**Supporting Information for**

**Rates of biome shift predict diversification dynamics in flowering plants.**

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**This PDF file includes:**

Figure S1 – S15

Table S1

Supporting text – label switching

SI references

**Figure S1:** (a) Here focal characters (orange, light green, and dark green) lead to increases or decreases in turnover rates throughout the clade. This is what is typically modeled by a BiSSE analysis. (b) Trait lability, here modeled as faster (black) or slower (grey) transition rates between the observed states, are positively associated with turnover rates, such that more labile lineages also experience higher speciation and extinction rates. This can be modeled using hidden Markov models, where the red and blue paintings are hidden states describing the dynamics of the observed states. (c) The reverse pattern shown in (b). Here, lineages with lower transition rates experience higher turnover rates.

A diagram of a graph

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**Figure S2:** (a) Backbone phylogeny used in the phylogenetic regression analyses. (b) Support for rate heterogeneity as calculated by the sum of the models which are concordant with a particular level of heterogenity. hidden\_incl is whether there is support for hidden rate classes at all. turn\_differ is whether there is evidence for differences in turnover between rate classes, but no differences in transition rates. trans\_differ is whether there is evidence for differences in transition rates between rate classes, but no differences in turnover rates. both\_differ is the support for models in which both transition rates and turnover rates differ between rate classes.

A graph of a number of different types of cells

Description automatically generated with medium confidence

**Figure S3:** Ancestral state reconstructions per clade: monocots. Green: closed-canopy biome, yellow: widespread, orange: open-canopy biome.

A screenshot of a graph

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**Figure S4:** Ancestral state reconstructions per clade: monocots (cont.). Green: closed-canopy biome, yellow: widespread, orange: open-canopy biome.

A screenshot of a computer screen

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**Figure S5:** Ancestral state reconstructions per clade: monocots (cont.). Green: closed-canopy biome, yellow: widespread, orange: open-canopy biome.

A screenshot of a computer screen

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**Figure S6:** Ancestral state reconstructions per clade: asterids. Green: closed-canopy biome, yellow: widespread, orange: open-canopy biome.

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**Figure S7:** Ancestral state reconstructions per clade: asterids (cont.). Green: closed-canopy biome, yellow: widespread, orange: open-canopy biome.

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**Figure S8:** Ancestral state reconstructions per clade: asterids (cont.). Green: closed-canopy biome, yellow: widespread, orange: open-canopy biome.

A screenshot of a computer screen

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**Figure S9:** Ancestral state reconstructions per clade: rosids. Green: closed-canopy biome, yellow: widespread, orange: open-canopy biome.

A screenshot of a graph

Description automatically generated

**Figure S10:** Ancestral state reconstructions per clade: rosids (cont.). Green: closed-canopy biome, yellow: widespread, orange: open-canopy biome.

A screenshot of a computer screen

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**Figure S11:** Ancestral state reconstructions per clade: rosids (cont.). Green: closed-canopy biome, yellow: widespread, orange: open-canopy biome.

A screenshot of a computer screen

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**Figure S12:** Ancestral state reconstructions per clade: asterids. Green: closed-canopy biome, yellow: widespread, orange: open-canopy biome.

A screenshot of a graph

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**Figure S13:** Ancestral state reconstructions per clade: asterids (cont.). Green: closed-canopy biome, yellow: widespread, orange: open-canopy biome.

A screenshot of a computer screen

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**Figure S14:** Ancestral state reconstructions per clade: asterids (cont.). Green: closed-canopy biome, yellow: widespread, orange: open-canopy biome.

A screenshot of a computer screen

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**Figure S15:** Ancestral state reconstructions per clade: other. Green: closed-canopy biome, yellow: widespread, orange: open-canopy biome.

A diagram of a tree

Description automatically generated with medium confidence

**Table S1:** Clade number (n), clade name, original study (reference), major group and ingroup number of tips (Ntips) and sampling fraction (Sf) for each clade.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| n | name | reference | group | Ntips ingroup | Sf ingroup |
| 1 | *Croton* (Euphorbiaceae) | Arevalo et al. (2017) | rosids | 307 | 0.24 |
| 2 | Chrysobalanaceae | Chave et al. (2020) | rosids | 164 | 0.29 |
| 3 | *Begonia* (Begoniaceae) | Moonlight et al. (2015) | rosids | 268 | 0.13 |
| 4 | Fagales | Xing et al. (2014) | rosids | 579 | 0.42 |
| 5 | *Ficus* (Moraceae) | Zhang et al. (2018) | rosids | 272 | 0.25 |
| 6 | *Lupinus* (Fabaceae) | Drummond et al. (2012) | rosids | 120 | 0.45 |
| 7 | Mimosoids (Fabaceae) | Ringelberg et al. (2023) | rosids | 2078 | 0.59 |
| 8 | *Chamaecrista* (Fabaceae) | Vasconcelos et al. (2020) | rosids | 108 | 0.32 |
| 9 | Thelypodieae (Brassicaceae) | Huang et al. (2019) | rosids | 128 | 0.46 |
| 10 | Arabideae (Brassicaceae) | Huang et al. (2019) | rosids | 347 | 0.6 |
| 11 | Alysseae (Brassicaceae) | Huang et al. (2019) | rosids | 156 | 0.52 |
| 12 | Erysimeae (Brassicaceae) | Huang et al. (2019) | rosids | 108 | 0.4 |
| 13 | Cardamineae (Brassicaceae) | Huang et al. (2019) | rosids | 159 | 0.37 |
| 14 | Lepidieae (Brassicaceae) | Huang et al. (2019) | rosids | 138 | 0.49 |
| 15 | Bombacoideae (Malvaceae) | Zizka et al. (2020) | rosids | 103 | 0.59 |
| 16 | Anarcardiaceae | Weeks et al. (2014) | rosids | 305 | 0.24 |
| 17 | Meliaceae | Koenen et al. (2015) | rosids | 254 | 0.34 |
| 18 | Melastomataceae | Reginato et al. (2022) | rosids | 2454 | 0.42 |
| 19 | Myrteae (Myrtaceae) | NMWG (2024) | rosids | 712 | 0.28 |
| 20 | *Eucalyptus* (Myrtaceae) | Thornhill et al. (2019) | rosids | 716 | 0.9 |
| 21 | Onagraceae | Freyman & Hohna (2018) | rosids | 292 | 0.45 |
| 22 | *Salvia* (Lamiaceae) | Kriebel et al. (2020) | asterids | 519 | 0.52 |
| 23 | *Ruellia* (Acanthaceae) | Tripp & Tsai (2012) | asterids | 172 | 0.43 |
| 24 | Bignonieae (Bignoniaceae) | Lohmann et al. (2012) | asterids | 105 | 0.26 |
| 25 | Antirrhineae (Plantaginaceae) | Gorospe et al. (2020) | asterids | 336 | 1 |
| 26 | Spermacoceae (Rubiaceae) | Neupane et al. (2017) | asterids | 365 | 0.36 |
| 27 | Vanguerieae (Rubiaceae) | Verstraete et al. (2017) | asterids | 163 | 0.25 |
| 28 | Apocynaceae | Fishbein et al. (2018) | asterids | 1041 | 0.21 |
| 29 | Solanaceae | Sarkinen et al. (2013) | asterids | 1075 | 0.4 |
| 30 | Lobelioideae (Campanulaceae) | Lagomarsino et al. (2017) | asterids | 153 | 0.39 |
| 31 | *Viburnum* (Adoxaceae) | Landis et al. (2021) | asterids | 163 | 1 |
| 32 | Apioideae (Apiaceae) | Banasiak et al. (2013) | asterids | 1194 | 0.41 |
| 33 | Primuloideae (Primulaceae) | De Vos et al. (2014) | asterids | 265 | 0.38 |
| 34 | Lysimachieae (Primulaceae) | Yan et al. (2018) | asterids | 126 | 0.5 |
| 35 | Lecythidaceae | Vargas & Dick (2020) | asterids | 110 | 0.55 |
| 36 | Ericaceae | Schwery et al. (2015) | asterids | 450 | 0.1 |
| 37 | *Hakea* (Proteaceae) | Cardillo et al. (2017) | other | 146 | 0.95 |
| 38 | *Heliconia* (Heliconiaceae) | Iles et al. (2017) | monocots | 203 | 0.77 |
| 39 | Arecaceae | Onstein et al. (2018) | monocots | 2539 | 1 |
| 40 | Poaceae | Spriggs et al. (2014) | monocots | 3595 | 0.33 |
| 41 | Restionaceae | Linder (2020) | monocots | 351 | 0.7 |
| 42 | *Paepalanthus* (Eriocaulaceae) | Vasconcelos et al. (2020) | monocots | 180 | 0.42 |
| 43 | *Carex* (Cyperaceae) | Martin-Bravo et al. (2019) | monocots | 1386 | 0.69 |
| 44 | Vrieseinae (Bromeliaceae) | Kessous et al. (2020) | monocots | 103 | 0.37 |
| 45 | *Allium* (Amaryllidaceae) | Han et al. (2019) | monocots | 484 | 0.46 |
| 46 | *Bulbophyllum* (Orchidaceae) | Gamisch & Comes (2019) | monocots | 319 | 0.16 |
| 47 | Cyclanthaceae | Leal et al. (2022) | monocots | 103 | 0.45 |
| 48 | Velloziaceae | Alcantara et al. (2018) | monocots | 151 | 0.57 |
| 49 | Annonaceae | Onstein et al. (2019) | other | 235 | 0.1 |

Supporting Information Text: Regression Distribution Results

## Label switching and the impact on regression results

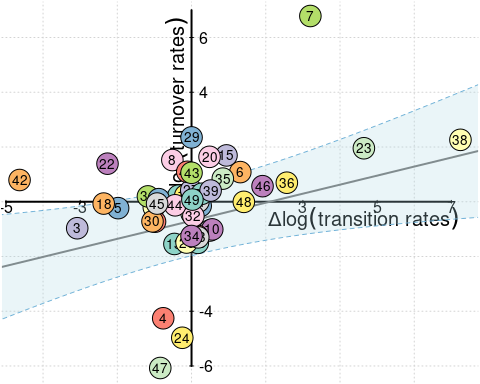
One of the quirks of hidden Markov models (HMMs) is that the labeling of rate classes is arbitrary. Not in the sense that labels are meaningless, but rate that it makes no difference whether something is labeled as A or B (a rate by any other name would smell as sweet).

This presents a problem for optimization since this means that there are two parameterizations with exactly the same likelihood (swapping rate class A and rate class B). Within packages like corHMM or hisse we have tried to circumvent this issue by generally forcing one rate class to be faster than another. This is done internally to help with the likelihood search but should also provide more consistency in the output results. Nonetheless, this issue could still impact our analysis of parameter estimates.

The impact on our regression estimates would be due to the fact that whether we are subtracting B from A is not consistent across our datasets. This means that you could comfortably flip, for any given clade, whether you are subtracting A from B or B from A. In this vignette, I will run a randomization test to determine whether the default results are trustworthy

Let’s review our initial results.

##   
## Call:  
## phylolm(formula = d\_turns ~ d\_trans, data = lm\_dat, phy = phy\_bb,   
## boot = 1000)  
##   
## AIC logLik   
## 197.12 -95.56   
##   
## Raw residuals:  
## Min 1Q Median 3Q Max   
## -5.1012 0.2260 0.7647 1.2625 6.4253   
##   
## Mean tip height: 135.9122  
## Parameter estimate(s) using ML:  
## sigma2: 0.0296571   
##   
## Coefficients:  
## Estimate StdErr t.value lowerbootCI upperbootCI p.value   
## (Intercept) -0.695293 0.609029 -1.141642 -1.861859 0.4518 0.25939   
## d\_trans 0.330045 0.135031 2.444214 0.083361 0.5882 0.01832 \*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## R-squared: 0.1128 Adjusted R-squared: 0.0939   
##   
## sigma2: 0.0296571  
## bootstrap mean: 0.02840432 (on raw scale)  
## 0.02778195 (on log scale, then back transformed)  
## bootstrap 95% CI: (0.01778029,0.04098993)  
##   
## Parametric bootstrap results based on 1000 fitted replicates



The results of our initial regression are shown above. We find a significant non-zero slope. However, as discussed above, for each clade, rate class a and rate class b are interchangeable. If we shuffle the rate classes around randomly, we will get a different result.

Let’s look at the raw data as a starting point. The data shown below are the transition rates for all possible transitions in our model with the order as follows:

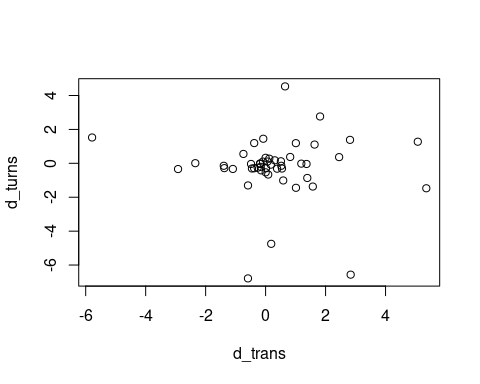
demo\_df <- data.frame( a = head(rate\_class\_a\_rate),  
 b = head(rate\_class\_b\_rate))  
print(demo\_df)

## a.1 a.2 a.3 a.4 b.1 b.2 b.3  
## 1 1.3326693 0.91372757 0.2759942 0.1598574 0.82861701 0.5864088 0.2800526  
## 2 4.9219393 5.42387691 79.7965024 34.8578563 4.85165113 5.0091649 79.5819495  
## 3 7.3769518 74.20552435 13.9641454 74.4910010 0.02403847 0.2138439 1.1785288  
## 4 1.3308422 12.88786020 0.4080388 9.9758091 0.42336915 3.9711361 0.4093351  
## 5 15.6736533 8.11807005 19.6690682 2.6754370 2.28548958 2.4752178 1.3565549  
## 6 0.1514647 0.09133707 0.3293246 0.1734857 1.24066757 0.9679194 0.4678052  
## b.4  
## 1 0.18960221  
## 2 34.95402507  
## 3 6.40132668  
## 4 6.66990903  
## 5 0.26680956  
## 6 0.09777796

## Random shuffling for a null distribution

To begin with let’s try and examine a null expectation. In this case, if we were to randomly shuffle all transition rates and turnover rates (mixing rate class A and B) we would not expect to find an association. By shuffling rate classes any estimated differences between rate class A and rate class B should be removed.

shuffled\_rates <- cbind(rate\_class\_a\_rate, rate\_class\_b\_rate)  
shuffled\_rates <- apply(shuffled\_rates, 1,   
 function(x) x[sample(1:8,8)])  
shuffled\_rate\_class\_a\_rate <- t(shuffled\_rates)[,1:4]  
shuffled\_rate\_class\_b\_rate <- t(shuffled\_rates)[,5:8]  
  
  
shuffled\_turns <- cbind(rate\_class\_a\_turn, rate\_class\_b\_turn)  
shuffled\_turns <- apply(shuffled\_turns, 1,   
 function(x) x[sample(1:6,6)])  
shuffled\_rate\_class\_a\_turn <- t(shuffled\_turns)[,1:3]  
shuffled\_rate\_class\_b\_turn <- t(shuffled\_turns)[,4:6]  
  
d\_turns <- d\_trans <- c()  
for(i in 1:49){  
 d\_trans <- (c(d\_trans, log(rowMeans(shuffled\_rate\_class\_b\_rate)[i]) -   
 log(rowMeans(shuffled\_rate\_class\_a\_rate)[i])))  
 d\_turns <- (c(d\_turns, log(rowMeans(shuffled\_rate\_class\_b\_turn)[i]) -   
 log(rowMeans(shuffled\_rate\_class\_a\_turn)[i])))  
}  
  
lm\_dat\_null <- data.frame(row.names = gsub(" .\*", "", plot\_data[,1]),  
 d\_trans = d\_trans,  
 d\_turns = d\_turns)  
fit\_null = phylolm(d\_turns ~ d\_trans, data=lm\_dat\_null, phy=phy\_bb, boot = 0)  
plot(lm\_dat\_null)



summary(fit\_null)

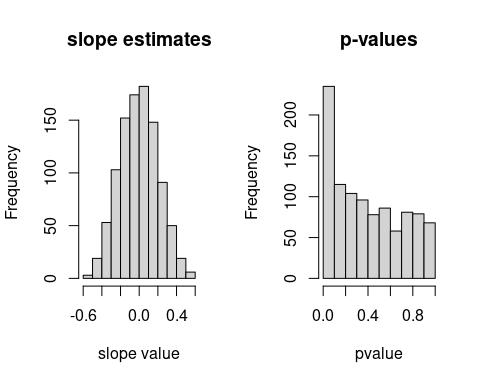
##   
## Call:  
## phylolm(formula = d\_turns ~ d\_trans, data = lm\_dat\_null, phy = phy\_bb,   
## boot = 0)  
##   
## AIC logLik   
## 213.4 -103.7   
##   
## Raw residuals:  
## Min 1Q Median 3Q Max   
## -6.9000 -0.4947 -0.1728 0.2577 4.5177   
##   
## Mean tip height: 135.9122  
## Parameter estimate(s) using ML:  
## sigma2: 0.04131173   
##   
## Coefficients:  
## Estimate StdErr t.value p.value  
## (Intercept) 0.068362 0.721982 0.0947 0.9250  
## d\_trans -0.076683 0.168277 -0.4557 0.6507  
##   
## R-squared: 0.004399 Adjusted R-squared: -0.01678

This suggests this shuffling procedure did succesfully remove the signal as the slope is not significantly different from 0. the Let’s iterate this shuffling procedure 1000 times and create a null distribution of slope estimates.

all\_fits\_shuffled <- list()  
for(j in 1:1000){  
 shuffled\_rates <- cbind(rate\_class\_a\_rate, rate\_class\_b\_rate)  
 shuffled\_rates <- apply(shuffled\_rates, 1,   
 function(x) x[sample(1:8,8)])  
 shuffled\_rate\_class\_a\_rate <- t(shuffled\_rates)[,1:4]  
 shuffled\_rate\_class\_b\_rate <- t(shuffled\_rates)[,5:8]  
   
   
 shuffled\_turns <- cbind(rate\_class\_a\_turn, rate\_class\_b\_turn)  
 shuffled\_turns <- apply(shuffled\_turns, 1,   
 function(x) x[sample(1:6,6)])  
 shuffled\_rate\_class\_a\_turn <- t(shuffled\_turns)[,1:3]  
 shuffled\_rate\_class\_b\_turn <- t(shuffled\_turns)[,4:6]  
   
 d\_turns <- d\_trans <- c()  
 for(i in 1:49){  
 d\_trans <- (c(d\_trans, log(rowMeans(shuffled\_rate\_class\_b\_rate)[i]) -   
 log(rowMeans(shuffled\_rate\_class\_a\_rate)[i])))  
 d\_turns <- (c(d\_turns, log(rowMeans(shuffled\_rate\_class\_b\_turn)[i]) -   
 log(rowMeans(shuffled\_rate\_class\_a\_turn)[i])))  
 }  
 lm\_dat\_shuffle <- data.frame(row.names = gsub(" .\*", "", plot\_data[,1]),  
 d\_trans = d\_trans,  
 d\_turns = d\_turns)  
 fit\_shuffle = phylolm(d\_turns ~ d\_trans, data=lm\_dat\_shuffle, phy=phy\_bb, boot = 0)  
 all\_fits\_shuffled[[j]] <- fit\_shuffle  
}

Distribution of the p-values and slope estimates.

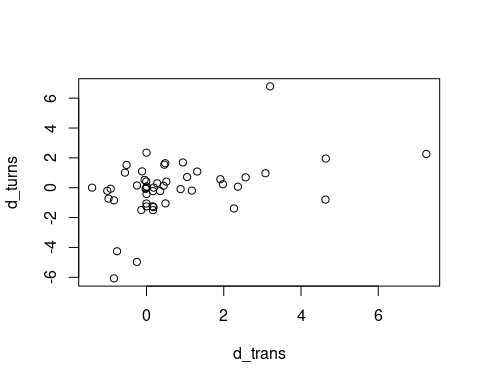
shuffled\_est <- lapply(all\_fits\_shuffled,   
 function(x) summary(x)$coefficients[2,c(1,4)])  
shuffled\_est\_df <- do.call(rbind,shuffled\_est)  
  
par(mfrow=c(1,2))  
hist(shuffled\_est\_df[,1], main = "slope estimates", xlab = "slope value")  
hist(shuffled\_est\_df[,2], main = "p-values", xlab = "pvalue")



## Random shuffling for robustness against label switching

With a null expectation established let’s shuffle rate classes in a way that should preserve the signal by randomly shuffling labels. The shuffling will randomly select between 1 and 49 clades and then randomly choose which of those clades will swap the labels on the rate class A and B.

no\_to\_swap <- sample(1:49, 1)  
to\_swap <- sample(1:49, no\_to\_swap, FALSE)  
d\_turns <- d\_trans <- c()  
for(i in 1:49){  
 if(i %in% to\_swap){  
 d\_trans <- (c(d\_trans, log(rowMeans(rate\_class\_a\_rate)[i]) -   
 log(rowMeans(rate\_class\_b\_rate)[i])))  
 d\_turns <- (c(d\_turns, log(rowMeans(rate\_class\_a\_turn)[i]) -   
 log(rowMeans(rate\_class\_b\_turn)[i])))  
 }else{  
 d\_trans <- (c(d\_trans, log(rowMeans(rate\_class\_b\_rate)[i]) -   
 log(rowMeans(rate\_class\_a\_rate)[i])))  
 d\_turns <- (c(d\_turns, log(rowMeans(rate\_class\_b\_turn)[i]) -   
 log(rowMeans(rate\_class\_a\_turn)[i])))  
 }  
}  
  
lm\_dat\_shuffle <- data.frame(row.names = gsub(" .\*", "", plot\_data[,1]),  
 d\_trans = d\_trans,  
 d\_turns = d\_turns)  
fit\_shuffle = phylolm(d\_turns ~ d\_trans, data=lm\_dat\_shuffle, phy=phy\_bb, boot = 0)  
plot(lm\_dat\_shuffle)



If we look at the data we can see that the data has been shuffled.

summary(fit\_shuffle)

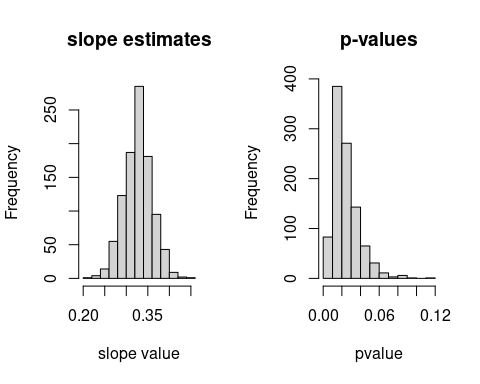
##   
## Call:  
## phylolm(formula = d\_turns ~ d\_trans, data = lm\_dat\_shuffle, phy = phy\_bb,   
## boot = 0)  
##   
## AIC logLik   
## 199.45 -96.73   
##   
## Raw residuals:  
## Min 1Q Median 3Q Max   
## -5.0231 -0.1293 0.5493 1.0316 6.2659   
##   
## Mean tip height: 135.9122  
## Parameter estimate(s) using ML:  
## sigma2: 0.03110491   
##   
## Coefficients:  
## Estimate StdErr t.value p.value   
## (Intercept) -0.72392 0.62892 -1.1511 0.2555   
## d\_trans 0.38879 0.14819 2.6236 0.0117 \*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## R-squared: 0.1277 Adjusted R-squared: 0.1092

However, we are still able to recover a significantly positive slope. Lets repeat this procedure 1000 times.

all\_fits <- list()  
for(j in 1:1000){  
 no\_to\_swap <- sample(1:49, 1)  
 to\_swap <- sample(1:49, no\_to\_swap, FALSE)  
 d\_turns <- d\_trans <- c()  
 for(i in 1:49){  
 if(i %in% to\_swap){  
 d\_trans <- (c(d\_trans, log(rowMeans(rate\_class\_a\_rate)[i]) -   
 log(rowMeans(rate\_class\_b\_rate)[i])))  
 d\_turns <- (c(d\_turns, log(rowMeans(rate\_class\_a\_turn)[i]) -   
 log(rowMeans(rate\_class\_b\_turn)[i])))  
 }else{  
 d\_trans <- (c(d\_trans, log(rowMeans(rate\_class\_b\_rate)[i]) -   
 log(rowMeans(rate\_class\_a\_rate)[i])))  
 d\_turns <- (c(d\_turns, log(rowMeans(rate\_class\_b\_turn)[i]) -   
 log(rowMeans(rate\_class\_a\_turn)[i])))  
 }  
 }  
   
 lm\_dat\_tmp <- data.frame(row.names = gsub(" .\*", "", plot\_data[,1]),  
 d\_trans = d\_trans,  
 d\_turns = d\_turns)  
 fit\_tmp = phylolm(d\_turns ~ d\_trans, data=lm\_dat\_tmp, phy=phy\_bb, boot = 0)  
 all\_fits[[j]] <- fit\_tmp  
}

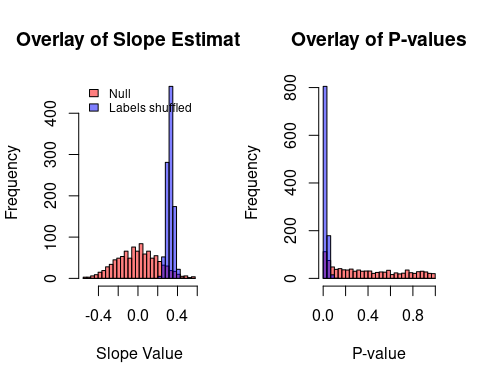
Let’s plot the resulting distributions.

est <- lapply(all\_fits,   
 function(x) summary(x)$coefficients[2,c(1,4)])  
est\_df <- do.call(rbind,est)  
  
par(mfrow=c(1,2))  
hist(est\_df[,1], main = "slope estimates", xlab = "slope value")  
hist(est\_df[,2], main = "p-values", xlab = "pvalue")



## Comparing distributions

# Calculate the combined range for the slope estimates  
min\_slope = min(c(shuffled\_est\_df[,1], est\_df[,1]))  
max\_slope = max(c(shuffled\_est\_df[,1], est\_df[,1]))  
  
# Calculate the combined range for the p-values  
min\_pvalue = min(c(shuffled\_est\_df[,2], est\_df[,2]))  
max\_pvalue = max(c(shuffled\_est\_df[,2], est\_df[,2]))  
  
# Define uniform break points for both datasets  
breaks\_slope = seq(min\_slope, max\_slope, length.out=31) # 30 bins, adjust number of breaks as needed  
breaks\_pvalue = seq(min\_pvalue, max\_pvalue, length.out=31) # 30 bins  
  
par(mfrow=c(1,2))  
# Plot histograms for slope estimates  
hist(shuffled\_est\_df[,1], breaks=breaks\_slope, main="Overlay of Slope Estimates", xlab="Slope Value", col=rgb(1, 0, 0, 0.5), ylim=c(0, max(c(hist(shuffled\_est\_df[,1], breaks=breaks\_slope, plot=FALSE)$counts, hist(est\_df[,1], breaks=breaks\_slope, plot=FALSE)$counts))))  
hist(est\_df[,1], breaks=breaks\_slope, add=TRUE, col=rgb(0, 0, 1, 0.5))  
legend("topleft", legend=c("Null", "Labels shuffled"), fill=c(rgb(1, 0, 0, 0.5), rgb(0, 0, 1, 0.5)),bty = "n", cex=0.75)  
  
# Plot histograms for p-values  
hist(shuffled\_est\_df[,2], breaks=breaks\_pvalue, main="Overlay of P-values", xlab="P-value", col=rgb(1, 0, 0, 0.5), ylim=c(0, max(c(hist(shuffled\_est\_df[,2], breaks=breaks\_pvalue, plot=FALSE)$counts, hist(est\_df[,2], breaks=breaks\_pvalue, plot=FALSE)$counts))))  
hist(est\_df[,2], breaks=breaks\_pvalue, add=TRUE, col=rgb(0, 0, 1, 0.5))



This suggests that our results are robust to the label switching problem with average estimates shown below.

## [1] "mean null"

## Estimate p.value   
## -0.001695969 0.398378729

## [1] "mean labels switched"

## Estimate p.value   
## 0.32737953 0.02430726

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