Predator phylogenetic diversity decreases predation rate via antagonistic interactions

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Introduction

We test three related hypotheses:

1. *species co-occurance*: closely-related predators occur together more frequently than less-related predators, due to their similar habitat requirements. Additionally, very closely related species never co-occur because they are too similar.

2. *diet similarity*: similarity in diet (as measured by feeding trials) decreases with phylogenetic distance.

3. *ecosystem-level effects*: similarity in the effect of predators on whole ecosystems declines with phylogenetic distance. Additionally, the non-additive effect of predators will have a greater absolute value when their phylogenetic diversity is larger.

Methods

Results

metabolic capacity and phylogenetic distance

```
## [1] "insects.to.leeches.csv"
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## [2] "odonata-Tabanidae.csv"
## [3] "tabanidae_culidicae_ie_Diptera.csv"
```

We identified 14 in the 2008 dataset as predators. These predators vary in taxonomic relatedness: from congeners (*Bezzia* sp. (Diptera:Ceratopogonidae) with two species, *Leptagrion* sp. (Odonata:Coenagrionidae) with three) to confamilials (three species of Tabanidae and two of Empididae, all Diptera). Three families of Diptera are represented by a single species each: Dolichopodidae, Corethrellidae and Chironomidae. The deepest taxonomic divide is between all insects present and a species of leech (Annelida:Hirudinidae). Node age data was available for all but the shallowest nodes of the tree, where either a lack of taxonomic information (e.g. Tabanidae) or a lack of phylogenetic studies (e.g. *Leptagrion*) prevented more information from being included. These branches were left as polytomies, and were all assigned identical, arbitrary and short branch lengths (15 Mya).

We obtained node age estimates for all 7 internal nodes of the tree. These were usually provided by only a single study, with more studies available for deeper nodes: Insecta–Hirudina (n=5, 543 to 700 Mya), Odonata–Tabanidae (n=4, 151 to 543 Mya) and Tabanidae–Diptera (n=7, 151 to 543 Mya). We used the median estimate of age for these nodes.

In 2008, insects were counted and measured in an observational study of 25 bromeliads. Across all bromeliads, predator species differed widely in metabolic capacity, from 0.0062 for a species of Empidid, to 0.4804 for the abundant predator *Leptagrion andromache*. Predators often co-occured in bromeliads (3.52 ± 3.1107 per plant). However, the euclidian distance between the total metabolic capacity of two predators did not show any relationship with phylogenetic distance between them ($F_{1,89}$=1.5558,P=0.2155).

diet similarity and phylogenetic distance

All predators showed a very generalist diet breadth. However, more phylogenetically distinct predators preferred slightly more distant prey, as measured by euclidian distance between

feeding trial outcomes ($F_{1,19}$=5.1641,P=0.0349) Regression was weighted by the number of trials conducted.

Ecosystem-level effects and phylogenetic distance

All increases in predator phylogenetic diversity beyond damselflies resulted in a reduction of prey mortality.

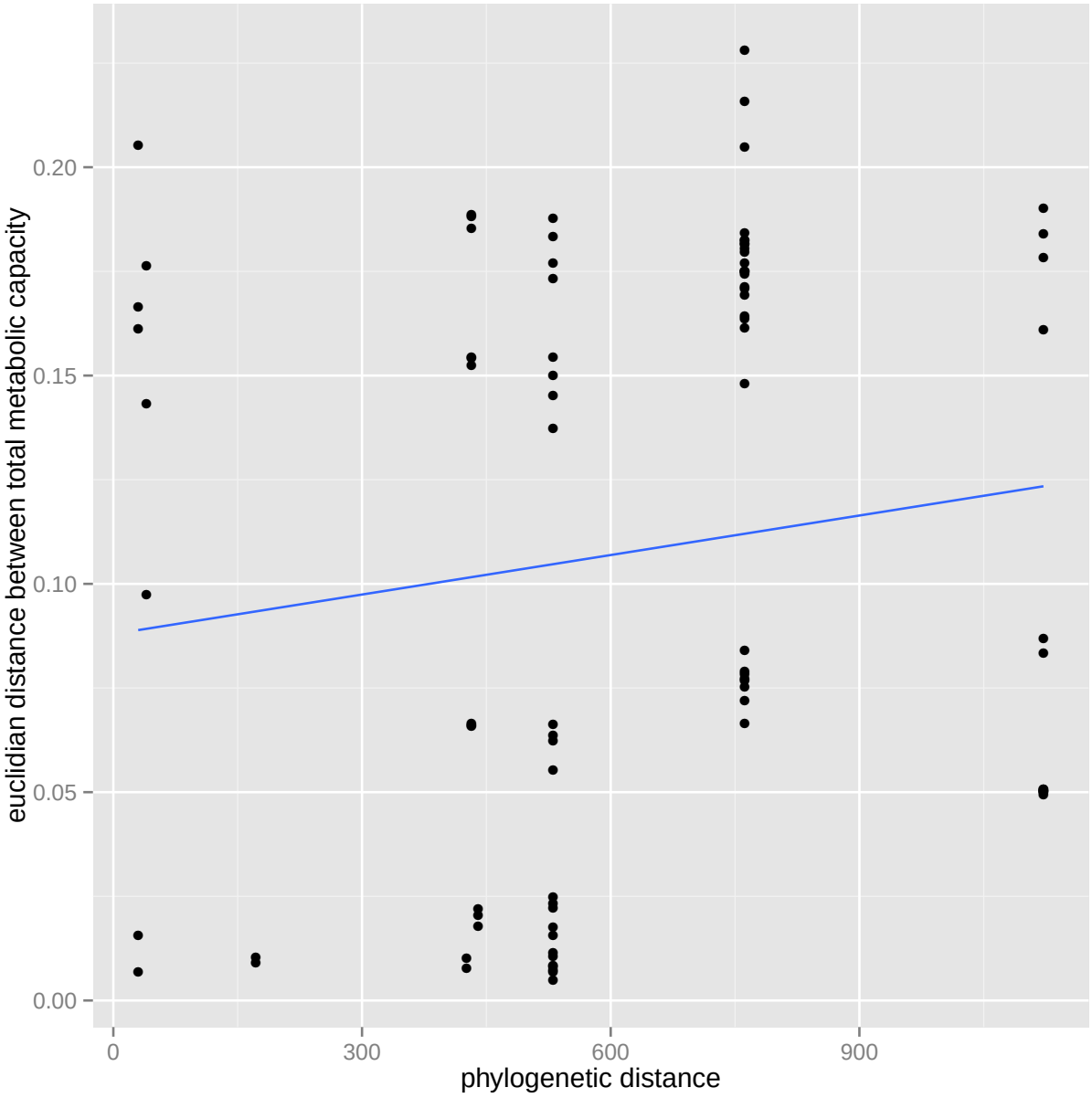
predator addition treatments did not differ strongly from predator-free controls. We did not find significant differences for FPOM, decompositon, or bromeliad growth. However, we did find results for N15 uptake into bromeliads. Our strongest differences were in insect survivorship, which decreased in all predator treatments relative to control.

Figures

controls not really differen

Discussion

Works Cited



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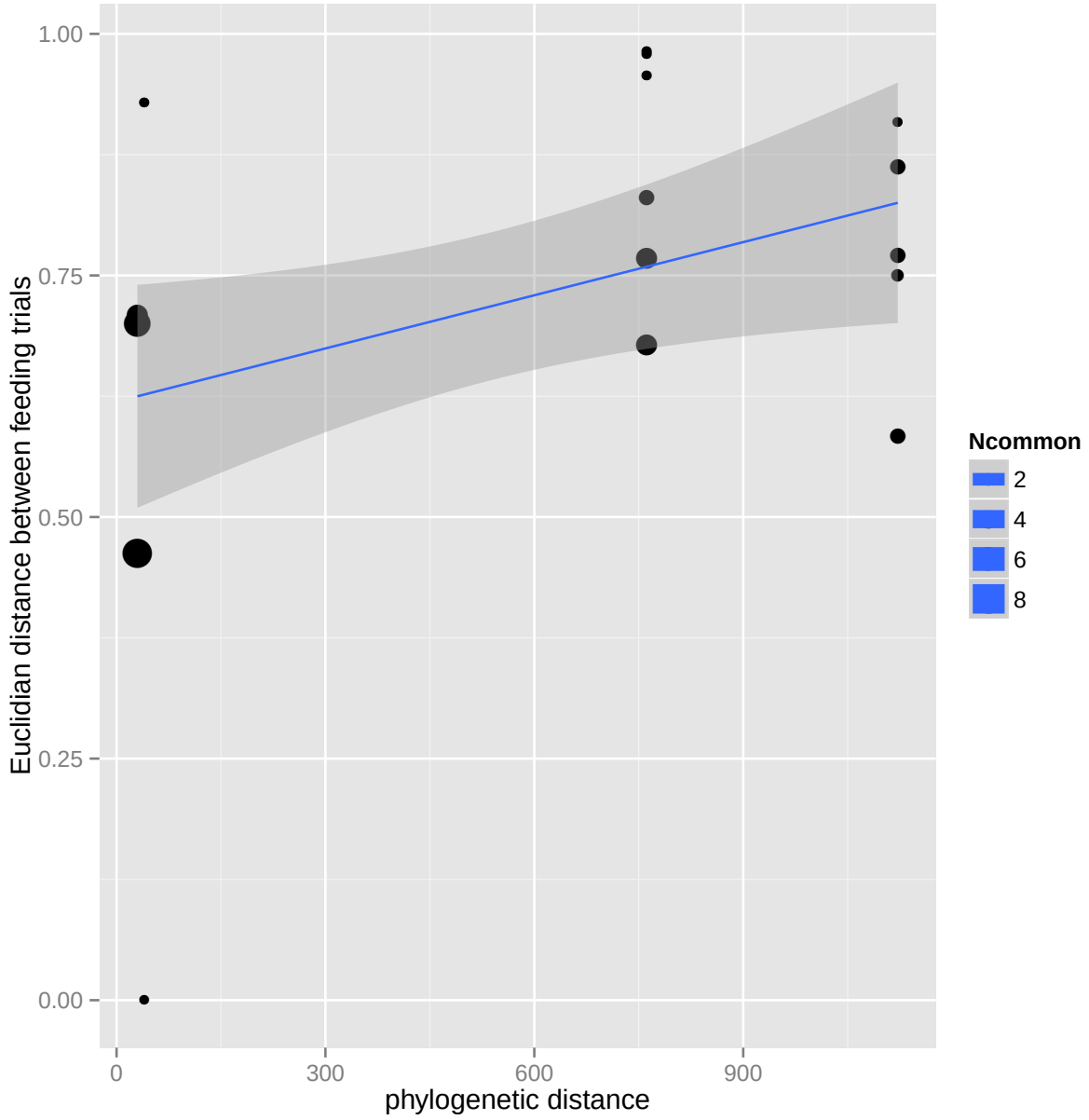

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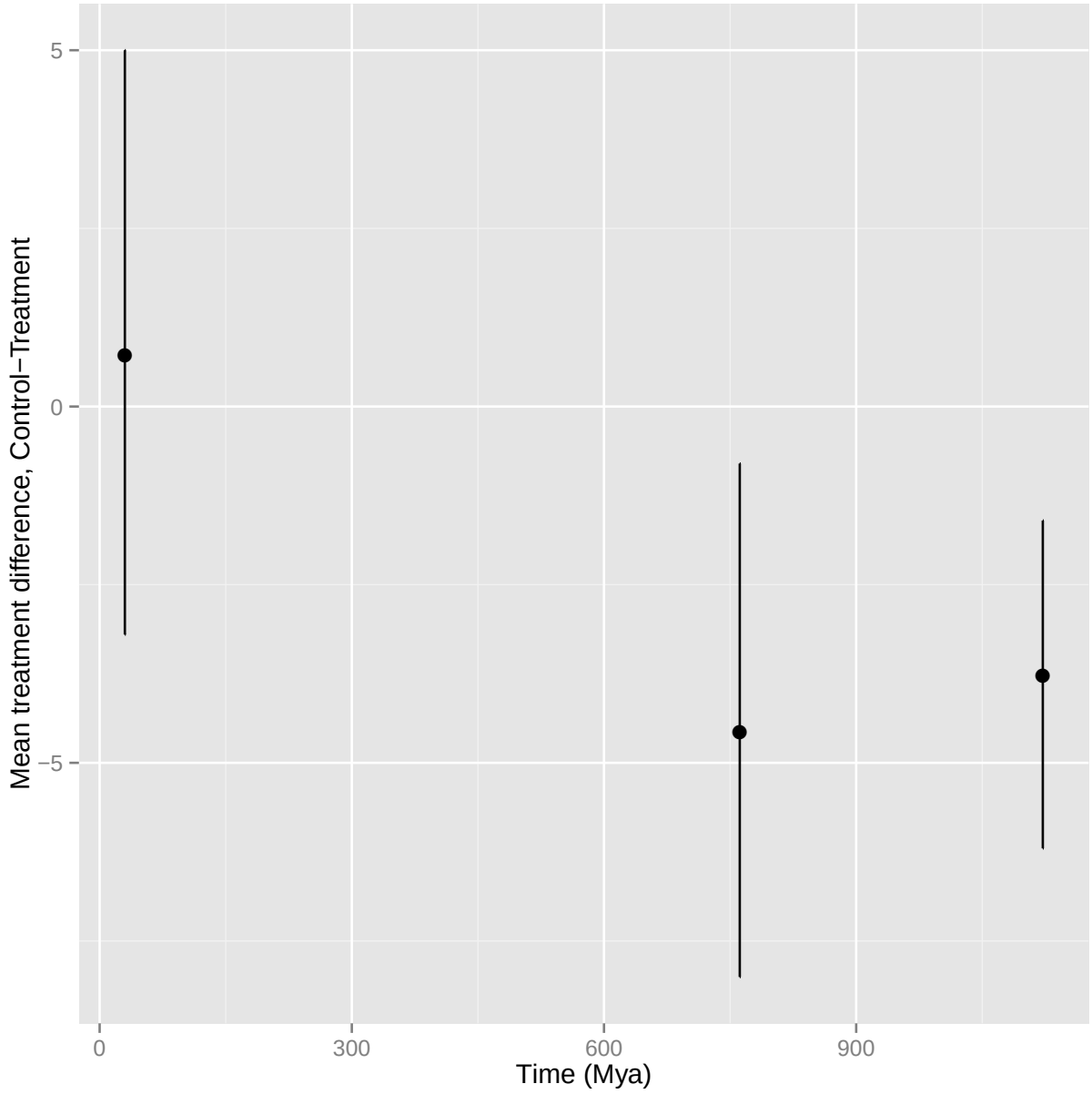

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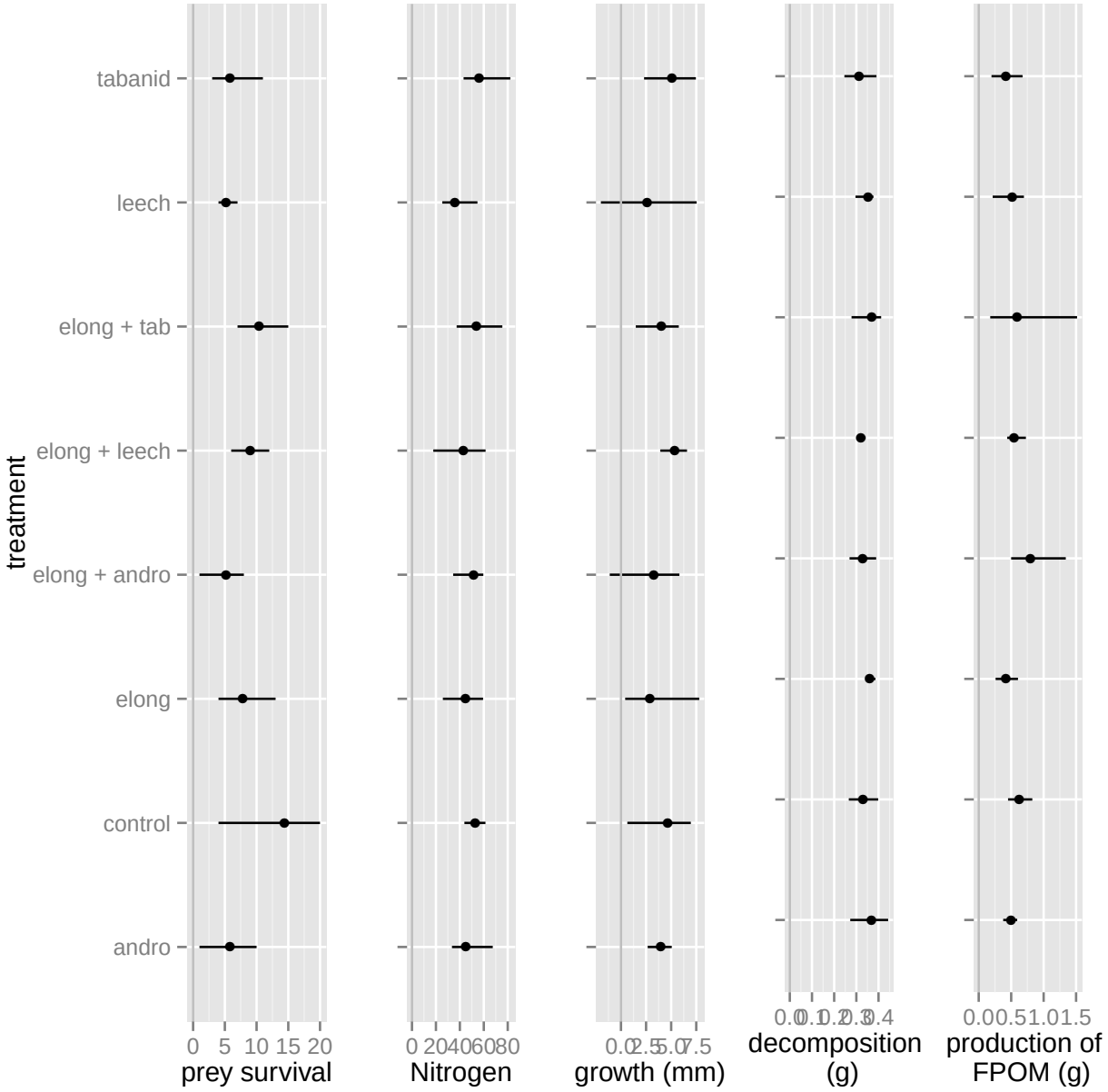

Figure 4: FALSE