Heidelberg Institute for Theoretical Studies

HITS

Phylogenetic Placement of Short Reads

Visualization, Species Delimitation and Taxonomic Annotation

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UniEuk 1st Implementation Meeting, Paris

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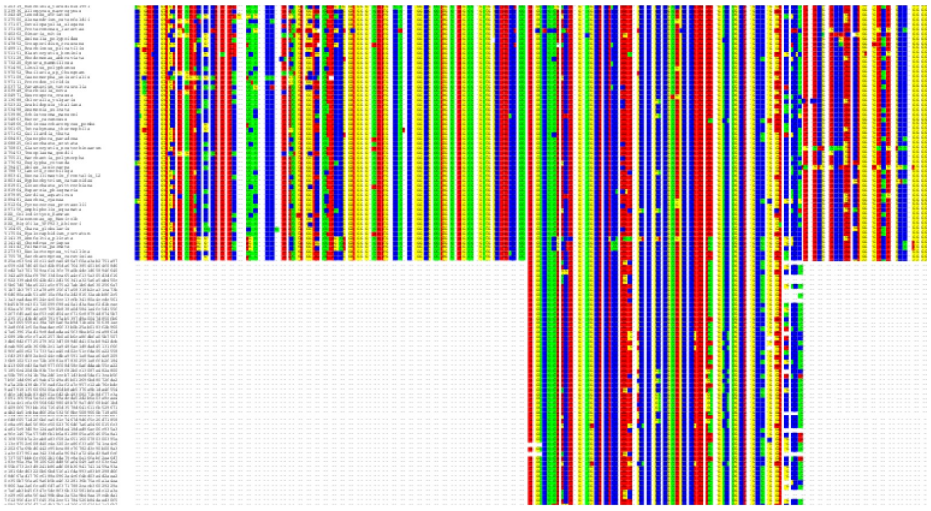
Input Data

Reference Tree



Reference Sequences

Query Sequences

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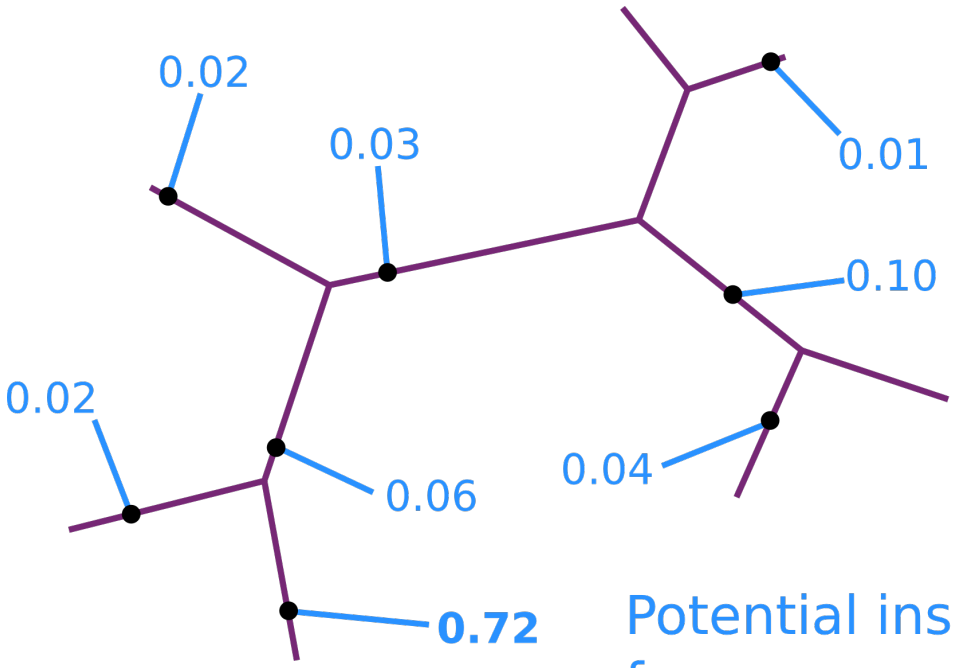
Evolutionary Placement (EPA)



Reference tree

Potential insertion positions ("placements")
for a query sequence with likelihood ratios

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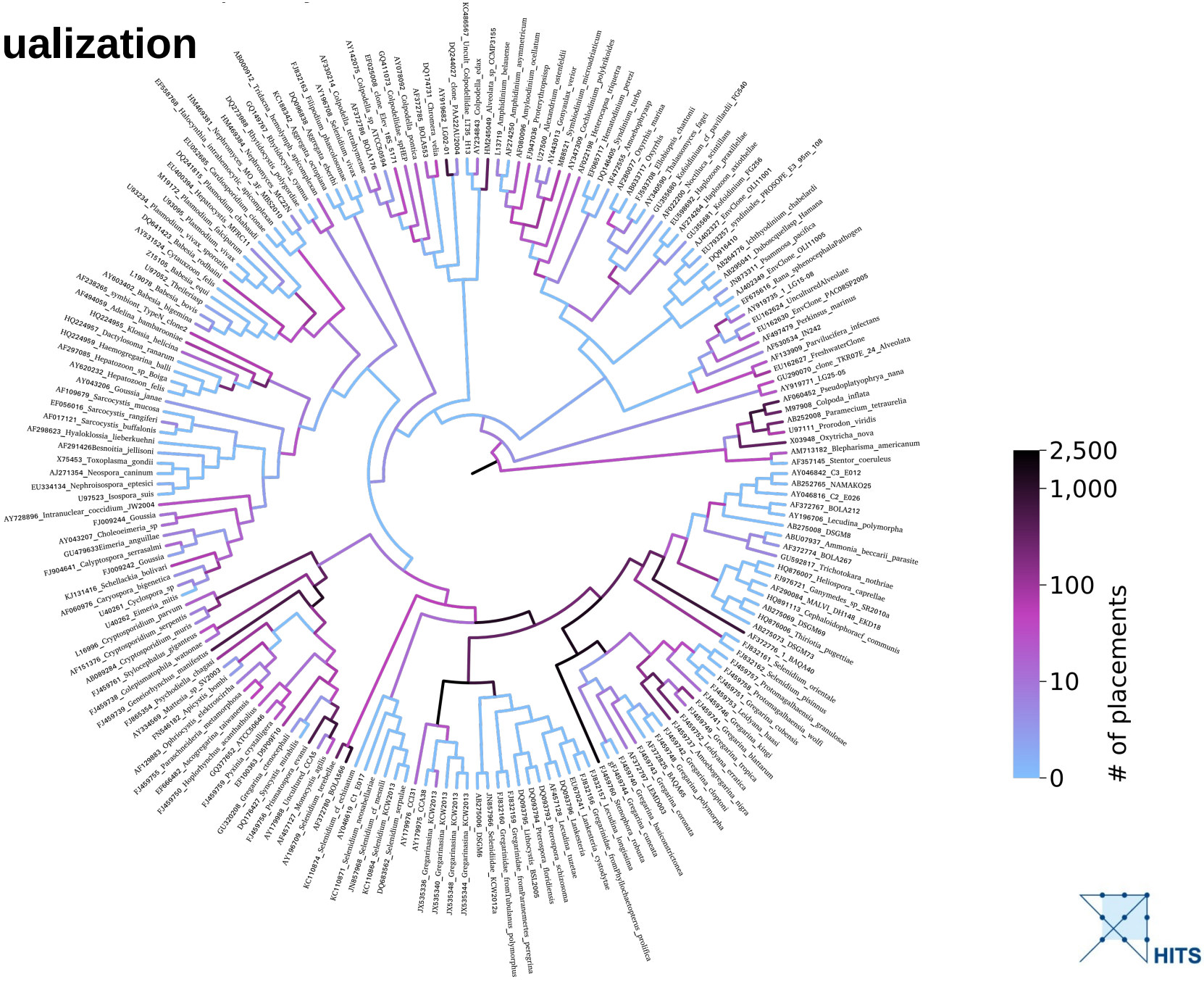
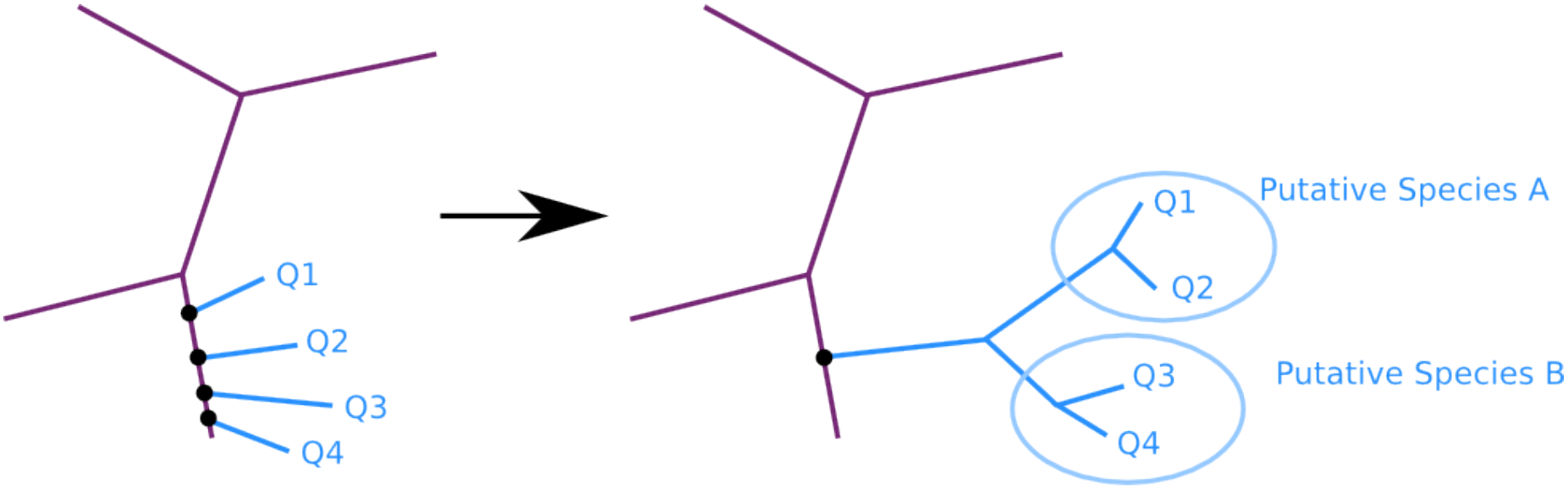
Visualization



Species Delimitation (PTP)



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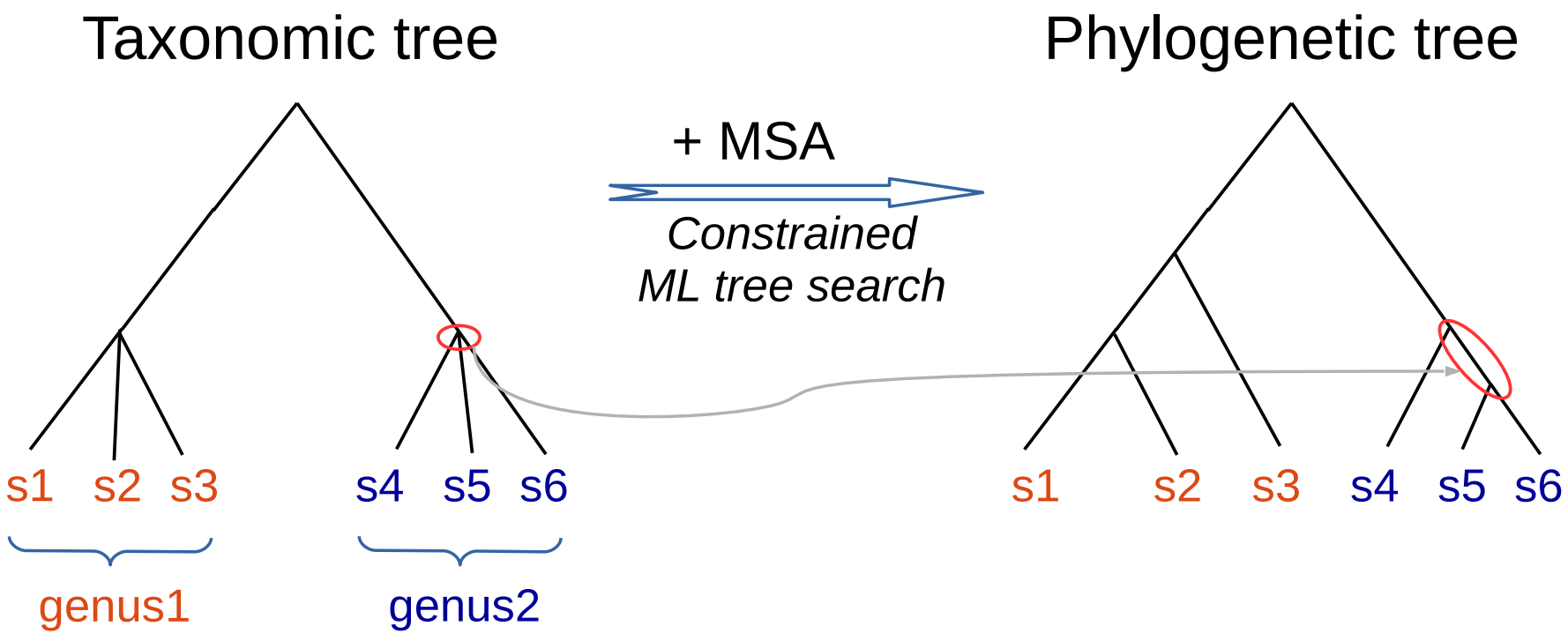
Taxonomic Annotation with EPA

Step 1: Build Reference Tree



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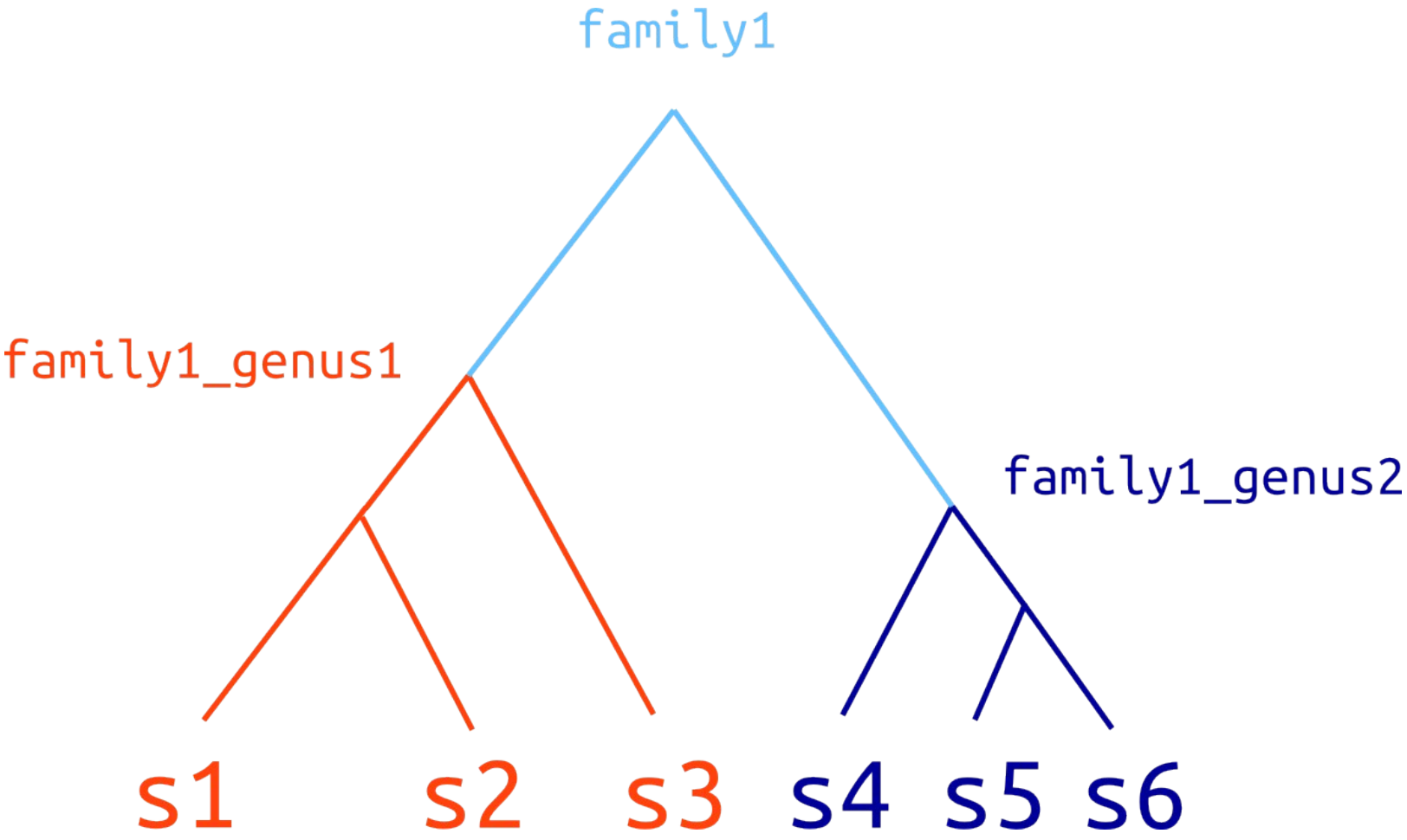
Step 2: Label the Branches



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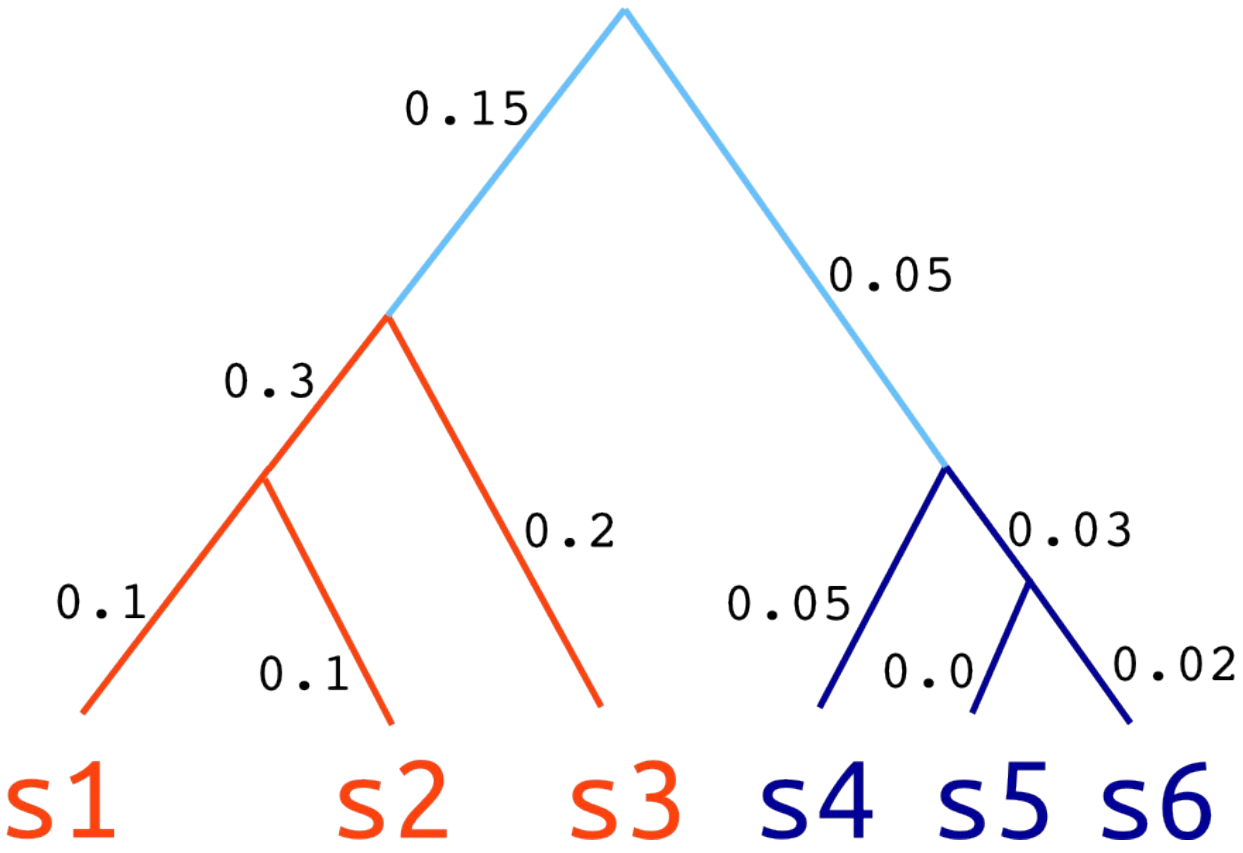
Step 3: Run EPA



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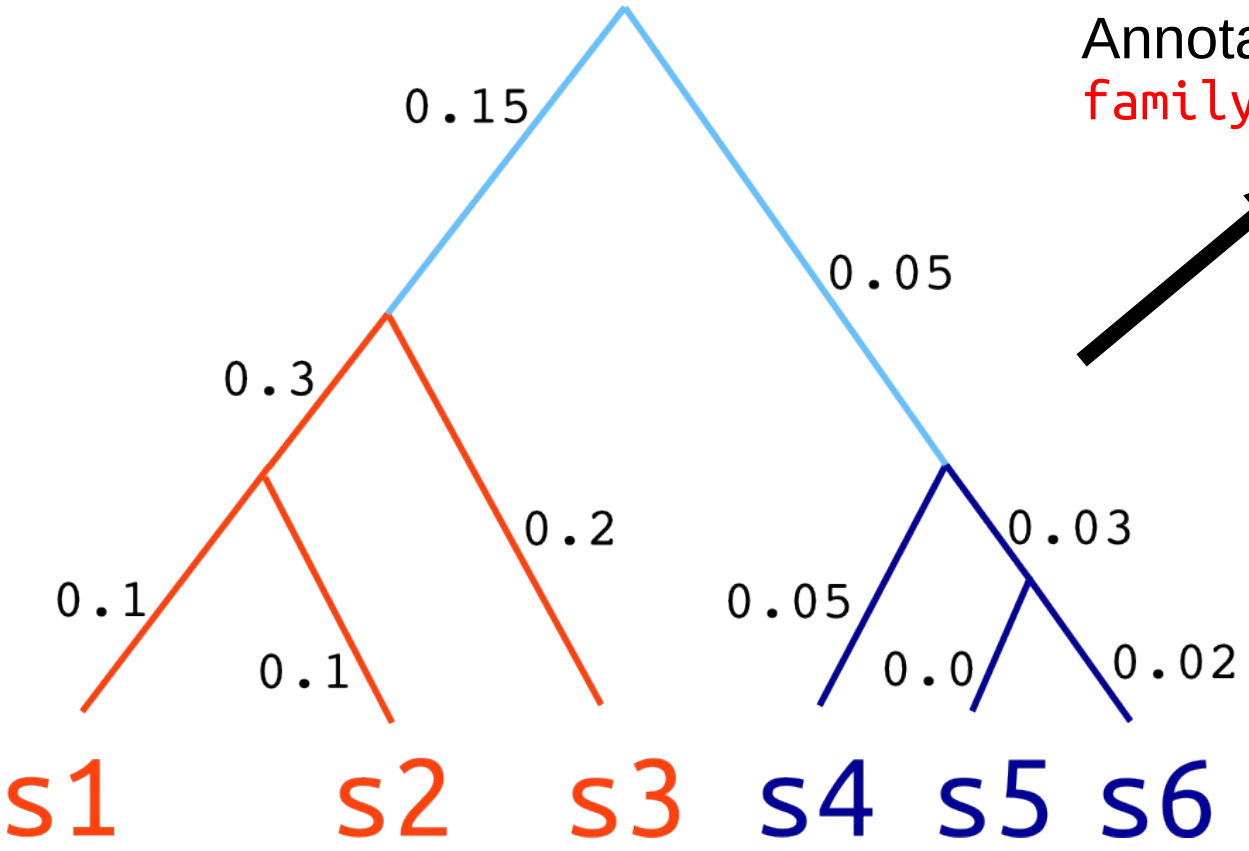
Taxonomic Annotation with EPA

Step 4: Derive Taxonomic Annotation



Annotation for Query:
family1_genus1

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Software

- PaPaRa: Align Short Reads to Reference MSA
  http://sco.h-its.org/exelixis/software
- RaxML-EPA: Phylogenetic Placement
  https://github.com/stamatak/standard-RAxML
- Genesis: Library for e.g. Clade Annotation and Visualization
  http://genesis-lib.org/
- SATIVA: Detect Taxonomically Mislabeled Sequences
  https://github.com/amkozlov/sativa
- PTP: Species Delimitation
  http://sco.h-its.org/exelixis/software
- PUmPER: Extend Trees with new Sequences from GenBank
  https://github.com/fizquierdo/perpetually-updated-trees

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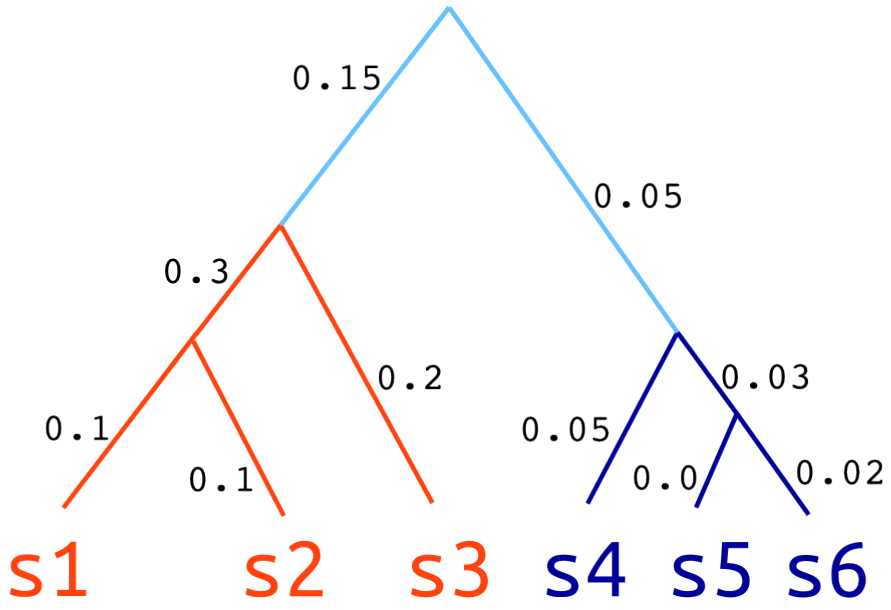
Taxonomic Annotation with EPA, Revisited



Per-rank LW score evaluation:

```
LW(family1_genus1) = 0.1  + 0.1 + 0.3 + 0.2 = 0.7
LW(family1)        = 0.15 + 0.05            = 0.2
LW(family1_genus2) = 0.05 + 0.03 + 0.02     = 0.1
```

Final assignment: `family1_genus1`

Confidence family / genus: `1.0 / 0.7`

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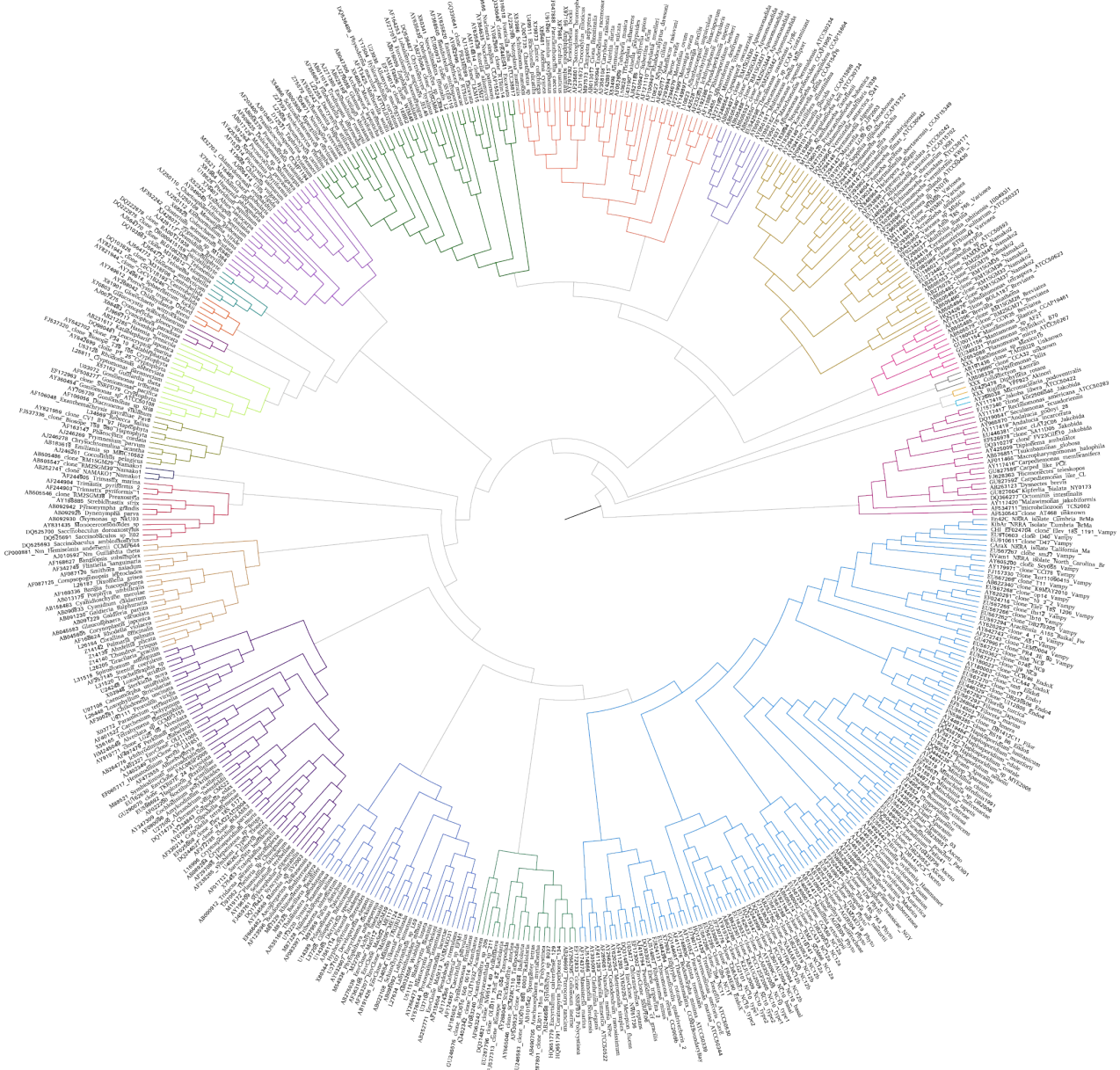
Clade Annotated Tree