

Lehrstuhl für **INFORMATIK I** Effiziente Algorithmen und wissensbasierte Systeme



# Advanced Algorithms

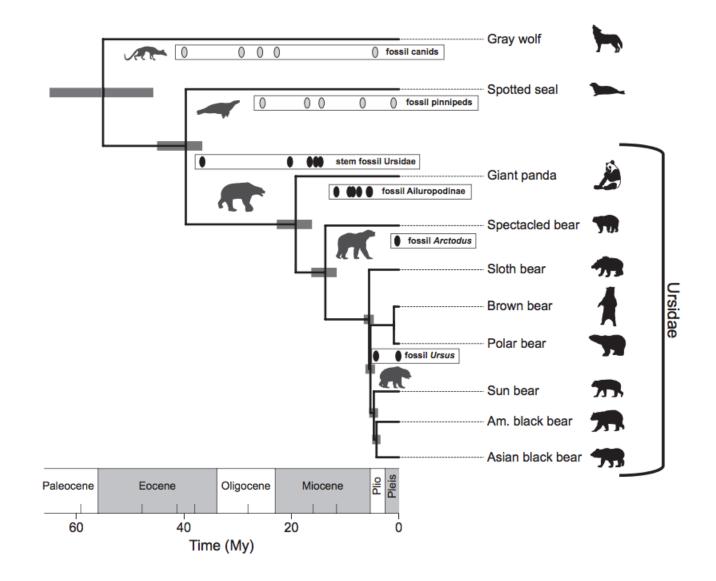
Winter term 2019/20

Lecture 12. Rearrangement distance of phylogenetic trees

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Chair for Computer Science I

# Phylogenetic trees



Phylogenetic trees

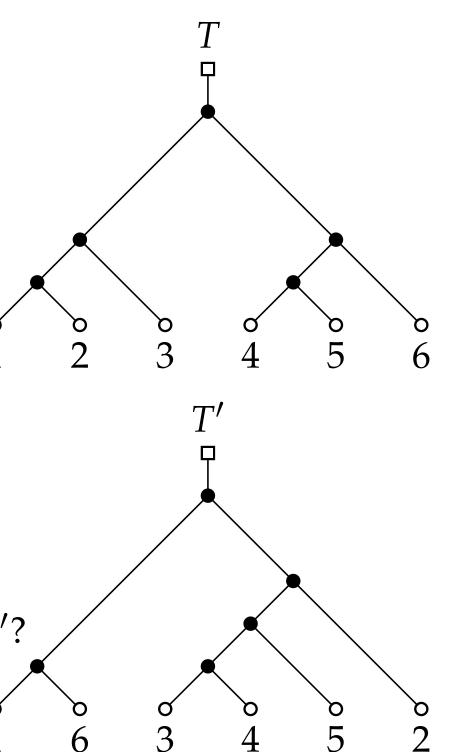
Let  $X = \{1, 2, ..., n\}.$ 

A phylogenetic tree *T* is a rooted, binary tree where the leaves are bijectively labelled with *X*.

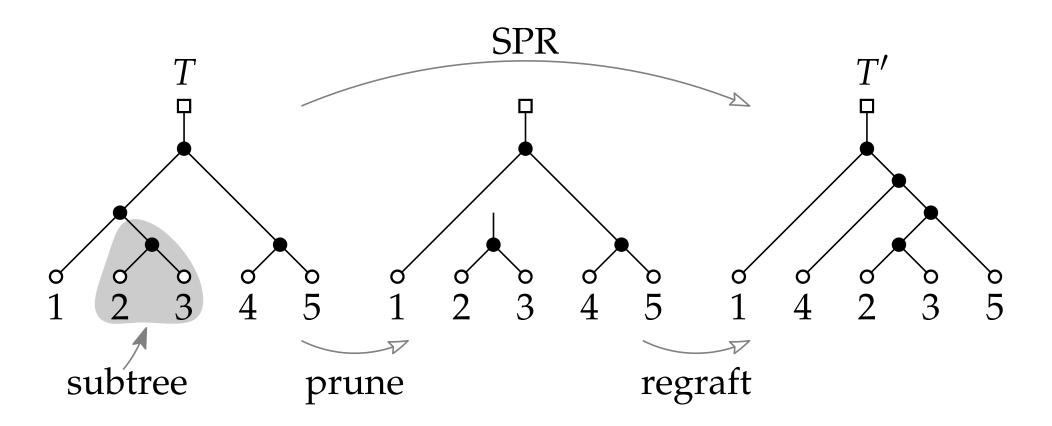
Inference methods compute a phylogenetic tree based on some model and data.

Different methods/models/data yield different phylogenetic trees.

How can we compare *T* and *T*'?
 We want a metric on phylogenetic trees.



#### Subtree Prune & Regraft (SPR)



Define SPR-rearrangement graph G = (V, E) with

•  $V = \{ all phylogenetic trees on X \} and$ 

•  $\{T, T'\} \in E$  if *T* can be transformed into *T'* with an SPR.

#### SPR-distance

Define the SPR-distance of *T* and *T'* as  $d_{SPR}(T, T') = \text{distance of } T \text{ and } T' \text{ in } G.$ 

**Lemma.** The SPR-rearrangement graph *G* is connected.

**Proof.** See blackboard (or exercise).

**Corollary.** The SPR-distance is a metric.

**Proof.** *G* is connected and undirected.

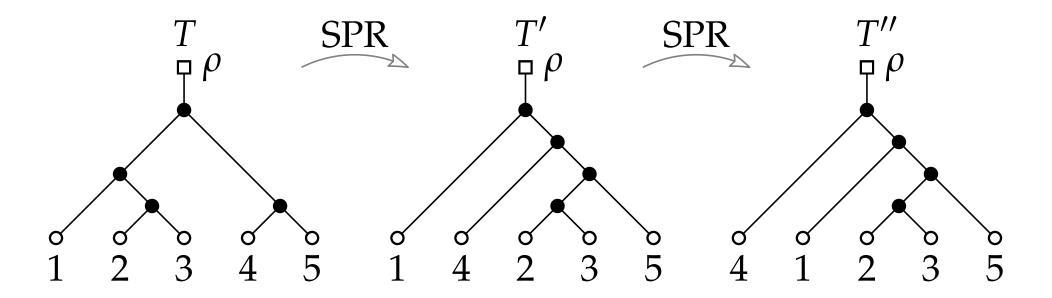
**Goal.** Compute the SPR-distance  $d_{SPR}(T, T')$ .

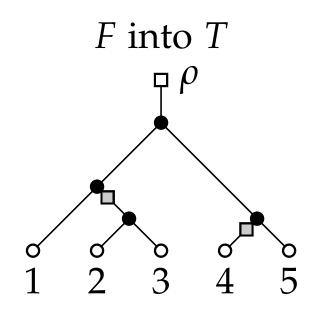
**Problem.** *G* is huge!

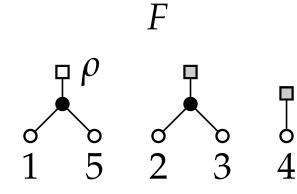
$$|V(G)| = (2n-3)!! = (2n-3) \cdot (2n-5) \cdot \ldots \cdot 5 \cdot 3$$

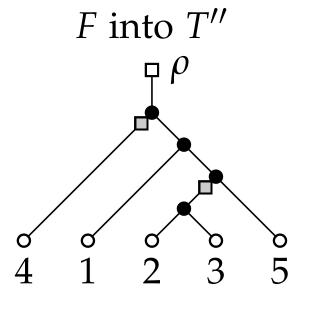
Can we rephrase the problem?

#### Maximum agreement forests

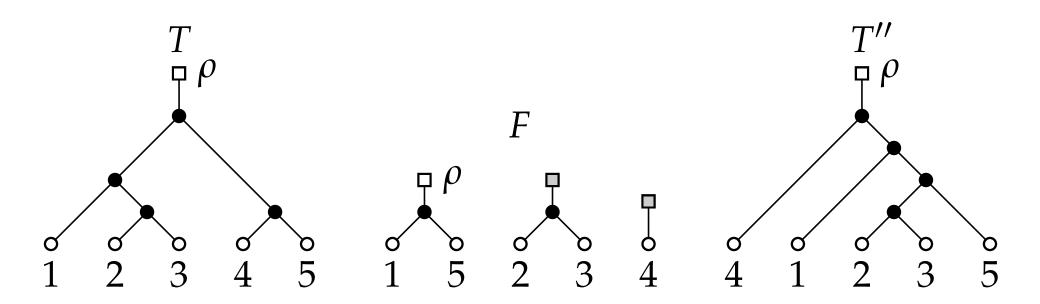








#### Maximum agreement forests



An agreement forest *F* of *T* and *T*<sup> $\prime\prime$ </sup> is a forest  $\{T_{\rho}, T_1, T_2, \ldots, T_k\}$  such that

- label sets of the  $T_i$  partition  $X \cup \{\rho\}$ ,
- $\rho$  is in label set of  $T_{\rho}$ , and
- there exist edge-disjoint embeddings of subdivisions of the *T<sub>i</sub>*'s into *T* and *T''* that cover all edges.

If *k* is minimal, *F* is a maximum agreement forest (MAF).

#### Characterisation

Let  $F = \{T_{\rho}, T_1, T_2, \dots, T_k\}$  be a MAF of T and T'. Then define

$$m(T,T')=k.$$

**Theorem.** Let *T* and *T'* be two phylogenetic trees on *X*. Then  $m(T,T') = d_{SPR}(T,T').$ 

**Proof.** See blackboard.

**Theorem.** Computing the SPR-distance of T and T' is NP-hard.

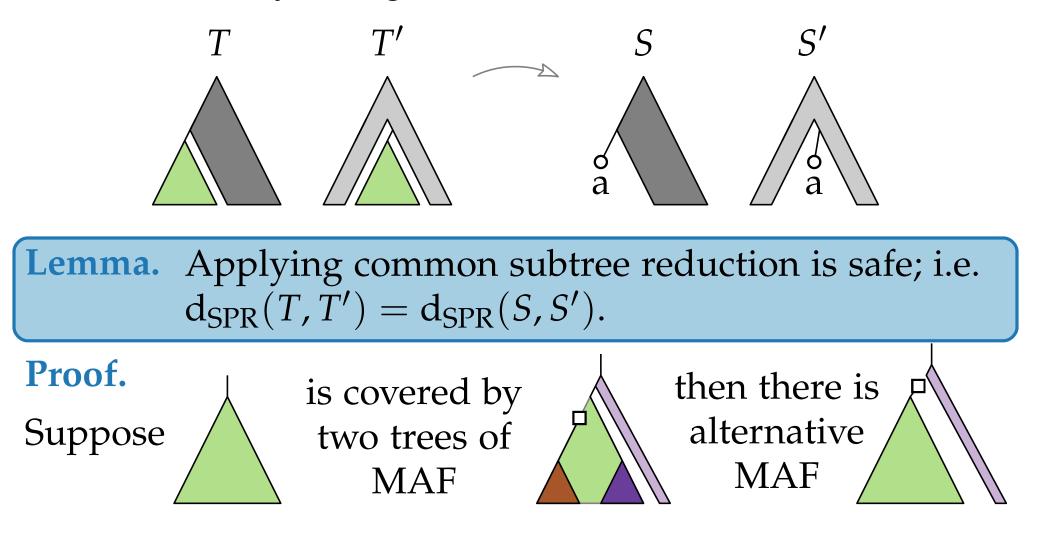
#### **Proof** is via reduction from Exact Cover by 3-Sets.

See Bordewich, Semple, "On the computational complexity of the rooted subtree prune and regraft distanc" and Hein et al., "On the complexity of comparing evolutionary trees" for details.

## Kernelisation (1 of 2)

#### Common subtree reduction:

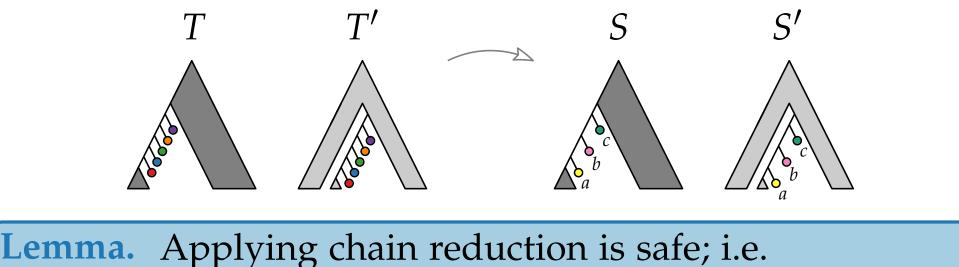
Replace any pendant subtree that occurs identically in both trees by a single leaf with a new label.



## Kernelisation (2 of 2)

#### Chain reduction:

Replace any chain of leaves that occurs identically in both trees by three new leaves.



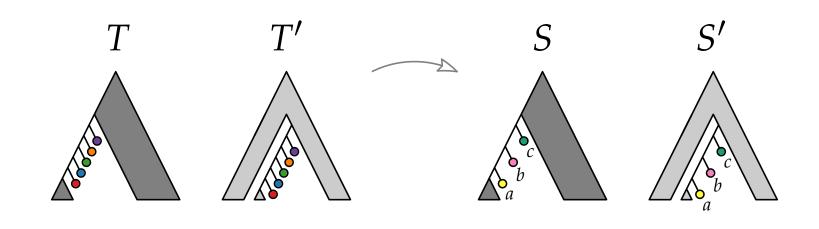
 $d_{\text{SPR}}(T,T') = d_{\text{SPR}}(S,S').$ 

**Proof.**Case 1 F into SShow there is a<br/>tree with abc-chain<br/>in a MAF.F

## Kernelisation (2 of 2)

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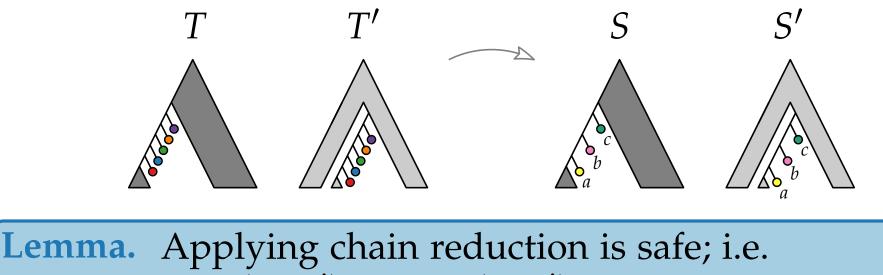
**Lemma.** Applying chain reduction is safe; i.e.  $d_{SPR}(T,T') = d_{SPR}(S,S')$ .

**Proof.** Case 2 *F* into *S* tree with abc-chain in a MAF. Case 2 F into *S*  $f_{a}^{b}$   $f_{a}^{b}$ 

## Kernelisation (2 of 2)

#### Chain reduction:

Replace any chain of leaves that occurs identically in both trees by three new leaves.



$$d_{\rm SPR}(T,T') = d_{\rm SPR}(S,S').$$

Proof.

Show there is a tree with abc-chain in a MAF.

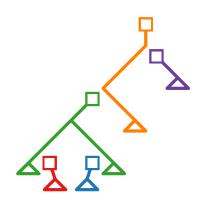
Swap abc-chain with original chain for MAF of T and T'.

**Theorem.** Reduce T and T' to S and S' by exhaustively applying the reduction rules. Let S and S' be on X'. Then

 $|X'| \leq 28 \operatorname{d}_{\operatorname{SPR}}(T, T').$ 

**Proof.** Let  $F = \{T_{\rho}, T_1, \ldots, T_k\}$  be MAF for *S* and *S'*.

Let  $n(T_i)$  be #  $T_j$  it overlaps with in embedding of F into T. Claim 1.  $\sum_{i=\rho}^{k} (n(T_i) + n'(T_i)) \le 4k = 4 \operatorname{d}_{\operatorname{SPR}}(T, T').$ 



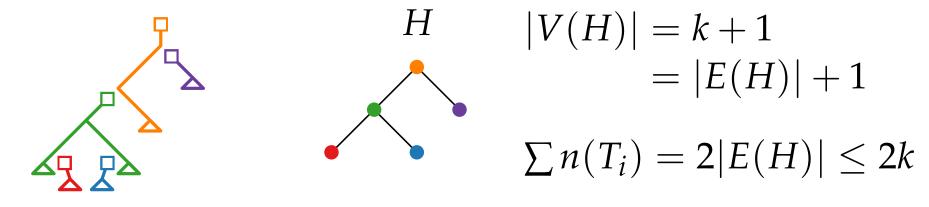
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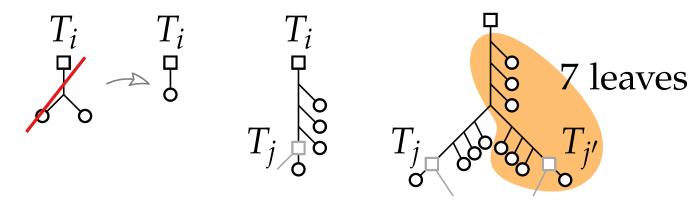
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Claim 2. # leaves of  $T_i \leq 7(n(T_i) + n'(T_i))$ .



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**Theorem.** Reduce T and T' to S and S' by exhaustively applying the reduction rules. Let S and S' be on X'. Then

 $|X'| \leq 28 \operatorname{d}_{\operatorname{SPR}}(T, T').$ 

**Corollary.** Computing  $d_{SPR}(T, T')$  is fixed-parameter tractable when parameterized by  $d_{SPR}(T, T')$ .

**Proof.** Reduce *T* and *T'* to *S* and *S'*. Let  $k = d_{SPR}(S, S')$ .

- S has at most 4|X'|<sup>2</sup> neighbours.
  S has ≤ 2|X'| edges to cut and attach to.
- Length-*k* BFS from *S* visits at most  $O((4|X'|^2)^k) = O((56k)^{2k})$  trees.

# Approximation algorithm

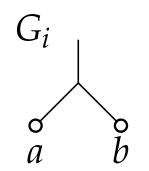
#### **Algorithm:** dSPRApprox(T, T')

 $i \leftarrow 1$ 

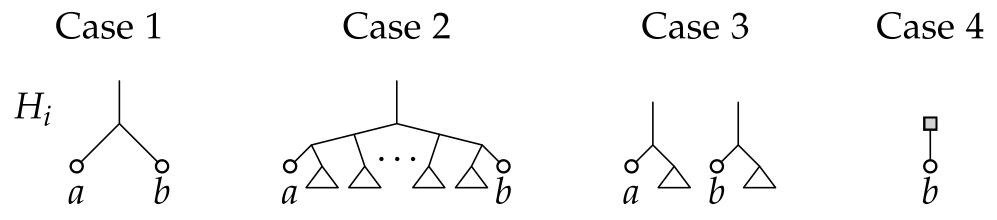
$$G_i \leftarrow T$$

 $H_i \leftarrow T'$ 

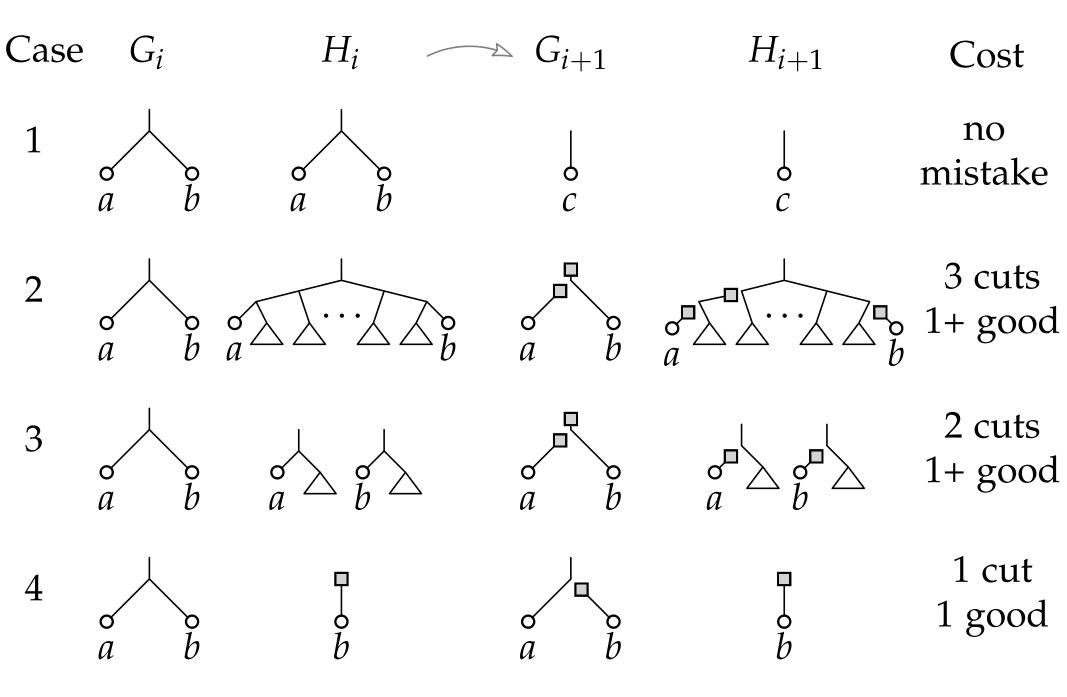
**while**  $\exists$  pair of sibling leaves *a* and *b* in *G<sub>i</sub>* **do** find the case that applies to *a* and *b* in *H<sub>i</sub>* apply the corresponding transaction to obtain *G<sub>i+1</sub>* from *G<sub>i</sub>* and *H<sub>i+1</sub>* from *H<sub>i</sub>* i + +



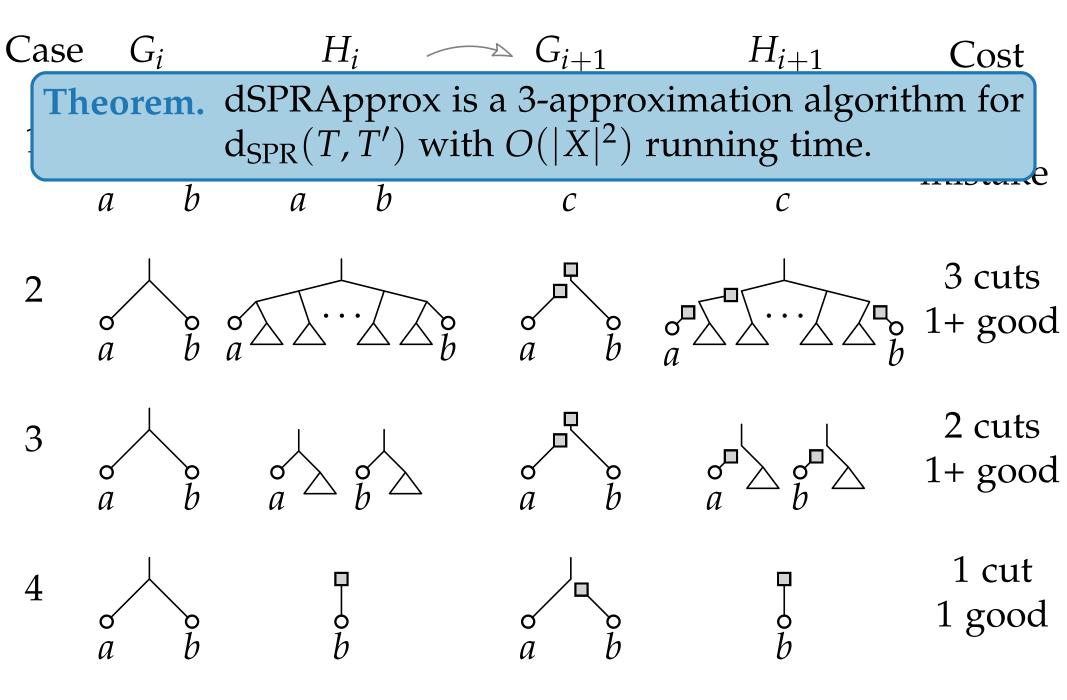
return H<sub>i</sub>



## Approximation algorithm



# Approximation algorithm



#### References

- Bordewich, Semple, "On the computational complexity of the rooted subtree prune and regraft distance", 2005 for SPR, MAF, characterisation, fpt, divide & conquer
- Hein et al., "On the complexity of comparing evolutionary trees", 1996 for NP-hardness proof
- Rodrigues et al., "The maximum agreement forest problem: Approximation algorithms and computational experiments", 2006