

BIOINFORMATICS  
INSTITUTE

# Implied weighting in TnT

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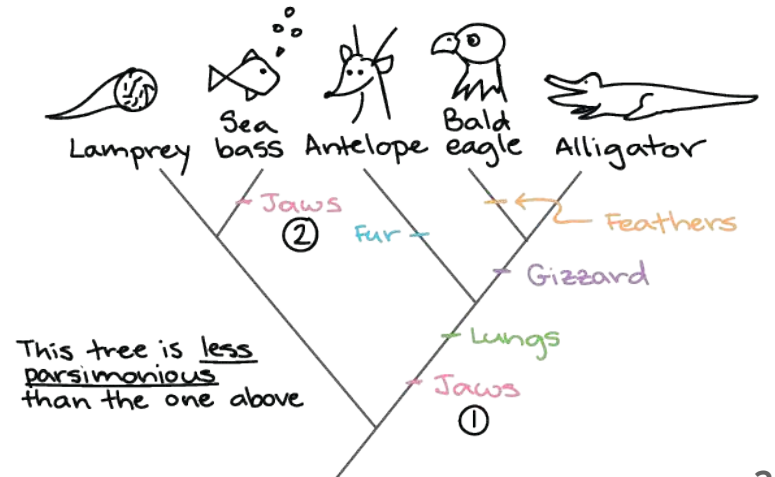
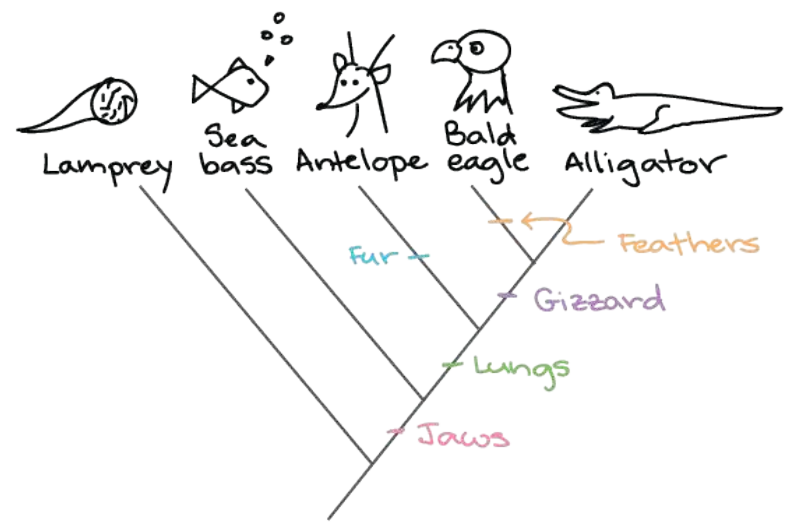
Faculty of Biology, St. Petersburg State University

# What is IW?

**Parsimony approach:** ideally we need to get the shortest tree (fewer changes).

**Problem:** for morphological trees some information is far more important than other.

**Approach:** what if we add weights to changes between clades and see how this would affect the tree.

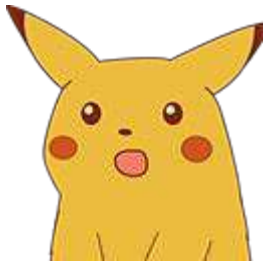


- **TnT** takes only one  $k$  value as an argument.
- **But TnT** allows to construct scripts with it's own script language.

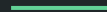
**program:** has bad documentation

**program:** doesn't follow its own documentation

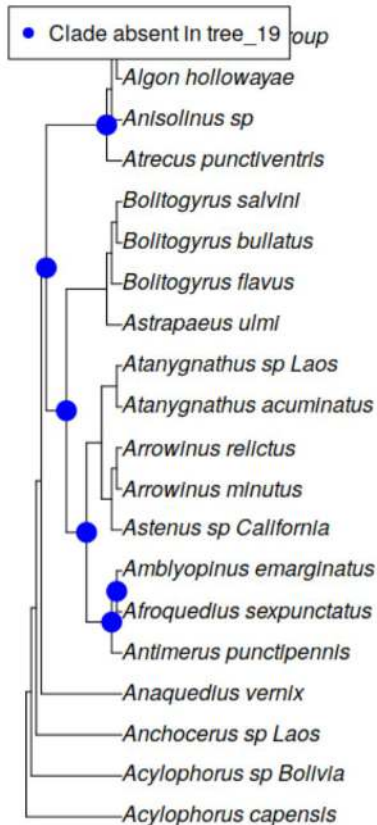
**user:**



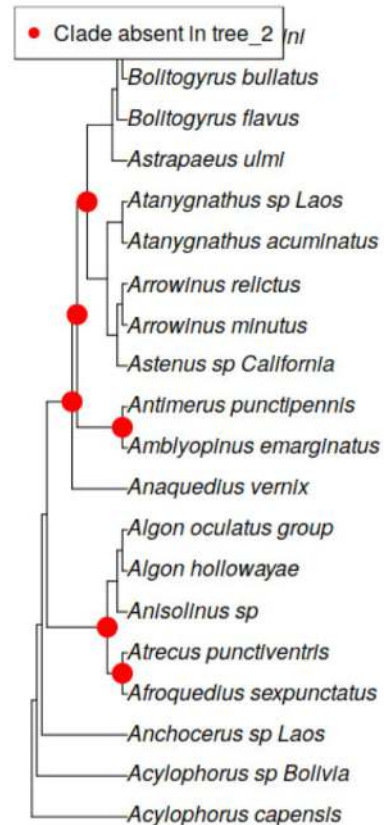
**Goal:** implement IW with different weights as a clade-support method.



tree\_2



tree\_19

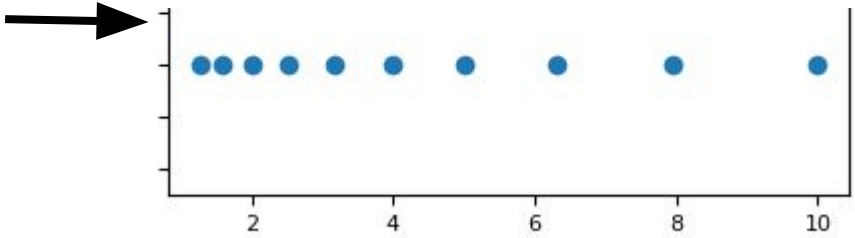
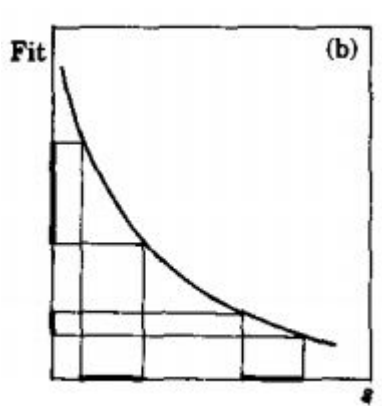


Examples of different tree topologies for different k values.  
Clades absent in other tree are colored.

# Done:

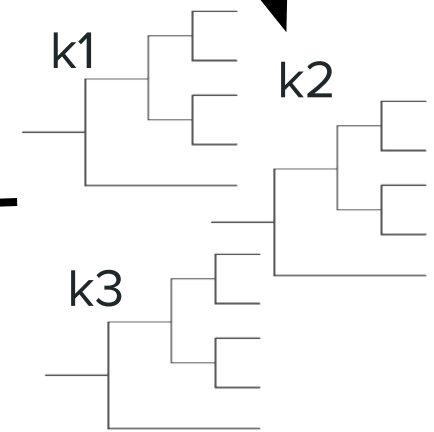
- Simple TnT script that can build trees for different k values.
- Python command-line script that can:
  - Read data in tnt-matrix or fasta format.
  - Take minimal and maximum k values (and number of steps is user wants do set it) and make log distribution.
  - Built consensus tree with clade support values.
  - Save resulting tree in different formats.
  - Draw resulting tree.

# Inside the script



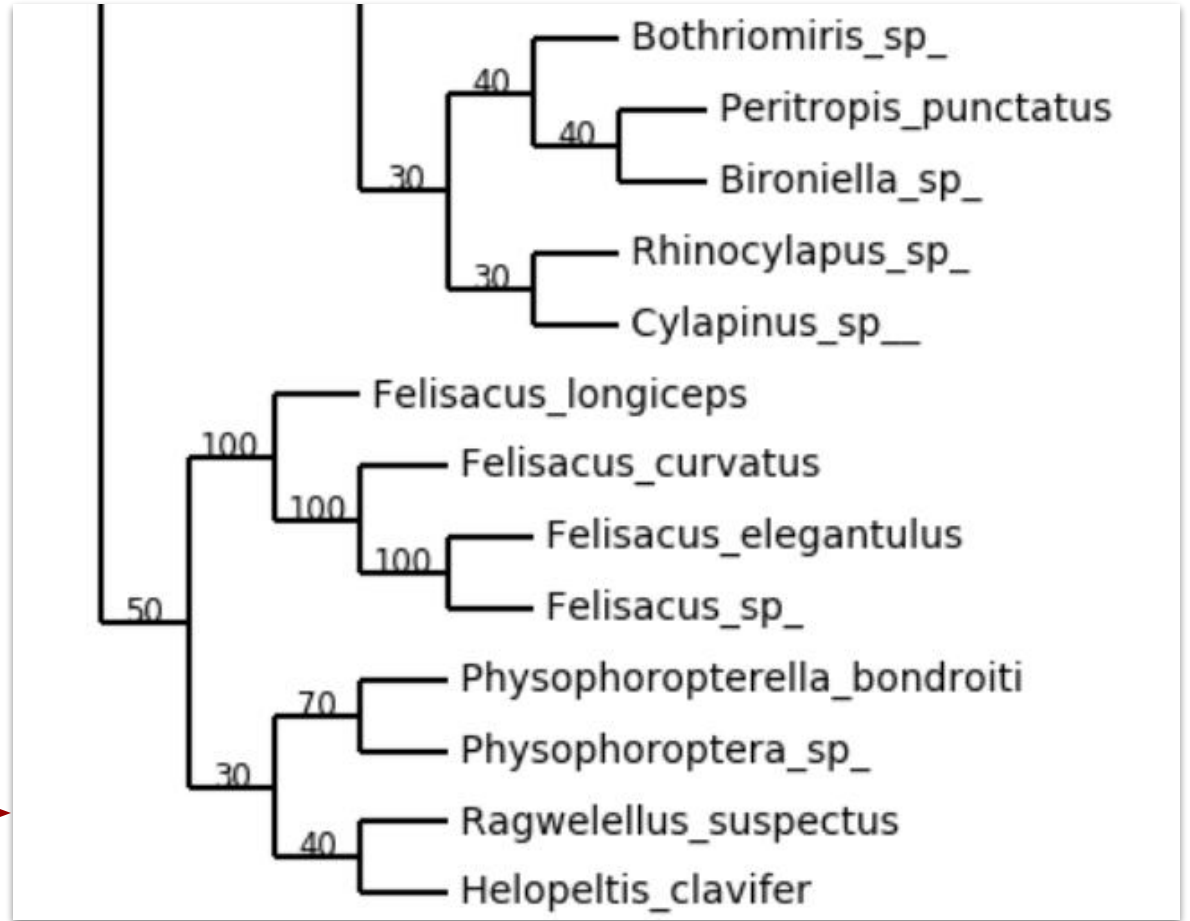
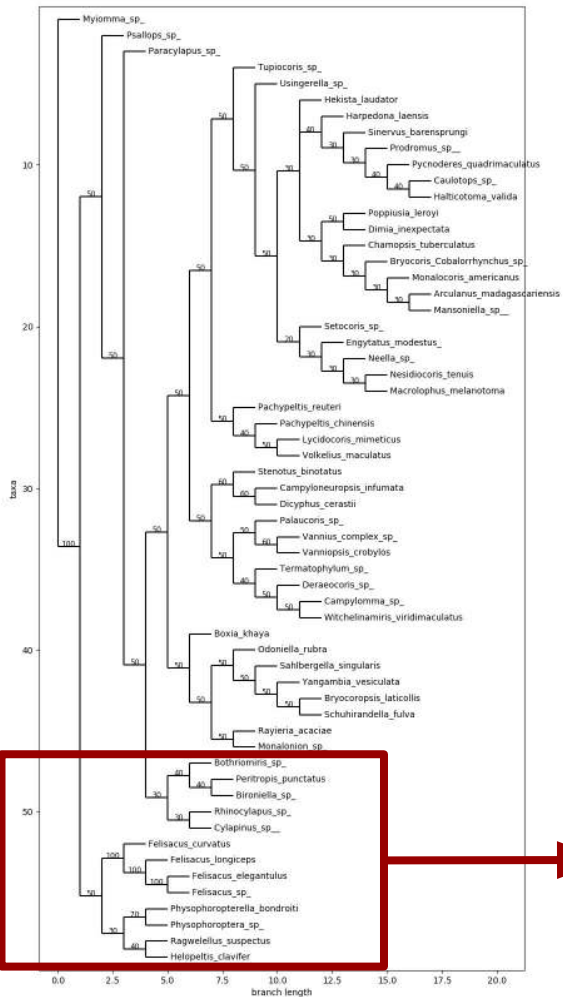
read data

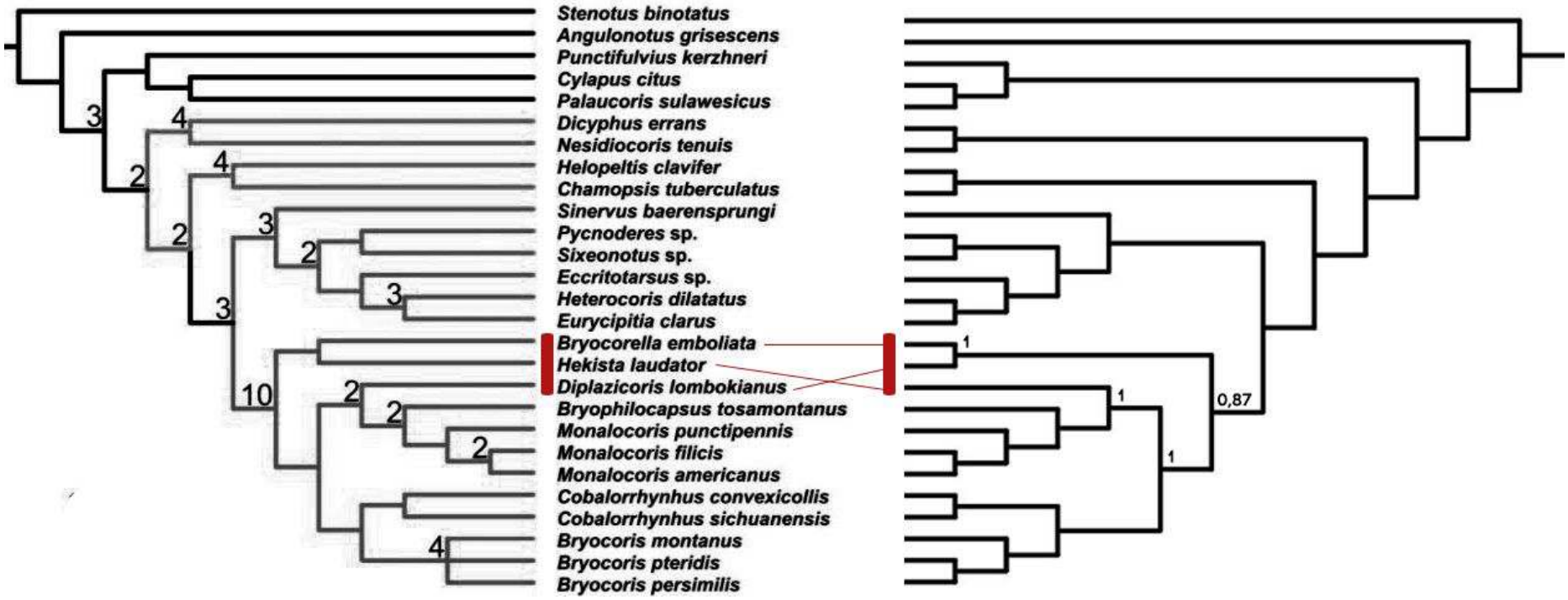
call TnT



consensus with branch support

Success!





Left: cladogram with Bremer support values.

Right: IW support.



Thank you for your attention

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<https://github.com/eksytnik/TnT-IW-branch-support>