

Repeat regularly

Download sequences
from Genbank:

- Whole plastomes



- 500 sequences
- 400 spp.
- 79 loci

Extract
sequences

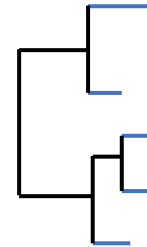
Resolve
taxonomy



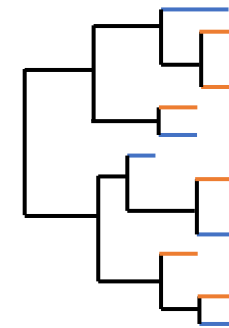
Align sequences
and concatenate



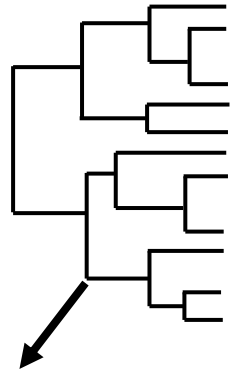
Backbone tree



Full tree



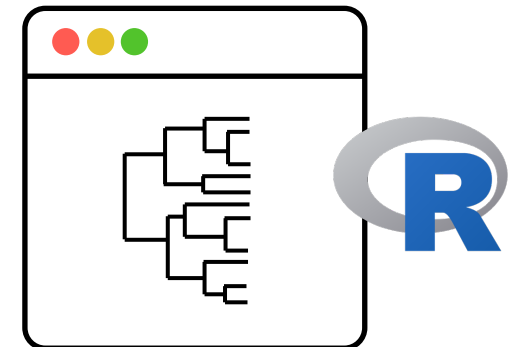
Dated tree



Inspect
tree,
remove
mis-IDs



- fernphy.github.io
- “ftolr” R package



- Sanger sequences



Extract
sequences

Resolve
taxonomy



Identify and
remove
rogues by all-
by-all BLAST



Align sequences
and concatenate

