

Phylogenetic Transfer Learning

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1 What is this paper?

2 The goal of this paper is to introduce PTL to a broad audience, extend the framework from being specific to
3 latent representation of networks (Strydom *et al.* 2022a, b) to arbitrary traits, and provide guidelines for when
4 PTL is appropriate and how to validate its prediction using both simulated and empirical data

5 What is Phylogenetic Transfer Learning

6 The goal of PTL is to take a species pool for which a given trait is only *partially* observed, and impute the value
7 of that trait for the rest of the species based on the evolutionary relatedness of each species.

8 Ancestral State Reconstruction

9 *Ancestral State Reconstruction* (ASR; also called ancestral character reconstruction, character estimation, or
10 character mapping) is a core topic in phylogenetics (Joy *et al.* 2016). The goal is, given an estimate of a
11 phylogeny \mathcal{P} and trait values T_i for each extant species in the phylogeny i , to estimate the value of that trait at
12 some historical point in the phylogeny (typically at the node representing the MRCA of a clade of interest).

13 To do this, one assumes a statistical model of evolution (and often tries to infer the best among a set of candidate
14 models). Depending on whether the trait of interest is discrete or continuous, the models are typically
15 discrete-space Markov chains (where the transition matrix is a target of inference) or, in the continuous setting,
16 either Brownian Motion or an Ornstein-Uhlenbeck (OU) process (where the parameters of the model are the
17 target of inference). The former is models neutral evolution and the latter is used when there is hypothesized
18 selection on the trait.

19 The methodology used to fit models has followed the historical progression from maximum parsimony models
20 (a naive approach that favors as few evolutionary changes as possible in discrete traits) to maximum likelihood
21 estimation. Modern methods revolve on using Bayesian methods, which has the direct benefit of including
22 uncertainty estimates in inferred ancestral states, and potentially uncertainty in the true topology of the
23 phylogeny itself (Huelsenbeck & Bollback 2001).

24 Typically rate of trait evolution is learned as a single value across the whole phylogeny, and branch length
25 enables ‘amount’ of evolution. Although in principle a hierarchical* model could be used to infer both a global
26 rate of evolution and rate values specific to each branch (*sadly ‘hierarchical’ in this is sense different than

27 ‘hierarchical’ as it is used in Huelsenbeck & Bollback (2001), which refers to different tree models but a single
28 set of parameters across all branches—this is because these models are constructed in the context of DNA
29 substitution rates, which are assumed to be fixed).

30 **Phylogenetic Transfer Learning**

31 The core goal of Phylogenetic Transfer Learning (PTL) is to take a phylogeny \mathcal{P} where the species pool consists
32 of two types of species: (1) species with trait observations, which we denote \mathcal{O} and call the *observed* species
33 and (2) species *without* trait observatoins, which we denote \mathcal{U} and call *unobserved*, and produce predicted trait
34 values for the unobserved species \mathcal{U} .

35 PTL does this by using ASR to infer a parameterized model of evolution and ancestral state of the partially
36 observed trait, and then to simulate the parameterized evolutionary model forward from the ancestral node to
37 get an estimate of trait values (with uncertainty) for each species in U .

38 The *transfer learning* component in particular comes from the first use of this methods to impute latent
39 representations of species based on their position in food-webs (Strydom *et al.* 2022a, b), although the method
40 is flexible enough to be applied to either latent or observed traits.

41 There are two possible models for PTL to be done in: (1) As in (Strydom *et al.* 2022a), the the evolutionary
42 model is inferred only from the observed trait values O . (2) The evolutionary model from a trait for which there
43 are observations available for the entire species pool. It may be the case that evolutionary dynamics inferred
44 with auxillary available information for every species (e.g. the raw sequences from which the tree is built) could
45 improve imputation accuracy.

46 **Substance of the paper**

47 The main substance of this paper is to provide guidelines on when PTL is robust, and diagnostics to validate
48 PTL estimates. This will be done in two parts: **(1)** using simulated phylogenies and trait values to compare
49 efficacy of PTL imputation across known “ground-truth” evolutionary dynamics, and **(2)** using published ASR
50 datasets, with known values for all extant species, to test imputation efficacy empirically.

51 **Simulated phylogenies**

52 First goal is to test predictive efficacy of PTL under various parameterizations of the “ground-truth”
53 evolutionary dynamics, e.g. - Rate of speciation - Rate of evolution - Trait dimensionality & correlation -
54 Frequency of “puntuactions” (i.e. pertubations to trait value at a speciation event)
55 and second to compare efficacy based on different properties of the data, e.g. - Proportion of species with trait
56 values - Predictive efficacy vs. distance to MRCA w/ data - Is there a set of traits for all species to infer
57 evolutionary dynaimcs? - How correlated are evolution between traits for all species vs. traits we want to impute

58 **Real data**

59 Thankfully there are lots of ACR studies out there with data for each extant species. So, in short, find as many
60 ACR studies as we can, and do crossvalidation where we drop the trait values for ~20% of the species and
61 inpute them with PTL, and compare.

62 **Questions to address**

- 63 • What phylogenetic scales can PTL give robust predictions?
 - 64 – There is a clear upper limit (if the MRCA for set of species is too long ago, there will be massive
 - 65 variance in predicted state at the tip)
 - 66 – There is also a lower limit (if there is horizontal-gene-transfer and the phylogeny is not a reliable
 - 67 proxy for how traits are evolving)
 - 68 – Robustness to noise in trait measurements?
 - 69 – How does this vary w/ amount and different types of selection
- 70 • When is PTL overkill?
 - 71 – Weighted average of neighbors by distance as alternative (ack. David Rolnick for idea)
- 72 • What diagnostics can we use to be confident a PTL inputated trait is statistically robust?

73 Possible Applications

74 The core idea of PTL is to fill in gaps for data-sparse processes in ecology, so naturally the applications are
75 going to be focused.

76 Link prediction in networks

77 This is the inciting question for which the idea was conceived(Strydom *et al.* 2022a). Interactions are hard to
78 sample (Catchen2022MisLin?). Not much to say here that isn't in (Strydom *et al.* 2022b).

79 Forecasting species range shifts

80 Many projections of species range shifts under climate change are based on statistical associations between
81 historical species observations and climatic conditions. The gap between so-called correlative vs. mechanistic
82 species distribution models (Shabani *et al.* 2016) is of critical interest for forecasting species ranges, but robust
83 mechanistic understandings about what and why climatic conditions limit where a species' range require
84 detailed sampling and potentially experimental conditions (Lee-Yaw *et al.* 2016), which are difficult to scale.
85 PTL could potentially alleviate this by giving good proxies of the physiological limitations of species ranges for
86 more species.

87 Connectivity and movement ecology

88 Reliable information about species movement is sparse, and PTL could fill this gap (Catchen *et al.* 2023).

89 Model species and ecological monitoring

90 There are a lot of species on Earth. Monitoring them all would be hard. Can we use single species a proxies for
91 larger groups of species? Maybe a little. PTL can guide us on what good proxy species are.

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