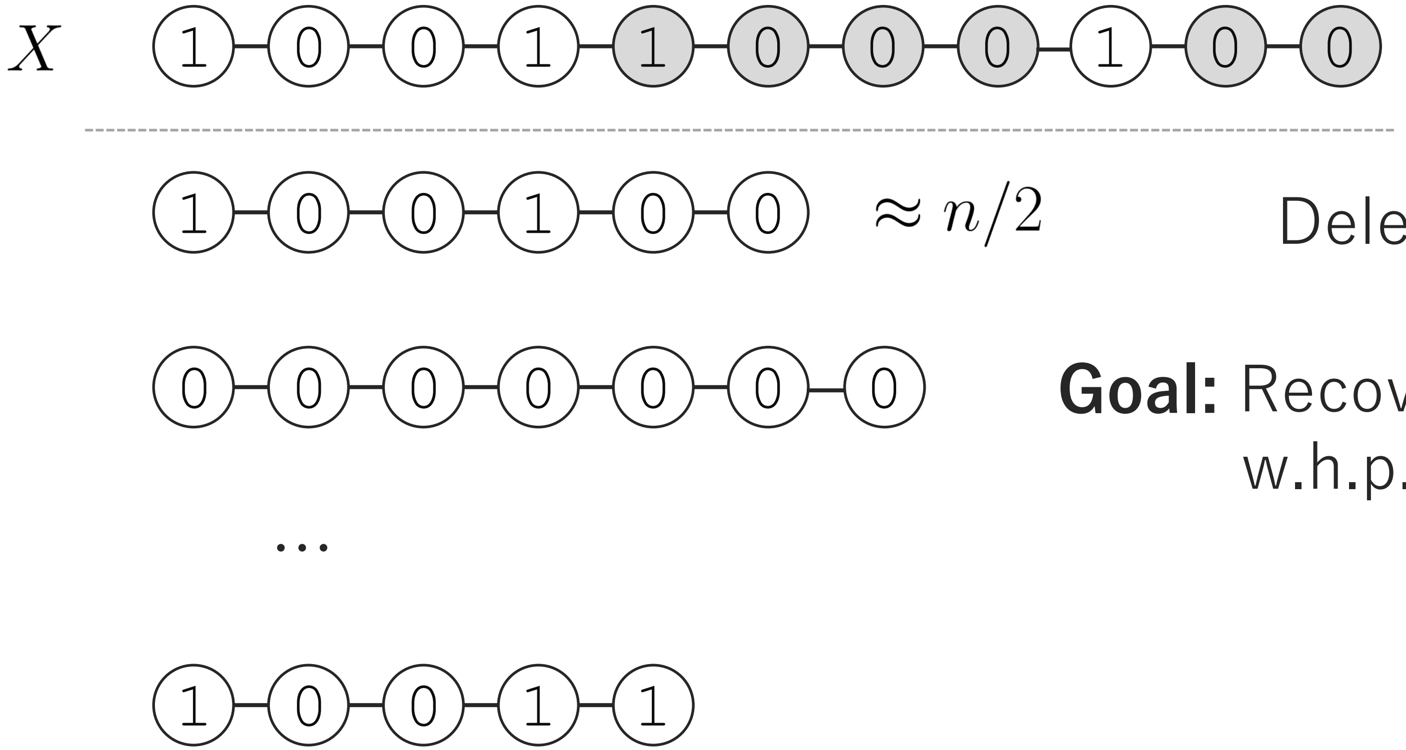

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Goal: Recover ***X*** exactly
w.h.p. using min # traces

Trace Reconstruction

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X 1 0 0 1 1 0 0 0 1 0 0

1 0 0 1 0 0

0 0 0 0 0 0 0

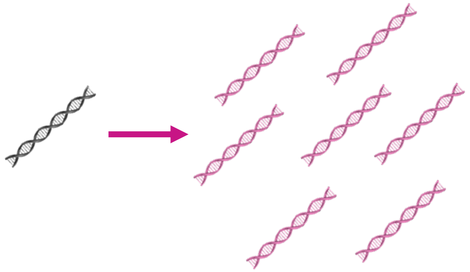
...

1 0 0 1 1

Motivation: Computational Biology

DNA Sequencing

illumina



DNA Data Storage

Past/ current work

Worst case:

- Batu, Kannan, Khanna, McGregor (2004):
  - Bitwise Majority Alignment (BMA) algorithm
  - $\Omega(n)$ traces needed when deletion probability is: $q \leq 1/n^{1/2+\varepsilon}$

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$$\mathbb{E}\left[\sum_{j\geq 0} \widetilde{a}_j w^j\right] = p \sum_{k=0}^{n-1} a_k \left(pw + q\right)^k$$

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- Holden, Lyons (2018); Chase (2019):
  - Improved lower bounds: $\widetilde{\Omega}(n^{3/2})$ traces needed

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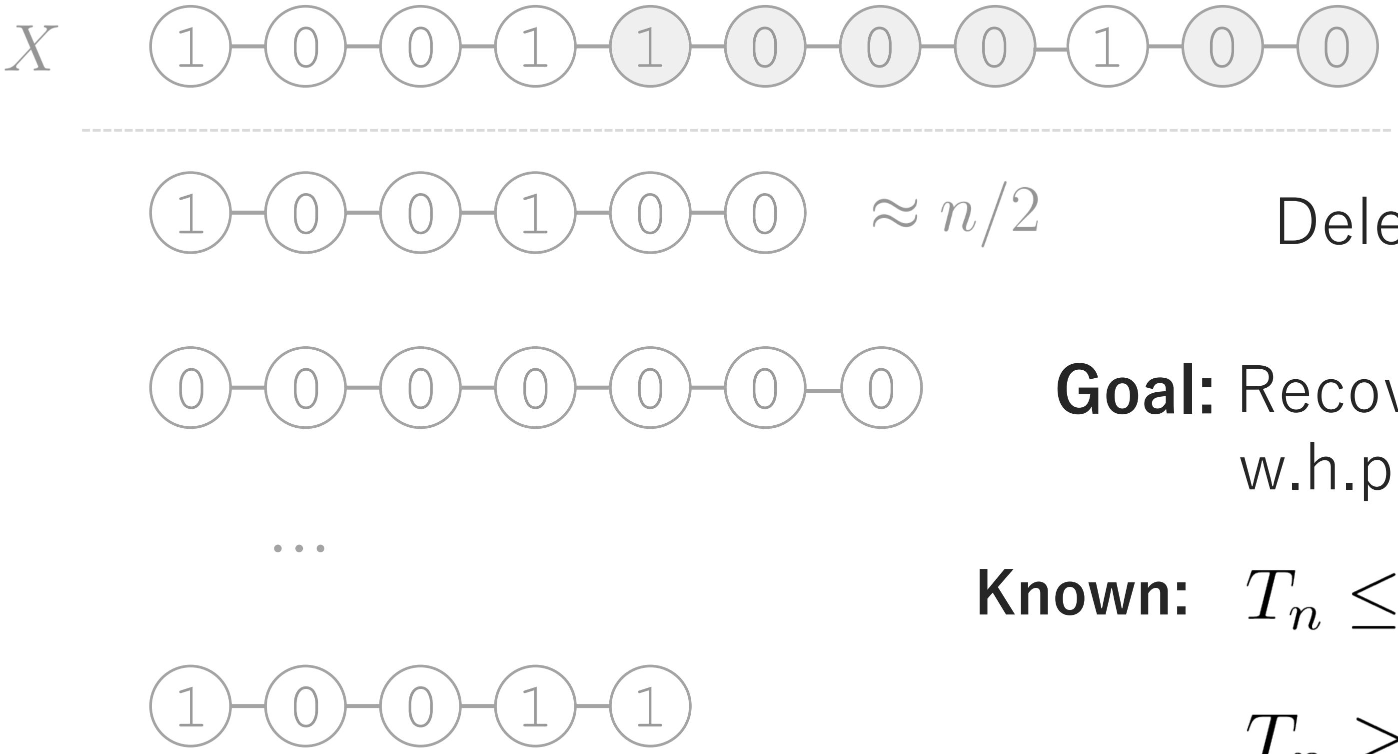

Deletion channel, probability q=0.5

Goal: Recover X **exactly**
w.h.p. using min # traces T_n

Known: $T_n \leq \exp(n^{1/3})$ [Nazarov, Peres '16; De, O'Donnell, Servedio '16]

$T_n \geq \widetilde{\Omega}(n^{3/2})$ [Holden, Lyons '18; Chase '19]

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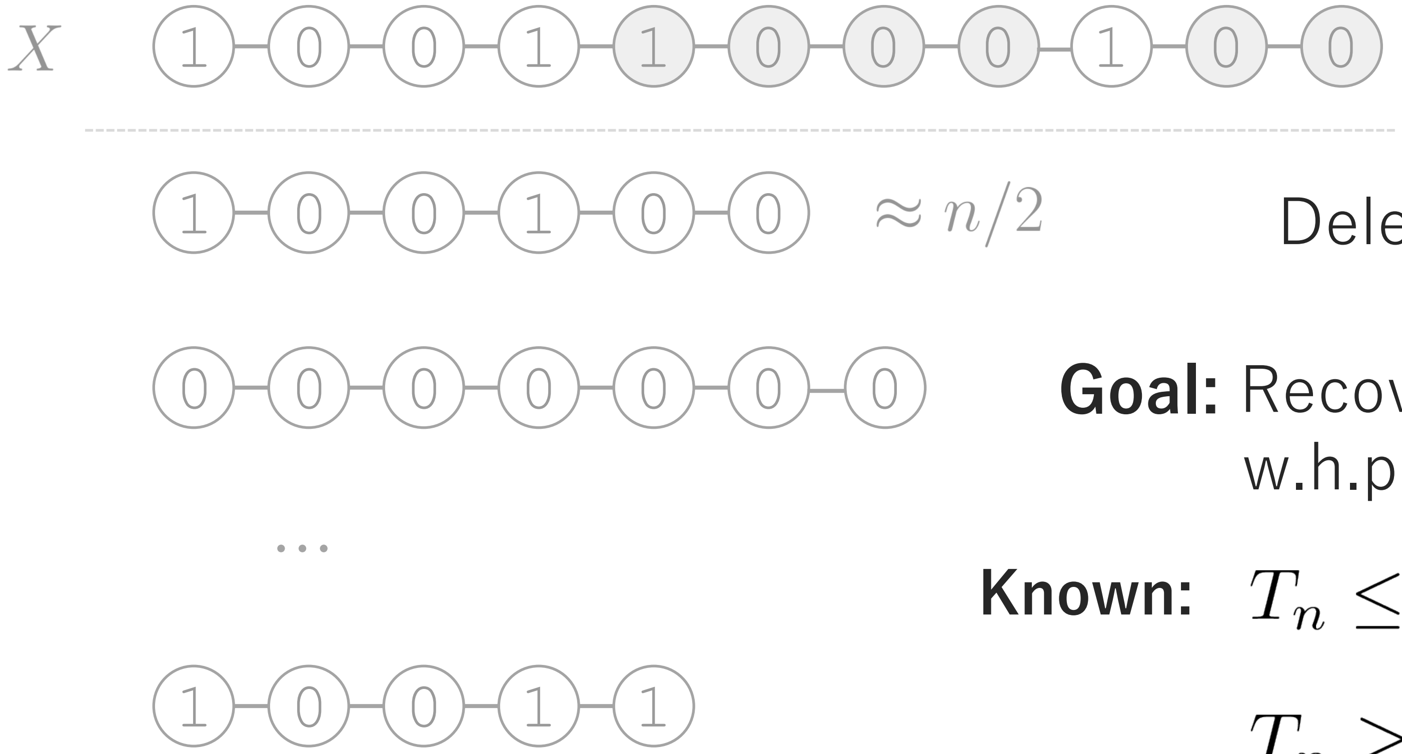

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Take away: huge gap between upper and lower bound! New ideas needed to improve upper bound

Trace Reconstruction Variants

- **coded TR:** encoded initial string X [Cheraghchi, Gabrys, Milenkovic, Ribeiro '19; Brakensiek, Li, Spang '19]
- **average-case:** X random → $\exp((\log n)^{1/3})$ [Peres-Zhai '17; Holden, Pemantle, Peres '18]
- **population recovery:** multiple unknown strings [Ban, Chen, Freilich, Servedio, Sinha '19]
- **matrix version:** delete random rows/cols [Krishnamurthy, Mazumdar, McGregor, Pal '19]
- **fixed # deletions:** e.g., 1, 2, 3, ... [Levenshtein '01; Gabrys, Yaakobi '18]
- **Tree TR:** reconstruct labelled trees **[Davies, Racz, Rashtchian '19]**

Deterministic Variants

- **k-deck:** reconstruct from all k-substrings $k \leq O(\sqrt{n})$ [Krasikov, Roditty '97]
- **Graph Reconstruction Conj:** all (n-1)-vertex subgraphs? [Kelly '57; Ulam '60]

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We'll come back to these later!

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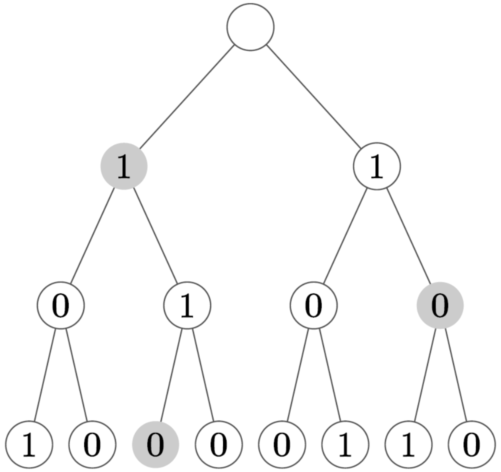
Generalization to Trees

(a) Original Tree



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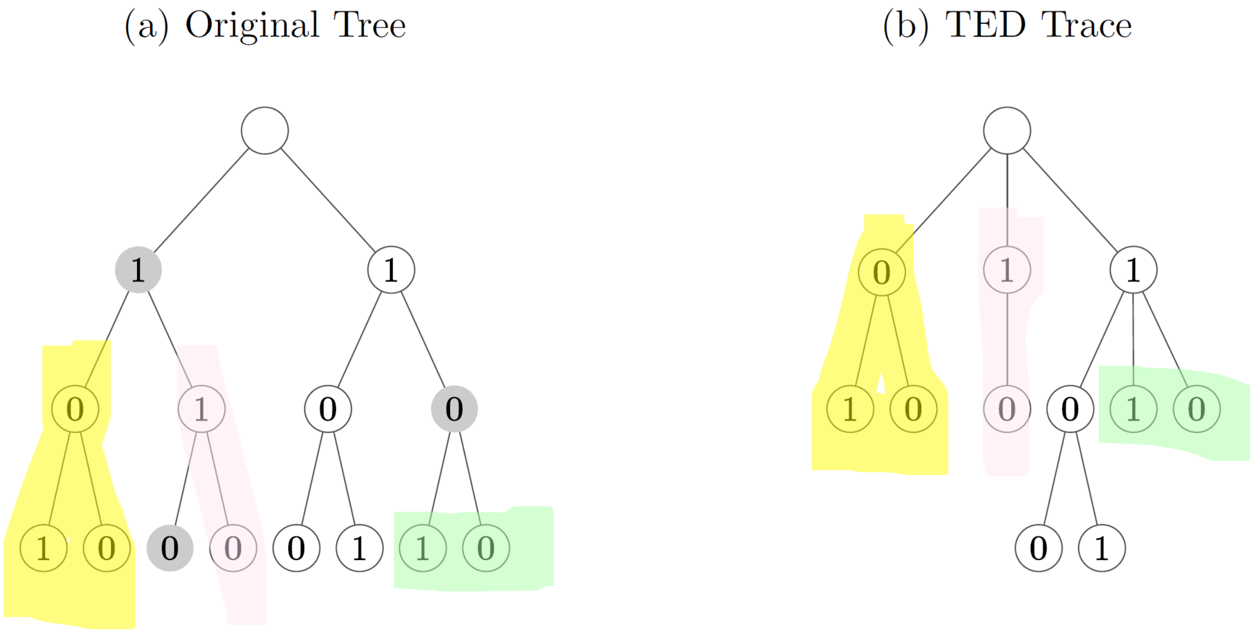
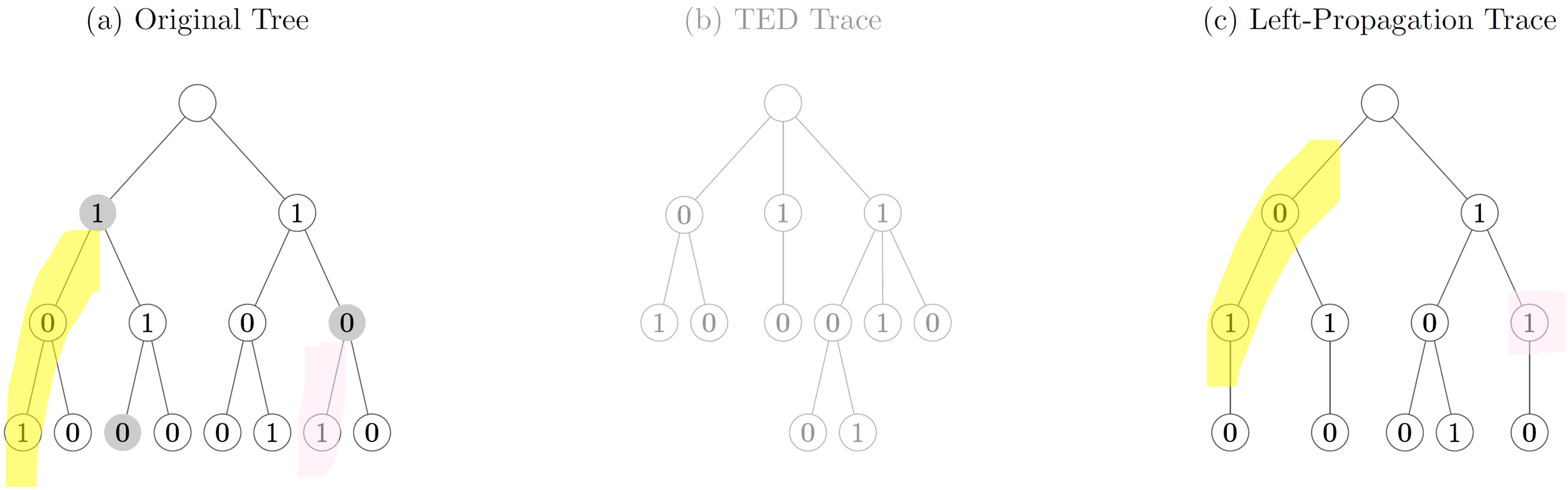


tree edit distance

children move up

degree may increase

Generalization to Trees



tree edit distance

children move up

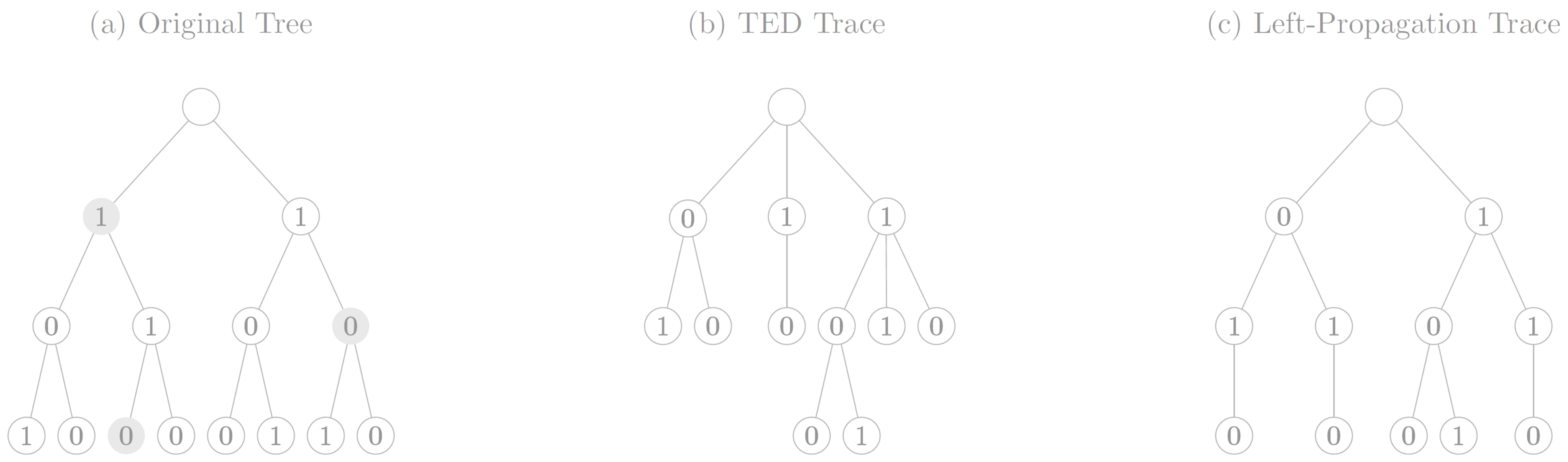
degree may increase

left propagation model

left child moves up

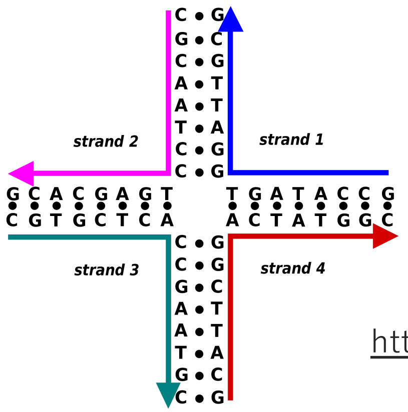
degree never increases

Why trees?



(Kind of, maybe) Practical interest

Tree-structured DNA



https://en.wikipedia.org/wiki/Holliday_junction

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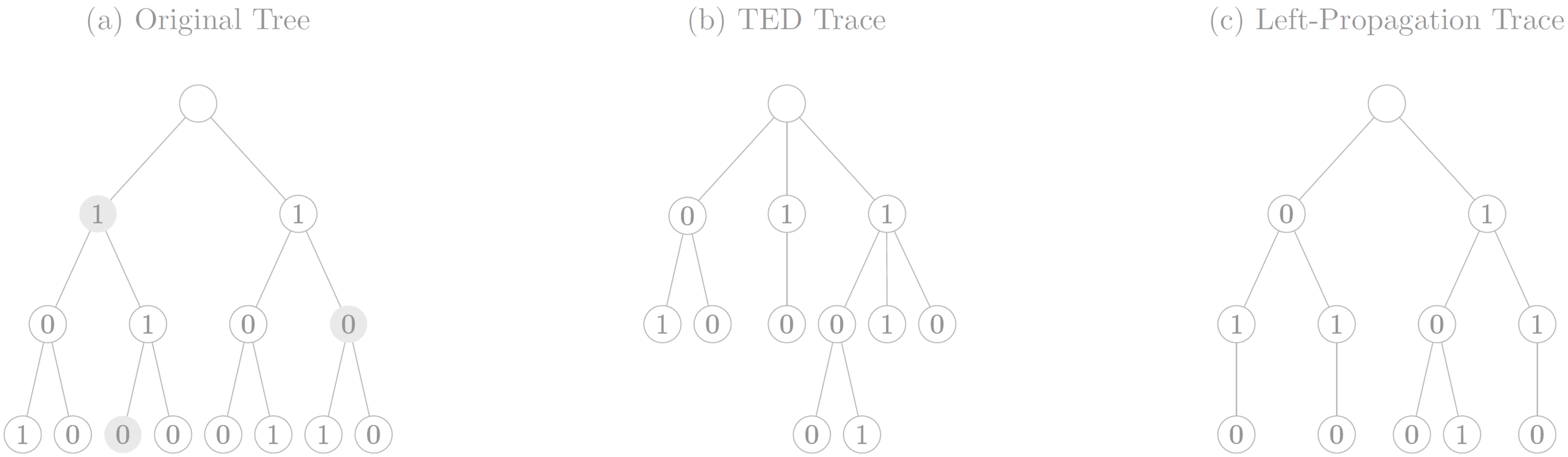
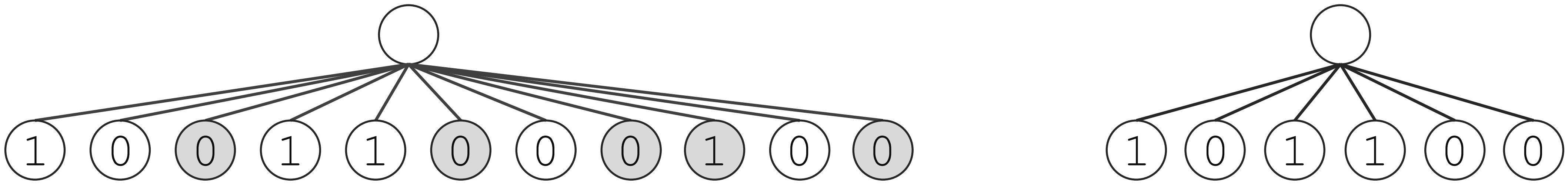


Theoretical interest

How does the addition of combinatorial structure allow us to move away from purely analytic methods (aka mean-based algorithms) in finding upper bounds for TR?

Generalization to Trees



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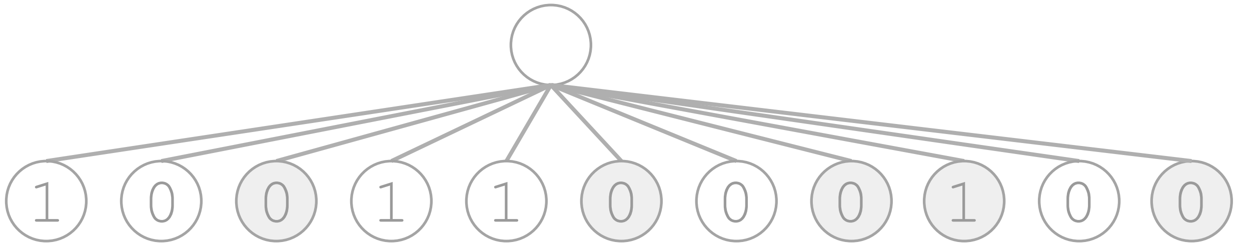

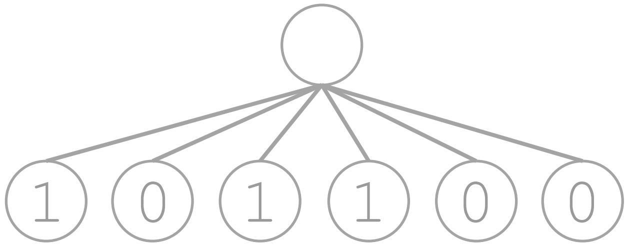

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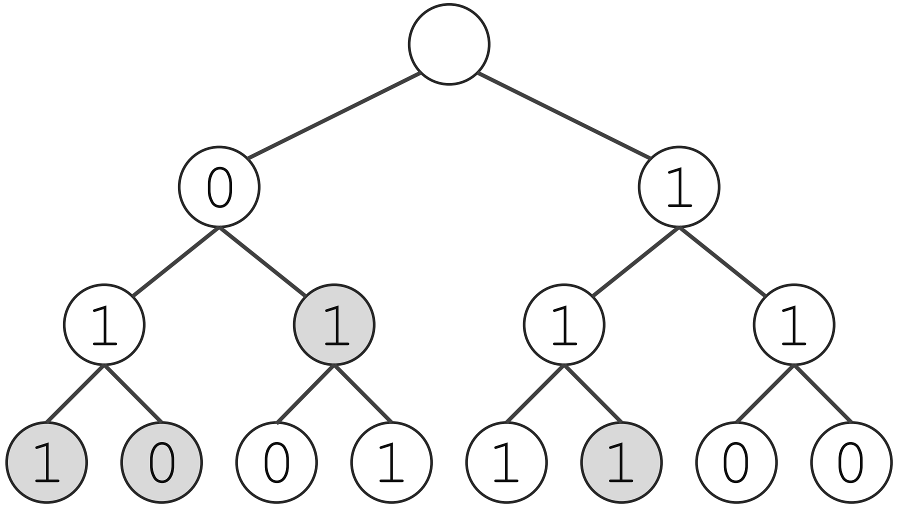
Tree Edit Distance (TED) Model

X



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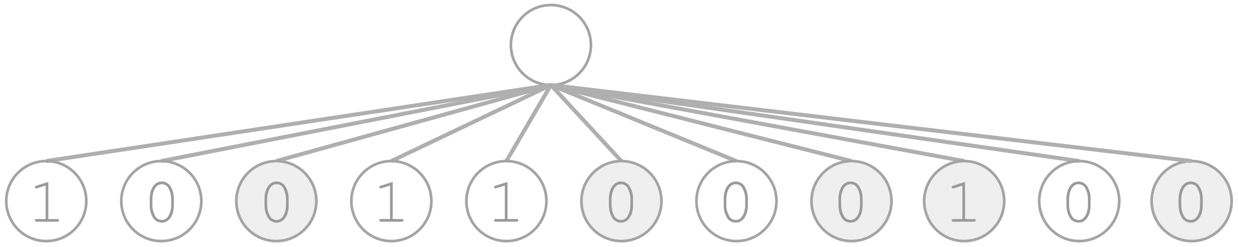
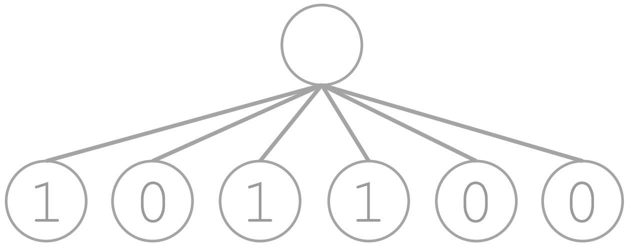
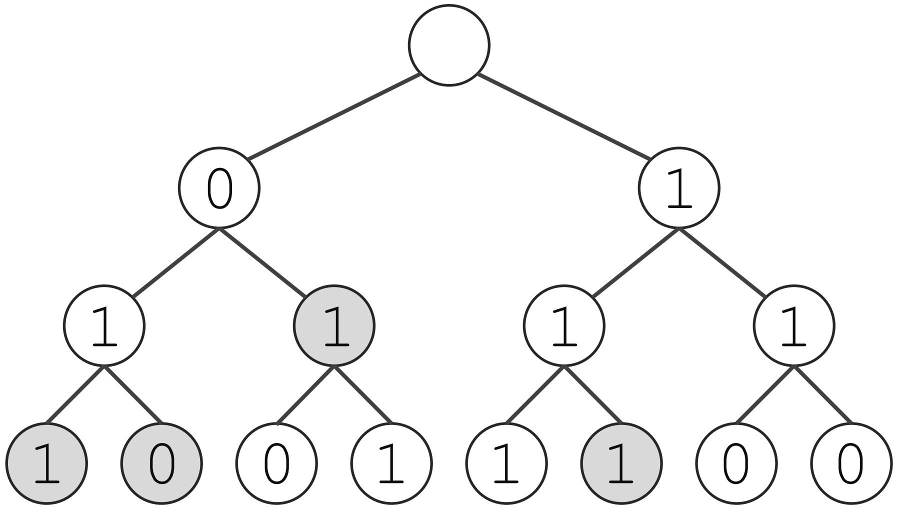


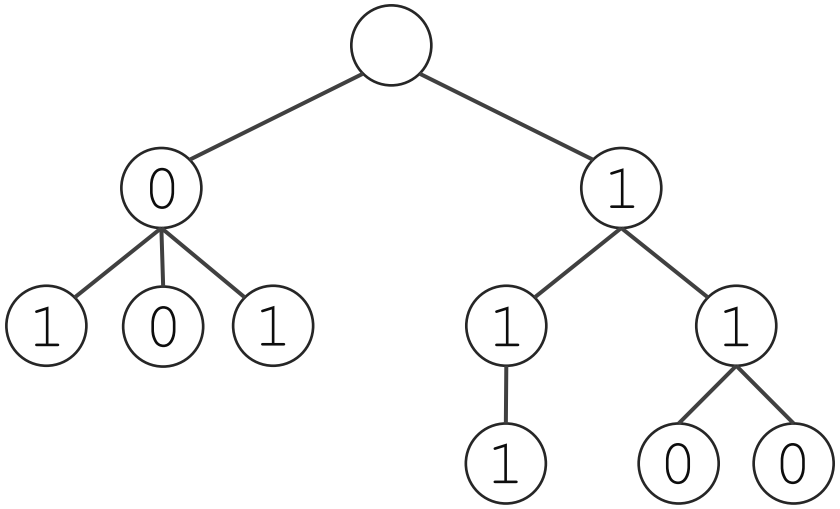


Tree Edit Distance (TED) Model

Vertex Deletion → Children Move Up
(fixed root)

X





Generalization to Trees

Fixed root w.l.o.g. → sample more traces

Consistent planar embedding (left-right)

Random tree “close” in Tree Edit Distance

Equivalent: contract edge, keep parent’s label

Tree Edit Distance (TED) Model

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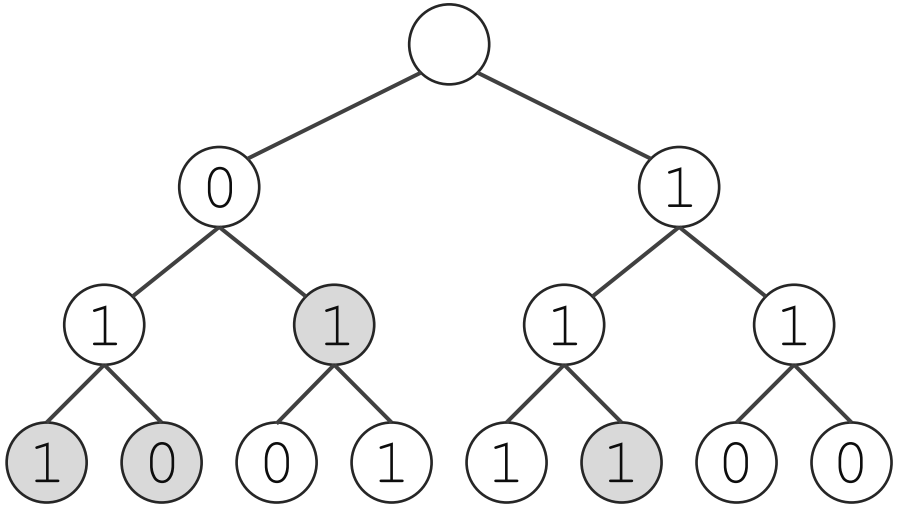

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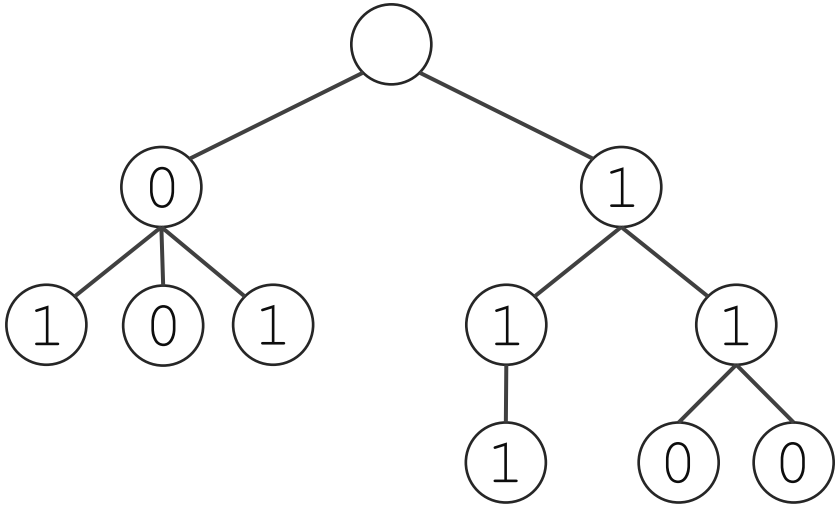

Our Results

unknown worst-case tree X with n vertices
deletion probability $q \in (0,1)$

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- $k = O(1)$
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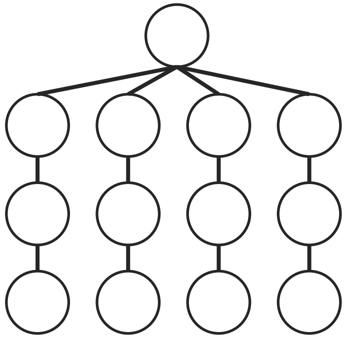

(n,d)-spider
n/d paths
depth d

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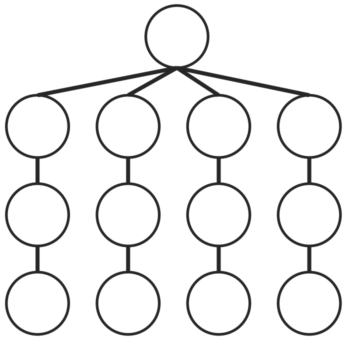

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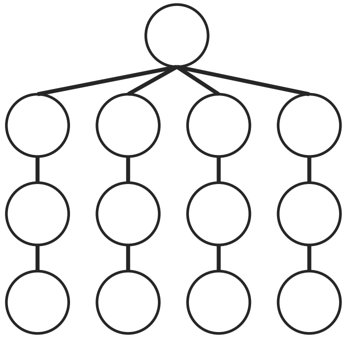
traces for **spiders**

$d = \alpha \log_{1/q}(n) \quad \alpha \in (0,1)$

- Previously $\exp\left(\widetilde{O}\left(n^{1-\alpha}\right)\right)$
- Our Result $\exp\left(\widetilde{O}\left(n^{\frac{1-\alpha}{3}}\right)\right)$



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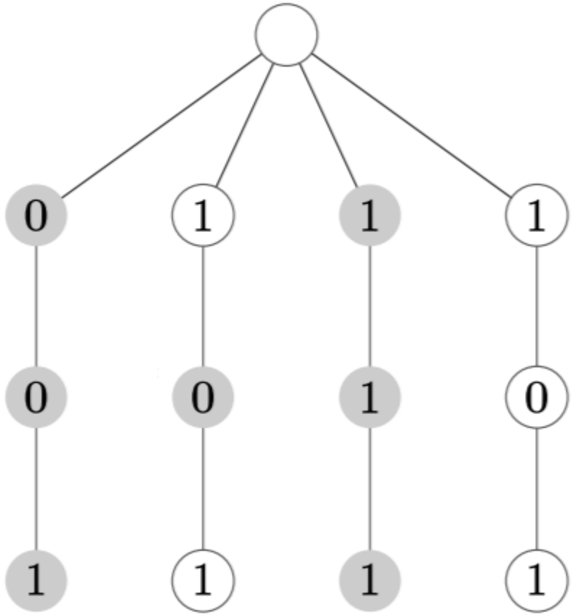
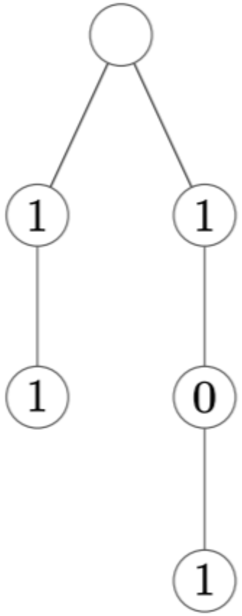
Spider Trees

original tree

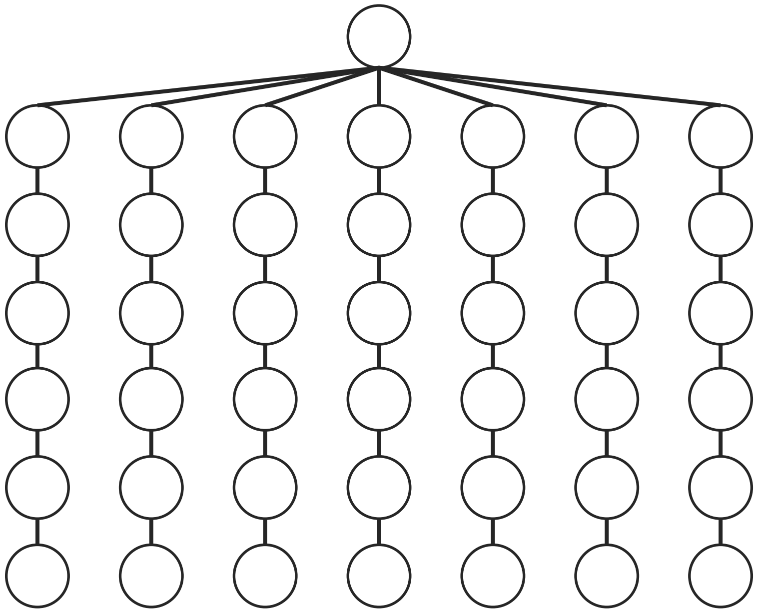


trace



Spider Trees

(n, d)-spider



depth d

n/d paths

Spider Trees

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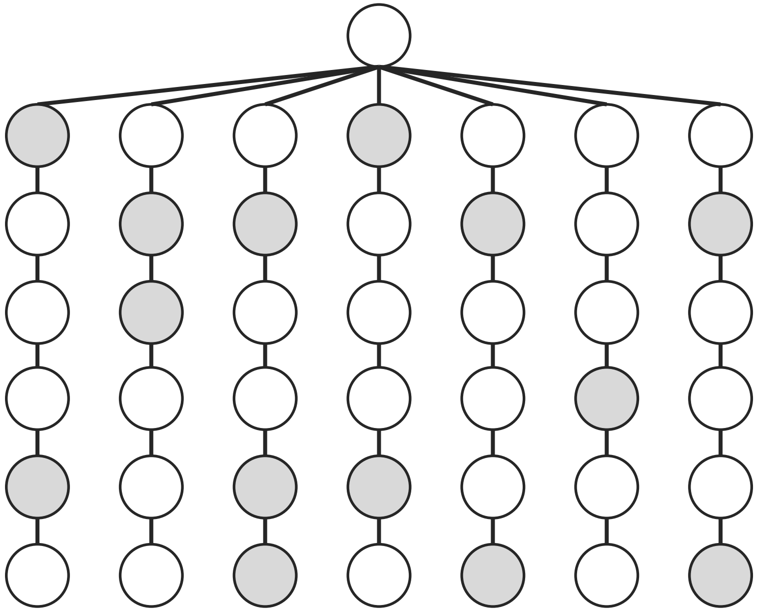

n/d paths

Easy regime: depth $d \geq \log(n)$

only keep traces with n/d paths

for each, use string TR

$$T_d \leq \exp(d^{1/3})$$

Spider Trees

(n, d)-spider

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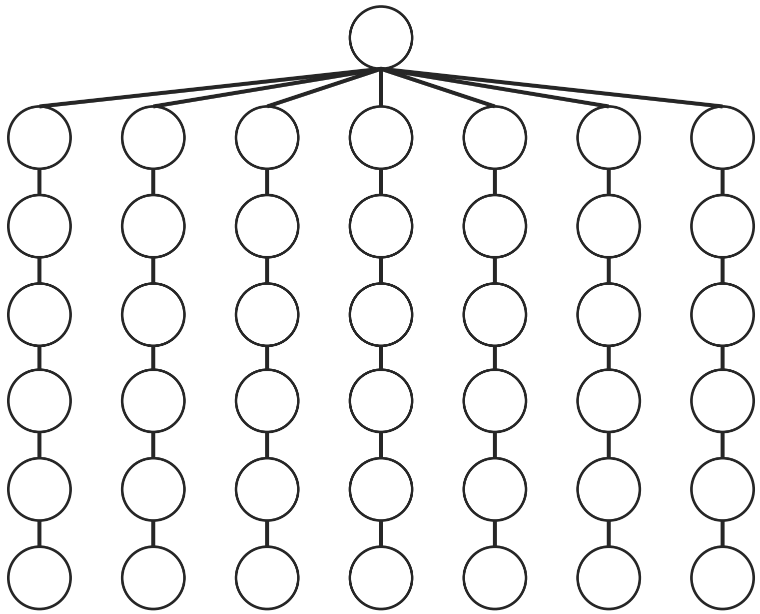

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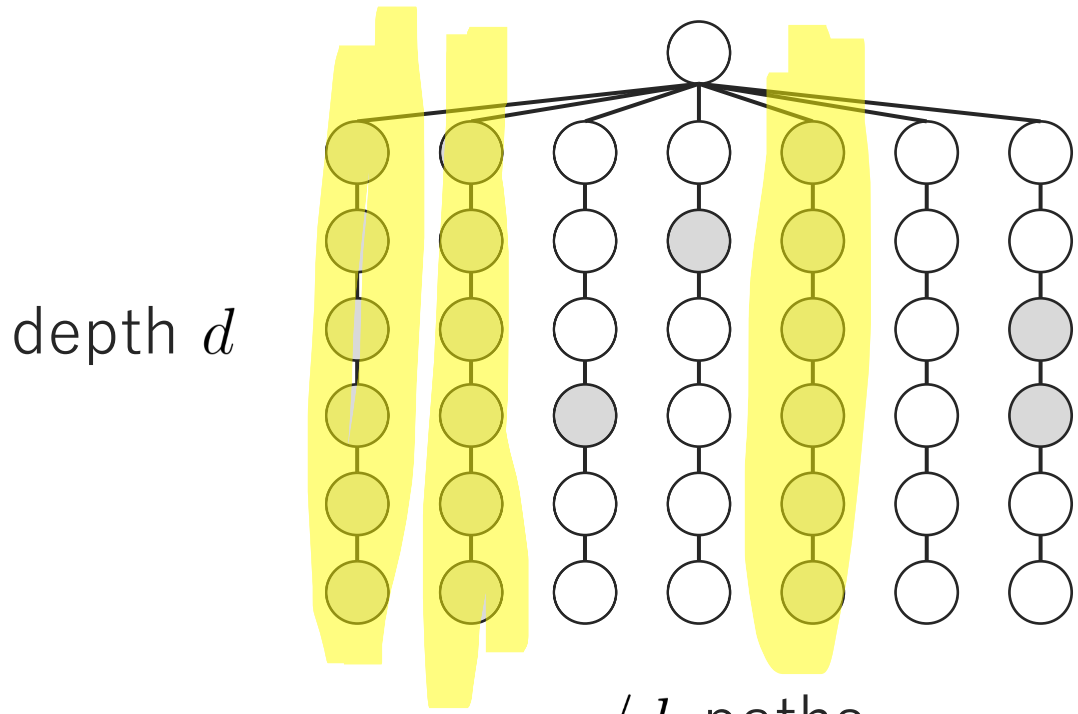

n/d paths

Deletion prob $0 < q \leq 0.7$

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only keep traces with n/d paths

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Hard regime: depth $d < \log(n)$

Full paths deleted

Theorem 3 $\exp\left(\tilde{O}\left(n^{1/3} q^{d/3}\right)\right)$ traces to reconstruct (n, d)-spiders $d \leq \log_{1/q}(n)$

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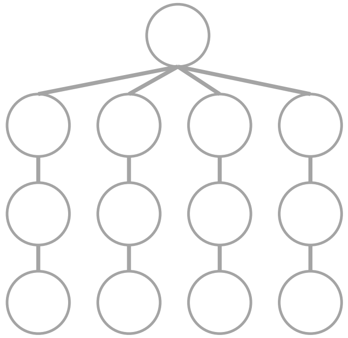

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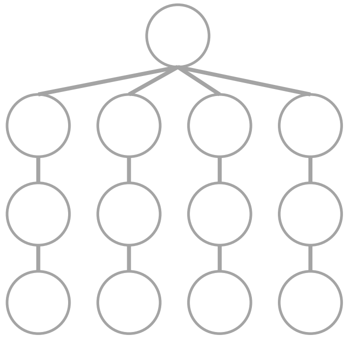

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Mean-based Algorithm [Nazarov-Peres '16; De, O'Donnell, Servedio '16]

X^1 vs. X^2 $\quad$ $\exists\, j$ such that average of j^{th} bit of trace differs by $\exp(-L)$

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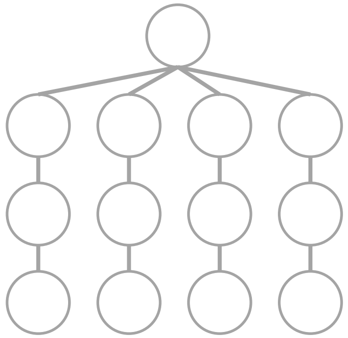

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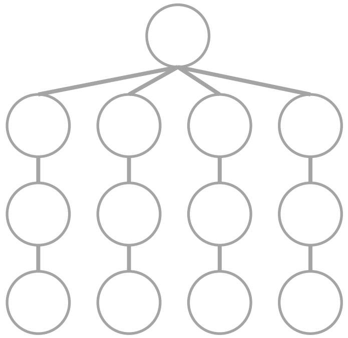

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union bound over all pairs of spiders

for every pair of spiders, $\exists$ a coordinate where in expectation traces look different

mean of this coordinate over traces tells us which of pair is more likely to be X

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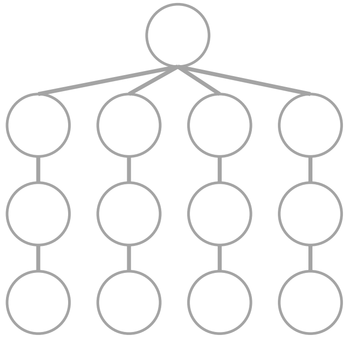

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Strings: easy to determine how original bits affect trace 😀

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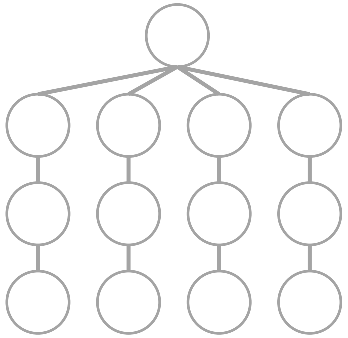

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Spiders: more complicated "two-dimensional" 🤔

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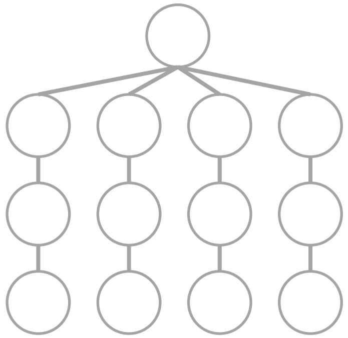

(n,d)-spider
n/d paths
depth d

Mean-based Algorithm [Nazarov-Peres '16; De, O'Donnell, Servedio '16]

X^1 vs. X^2 $\exists\, j$ such that average of j^{th} bit of trace differs by $\exp(-L)$ $\implies$ $\exp\left(O(L)\right)$ traces suffice

Strings: easy to determine how original bits affect trace 😀

Spiders: more complicated "two-dimensional" 🤔

General trees: no idea... 😔

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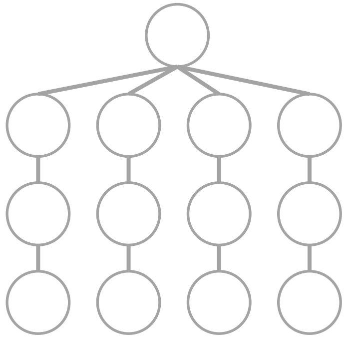

Generating function

$w \in \mathbb{C}$

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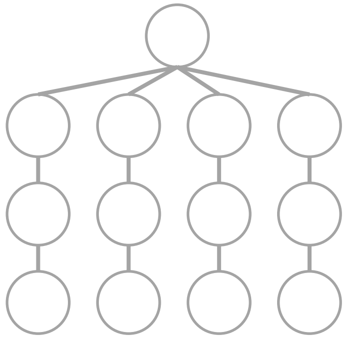

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n/d paths

depth d

DFS indexing

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original labels $a = a_0, a_1, \dots, a_{n-1}$

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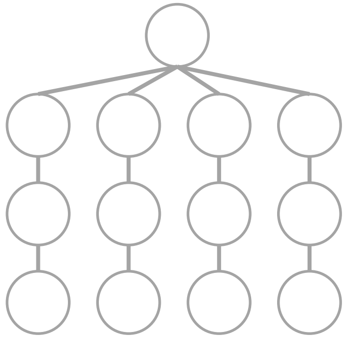

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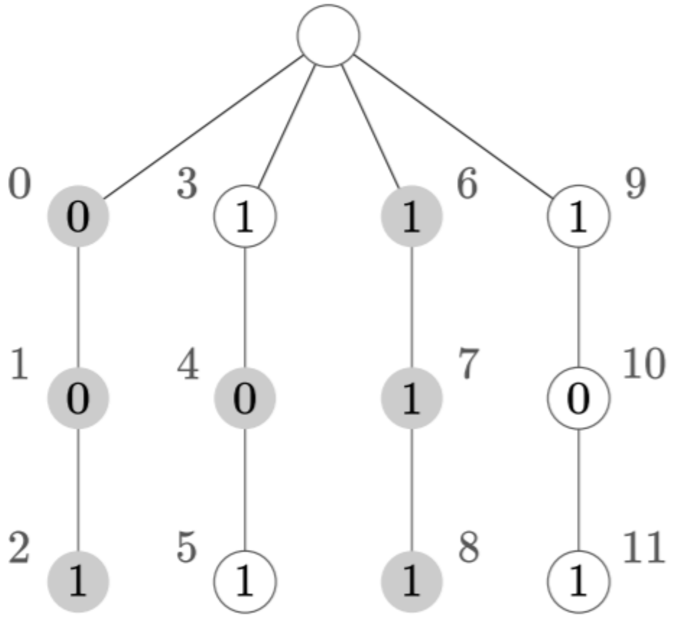

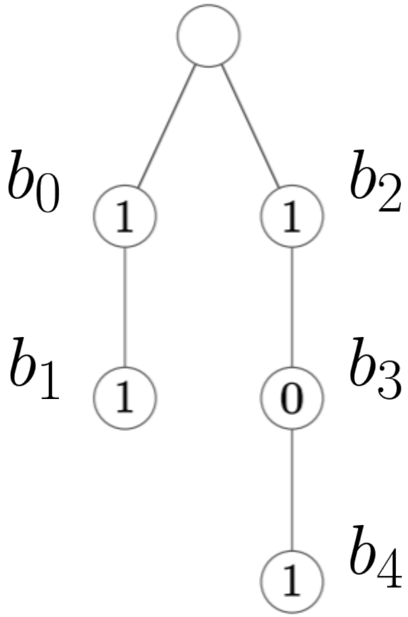

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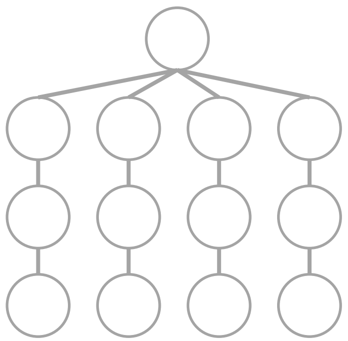

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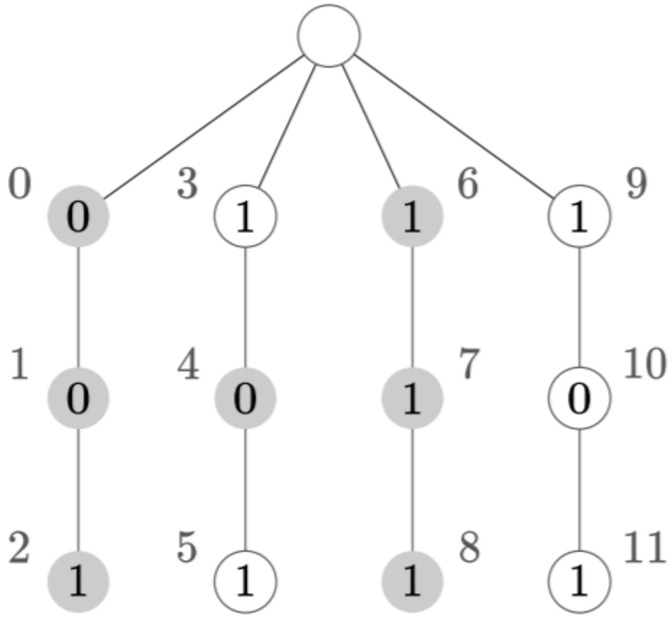

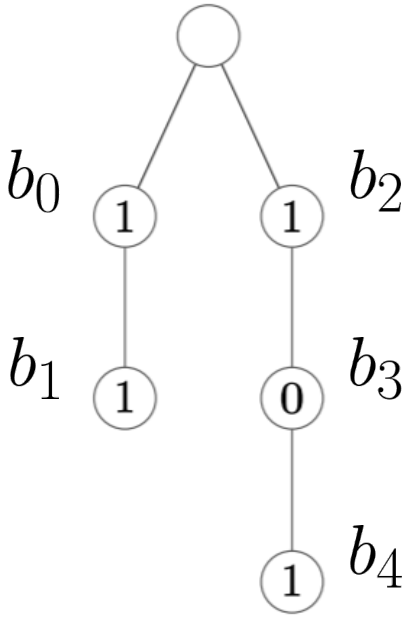

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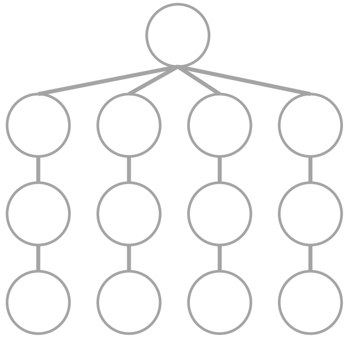

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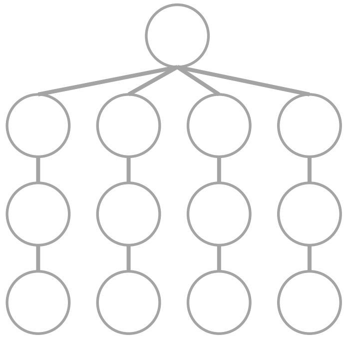

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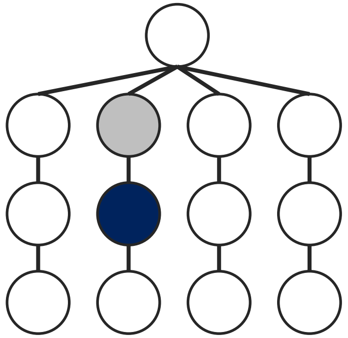

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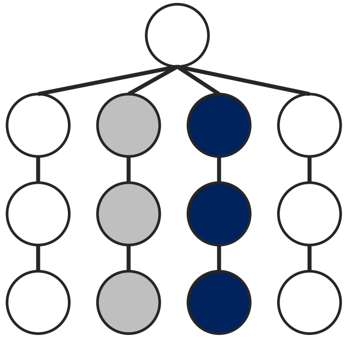

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n/d paths

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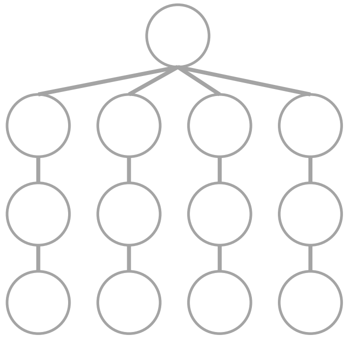

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X^1 vs. X^2

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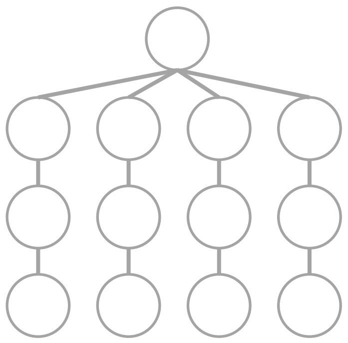

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$$|A(w^*)| \ge \exp(-L)$$

$$L = \widetilde{O}\left(n^{1/3}q^{d/3}\right)$$

$|w^*| = 1$

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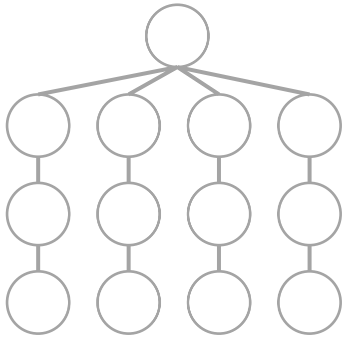

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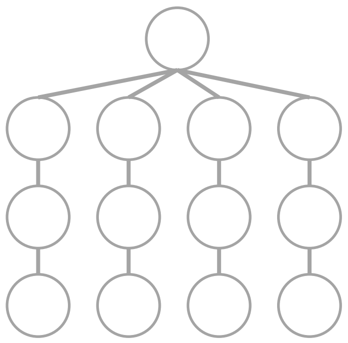

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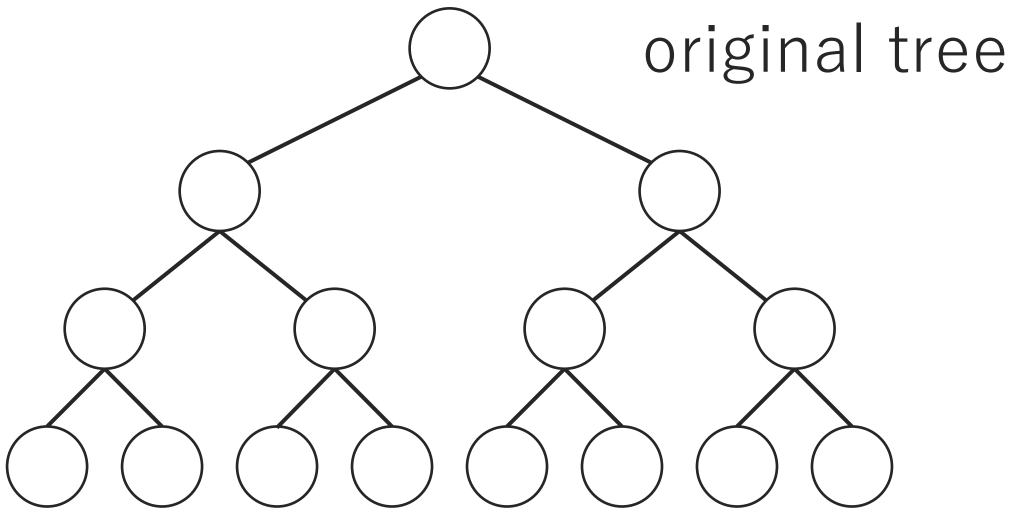
Littlewood-like polynomials

Inspired by

[Borwein and Erdélyi '97]

[Hartung, Holden, Peres '18]

Theorem 1 $\exp\left(k \log_k n\right)$ traces to reconstruct complete k-ary trees



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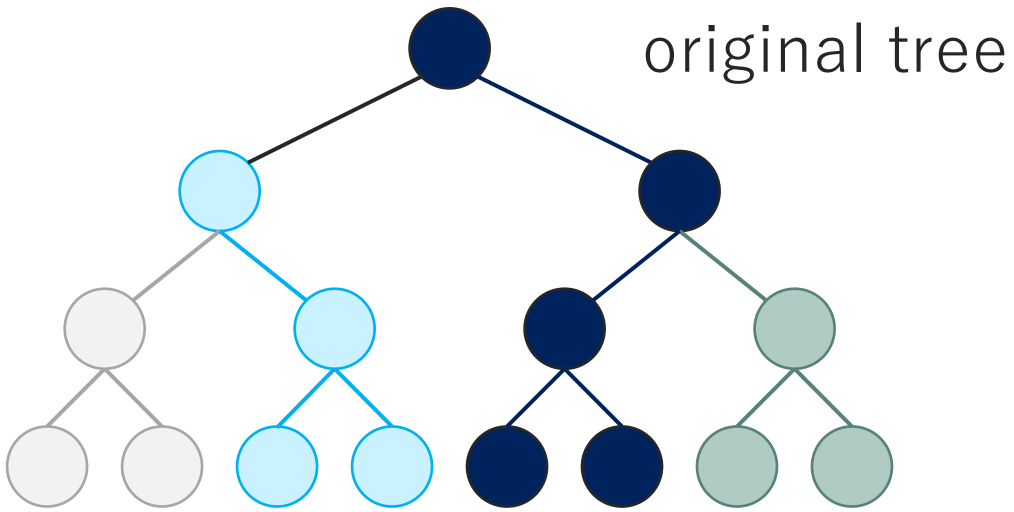
Proof: partition X into subtrees



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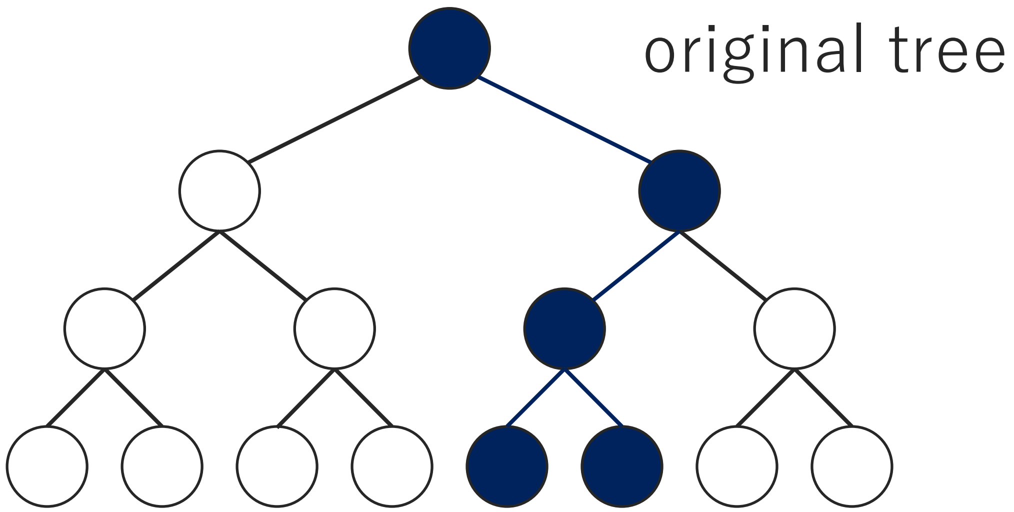

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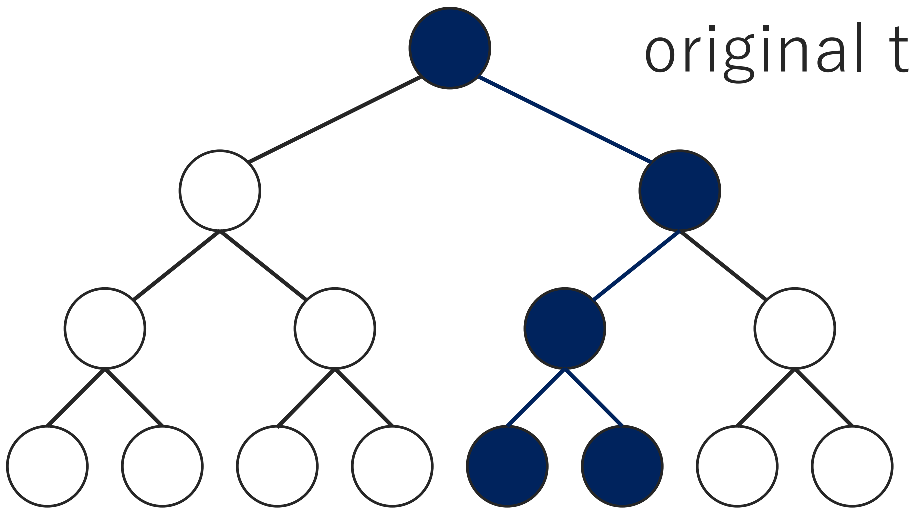
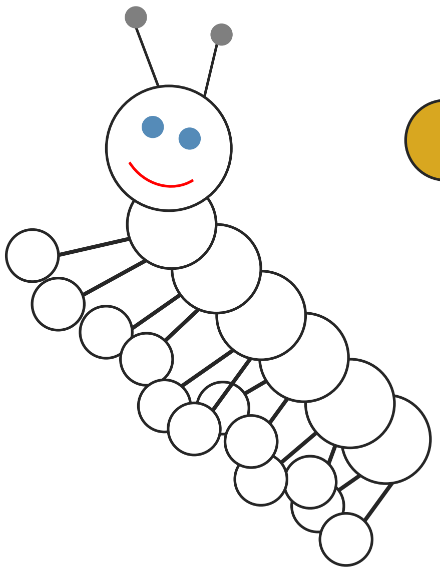
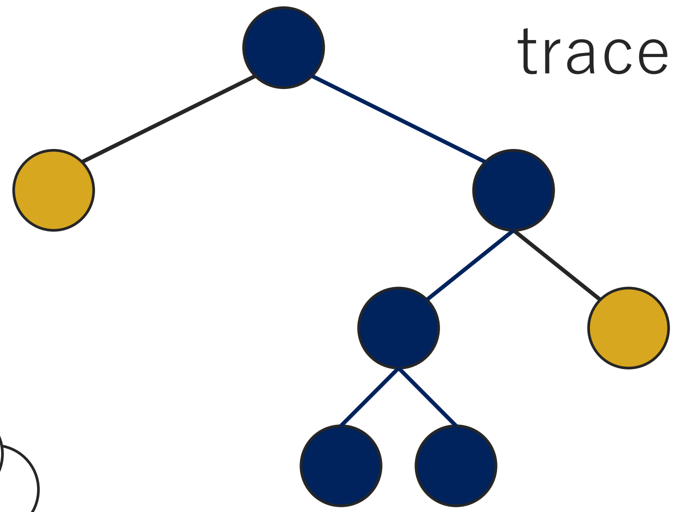
Lemma
if trace contains caterpillar, then subtree labels are usually correct



original tree





trace

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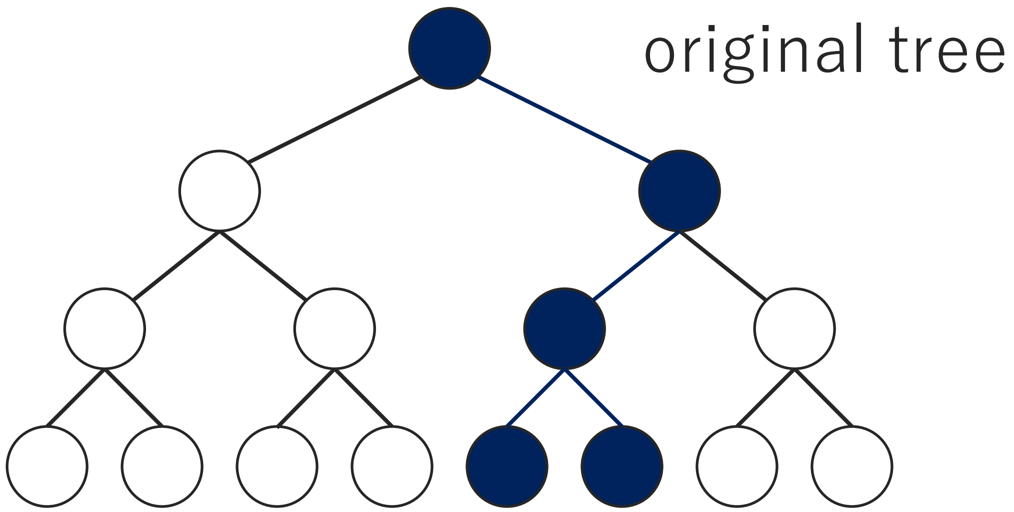

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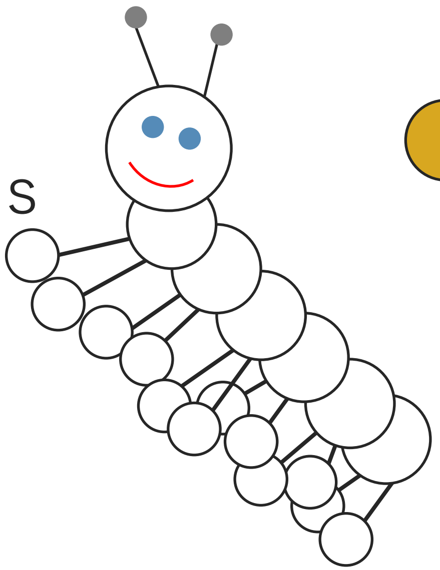
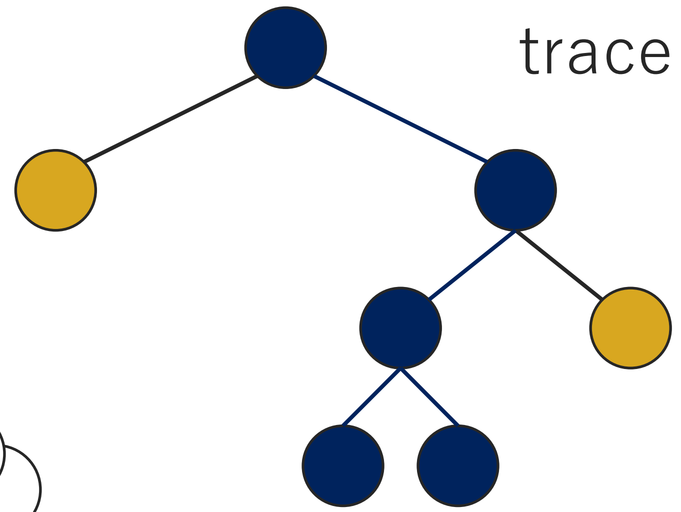
Extra nodes witness correct positions





Labels correct with prob > 2/3

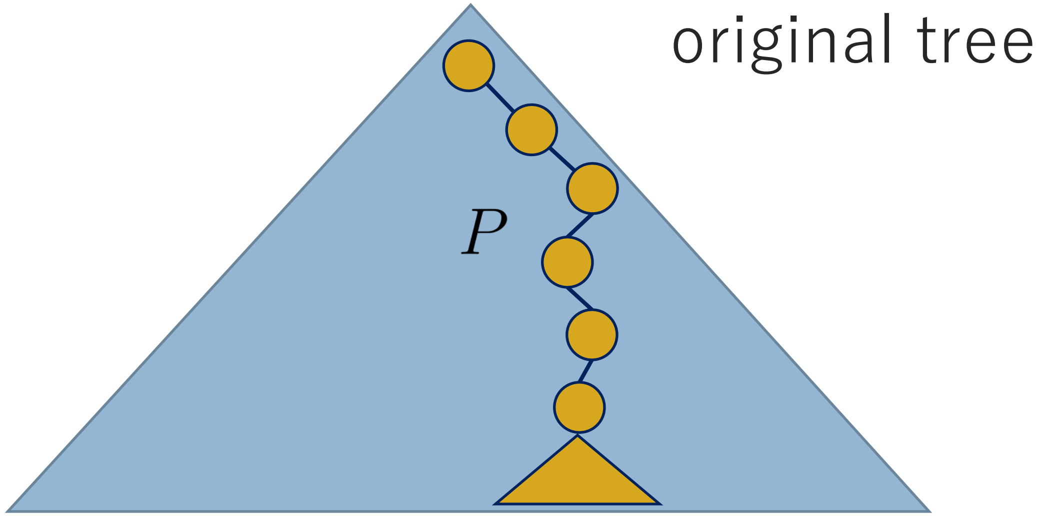
Majority vote O(log n) traces

Theorem 2 $\exp\left(k^{1/3} + \log_k n\right)$ traces to reconstruct complete k-ary trees if $k \geq c \log^2(n)$

When k is large, Theorem 1 is expensive (wait a long time to see a trace preserving a caterpillar)

Theorem 2 $\exp\left(k^{1/3} + \log_k n\right)$ traces to reconstruct complete k-ary trees if $k \geq c\log^2(n)$

Proof: cover X by subtrees



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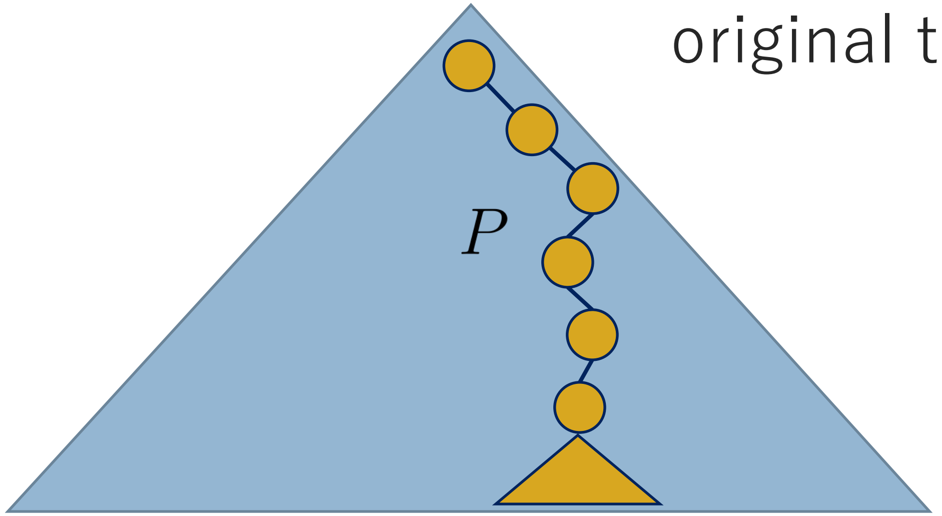

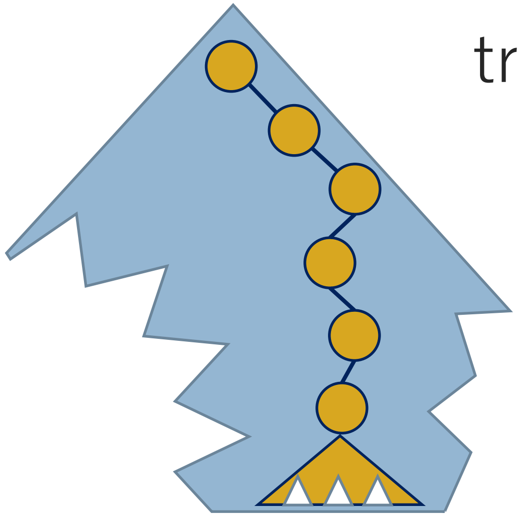

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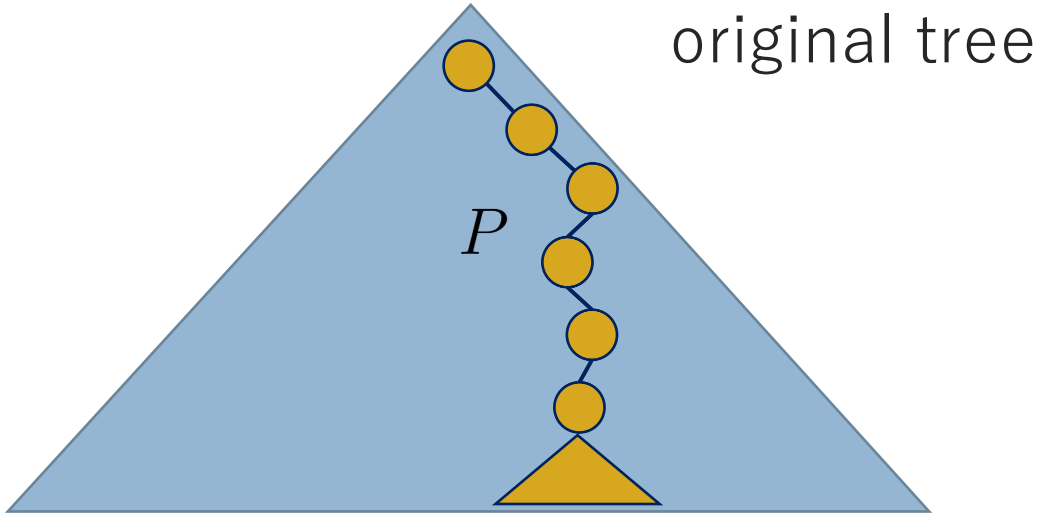

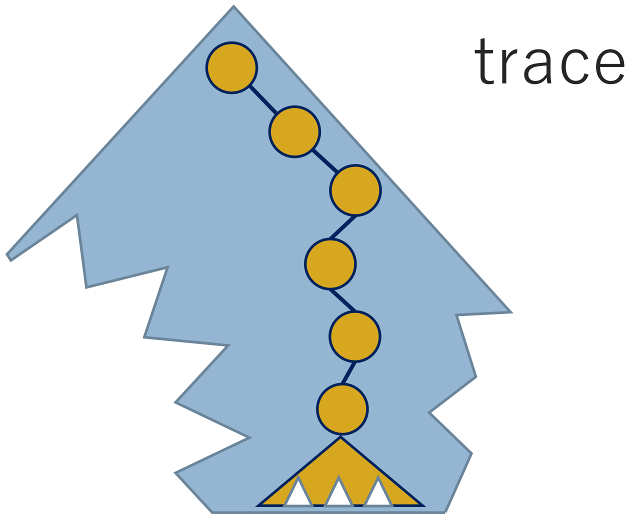

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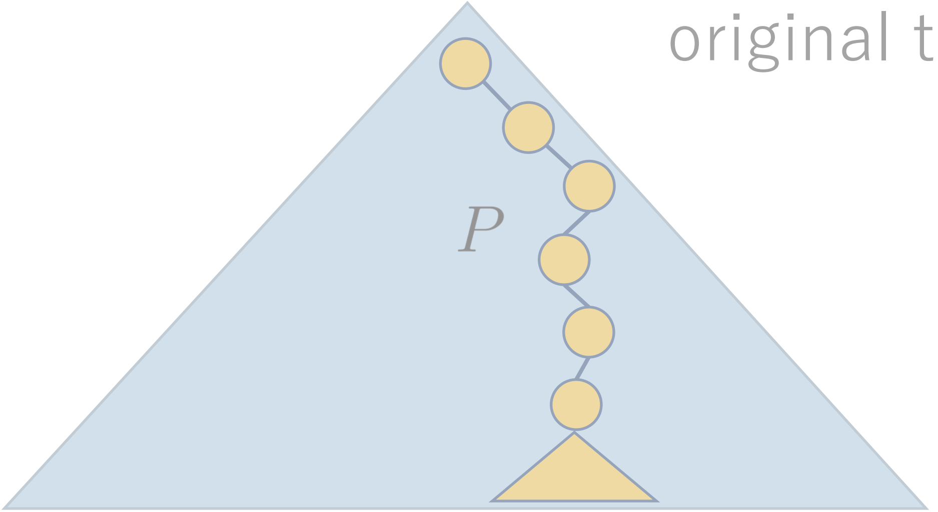

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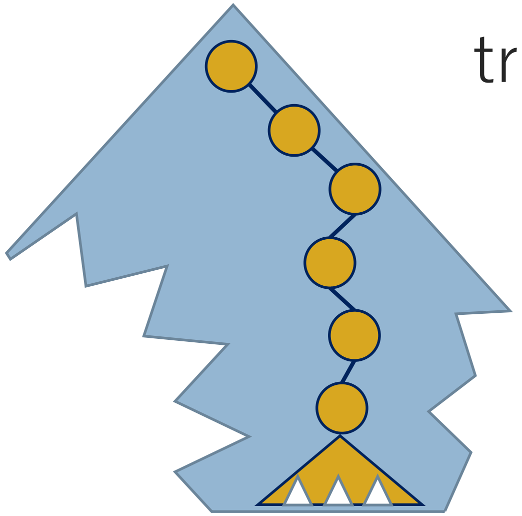
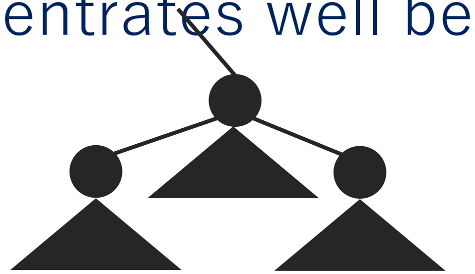


Idea: estimate # deleted nodes at every level, concentrates well because k is large!



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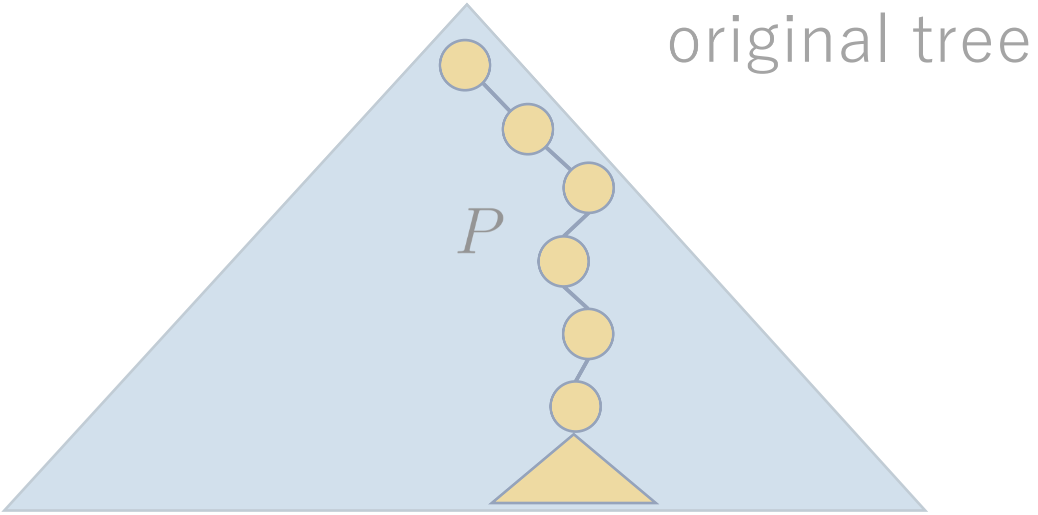
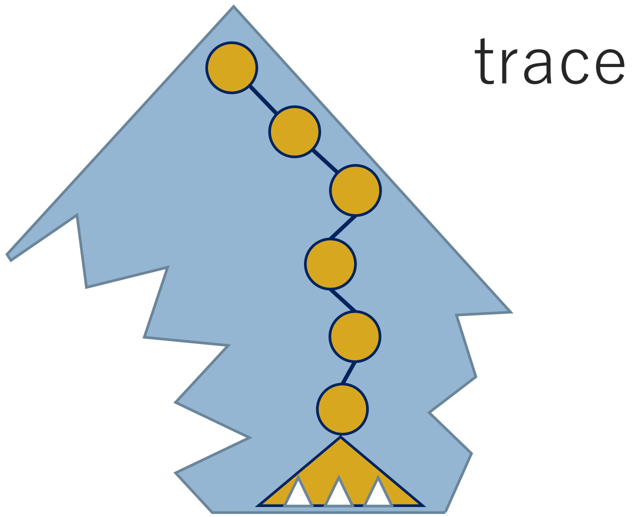
Lemma 2
Reconstruct k leaves w.h.p. using T_k traces

$$T_k \leq \exp\left(k^{1/3}\right)$$





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Trace Reconstruction Variants

- **coded TR:** encoded initial string X [Cheraghchi, Gabrys, Milenkovic, Ribeiro '19; Brakensiek, Li, Spang '19]
- **average-case:** X random → $\exp((\log n)^{1/3})$ [Peres-Zhai '17; Holden, Pemantle, Peres '18]
- **population recovery:** multiple unknown strings [Ban, Chen, Freilich, Servedio, Sinha '19]
- **matrix version:** delete random rows/cols [Krishnamurthy, Mazumdar, McGregor, Pal '19]
- **fixed # deletions:** e.g., 1, 2, 3, ... [Levenshtein '01; Gabrys, Yaakobi '18]
- **Tree TR:** reconstruct labelled trees **[Davies, Racz, Rashtchian '19]**

Deterministic Variants

- **k-deck:** reconstruct from all k-substrings $k \leq O(\sqrt{n})$ [Krasikov, Roditty '97]
- **Graph Reconstruction Conj:** all (n-1)-vertex subgraphs? [Kelly '57; Ulam '60]

Average case

Assume X is drawn uniformly at random from $\{0,1\}^n$

Know $\exp(\log^{1/3}(n))$ traces suffice

Can't improve avg. case upper bound w/out also improving worst case upper bound

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Design codes which require less traces to reconstruct

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Coded TR

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Population recovery

Multiple unknown strings to learn

Algorithm observes traces, but doesn't know which original string they are from

When strings are random, this is just a clustering problem, then avg. case result applies

What's up with the *k*-deck?

The ***k*-deck** of a string X is the multi-set of all length k substrings
Strings with the same k-deck are ***k*-equivalent**
K-decks are unique when $k \geq Cn^{1/2}$. **Improvements here very interesting**

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Strings with the same k-deck are ***k*-equivalent**
K-decks are unique when $k \geq Cn^{1/2}$. **Improvements here very interesting**

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So, we already know that we can distinguish between strings with small Hamming distance using only traces from the deletion channel.
Are there better lower bounds using strings whose hamming distance is say, log(n).

Other Open Questions

- Families of graphs needing only $\text{polylog}(n)$ traces?
- **Approximate TR let εn bits of string be incorrect.**
- More practical deletion models for string TR (burst insertions/ deletions)
- Other useful structure for trace reconstruction?
- Applications for Tree TR to computational biology or sensors or … ?

Thanks!

Sami Davies
www.samidavies.com
daviess@uw.edu