

Machine learning models accurately predict clades of proteocephalidean tapeworms based on host and zoogeographical data

PVA, RJdS, AdC, JLL, AD, DJ, DJM

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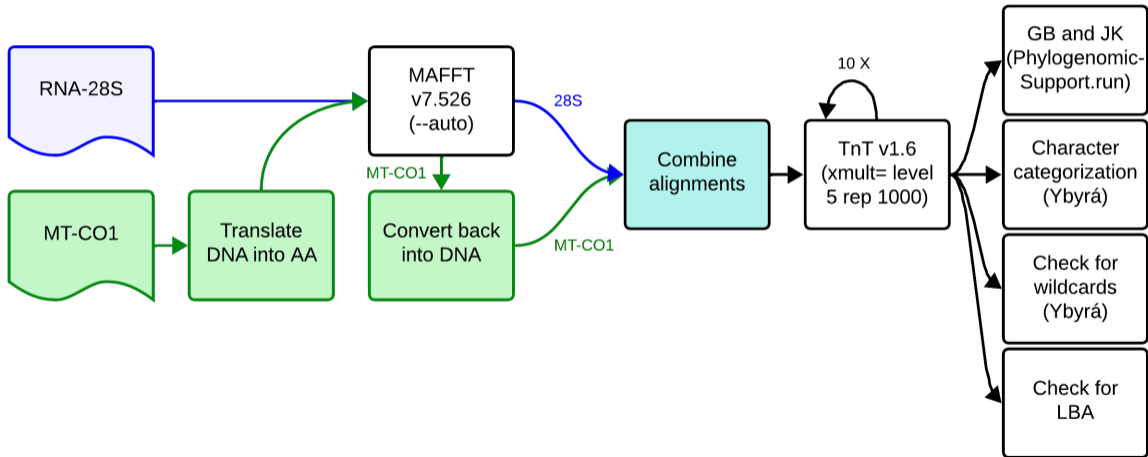


Species selection and DNA data

- ▶ Our matrix of **28S rRNA** (510 terminals) and **MT-CO1** (253 terminals) contained a total of **537 terminals**.
- ▶ 58 terminals were sequenced for the first time to generate **85 new sequences** (56 for 28S and 29 for MT-CO1).
- ▶ This matrix represents **222 parasite species** from **194 host species**.
- ▶ Our **outgroup (87 terminals)** comprises *Acanthobothrium* (18 species), *Clistobothrium* (1; our root), *Matticestus* (2), *Pachybothrium* (1), and *Potamotrygonocestus* (2).
- ▶ Our **ingroup (450 terminals)** contains 63 genera of proteocephalids.

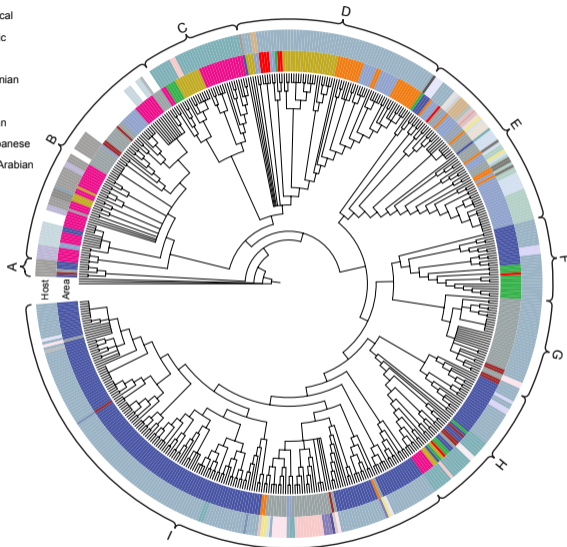


Phylogenetics workflow



Area

- Afrotropical
- Neotropical
- Palaearctic
- Nearctic
- Panamanian
- Oriental
- Australian
- Sino-Japanese
- Saharo-Arabian

**Hosts**

- Amiiformes
- Anguilliformes
- Anura
- Centrarchiformes
- Characiformes
- Cichliformes
- Cypriniformes
- Cyprinodontiformes
- Didelphimorphia
- Esociformes
- Gobiiformes
- Gymnotiformes
- Heterodontiformes
- Myliobatiformes
- Orectolobiformes
- Osmeriformes
- Osteoglossiformes
- Perciformes
- Rajiformes
- Rhinopristiformes
- Salmoniformes
- Scorpaeniformes
- Siluriformes
- Squaliformes
- Squamata
- Synbranchiformes
- Testudines
- Urodela



Host and biogeographical data

Ten different features (5,040 data points):

▶ Host taxonomy:

- ▶ class (5)
- ▶ order (29)
- ▶ family (66)
- ▶ genus (120)
- ▶ species (176)

▶ Environment and habitat:

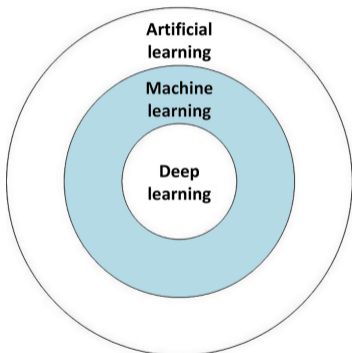
- ▶ terrestrial or aquatic (2)
- ▶ freshwater, brackish, or saltwater (3)

▶ Locality:

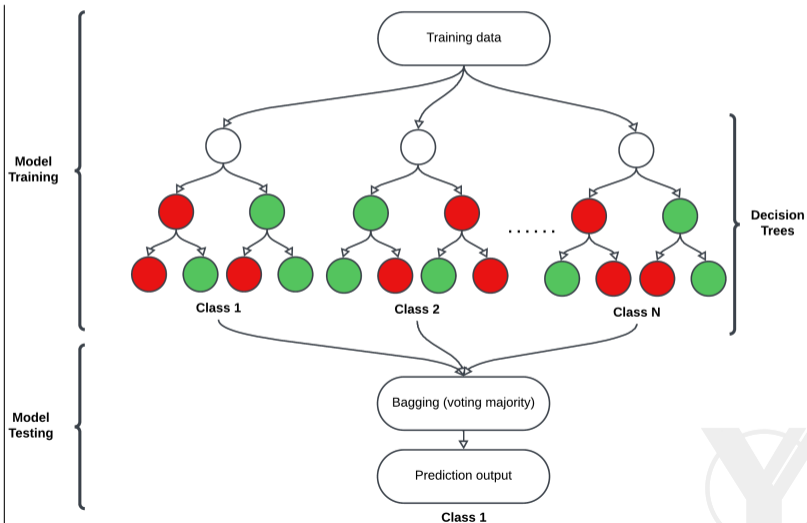
- ▶ zoogeographical region (10)
- ▶ continent (7)
- ▶ country or river basin (42)



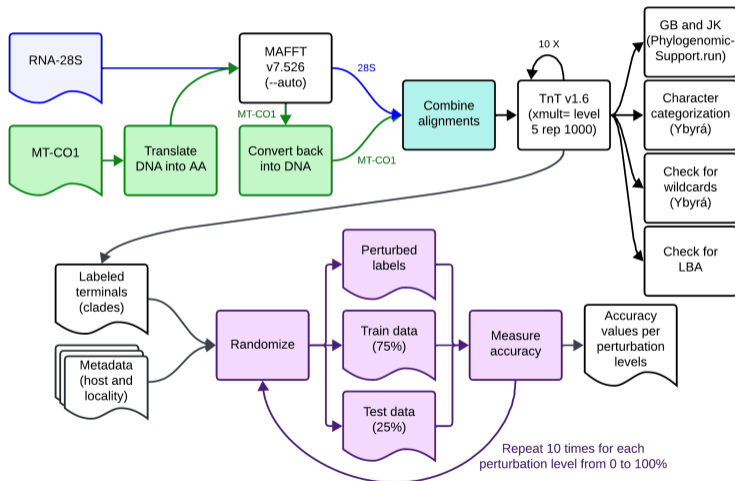
What are machine learning and random forests?



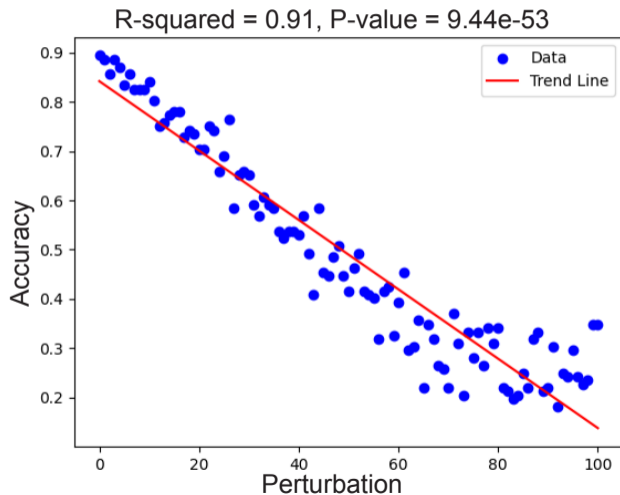
Modified from Fig. 1 from Jakhar & Kaur (2020; DOI: 10.1111/ced.14029).



Our random forest experiment



The effect of clade perturbation over accuracy



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Example application of random forests

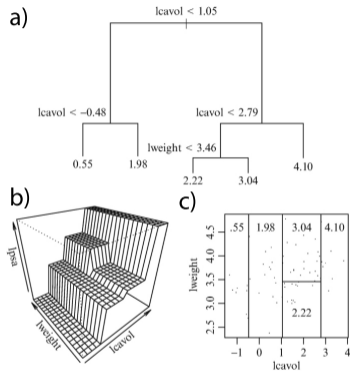


Fig. 3 from Cutler *et al.* (2012; DOI: 10.1007/978-1-4419-9326-7_5).

Prostate cancer data comes from a prostate cancer study (Stamey *et al.* 1989; Hastie *et al.* 2009).

a) Tree diagram.

b) A perspective plot of the fitted regression surface.

c) Partitioning of the predictor space.

Response variable: level of prostate-specific antigen ($lpsa$). **Predictor variables:** log cancer volume ($lcaivol$), log prostate weight ($lweight$), age, log of the amount of benign prostatic hyperplasia ($lbph$), seminal vesicle invasion (svi), log of capsular penetration (lcp), Gleason score ($gleason$), and percentage of Gleason scores 4 or 5 ($pgg45$).

A closer view into our random forests

