

## Introduction

Phylogenetic trees estimate the evolutionary history among species.

**Phylogenetic diversity (PD)** measures the total length of a tree: each time a species goes extinct, *PD* is lost (Figure 1). **Extinction risk (*p*)** can be assigned to species and used to calculate the projected *PD* of a tree<sup>1</sup>. Extinction risk is often **clumped** and high projected losses are ascribed at least in part to this clumpiness<sup>2,3,4</sup>.

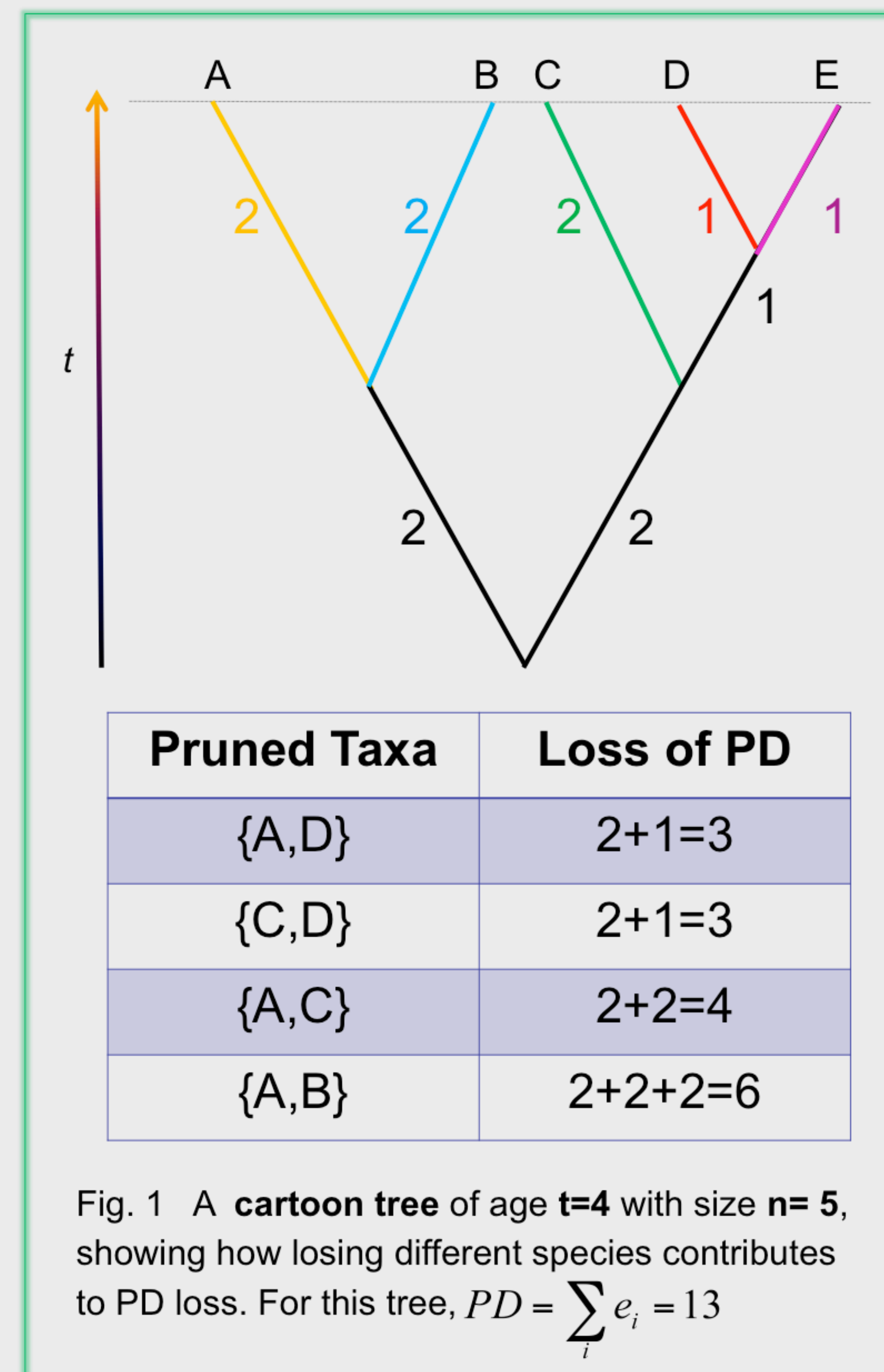
Here we quantify the loss of *PD* due to clumped extinction risk<sup>5</sup> on model trees.

## Methods

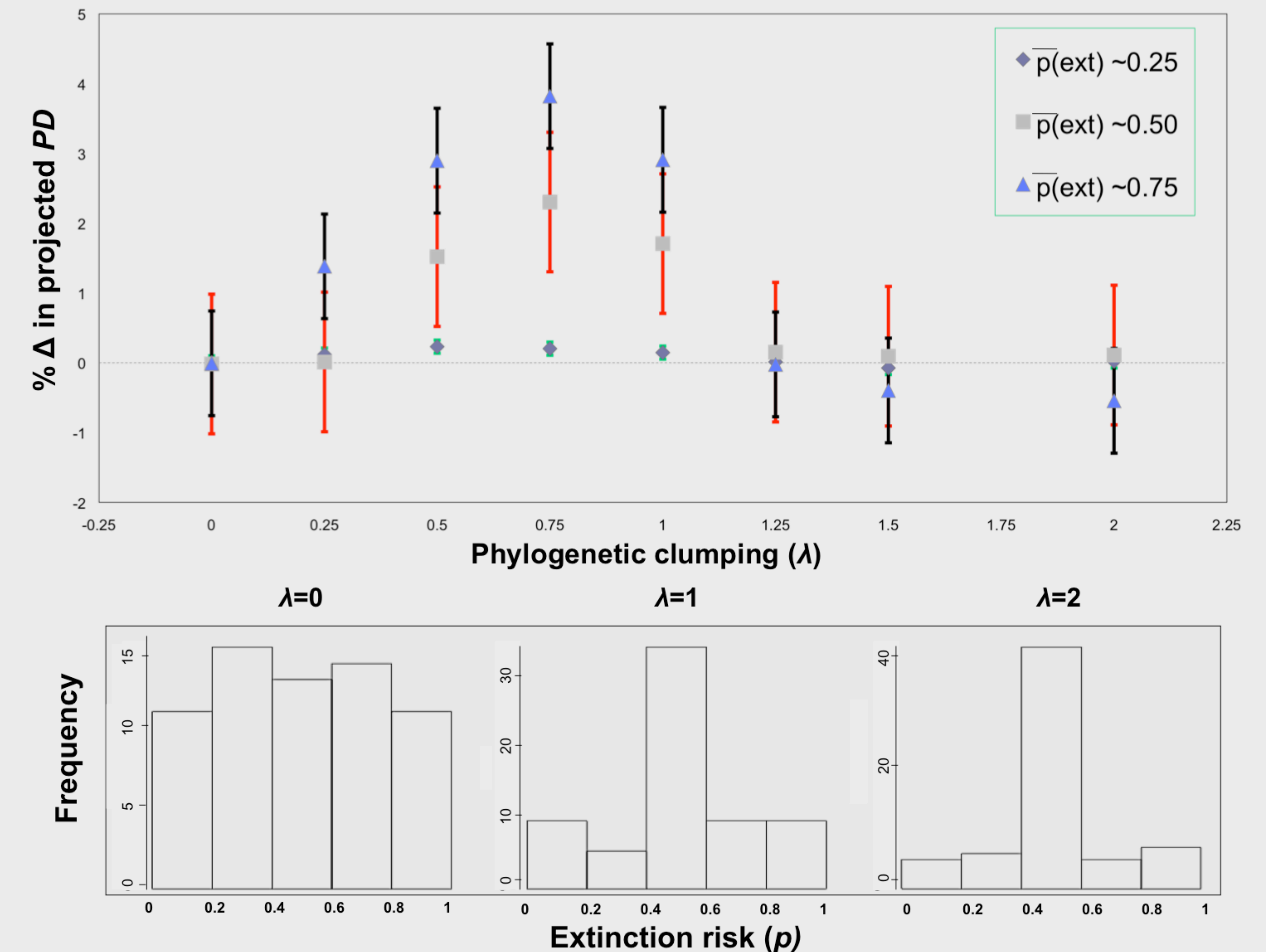
1. We simulated continuous traits on each of 1000 64-tip Yule trees<sup>6</sup> under the Brownian motion model.
2. We transformed these species traits into extinction risk (*p*).
3. We used *p* and the edge lengths (*e*) to calculate the projected *PD* [*E*(*PD*)] of a tree<sup>1</sup>, where *j* tips subtend each of *i* edges:

$$E(PD) = \sum_i e_i (1 - \prod_j p_j)$$

4. %  $\Delta$  in projected *PD* compares projected *PD* with the *PD* when the same *p*'s are randomly shuffled on the tree, i.e. there is no clumpiness.
5. We repeated steps 1 - 4 to model loss at various levels of clumpiness ( $\lambda$ )<sup>7</sup>.



## Results



## Discussion

Clumping causes very minimal extra loss of *PD* (%  $\Delta$  in projected *PD* <4%). Extreme levels of clumping leads to even less extra loss, due to the change in distribution of extinction risks across the tips. Other diversification models (not shown) produce similar results.

Thus, factors other than clumping alone, like tree topology<sup>5</sup> and the fact that high *p* values are concentrated in species-poor regions<sup>8</sup> of trees are more important in explaining recent high projected losses of *PD*.