PGLS locomtor performance

Phylogenetic analysis of locomotor performance across all life.

```
library(phylolm)
```

```
## Loading required package: ape
```

```
library(treeplyr)
```

```
## Loading required package: dplyr
```

```
##
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
##
## Attaching package: 'treeplyr'
```

```
## The following object is masked from 'package:stats':
##
##     reorder
```

```
library(foreach)
library(doParallel)
```

```
## Loading required package: iterators
```

```
## Loading required package: parallel
```

```
library(phytools)
```

```
## Loading required package: maps
```

```
registerDoParallel(cores=50)
tds <- readRDS("../output/fullTreeTreeDataObjects.rds")
tds[[1]]
```

```
## $phy
##
## Phylogenetic tree with 38 tips and 37 internal nodes.
##
## Tip labels:
##  Zalophus_californianus, Inia_geoffrensis, Delphinapterus_leucas, Lagenorhynchus_obliquidens, Cephal
## Node labels:
##  , , , , , , ...
##
## Rooted; includes branch lengths.
##
## $dat
## # A tibble: 38 x 10
##      SI_Mass    LnMass Locomotor.Trait TraitValue TempTraitValue
```

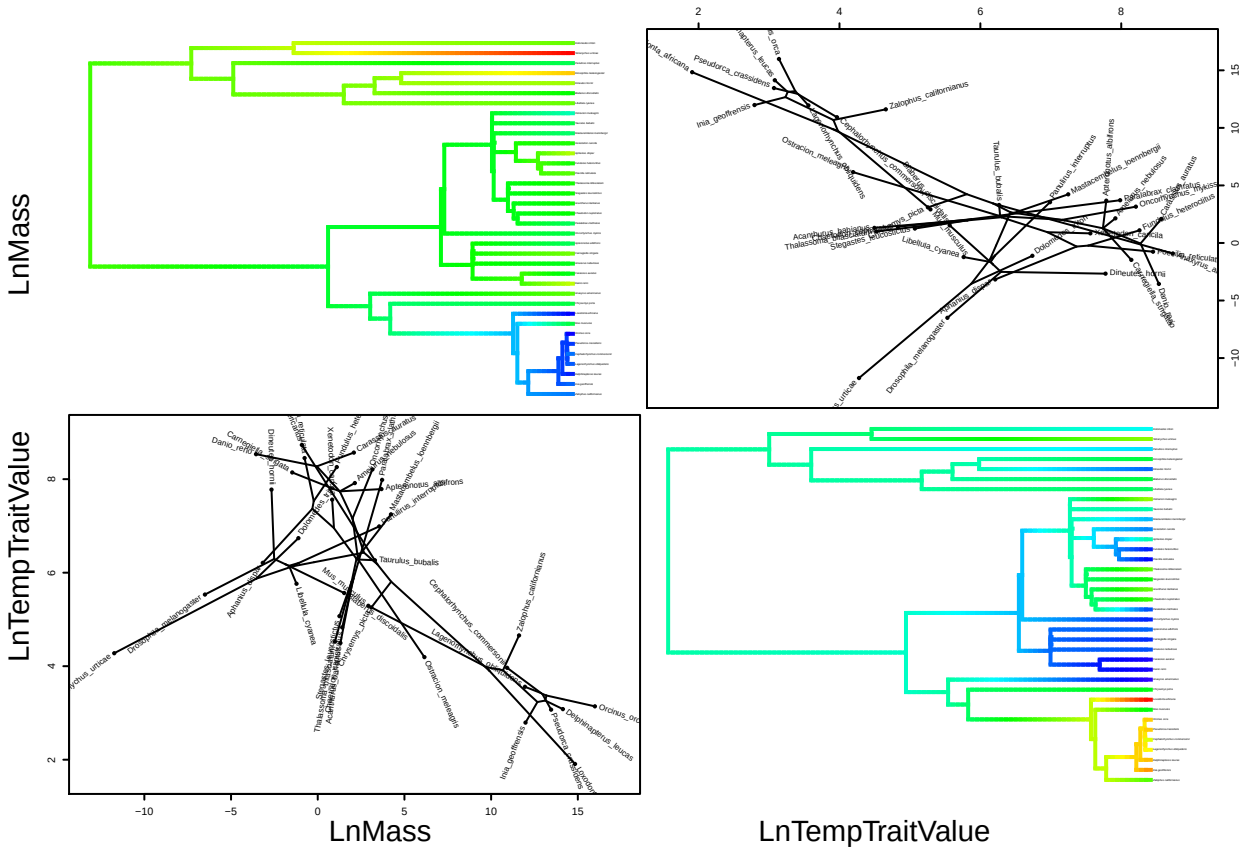
```
##  *     <dbl>     <dbl>          <fctr>      <dbl>          <dbl>
##  1  113000.0 11.610051   Angular Speed    675.000     105.412367
##  2  160000.0 11.982929   Angular Speed    104.625      16.338917
##  3 1381640.0 14.138782   Angular Speed    139.620      21.803962
##  4  155000.0 11.951180   Angular Speed    225.000      35.137456
##  5   55500.0 10.924138   Angular Speed    337.500      52.706183
##  6  700000.0 13.458836   Angular Speed    138.000      21.550973
##  7 8750000.0 15.984564   Angular Speed    148.130      23.132939
##  8      18.5  2.917771   Angular Speed   1272.000     198.643749
##  9 2780000.0 14.837961   Angular Speed     43.200       6.746391
## 10       NaN       NaN   Angular Speed    230.770      95.912526
## # ... with 28 more rows, and 5 more variables: Temperature <dbl>,
## #   TempType <fctr>, Environment <fctr>, Thermy <fctr>,
## #   TrophicGroup <fctr>
```

Single variable fits w/Brownian Motion

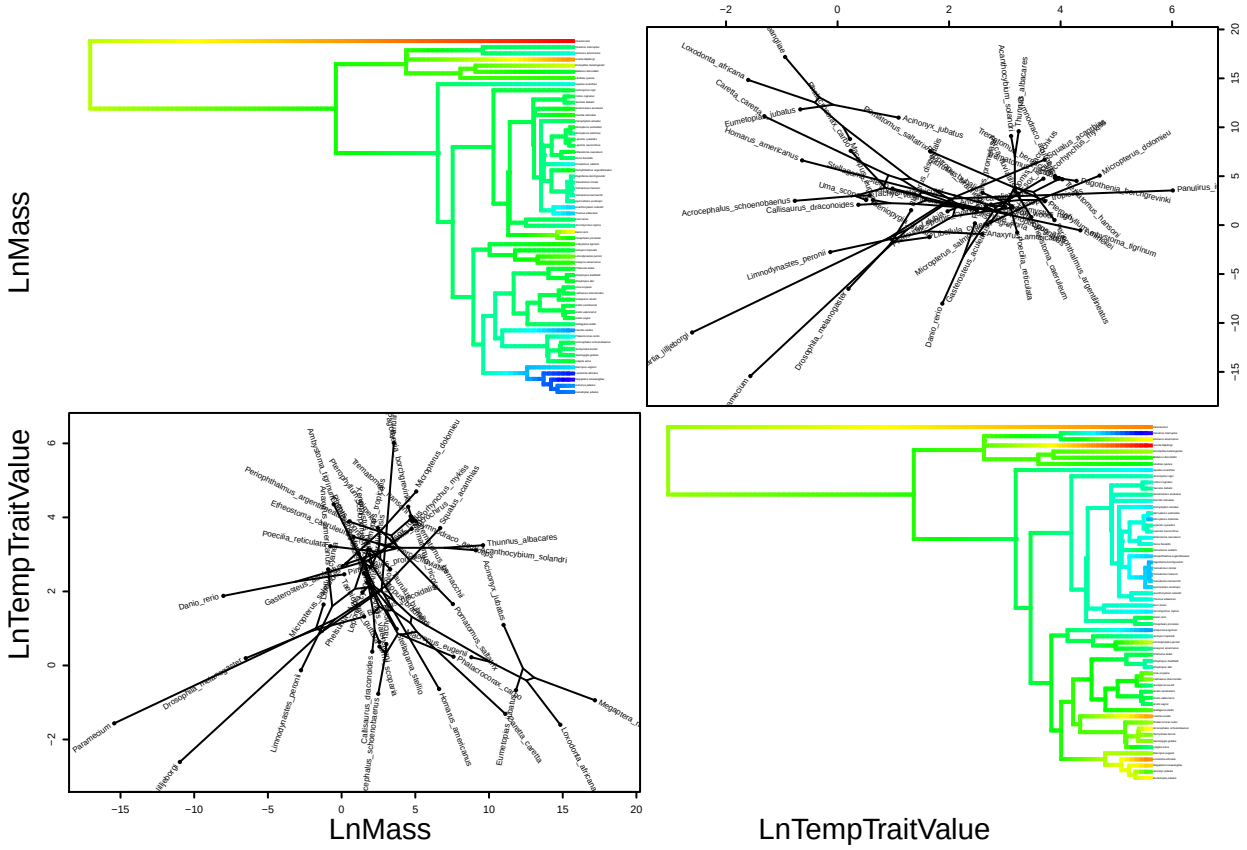
```
singlefits <- foreach(i=1:length(tds)) %do% {
  td <- filter(tds[[i]], !is.na(TempTraitValue), !is.na(LnMass))
  td$dat <- mutate(td$dat, "LnTempTraitValue"=log(TempTraitValue))
  LnTempTraitValue <- td$dat[['LnTempTraitValue']]
  LnMass <- td$dat[['LnMass']]
  vizdat <- cbind(LnMass, LnTempTraitValue)
  rownames(vizdat) <- td$phy$tip.label
  fancyTree(td$phy, type="scattergram", X = as.matrix(vizdat), fsize=0.3)
  phylolm(LnTempTraitValue~LnMass, phy=td$phy, model="BM")

}
```

```
## Computing multidimensional phylogenetic scatterplot matrix...
```

```
## Warning in phylolm(LnTempTraitValue ~ LnMass, phy = td$phy, model = "BM"): data names do not match w
```

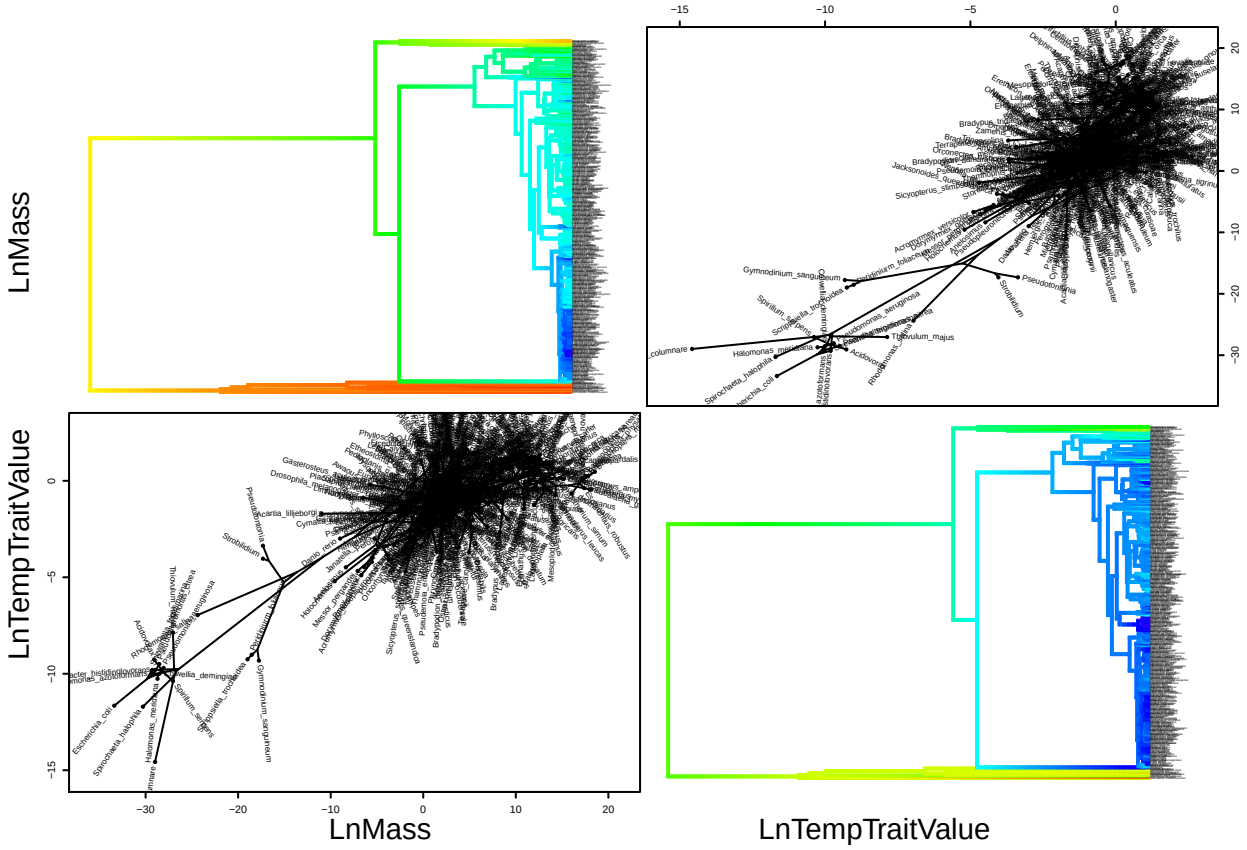



```
## Computing multidimensional phylogenetic scatterplot matrix...
## Warning in phylolm(LnTempTraitValue ~ LnMass, phy = td$phy, model = "BM"): data names do not match wi
```



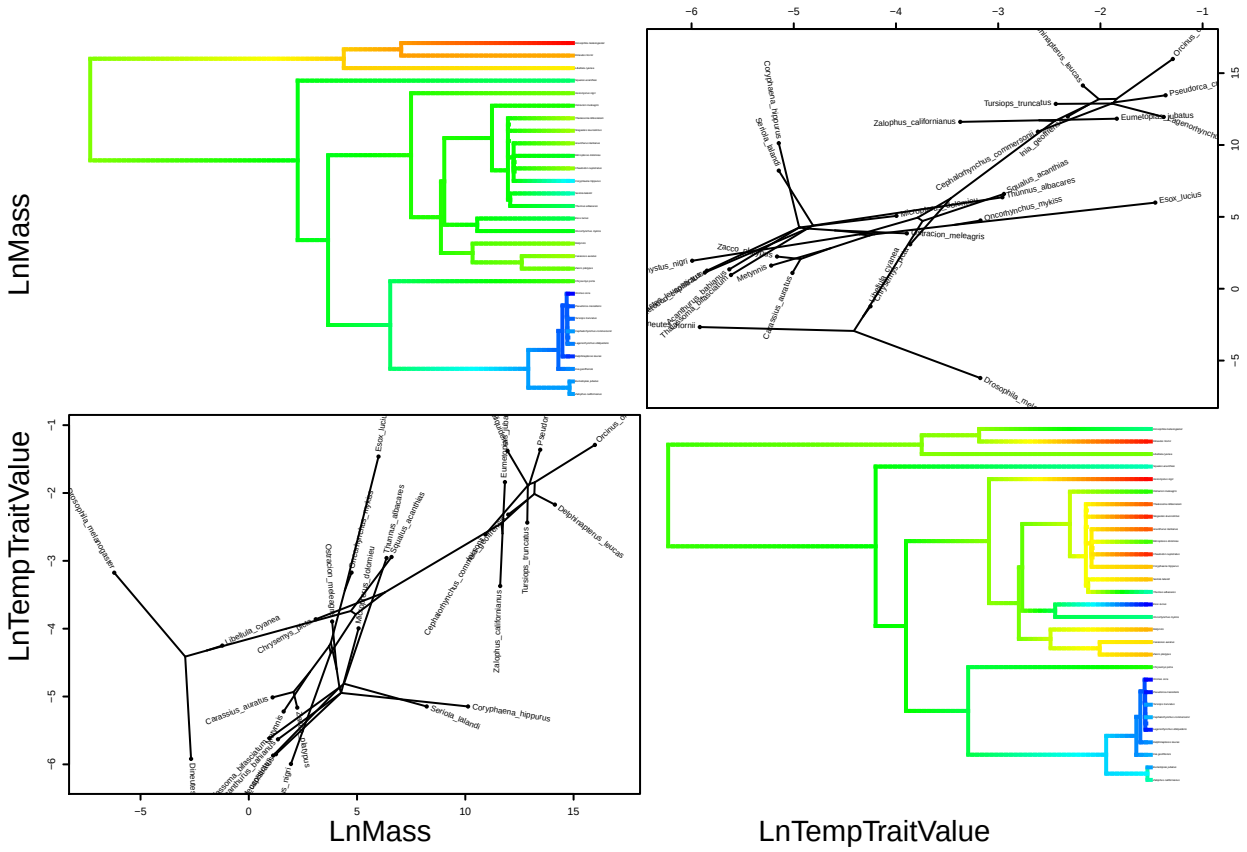

```
## Computing multidimensional phylogenetic scatterplot matrix...
```

```
## Warning in phylolm(LnTempTraitValue ~ LnMass, phy = td$phy, model = "BM"): data names do not match wi
```

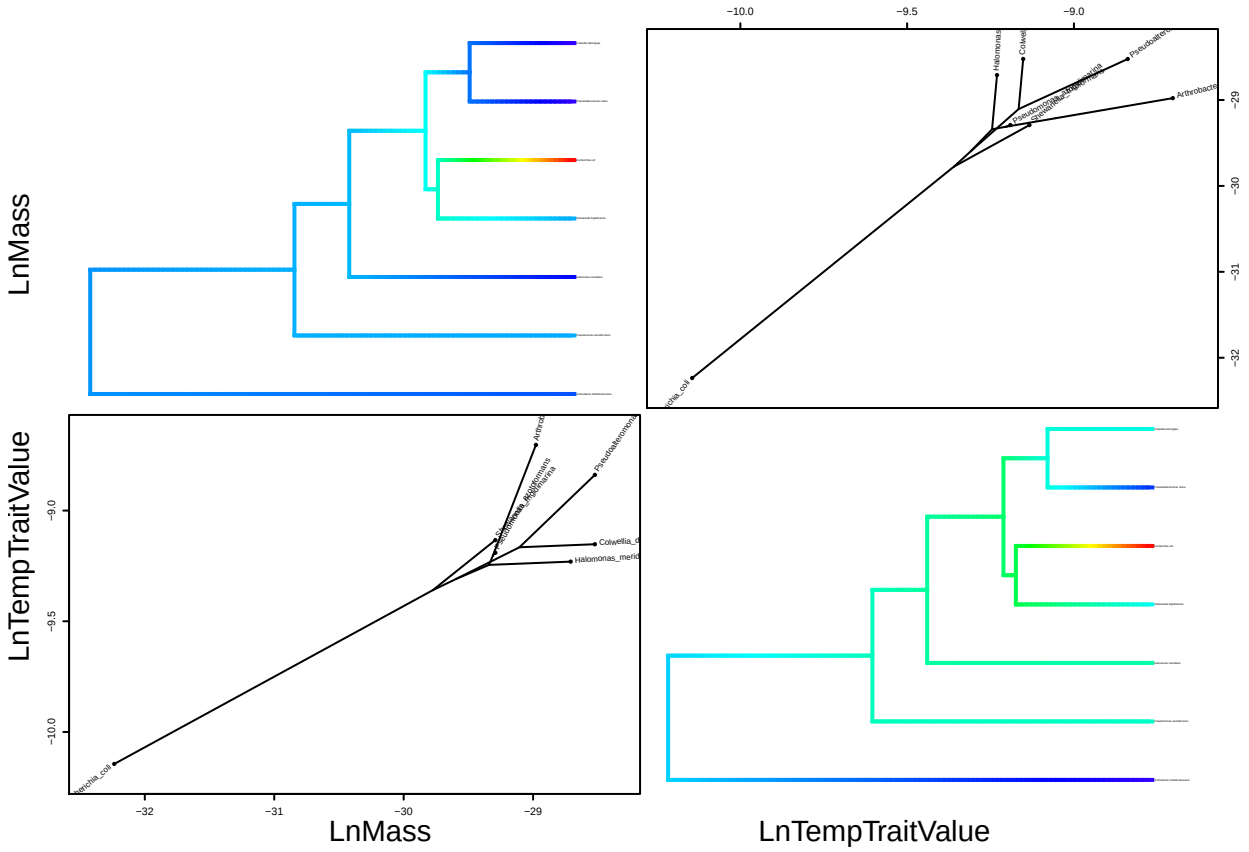



```
## Computing multidimensional phylogenetic scatterplot matrix...
```

```
## Warning in phylolm(LnTempTraitValue ~ LnMass, phy = td$phy, model = "BM"): data names do not match wi
```

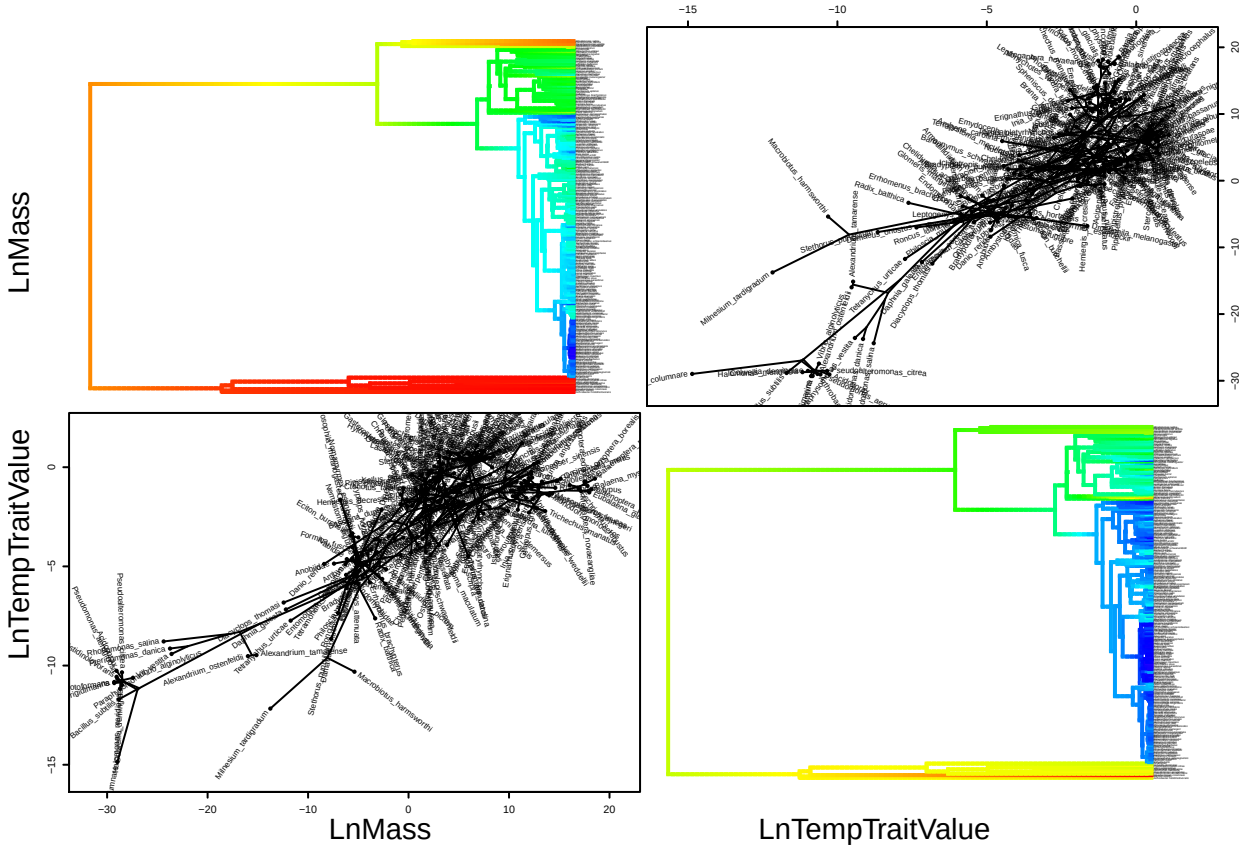



```
## Computing multidimensional phylogenetic scatterplot matrix...
## Warning in phylolm(LnTempTraitValue ~ LnMass, phy = td$phy, model = "BM"): data names do not match wi
```




```
## Computing multidimensional phylogenetic scatterplot matrix...
```

```
## Warning in phylolm(LnTempTraitValue ~ LnMass, phy = td$phy, model = "BM"): data names do not match wi
```




```
names(singlefits) <- sapply(tds, function(x) x$dat$Locomotor.Trait[1])
lapply(singlefits, summary)
```

```
## $`Angular Speed`
##
## Call:
## phylolm(formula = LnTempTraitValue ~ LnMass, phy = td$phy, model = "BM")
##
##    AIC logLik
## 132.95 -63.48
##
## Raw residuals:
##     Min      1Q  Median      3Q     Max
## -3.3159 -1.2309 -0.4079  1.8062  2.6180
##
## Mean tip height: 846.9994
## Parameter estimate(s) using ML:
## sigma2: 0.01064946
##
## Coefficients:
##             Estimate    StdErr t.value   p.value
## (Intercept)  6.197813  1.533536  4.0415 0.0002874 ***
## LnMass      -0.118930  0.056133 -2.1187 0.0415007 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $`Maximum Acceleration`
```

```
##
## Call:
## phylolm(formula = LnTempTraitValue ~ LnMass, phy = td$phy, model = "BM")
##
##    AIC logLik
##  207.8 -100.9
##
## Raw residuals:
##     Min      1Q  Median      3Q     Max
## -3.1946 -0.2347  1.8377  2.3809  5.1366
##
## Mean tip height: 1724.729
## Parameter estimate(s) using ML:
## sigma2: 0.01201646
##
## Coefficients:
##             Estimate   StdErr t.value p.value
## (Intercept) 0.650905 2.898373  0.2246  0.8231
## LnMass      0.063451 0.049765  1.2750  0.2076
##
## $`Maximum Speed`
##
## Call:
## phylolm(formula = LnTempTraitValue ~ LnMass, phy = td$phy, model = "BM")
##
##    AIC logLik
## 1207.7 -600.8
##
## Raw residuals:
##    Min     1Q Median     3Q    Max
## -5.636  3.260  3.835  4.331  6.752
##
## Mean tip height: 4246.667
## Parameter estimate(s) using ML:
## sigma2: 0.01730968
##
## Coefficients:
##              Estimate    StdErr t.value   p.value
## (Intercept) -5.024015  4.373374 -1.1488    0.2513
## LnMass       0.135032  0.022184  6.0869 2.548e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $`Minimum Turn Radius`
##
## Call:
## phylolm(formula = LnTempTraitValue ~ LnMass, phy = td$phy, model = "BM")
##
##    AIC logLik
## 109.66 -51.83
##
## Raw residuals:
##     Min      1Q  Median      3Q     Max
## -2.7526 -1.2613 -0.5446  0.1553  2.3438
```

```
##
## Mean tip height: 846.9994
## Parameter estimate(s) using ML:
## sigma2: 0.01473165
##
## Coefficients:
##             Estimate   StdErr t.value p.value
## (Intercept) -4.33057  2.07062 -2.0914 0.04603 *
## LnMass       0.19122  0.07725  2.4754 0.01988 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $`Routine Accleration`
##
## Call:
## phylolm(formula = LnTempTraitValue ~ LnMass, phy = td$phy, model = "BM")
##
##    AIC logLik
##  3.152  1.424
##
## Raw residuals:
##      Min       1Q   Median       3Q      Max
## -0.33153 -0.23082 -0.11082 -0.02578  0.27879
##
## Mean tip height: 3091.214
## Parameter estimate(s) using ML:
## sigma2: 2.052773e-05
##
## Coefficients:
##             Estimate   StdErr t.value p.value
## (Intercept) 0.016178 1.581583  0.0102 0.99223
## LnMass      0.310527 0.053777  5.7744 0.00219 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $`Routine Speed`
##
## Call:
## phylolm(formula = LnTempTraitValue ~ LnMass, phy = td$phy, model = "BM")
##
##    AIC logLik
##  697.6 -345.8
##
## Raw residuals:
##    Min     1Q Median     3Q    Max
## -3.691  2.165  3.069  4.789  6.130
##
## Mean tip height: 4246.667
## Parameter estimate(s) using ML:
## sigma2: 0.009635771
##
## Coefficients:
##              Estimate    StdErr t.value p.value
## (Intercept) -6.046706  3.327419 -1.8172 0.07041 .
```

```
## LnMass       0.176799  0.020021  8.8305 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Quadratic fits

```
par(mfrow=c(3,2))
quadfits <- foreach(i=1:length(tds)) %do% {
  td <- filter(tds[[i]], !is.na(TempTraitValue), !is.na(LnMass))
  td$dat <- mutate(td$dat, "LnTempTraitValue"=log(TempTraitValue))
  LnTempTraitValue <- td$dat[['LnTempTraitValue']]
  LnMass <- td$dat[['LnMass']]
  LnMass2 <- LnMass^2
  phylolm(LnTempTraitValue~LnMass + LnMass2, phy=td$phy, model="BM")

}
```

```
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2, phy = td$phy, model = "BM"): data names do n

## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2, phy = td$phy, model = "BM"): data names do n

## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2, phy = td$phy, model = "BM"): data names do n

## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2, phy = td$phy, model = "BM"): data names do n

## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2, phy = td$phy, model = "BM"): data names do n

## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2, phy = td$phy, model = "BM"): data names do n
```

```
names(quadfits) <- sapply(tds, function(x) x$dat$Locomotor.Trait[1])
lapply(quadfits, summary)
```

```
## $`Angular Speed`
##
## Call:
## phylolm(formula = LnTempTraitValue ~ LnMass + LnMass2, phy = td$phy,
##     model = "BM")
##
##    AIC logLik
## 131.09 -61.54
##
## Raw residuals:
##    Min     1Q Median     3Q    Max
## -2.860 -1.643 -0.658  1.369  2.225
##
## Mean tip height: 846.9994
## Parameter estimate(s) using ML:
## sigma2: 0.009565361
##
## Coefficients:
##               Estimate     StdErr t.value   p.value
## (Intercept)  6.5211432  1.4846858  4.3923 0.0001091 ***
## LnMass       0.0077352  0.0848862  0.0911 0.9279451
## LnMass2     -0.0084778  0.0043837 -1.9339 0.0617358 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## $`Maximum Acceleration`
##
## Call:
## phylolm(formula = LnTempTraitValue ~ LnMass + LnMass2, phy = td$phy,
##     model = "BM")
##
##    AIC logLik
## 201.15 -96.58
##
## Raw residuals:
##     Min      1Q  Median      3Q     Max
## -3.9625 -1.8874 -0.3752  0.4900  2.8303
##
## Mean tip height: 1724.729
## Parameter estimate(s) using ML:
## sigma2: 0.01035881
##
## Coefficients:
##               Estimate     StdErr t.value  p.value
## (Intercept)  2.8477560  2.8145578  1.0118 0.316067
## LnMass       0.1467301  0.0544220  2.6962 0.009290 **
## LnMass2     -0.0147857  0.0049839 -2.9667 0.004448 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $`Maximum Speed`
##
## Call:
## phylolm(formula = LnTempTraitValue ~ LnMass + LnMass2, phy = td$phy,
##     model = "BM")
##
##    AIC logLik
## 1205.8 -598.9
##
## Raw residuals:
##     Min      1Q  Median      3Q     Max
## -4.4068  0.1482  0.6476  1.1843  3.4769
##
## Mean tip height: 4246.667
## Parameter estimate(s) using ML:
## sigma2: 0.01715376
##
## Coefficients:
##               Estimate     StdErr t.value   p.value
## (Intercept) -1.7933675  4.6549400 -0.3853   0.70023
## LnMass       0.1694077  0.0281276  6.0228 3.682e-09 ***
## LnMass2     -0.0041244  0.0020861 -1.9770   0.04868 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $`Minimum Turn Radius`
##
## Call:
```

```
## phylolm(formula = LnTempTraitValue ~ LnMass + LnMass2, phy = td$phy,
##     model = "BM")
##
##    AIC logLik
##  111.6  -51.8
##
## Raw residuals:
##     Min      1Q  Median      3Q     Max
## -2.5837 -1.1908 -0.4158  0.2802  2.0482
##
## Mean tip height: 846.9994
## Parameter estimate(s) using ML:
## sigma2: 0.01470449
##
## Coefficients:
##               Estimate     StdErr t.value p.value
## (Intercept) -4.3303842  2.1081200 -2.0541 0.05014 .
## LnMass       0.1554193  0.1813238  0.8571 0.39920
## LnMass2      0.0018870  0.0086107  0.2191 0.82825
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $`Routine Accleration`
##
## Call:
## phylolm(formula = LnTempTraitValue ~ LnMass + LnMass2, phy = td$phy,
##     model = "BM")
##
##    AIC logLik
##  4.449  1.776
##
## Raw residuals:
##      Min       1Q   Median       3Q      Max
## -0.29385 -0.20030 -0.10942 -0.01507  0.27010
##
## Mean tip height: 3091.214
## Parameter estimate(s) using ML:
## sigma2: 1.856646e-05
##
## Coefficients:
##               Estimate     StdErr t.value p.value
## (Intercept) -49.358059  75.975409 -0.6497  0.5513
## LnMass       -2.939243   4.999739 -0.5879  0.5882
## LnMass2      -0.053338   0.082054 -0.6500  0.5511
##
## $`Routine Speed`
##
## Call:
## phylolm(formula = LnTempTraitValue ~ LnMass + LnMass2, phy = td$phy,
##     model = "BM")
##
##    AIC logLik
##  685.5 -338.7
##
```

```
## Raw residuals:
##     Min      1Q  Median      3Q     Max
## -8.4814 -3.1108 -2.2443 -0.7462  2.7294
##
## Mean tip height: 4246.667
## Parameter estimate(s) using ML:
## sigma2: 0.009100017
##
## Coefficients:
##               Estimate     StdErr t.value   p.value
## (Intercept) -0.3297580  3.5754293 -0.0922 0.9265921
## LnMass       0.2430368  0.0262069  9.2738 < 2.2e-16 ***
## LnMass2     -0.0066373  0.0017548 -3.7824 0.0001956 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Environmental effects

```
par(mfrow=c(3,2))
varenv <- which(sapply(tds, function(x) length(unique(x[['Environment']]))>1))

envfits <- foreach(i=1:length(tds)) %do% {
  if(i %in% varenv){
  td <- filter(tds[[i]], !is.na(TempTraitValue), !is.na(LnMass))
  td$dat <- mutate(td$dat, "LnTempTraitValue"=log(TempTraitValue))
  LnTempTraitValue <- td$dat[['LnTempTraitValue']]
  LnMass <- td$dat[['LnMass']]
  Environment <- td$dat[['Environment']]
  phylolm(LnTempTraitValue~LnMass+Environment, phy=td$phy, model="BM")
  } else {
    list()
  }

}
```

```
## Warning in phylolm(LnTempTraitValue ~ LnMass + Environment, phy = td$phy, : data names do not match w

## Warning in phylolm(LnTempTraitValue ~ LnMass + Environment, phy = td$phy, : data names do not match w

## Warning in phylolm(LnTempTraitValue ~ LnMass + Environment, phy = td$phy, : data names do not match w

## Warning in phylolm(LnTempTraitValue ~ LnMass + Environment, phy = td$phy, : data names do not match w

## Warning in phylolm(LnTempTraitValue ~ LnMass + Environment, phy = td$phy, : data names do not match w
```

```
names(envfits) <-  sapply(tds, function(x) x$dat$Locomotor.Trait[1])
```

```
lapply(envfits, summary)
```

```
## $`Angular Speed`
##
## Call:
## phylolm(formula = LnTempTraitValue ~ LnMass + Environment, phy = td$phy,
##     model = "BM")
##
##    AIC logLik
```

```
## 134.75 -62.37
##
## Raw residuals:
##      Min       1Q   Median       3Q      Max
## -2.99923 -1.70536 -0.07465  1.14994  2.02088
##
## Mean tip height: 846.9994
## Parameter estimate(s) using ML:
## sigma2: 0.0100167
##
## Coefficients:
##                   Estimate    StdErr t.value p.value
## (Intercept)       4.851097  2.213022  2.1921 0.03576 *
## LnMass           -0.133438  0.057039 -2.3394 0.02572 *
## EnvironmentLand   0.859767  1.888605  0.4552 0.65201
## EnvironmentWater  1.974035  1.874571  1.0531 0.30020
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $`Maximum Acceleration`
##
## Call:
## phylolm(formula = LnTempTraitValue ~ LnMass + Environment, phy = td$phy,
##     model = "BM")
##
##    AIC logLik
##  211.6 -100.8
##
## Raw residuals:
##     Min      1Q  Median      3Q     Max
## -3.4318 -0.3885  1.7713  2.4020  5.1562
##
## Mean tip height: 1724.729
## Parameter estimate(s) using ML:
## sigma2: 0.01199357
##
## Coefficients:
##                   Estimate    StdErr t.value p.value
## (Intercept)       0.764469  3.226678  0.2369  0.8136
## LnMass            0.065634  0.051328  1.2787  0.2065
## EnvironmentLand   0.091221  1.440540  0.0633  0.9497
## EnvironmentWater -0.140883  1.454366 -0.0969  0.9232
##
## $`Maximum Speed`
##
## Call:
## phylolm(formula = LnTempTraitValue ~ LnMass + Environment, phy = td$phy,
##     model = "BM")
##
##    AIC logLik
## 1201.6 -595.8
##
## Raw residuals:
##    Min     1Q Median     3Q    Max
```

```
## -5.411  2.802  3.374  3.832  6.292
##
## Mean tip height: 4246.667
## Parameter estimate(s) using ML:
## sigma2: 0.0169114
##
## Coefficients:
##                   Estimate    StdErr t.value   p.value
## (Intercept)      -3.078341  4.403988 -0.6990   0.48494
## LnMass            0.142141  0.022132  6.4225 3.564e-10 ***
## EnvironmentLand  -1.497130  0.782007 -1.9145   0.05622 .
## EnvironmentWater -1.964095  0.795193 -2.4700   0.01390 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $`Minimum Turn Radius`
##
## Call:
## phylolm(formula = LnTempTraitValue ~ LnMass + Environment, phy = td$phy,
##     model = "BM")
##
##    AIC logLik
## 110.64 -51.32
##
## Raw residuals:
##     Min      1Q  Median      3Q     Max
## -2.0574 -0.6936  0.1067  0.7178  2.4520
##
## Mean tip height: 846.9994
## Parameter estimate(s) using ML:
## sigma2: 0.01422062
##
## Coefficients:
##                   Estimate    StdErr t.value p.value
## (Intercept)      -2.652074  2.704303 -0.9807 0.33579
## LnMass            0.199676  0.077837  2.5653 0.01643 *
## EnvironmentWater -2.459276  2.544222 -0.9666 0.34264
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $`Routine Accleration`
## Length  Class   Mode
##      0   list   list
##
## $`Routine Speed`
##
## Call:
## phylolm(formula = LnTempTraitValue ~ LnMass + Environment, phy = td$phy,
##     model = "BM")
##
##    AIC logLik
##  645.0 -317.5
##
## Raw residuals:
```

```
##    Min     1Q Median     3Q    Max
## -3.613  1.404  2.005  2.923  5.680
##
## Mean tip height: 4246.667
## Parameter estimate(s) using ML:
## sigma2: 0.007655838
##
## Coefficients:
##                    Estimate    StdErr t.value   p.value
## (Intercept)      -2.475444  3.019654 -0.8198    0.4131
## LnMass            0.199734  0.018163 10.9968 < 2.2e-16 ***
## EnvironmentLand  -3.821115  0.483018 -7.9109 9.119e-14 ***
## EnvironmentWater -2.984118  0.434781 -6.8635 5.602e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Interaction with environment

```
par(mfrow=c(3,2))
varenv <- which(sapply(tds, function(x) length(unique(x[['Environment']]))>1))

envIntfits <- foreach(i=1:length(tds)) %do% {
  if(i %in% varenv){
  td <- filter(tds[[i]], !is.na(TempTraitValue), !is.na(LnMass))
  td$dat <- mutate(td$dat, "LnTempTraitValue"=log(TempTraitValue))
  LnTempTraitValue <- td$dat[['LnTempTraitValue']]
  LnMass <- td$dat[['LnMass']]
  Environment <- td$dat[['Environment']]
  phylolm(LnTempTraitValue~LnMass*Environment, phy=td$phy, model="BM")
  } else {
    list()
  }

}
```

```
## Warning in phylolm(LnTempTraitValue ~ LnMass * Environment, phy = td$phy, : data names do not match w

## Warning in phylolm(LnTempTraitValue ~ LnMass * Environment, phy = td$phy, : data names do not match w

## Warning in phylolm(LnTempTraitValue ~ LnMass * Environment, phy = td$phy, : data names do not match w

## Warning in phylolm(LnTempTraitValue ~ LnMass * Environment, phy = td$phy, : data names do not match w

## Warning in phylolm(LnTempTraitValue ~ LnMass * Environment, phy = td$phy, : data names do not match w
```

```
names(envIntfits) <-  sapply(tds, function(x) x$dat$Locomotor.Trait[1])
```

```
lapply(envIntfits, summary)
```

```
## $`Angular Speed`
##
## Call:
## phylolm(formula = LnTempTraitValue ~ LnMass * Environment, phy = td$phy,
##     model = "BM")
##
##    AIC logLik
```

```
## 138.55 -62.28
##
## Raw residuals:
##     Min      1Q  Median      3Q     Max
## -3.3165 -1.5750  0.0075  1.2836  2.1338
##
## Mean tip height: 846.9994
## Parameter estimate(s) using ML:
## sigma2: 0.009962018
##
## Coefficients:
##                           Estimate    StdErr t.value p.value
## (Intercept)               5.651036  3.311466  1.7065 0.09825 .
## LnMass                    0.064809  0.582890  0.1112 0.91221
## EnvironmentLand           0.122971  3.157734  0.0389 0.96919
## EnvironmentWater          1.050589  3.157994  0.3327 0.74169
## LnMass:EnvironmentLand   -0.219897  0.594204 -0.3701 0.71393
## LnMass:EnvironmentWater -0.193160  0.585310 -0.3300 0.74368
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $`Maximum Acceleration`
##
## Call:
## phylolm(formula = LnTempTraitValue ~ LnMass * Environment, phy = td$phy,
##     model = "BM")
##
##    AIC logLik
##  214.8 -100.4
##
## Raw residuals:
##     Min      1Q  Median      3Q     Max
## -3.8240 -0.0788  1.8244  2.3852  5.1307
##
## Mean tip height: 1724.729
## Parameter estimate(s) using ML:
## sigma2: 0.01181695
##
## Coefficients:
##                           Estimate    StdErr t.value p.value
## (Intercept)               0.814040  3.276497  0.2484  0.8048
## LnMass                   -0.082432  0.189262 -0.4355  0.6650
## EnvironmentLand          -0.183477  1.548366 -0.1185  0.9061
## EnvironmentWater         -0.190648  1.506110 -0.1266  0.8998
## LnMass:EnvironmentLand    0.189677  0.215847  0.8788  0.3836
## LnMass:EnvironmentWater   0.155303  0.194514  0.7984  0.4283
##
## $`Maximum Speed`
##
## Call:
## phylolm(formula = LnTempTraitValue ~ LnMass * Environment, phy = td$phy,
##     model = "BM")
##
##    AIC logLik
```

```
## 1205.3 -595.7
##
## Raw residuals:
##    Min     1Q Median     3Q    Max
## -5.351  2.563  3.160  3.640  6.063
##
## Mean tip height: 4246.667
## Parameter estimate(s) using ML:
## sigma2: 0.01690045
##
## Coefficients:
##                            Estimate     StdErr t.value p.value
## (Intercept)             -2.8808859  4.4374539 -0.6492 0.51654
## LnMass                   0.1329619  0.1555107  0.8550 0.39303
## EnvironmentLand         -1.4368241  0.8359845 -1.7187 0.08639 .
## EnvironmentWater        -1.9918234  0.8367728 -2.3804 0.01773 *
## LnMass:EnvironmentLand  -0.0023155  0.1573517 -0.0147 0.98827
## LnMass:EnvironmentWater  0.0171282  0.1570107  0.1091 0.91318
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $`Minimum Turn Radius`
##
## Call:
## phylolm(formula = LnTempTraitValue ~ LnMass * Environment, phy = td$phy,
##     model = "BM")
##
##    AIC logLik
## 112.24 -51.12
##
## Raw residuals:
##      Min       1Q   Median       3Q      Max
## -2.18872 -0.71582 -0.03688  0.53301  2.33906
##
## Mean tip height: 846.9994
## Parameter estimate(s) using ML:
## sigma2: 0.0140252
##
## Coefficients:
##                          Estimate   StdErr t.value p.value
## (Intercept)             -4.33904  3.95868 -1.0961  0.2835
## LnMass                  -0.22353  0.72137 -0.3099  0.7592
## EnvironmentWater        -0.68613  3.95796 -0.1734  0.8638
## LnMass:EnvironmentWater  0.42766  0.72461  0.5902  0.5604
##
## $`Routine Accleration`
## Length  Class   Mode
##      0   list   list
##
## $`Routine Speed`
##
## Call:
## phylolm(formula = LnTempTraitValue ~ LnMass * Environment, phy = td$phy,
##     model = "BM")
```

```
##
##    AIC logLik
##  647.5 -316.8
##
## Raw residuals:
##    Min     1Q Median     3Q    Max
## -3.578  1.284  1.848  2.794  5.521
##
## Mean tip height: 4246.667
## Parameter estimate(s) using ML:
## sigma2: 0.007611281
##
## Coefficients:
##                            Estimate    StdErr t.value   p.value
## (Intercept)              -2.041485  3.063575 -0.6664   0.50581
## LnMass                    0.136527  0.056502  2.4163   0.01643 *
## EnvironmentLand          -4.114317  0.543460 -7.5706 7.965e-13 ***
## EnvironmentWater         -3.282397  0.516048 -6.3606 1.007e-09 ***
## LnMass:EnvironmentLand    0.071048  0.065687  1.0816   0.28051
## LnMass:EnvironmentWater   0.069103  0.060156  1.1487   0.25181
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
par(mfrow=c(3,2))
varenv <- which(sapply(tds, function(x) length(unique(x[['Environment']]))>1))

envQuadfits <- foreach(i=1:length(tds)) %do% {
  if(i %in% varenv){
  td <- filter(tds[[i]], !is.na(TempTraitValue), !is.na(LnMass))
  td$dat <- mutate(td$dat, "LnTempTraitValue"=log(TempTraitValue))
  LnTempTraitValue <- td$dat[['LnTempTraitValue']]
  LnMass <- td$dat[['LnMass']]
  LnMass2 <- LnMass^2
  Environment <- td$dat[['Environment']]
  phylolm(LnTempTraitValue~LnMass+LnMass2+Environment, phy=td$phy, model="BM")
  } else {
    list()
  }

}
```

```
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2 + Environment, phy = td$phy, : data names do n

## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2 + Environment, phy = td$phy, : data names do n

## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2 + Environment, phy = td$phy, : data names do n

## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2 + Environment, phy = td$phy, : data names do n

## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2 + Environment, phy = td$phy, : data names do n
```

```
names(envQuadfits) <-  sapply(tds, function(x) x$dat$Locomotor.Trait[1])
```

```
lapply(envQuadfits, summary)
```

```
## $`Angular Speed`
```

```
##
## Call:
## phylolm(formula = LnTempTraitValue ~ LnMass + LnMass2 + Environment,
##     phy = td$phy, model = "BM")
##
##    AIC logLik
## 133.53 -60.77
##
## Raw residuals:
##     Min      1Q  Median      3Q     Max
## -2.9121 -1.9907 -0.5101  0.9609  1.7259
##
## Mean tip height: 846.9994
## Parameter estimate(s) using ML:
## sigma2: 0.009160403
##
## Coefficients:
##                    Estimate     StdErr t.value p.value
## (Intercept)       5.5780095  2.1921717  2.5445 0.01614 *
## LnMass           -0.0160079  0.0884868 -0.1809 0.85762
## LnMass2          -0.0076645  0.0045024 -1.7023 0.09871 .
## EnvironmentLand   0.4532140  1.8504511  0.2449 0.80813
## EnvironmentWater  1.4200369  1.8501859  0.7675 0.44858
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $`Maximum Acceleration`
##
## Call:
## phylolm(formula = LnTempTraitValue ~ LnMass + LnMass2 + Environment,
##     phy = td$phy, model = "BM")
##
##    AIC logLik
## 204.96 -96.48
##
## Raw residuals:
##     Min      1Q  Median      3Q     Max
## -4.0225 -1.8215 -0.2911  0.3641  2.7081
##
## Mean tip height: 1724.729
## Parameter estimate(s) using ML:
## sigma2: 0.01032432
##
## Coefficients:
##                    Estimate     StdErr t.value  p.value
## (Intercept)       2.6619959  3.0905795  0.8613 0.392939
## LnMass            0.1466833  0.0554727  2.6442 0.010747 *
## LnMass2          -0.0153440  0.0052417 -2.9273 0.005028 **
## EnvironmentLand   0.0326734  1.3492379  0.0242 0.980771
## EnvironmentWater  0.3150824  1.3709157  0.2298 0.819106
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $`Maximum Speed`
```

```
##
## Call:
## phylolm(formula = LnTempTraitValue ~ LnMass + LnMass2 + Environment,
##     phy = td$phy, model = "BM")
##
##    AIC logLik
## 1201.0 -594.5
##
## Raw residuals:
##     Min      1Q  Median      3Q     Max
## -4.4202  0.2848  0.7692  1.2833  3.6247
##
## Mean tip height: 4246.667
## Parameter estimate(s) using ML:
## sigma2: 0.01680822
##
## Coefficients:
##                    Estimate     StdErr t.value   p.value
## (Intercept)      -0.5859550  4.6568570 -0.1258   0.89993
## LnMass            0.1698001  0.0279134  6.0831 2.617e-09 ***
## LnMass2          -0.0033833  0.0020874 -1.6209   0.10578
## EnvironmentLand  -1.3576974  0.7852542 -1.7290   0.08453 .
## EnvironmentWater -1.8048685  0.7997450 -2.2568   0.02452 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $`Minimum Turn Radius`
##
## Call:
## phylolm(formula = LnTempTraitValue ~ LnMass + LnMass2 + Environment,
##     phy = td$phy, model = "BM")
##
##    AIC logLik
## 112.64 -51.32
##
## Raw residuals:
##      Min       1Q   Median       3Q      Max
## -2.07223 -0.69205  0.09406  0.74097  2.43994
##
## Mean tip height: 846.9994
## Parameter estimate(s) using ML:
## sigma2: 0.01422028
##
## Coefficients:
##                     Estimate      StdErr t.value p.value
## (Intercept)      -2.64061912  2.79712230 -0.9440  0.3542
## LnMass            0.20388938  0.18928092  1.0772  0.2917
## LnMass2          -0.00021899  0.00893199 -0.0245  0.9806
## EnvironmentWater -2.47609013  2.68368602 -0.9226  0.3650
##
## $`Routine Accleration`
## Length  Class   Mode
##      0   list   list
##
```

```
## $`Routine Speed`
##
## Call:
## phylolm(formula = LnTempTraitValue ~ LnMass + LnMass2 + Environment,
##     phy = td$phy, model = "BM")
##
##    AIC logLik
##  631.0 -309.5
##
## Raw residuals:
##    Min     1Q Median     3Q    Max
## -7.799 -3.738 -3.179 -2.040  2.716
##
## Mean tip height: 4246.667
## Parameter estimate(s) using ML:
## sigma2: 0.007173008
##
## Coefficients:
##                    Estimate     StdErr t.value   p.value
## (Intercept)       2.8478102  3.2133322  0.8862    0.3764
## LnMass            0.2623784  0.0235007 11.1647 < 2.2e-16 ***
## LnMass2          -0.0063332  0.0015724 -4.0277 7.552e-05 ***
## EnvironmentLand  -3.7650875  0.4687145 -8.0328 4.231e-14 ***
## EnvironmentWater -2.8592432  0.4228576 -6.7617 1.022e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Determine which is the best

```
aic1 <- sapply(singlefits, function(x) x$aic)
aic2 <- sapply(quadfits, function(x) x$aic)
aic3 <- sapply(envfits, function(x) x$aic)
aic4 <- sapply(envIntfits, function(x) x$aic)
aic5 <- sapply(envQuadfits, function(x) x$aic)
aicTable <- do.call(rbind, list(aic1, aic2, aic3, aic4, aic5))
rownames(aicTable) <- c("singlefits", "quadfits", "envfits", "envIntfits", "envQuadfits")

aicTable
```

```
##             Angular Speed Maximum Acceleration Maximum Speed
## singlefits  132.9534      207.7595             1207.694
## quadfits    131.0884      201.15               1205.776
## envfits     134.7482      211.649              1201.614
## envIntfits  138.5511      214.7885             1205.334
## envQuadfits 133.5311      204.9566             1200.965
##             Minimum Turn Radius Routine Accleration Routine Speed
## singlefits  109.6635            3.151593            697.5601
## quadfits    111.61              4.448655            685.4875
## envfits     110.6396            NULL                644.9767
## envIntfits  112.2383            NULL                647.5408
## envQuadfits 112.6389            NULL                630.9515
```

For the following models, it looks like these are the best fits: Angular speed: Quadratic w/ lnMass Maximum acceleration: Quadratic w/ lnMass Maximum Speed: Separate environment intercepts Minimum turn radius: Linear with lnMass Routine Acceleration: Linear with lnMass Routine Speed: Separate environment intercepts

Compare different residual structures

Make it one big function

```
fitModels <- function(model){
  singlefits <- foreach(i=1:length(tds)) %do% {
    td <- filter(tds[[i]], !is.na(TempTraitValue), !is.na(LnMass))
    td$dat <- mutate(td$dat, "LnTempTraitValue"=log(TempTraitValue))
    LnTempTraitValue <- td$dat[['LnTempTraitValue']]
    LnMass <- td$dat[['LnMass']]
    phylolm(LnTempTraitValue~LnMass, phy=td$phy, model=model)
  }
  quadfits <- foreach(i=1:length(tds)) %do% {
    td <- filter(tds[[i]], !is.na(TempTraitValue), !is.na(LnMass))
    td$dat <- mutate(td$dat, "LnTempTraitValue"=log(TempTraitValue))
    LnTempTraitValue <- td$dat[['LnTempTraitValue']]
    LnMass <- td$dat[['LnMass']]
    LnMass2 <- LnMass^2
    phylolm(LnTempTraitValue~LnMass + LnMass2, phy=td$phy, model=model)
  }
  names(singlefits) <- names(quadfits) <-sapply(tds, function(x) x$dat$Locomotor.Trait[1])

varenv <- which(sapply(tds, function(x) length(unique(x[['Environment']]))>1))

envfits <- foreach(i=1:length(tds)) %do% {
  if(i %in% varenv){
  td <- filter(tds[[i]], !is.na(TempTraitValue), !is.na(LnMass))
  td$dat <- mutate(td$dat, "LnTempTraitValue"=log(TempTraitValue))
  LnTempTraitValue <- td$dat[['LnTempTraitValue']]
  LnMass <- td$dat[['LnMass']]
  Environment <- td$dat[['Environment']]
  phylolm(LnTempTraitValue~LnMass+Environment, phy=td$phy, model=model)
  } else {
    list()
  }

}
names(envfits) <-  sapply(tds, function(x) x$dat$Locomotor.Trait[1])

envIntfits <- foreach(i=1:length(tds)) %do% {
  if(i %in% varenv){
  td <- filter(tds[[i]], !is.na(TempTraitValue), !is.na(LnMass))
  td$dat <- mutate(td$dat, "LnTempTraitValue"=log(TempTraitValue))
  LnTempTraitValue <- td$dat[['LnTempTraitValue']]
  LnMass <- td$dat[['LnMass']]
  Environment <- td$dat[['Environment']]
  phylolm(LnTempTraitValue~LnMass*Environment, phy=td$phy, model=model)
  } else {
    list()
  }

}
names(envIntfits) <-  sapply(tds, function(x) x$dat$Locomotor.Trait[1])

envQuadfits <- foreach(i=1:length(tds)) %do% {
```

```
  if(i %in% varenv){
  td <- filter(tds[[i]], !is.na(TempTraitValue), !is.na(LnMass))
  td$dat <- mutate(td$dat, "LnTempTraitValue"=log(TempTraitValue))
  LnTempTraitValue <- td$dat[['LnTempTraitValue']]
  LnMass <- td$dat[['LnMass']]
  LnMass2 <- LnMass^2
  Environment <- td$dat[['Environment']]
  phylolm(LnTempTraitValue~LnMass+LnMass2+Environment, phy=td$phy, model=model)
  } else {
    list()
  }

}
names(envQuadfits) <-  sapply(tds, function(x) x$dat$Locomotor.Trait[1])

return(list(singlefits=singlefits, quadfits=quadfits, envfits=envfits, envIntfits=envIntfits, envQuadfi
}
```

Run it over different error structures

```
fitsOUr <- fitModels("OUrandomRoot")
```

```
## Warning in phylolm(LnTempTraitValue ~ LnMass, phy = td$phy, model = model): data names do not match w

## Warning in phylolm(LnTempTraitValue ~ LnMass, phy = td$phy, model = model): data names do not match w

## Warning in phylolm(LnTempTraitValue ~ LnMass, phy = td$phy, model = model): data names do not match w

## Warning in phylolm(LnTempTraitValue ~ LnMass, phy = td$phy, model = model): data names do not match w

## Warning in phylolm(LnTempTraitValue ~ LnMass, phy = td$phy, model = model): data names do not match w

## Warning in phylolm(LnTempTraitValue ~ LnMass, phy = td$phy, model = model): data names do not match w
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2, phy = td$phy, model = model): data names do n

## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2, phy = td$phy, model = model): data names do n

## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2, phy = td$phy, model = model): data names do n

## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2, phy = td$phy, model = model): data names do n
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2, phy = td$phy, model = model): the estimation
##                            You may change the bounds using options "upper.bound" and "lower.bound".
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2, phy = td$phy, model = model): data names do n

## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2, phy = td$phy, model = model): data names do n
## Warning in phylolm(LnTempTraitValue ~ LnMass + Environment, phy = td$phy, : data names do not match w

## Warning in phylolm(LnTempTraitValue ~ LnMass + Environment, phy = td$phy, : data names do not match w

## Warning in phylolm(LnTempTraitValue ~ LnMass + Environment, phy = td$phy, : data names do not match w

## Warning in phylolm(LnTempTraitValue ~ LnMass + Environment, phy = td$phy, : data names do not match w
```

```
## Warning in phylolm(LnTempTraitValue ~ LnMass + Environment, phy = td$phy, : the estimation of alpha r
##                            You may change the bounds using options "upper.bound" and "lower.bound".
## Warning in phylolm(LnTempTraitValue ~ LnMass + Environment, phy = td$phy, : data names do not match w
## Warning in phylolm(LnTempTraitValue ~ LnMass * Environment, phy = td$phy, : data names do not match w
## Warning in phylolm(LnTempTraitValue ~ LnMass * Environment, phy = td$phy, : data names do not match w
## Warning in phylolm(LnTempTraitValue ~ LnMass * Environment, phy = td$phy, : data names do not match w
## Warning in phylolm(LnTempTraitValue ~ LnMass * Environment, phy = td$phy, : data names do not match w
## Warning in phylolm(LnTempTraitValue ~ LnMass * Environment, phy = td$phy, : the estimation of alpha r
##                            You may change the bounds using options "upper.bound" and "lower.bound".
## Warning in phylolm(LnTempTraitValue ~ LnMass * Environment, phy = td$phy, : data names do not match w
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2 + Environment, phy = td$phy, : data names do n
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2 + Environment, phy = td$phy, : data names do n
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2 + Environment, phy = td$phy, : data names do n
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2 + Environment, phy = td$phy, : the estimation
##                            You may change the bounds using options "upper.bound" and "lower.bound".
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2 + Environment, phy = td$phy, : data names do n
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2 + Environment, phy = td$phy, : the estimation
##                            You may change the bounds using options "upper.bound" and "lower.bound".
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2 + Environment, phy = td$phy, : data names do n
fitsOUf <- fitModels("OUfixedRoot")
## Warning in phylolm(LnTempTraitValue ~ LnMass, phy = td$phy, model = model): data names do not match w
## Warning in phylolm(LnTempTraitValue ~ LnMass, phy = td$phy, model = model): data names do not match w
## Warning in phylolm(LnTempTraitValue ~ LnMass, phy = td$phy, model = model): data names do not match w
## Warning in phylolm(LnTempTraitValue ~ LnMass, phy = td$phy, model = model): data names do not match w
## Warning in phylolm(LnTempTraitValue ~ LnMass, phy = td$phy, model = model): data names do not match w
## Warning in phylolm(LnTempTraitValue ~ LnMass, phy = td$phy, model = model): the estimation of alpha r
##                            You may change the bounds using options "upper.bound" and "lower.bound".
## Warning in phylolm(LnTempTraitValue ~ LnMass, phy = td$phy, model = model): data names do not match w
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2, phy = td$phy, model = model): data names do n
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2, phy = td$phy, model = model): data names do n
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2, phy = td$phy, model = model): data names do n
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2, phy = td$phy, model = model): data names do n
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2, phy = td$phy, model = model): the estimation
##                            You may change the bounds using options "upper.bound" and "lower.bound".
```

```
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2, phy = td$phy, model = model): data names do n
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2, phy = td$phy, model = model): the estimation
##                            You may change the bounds using options "upper.bound" and "lower.bound".
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2, phy = td$phy, model = model): data names do n
## Warning in phylolm(LnTempTraitValue ~ LnMass + Environment, phy = td$phy, : data names do not match w
## Warning in phylolm(LnTempTraitValue ~ LnMass + Environment, phy = td$phy, : data names do not match w
## Warning in phylolm(LnTempTraitValue ~ LnMass + Environment, phy = td$phy, : data names do not match w
## Warning in phylolm(LnTempTraitValue ~ LnMass + Environment, phy = td$phy, : data names do not match w
## Warning in phylolm(LnTempTraitValue ~ LnMass + Environment, phy = td$phy, : the estimation of alpha n
##                            You may change the bounds using options "upper.bound" and "lower.bound".
## Warning in phylolm(LnTempTraitValue ~ LnMass + Environment, phy = td$phy, : data names do not match w
## Warning in phylolm(LnTempTraitValue ~ LnMass * Environment, phy = td$phy, : data names do not match w
## Warning in phylolm(LnTempTraitValue ~ LnMass * Environment, phy = td$phy, : data names do not match w
## Warning in phylolm(LnTempTraitValue ~ LnMass * Environment, phy = td$phy, : data names do not match w
## Warning in phylolm(LnTempTraitValue ~ LnMass * Environment, phy = td$phy, : data names do not match w
## Warning in phylolm(LnTempTraitValue ~ LnMass * Environment, phy = td$phy, : the estimation of alpha n
##                            You may change the bounds using options "upper.bound" and "lower.bound".
## Warning in phylolm(LnTempTraitValue ~ LnMass * Environment, phy = td$phy, : data names do not match w
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2 + Environment, phy = td$phy, : data names do n
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2 + Environment, phy = td$phy, : data names do n
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2 + Environment, phy = td$phy, : data names do n
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2 + Environment, phy = td$phy, : the estimation
##                            You may change the bounds using options "upper.bound" and "lower.bound".
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2 + Environment, phy = td$phy, : data names do n
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2 + Environment, phy = td$phy, : the estimation
##                            You may change the bounds using options "upper.bound" and "lower.bound".
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2 + Environment, phy = td$phy, : data names do n
fitsLambda <- fitModels("lambda")
## Warning in phylolm(LnTempTraitValue ~ LnMass, phy = td$phy, model = model): data names do not match w
## Warning in phylolm(LnTempTraitValue ~ LnMass, phy = td$phy, model = model): data names do not match w
## Warning in phylolm(LnTempTraitValue ~ LnMass, phy = td$phy, model = model): data names do not match w
## Warning in phylolm(LnTempTraitValue ~ LnMass, phy = td$phy, model = model): data names do not match w
## Warning in phylolm(LnTempTraitValue ~ LnMass, phy = td$phy, model = model): data names do not match w
## Warning in phylolm(LnTempTraitValue ~ LnMass, phy = td$phy, model = model): data names do not match w
```

```
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2, phy = td$phy, model = model): data names do n
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2, phy = td$phy, model = model): the estimation
##                            You may change the bounds using options "upper.bound" and "lower.bound".
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2, phy = td$phy, model = model): data names do n
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2, phy = td$phy, model = model): data names do n
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2, phy = td$phy, model = model): data names do n
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2, phy = td$phy, model = model): the estimation
##                            You may change the bounds using options "upper.bound" and "lower.bound".
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2, phy = td$phy, model = model): data names do n
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2, phy = td$phy, model = model): data names do n
## Warning in phylolm(LnTempTraitValue ~ LnMass + Environment, phy = td$phy, : data names do not match w
## Warning in phylolm(LnTempTraitValue ~ LnMass + Environment, phy = td$phy, : data names do not match w
## Warning in phylolm(LnTempTraitValue ~ LnMass + Environment, phy = td$phy, : data names do not match w
## Warning in phylolm(LnTempTraitValue ~ LnMass + Environment, phy = td$phy, : data names do not match w
## Warning in phylolm(LnTempTraitValue ~ LnMass + Environment, phy = td$phy, : the estimation of lambda
##                            You may change the bounds using options "upper.bound" and "lower.bound".
## Warning in phylolm(LnTempTraitValue ~ LnMass + Environment, phy = td$phy, : data names do not match w
## Warning in phylolm(LnTempTraitValue ~ LnMass * Environment, phy = td$phy, : data names do not match w
## Warning in phylolm(LnTempTraitValue ~ LnMass * Environment, phy = td$phy, : the estimation of lambda
##                            You may change the bounds using options "upper.bound" and "lower.bound".
## Warning in phylolm(LnTempTraitValue ~ LnMass * Environment, phy = td$phy, : data names do not match w
## Warning in phylolm(LnTempTraitValue ~ LnMass * Environment, phy = td$phy, : data names do not match w
## Warning in phylolm(LnTempTraitValue ~ LnMass * Environment, phy = td$phy, : data names do not match w
## Warning in phylolm(LnTempTraitValue ~ LnMass * Environment, phy = td$phy, : the estimation of lambda
##                            You may change the bounds using options "upper.bound" and "lower.bound".
## Warning in phylolm(LnTempTraitValue ~ LnMass * Environment, phy = td$phy, : data names do not match w
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2 + Environment, phy = td$phy, : data names do n
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2 + Environment, phy = td$phy, : the estimation
##                            You may change the bounds using options "upper.bound" and "lower.bound".
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2 + Environment, phy = td$phy, : data names do n
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2 + Environment, phy = td$phy, : the estimation
##                            You may change the bounds using options "upper.bound" and "lower.bound".
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2 + Environment, phy = td$phy, : data names do n
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2 + Environment, phy = td$phy, : data names do n
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2 + Environment, phy = td$phy, : the estimation
##                            You may change the bounds using options "upper.bound" and "lower.bound".
```

```
## Warning in phylolm(LnTempTraitValue ~ LnMass + LnMass2 + Environment, phy = td$phy, : data names do n
```

```
print("BM")
```

```
## [1] "BM"
```

```
aicTable
```

```
##             Angular Speed Maximum Acceleration Maximum Speed
## singlefits  132.9534      207.7595             1207.694
## quadfits    131.0884      201.15               1205.776
## envfits     134.7482      211.649              1201.614
## envIntfits  138.5511      214.7885             1205.334
## envQuadfits 133.5311      204.9566             1200.965
##             Minimum Turn Radius Routine Accleration Routine Speed
## singlefits  109.6635            3.151593            697.5601
## quadfits    111.61              4.448655            685.4875
## envfits     110.6396            NULL                644.9767
## envIntfits  112.2383            NULL                647.5408
## envQuadfits 112.6389            NULL                630.9515
```

```
print("OUrandomRoot")
```

```
## [1] "OUrandomRoot"
```

```
do.call(rbind, lapply(fitsOUr, function(x) sapply(x, function(y) y$aic)))
```

```
##             Angular Speed Maximum Acceleration Maximum Speed
## singlefits  130.1423      204.3471             1143.064
## quadfits    125.6062      191.7894             1093.592
## envfits     128.3004      208.2988             1115.908
## envIntfits  130.8364      211.8483             1117.419
## envQuadfits 125.0921      187.935              1074.416
##             Minimum Turn Radius Routine Accleration Routine Speed
## singlefits  95.10456            4.72215             666.8413
## quadfits    94.68196            5.745505            659.2593
## envfits     89.80194            NULL                612.7989
## envIntfits  88.8732             NULL                614.5432
## envQuadfits 91.71864            NULL                604.2794
```

```
print("OUfixedRoot")
```

```
## [1] "OUfixedRoot"
```

```
do.call(rbind, lapply(fitsOUf, function(x) sapply(x, function(y) y$aic)))
```

```
##             Angular Speed Maximum Acceleration Maximum Speed
## singlefits  130.0926      204.3419             1143.064
## quadfits    125.5998      191.7894             1093.592
## envfits     128.2987      208.2944             1115.908
## envIntfits  130.8362      211.8427             1117.419
## envQuadfits 125.0918      187.935              1074.416
##             Minimum Turn Radius Routine Accleration Routine Speed
## singlefits  95.10456            4.72215             666.8413
## quadfits    94.68196            5.745505            659.2593
## envfits     89.80194            NULL                612.7989
## envIntfits  88.8732             NULL                614.5432
## envQuadfits 91.71864            NULL                604.2794
```

```
print("Lambda")
```

```
## [1] "Lambda"
```

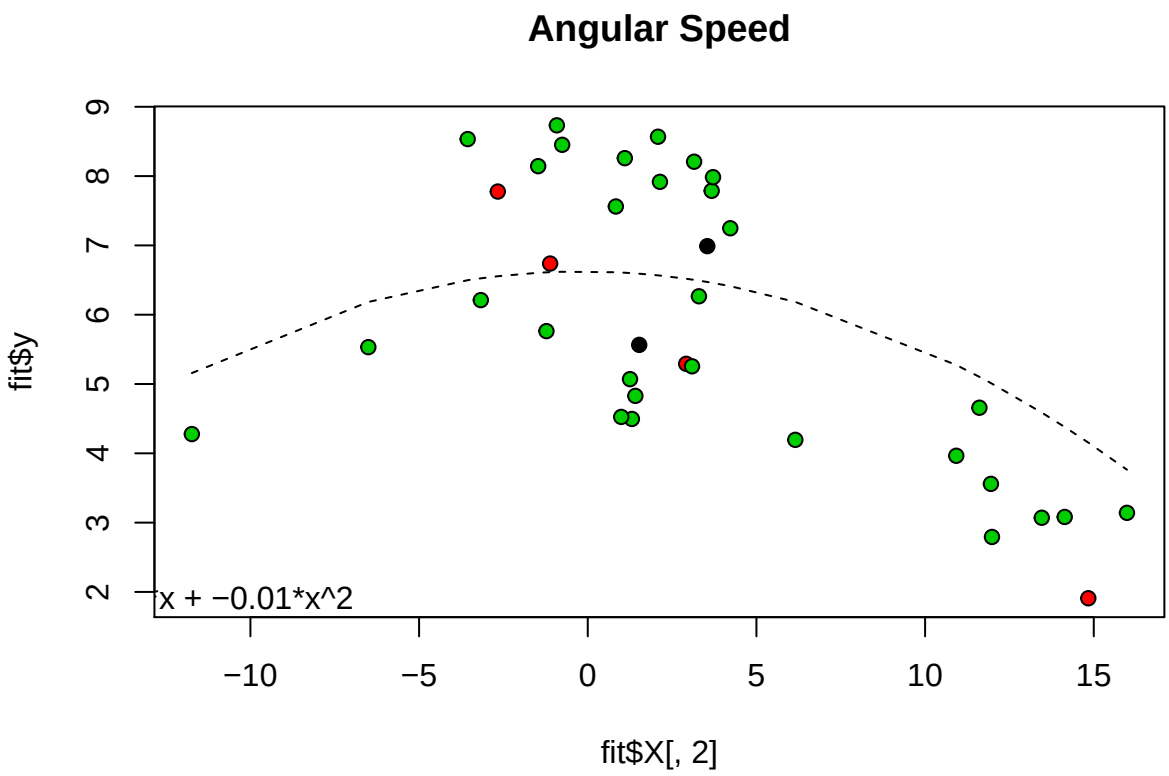
```
do.call(rbind, lapply(fitsLambda, function(x) sapply(x, function(y) y$aic)))
```

```
##             Angular Speed Maximum Acceleration Maximum Speed
## singlefits  134.9534      203.6839             1033.085
## quadfits    129.7642      192.606              1021.156
## envfits     136.7482      207.6027             1012.016
## envIntfits  135.7524      211.0994             1014.242
## envQuadfits 128.7389      192.0583             1004.829
##             Minimum Turn Radius Routine Accleration Routine Speed
## singlefits  93.64496             4.426986            695.6495
## quadfits    94.24958             5.637119            683.4688
## envfits     89.45079             NULL                633.0971
## envIntfits  88.22818             NULL                635.693
## envQuadfits 91.24044             NULL                619.9154
```

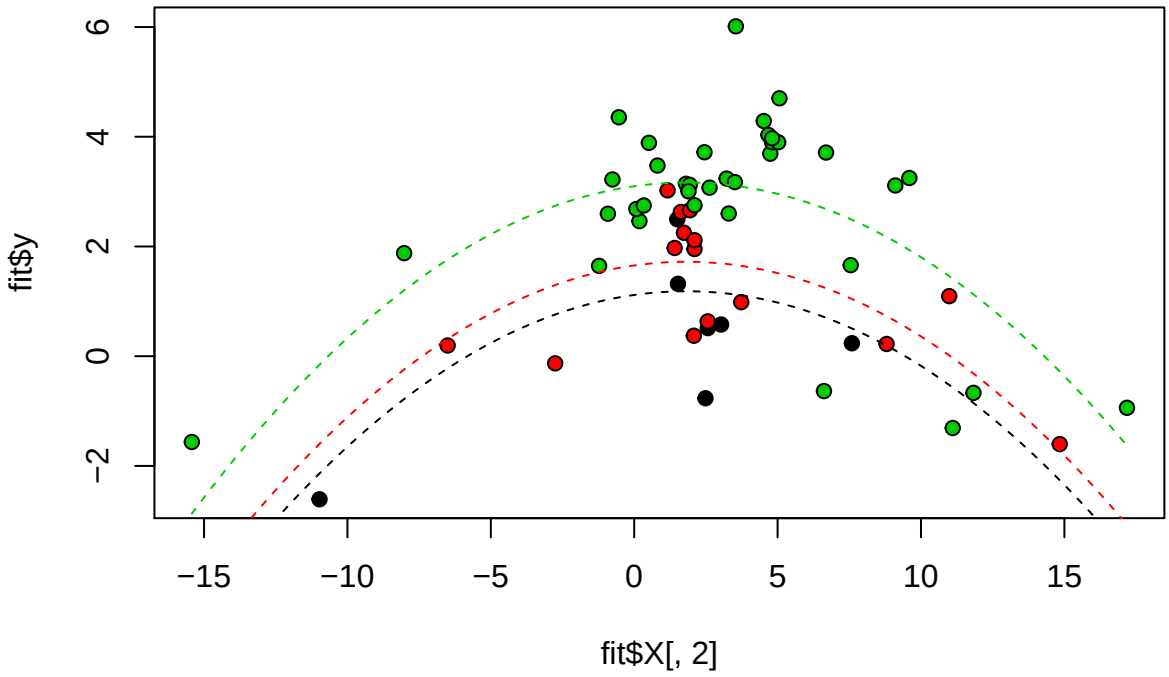
For the following models, it looks like these are the best fits: Angular speed: Quadratic w/OU residuals Maximum acceleration: Quadratic & environment w/ OU residuals Maximum Speed: Quadratic & environment w/Lambda residuals Minimum turn radius: Environment with either OU or Lambda residuals Routine Acceleration: Linear with BM residuals Routine Speed: Environment and Quadratic with OU residuals

Plotting fitted models

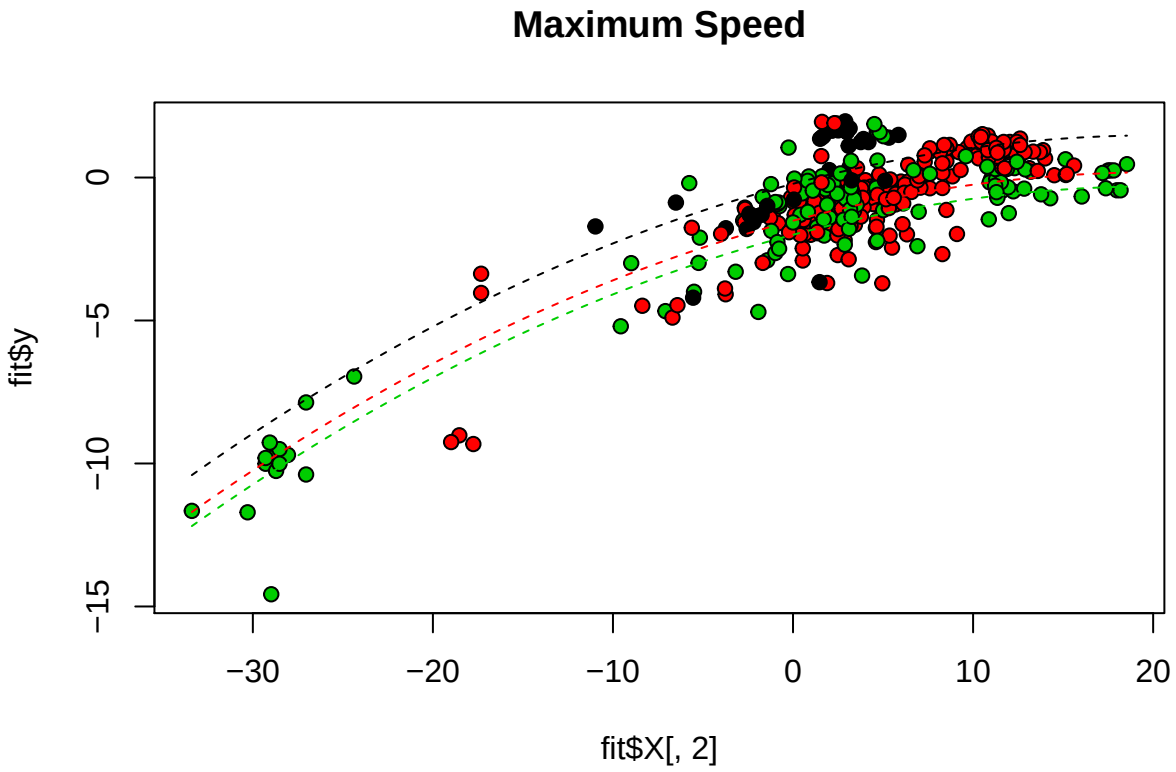
```
## Angular Speed
fit <- fitsOUr$quadfits$`Angular Speed`
plot(fit$X[,2], fit$y, main="Angular Speed", pch=21, bg=tds[[1]]$dat$Environment)
o <- order(fit$X[,2])
lines(fit$X[o,2], fit$fitted.values[o], lty=2)
coef <- round(fit$coefficients,2)
text(min(fit$X[,2]), min(fit$y), labels=paste(coef[1], " + ",coef[2], "*x + ", coef[3],"*x^2", sep=""))
```



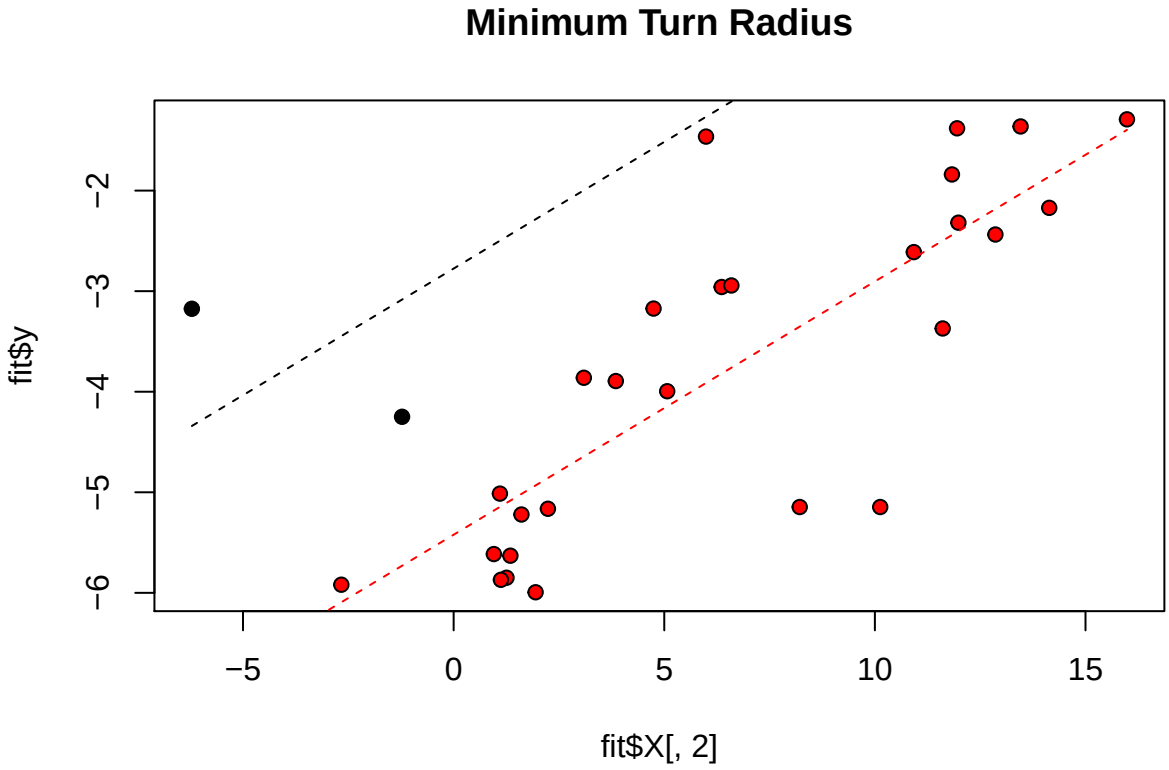

```
## Maximum Acceleration
fit <- fitsOUr$envQuadfits$`Maximum Acceleration`
plot(fit$X[,2], fit$y, main="Maximum Acceleration", pch=21, bg=tds[[2]]$dat$Environment)
o <- order(fit$X[,2])
coef <- fit$coefficients
curve(coef[1]+coef[2]*x+coef[3]*x^2, add=TRUE, lty=2, col=1)
curve(coef[1]+coef[2]*x+coef[3]*x^2+coef[4], add=TRUE, lty=2, col=2)
curve(coef[1]+coef[2]*x+coef[3]*x^2+coef[5], add=TRUE, lty=2, col=3)
```



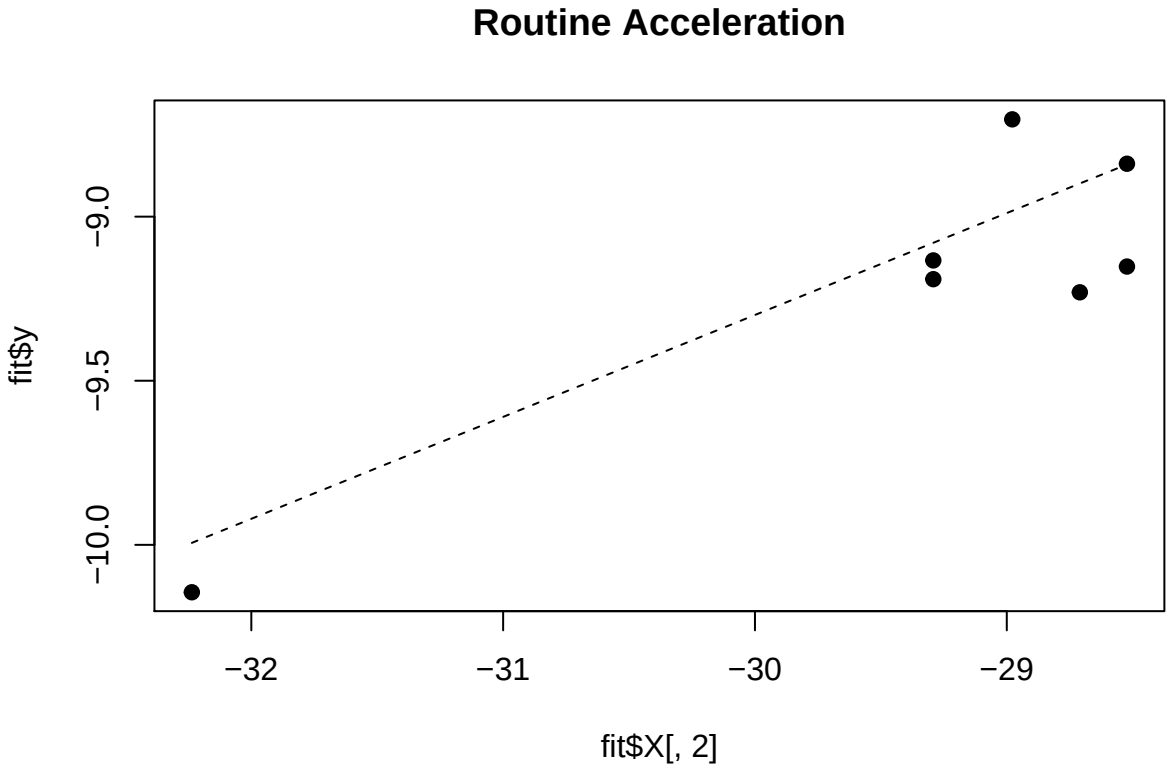

```
## Maximum Speed
fit <- fitsLambda$envQuadfits$`Maximum Speed`
plot(fit$X[,2], fit$y, main="Maximum Speed", pch=21, bg=tds[[3]]$dat$Environment)
o <- order(fit$X[,2])
coef <- fit$coefficients
curve(coef[1]+coef[2]*x+coef[3]*x^2, add=TRUE, lty=2, col=1)
curve(coef[1]+coef[2]*x+coef[3]*x^2+coef[4], add=TRUE, lty=2, col=2)
curve(coef[1]+coef[2]*x+coef[3]*x^2+coef[5], add=TRUE, lty=2, col=3)
```



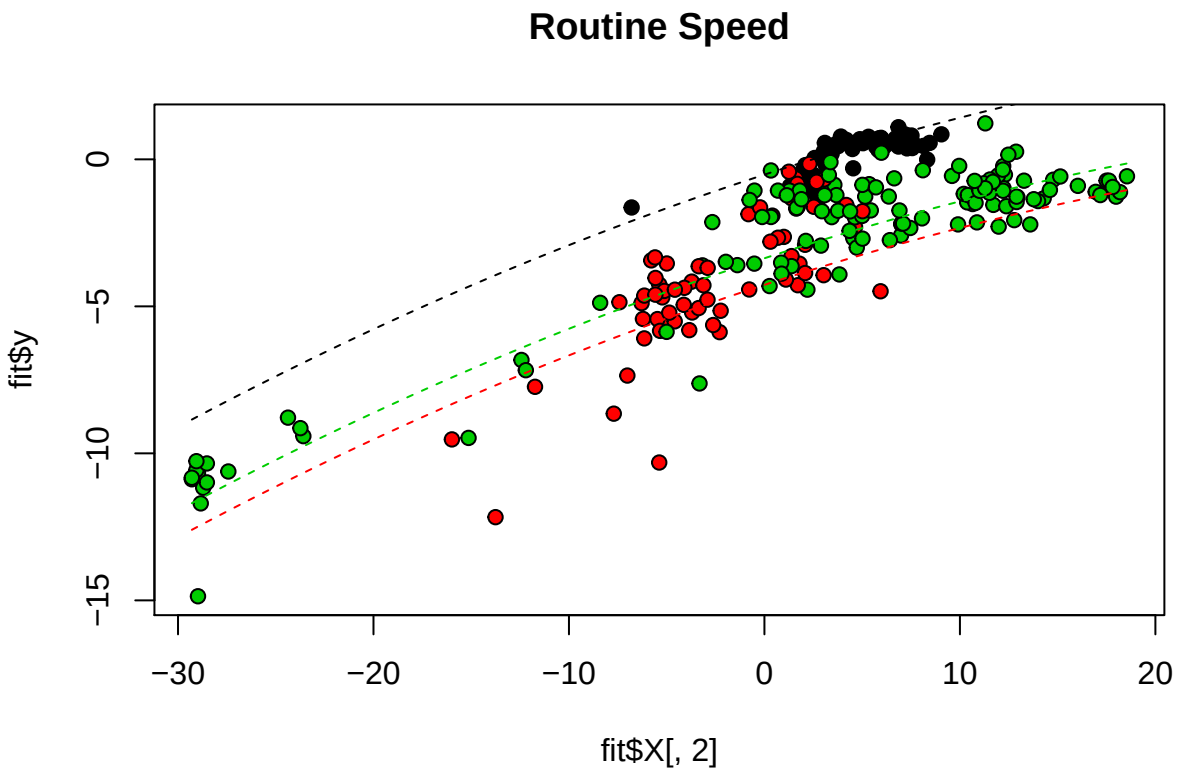

```
## Minimum turn radius
fit <- fitsLambda$envfits$`Minimum Turn Radius`
plot(fit$X[,2], fit$y, main="Minimum Turn Radius", pch=21, bg=tds[[4]]$dat$Environment)
o <- order(fit$X[,2])
coef <- fit$coefficients
curve(coef[1]+coef[2]*x, add=TRUE, lty=2, col=1)
curve(coef[1]+coef[2]*x+coef[3], add=TRUE, lty=2, col=2)
curve(coef[1]+coef[2]*x+coef[4], add=TRUE, lty=2, col=3)
```




```
## Routine acceleration
fit <- singlefits$`Routine Accleration`
plot(fit$X[,2], fit$y, main="Routine Acceleration", pch=21, bg=tds[[5]]$dat$Environment)
o <- order(fit$X[,2])
coef <- fit$coefficients
curve(coef[1]+coef[2]*x, add=TRUE, lty=2, col=1)
```




```
## Routine Speed
fit <- fitsOUr$envQuadfits$`Routine Speed`
plot(fit$X[,2], fit$y, main="Routine Speed", pch=21, bg=tds[[6]]$dat$Environment)
o <- order(fit$X[,2])
coef <- fit$coefficients
curve(coef[1]+coef[2]*x+coef[3]*x^2, add=TRUE, lty=2, col=1)
curve(coef[1]+coef[2]*x+coef[3]*x^2+coef[4], add=TRUE, lty=2, col=2)
curve(coef[1]+coef[2]*x+coef[3]*x^2+coef[5], add=TRUE, lty=2, col=3)
```



Phylogenetic versions of regressions featured in the manuscript (currently)

Figure 1

```
#A) Exploratory Speed (Routine speed?)
td <- tds[[6]]
td <- filter(td, !is.na(LnMass), !is.na(TempTraitValue))
M <- td[['LnMass']]
y <- log(td[['TempTraitValue']])
lmF1A <- phylolm(y~M, phy=td$phy, model="OUrandomRoot")
summary(lmF1A)
```

```
##
## Call:
## phylolm(formula = y ~ M, phy = td$phy, model = "OUrandomRoot")
##
##    AIC logLik
##  666.8 -329.4
##
## Raw residuals:
##     Min      1Q  Median      3Q     Max
## -4.6061  0.5106  1.5644  3.3508  4.6299
##
## Mean tip height: 4246.667
## Parameter estimate(s) using ML:
## alpha: 0.002030998
## sigma2: 0.01271395
```

```
##
## Coefficients:
##             Estimate   StdErr t.value   p.value
## (Intercept) -4.67610  0.44129 -10.596 < 2.2e-16 ***
## M            0.20992  0.01672  12.555 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Note: p-values are conditional on alpha=0.002030998.
```

```
print(paste("N=", length(y)))
```

```
## [1] "N= 246"
```

```
#B) Maximum Speed
td <- tds[[3]]
td <- filter(td, !is.na(LnMass), !is.na(TempTraitValue))
M <- td[['LnMass']]
y <- log(td[['TempTraitValue']])
lmF1B <- phylolm(y~M, phy=td$phy, model="OUrandomRoot")
summary(lmF1B)
```

```
##
## Call:
## phylolm(formula = y ~ M, phy = td$phy, model = "OUrandomRoot")
##
##    AIC logLik
## 1143.1 -567.5
##
## Raw residuals:
##     Min      1Q  Median      3Q     Max
## -5.4023 -0.6526  0.0449  0.5949  3.2682
##
## Mean tip height: 4246.667
## Parameter estimate(s) using ML:
## alpha: 0.007578025
## sigma2: 0.02756155
##
## Coefficients:
##             Estimate    StdErr t.value   p.value
## (Intercept) -1.735603  0.166140 -10.447 < 2.2e-16 ***
## M            0.256564  0.011065  23.188 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Note: p-values are conditional on alpha=0.007578025.
```

```
print(paste("N=", length(y)))
```

```
## [1] "N= 433"
```

```
#C) Acceleration
td <- tds[[2]]
td <- filter(td, !is.na(LnMass), !is.na(TempTraitValue))
M <- td[['LnMass']]
y <- log(td[['TempTraitValue']])
lmF1C <- phylolm(y~M, phy=td$phy, model="OUrandomRoot")
```

```r
summary(lmF1C)
```

```
##
## Call:
## phylolm(formula = y ~ M, phy = td$phy, model = "OUrandomRoot")
##
##    AIC logLik
## 204.35 -98.17
##
## Raw residuals:
##     Min      1Q  Median      3Q     Max
## -3.7258 -0.7812  1.2707  1.8189  4.5763
##
## Mean tip height: 1724.729
## Parameter estimate(s) using ML:
## alpha: 0.002142062
## sigma2: 0.01736926
##
## Coefficients:
##             Estimate   StdErr t.value p.value
## (Intercept) 1.220296 0.718017  1.6995 0.09477 .
## M           0.060879 0.046567  1.3073 0.19644
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Note: p-values are conditional on alpha=0.002142062.
```

```r
print(paste("N=", length(y)))
```

```
## [1] "N= 58"
```

```r
#D) Min Turn Radius
td <- tds[[4]]
td <- filter(td, !is.na(LnMass), !is.na(TempTraitValue))
M <- td[['LnMass']]
y <- log(td[['TempTraitValue']])
lmF1D <- phylolm(y~M, phy=td$phy, model="BM")
summary(lmF1D)
```

```
##
## Call:
## phylolm(formula = y ~ M, phy = td$phy, model = "BM")
##
##    AIC logLik
## 109.66 -51.83
##
## Raw residuals:
##     Min      1Q  Median      3Q     Max
## -2.7526 -1.2613 -0.5446  0.1553  2.3438
##
## Mean tip height: 846.9994
## Parameter estimate(s) using ML:
## sigma2: 0.01473165
##
## Coefficients:
```

```
##             Estimate   StdErr t.value p.value
## (Intercept) -4.33057  2.07062 -2.0914 0.04603 *
## M            0.19122  0.07725  2.4754 0.01988 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
print(paste("N=", length(y)))
```

```
## [1] "N= 29"
```

```
#E) Angular Speed
td <- tds[[1]]
td <- filter(td, !is.na(LnMass), !is.na(TempTraitValue))
M <- td[['LnMass']]
y <- log(td[['TempTraitValue']])
lmF1E <- phylolm(y~M, phy=td$phy, model="OUrandomRoot")
summary(lmF1E)
```

```
##
## Call:
## phylolm(formula = y ~ M, phy = td$phy, model = "OUrandomRoot")
##
##    AIC logLik
## 130.14 -61.07
##
## Raw residuals:
##     Min      1Q  Median      3Q     Max
## -3.1786 -1.4448 -0.4746  1.7714  2.5238
##
## Mean tip height: 846.9994
## Parameter estimate(s) using ML:
## alpha: 0.003209977
## sigma2: 0.01860283
##
## Coefficients:
##              Estimate    StdErr t.value   p.value
## (Intercept)  6.257101  0.544317  11.495 2.928e-13 ***
## M           -0.102181  0.056235  -1.817   0.07804 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Note: p-values are conditional on alpha=0.003209977.
```

```
print(paste("N=", length(y)))
```

```
## [1] "N= 36"
```

Figure 2

```
#A) Routine Speed
td <- tds[[6]]
td <- filter(td, !is.na(LnMass), !is.na(TempTraitValue), !is.na(Environment)) %>% mutate(., LnTTV = log

sumTableA <- summarise(td, Int=phylolm(LnTTV~LnMass, phy=phy, model="OUrandomRoot")$coef[1], Slope=phylo
                       p.slope=round(summary(phylolm(LnTTV~LnMass, phy=phy, model="OUrandomRoot"))$coeffi
```

```
## Warning in phylolm(LnTTV ~ LnMass, phy = phy, model = "OUrandomRoot"): data names do not match with t

## Warning in phylolm(LnTTV ~ LnMass, phy = phy, model = "OUrandomRoot"): data names do not match with t

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## Warning in phylolm(LnTTV ~ LnMass, phy = phy, model = "OUrandomRoot"): data names do not match with t

## Warning in phylolm(LnTTV ~ LnMass, phy = phy, model = "OUrandomRoot"): data names do not match with t

## Warning in phylolm(LnTTV ~ LnMass, phy = phy, model = "OUrandomRoot"): data names do not match with t
```

```
sumTableA
```

```
##   Environment        Int     Slope   N      p.slope
## 1         Air -0.5825912 0.1679678  51 4.89293e-05
## 2        Land -4.5706163 0.2395115  66 2.38800e-07
## 3       Water -3.5428488 0.2551563 129 0.00000e+00
```

```
#B) Maximum Speed
td <- tds[[3]]
td <- filter(td, !is.na(LnMass), !is.na(TempTraitValue), !is.na(Environment)) %>% mutate(., LnTTV = log
model <- "OUrandomRoot"
sumTableB <- summarise(td, Int=phylolm(LnTTV~LnMass, phy=phy, model=model)$coef[1], Slope=phylolm(LnTTV
                      p.slope=round(summary(phylolm(LnTTV~LnMass, phy=phy, model=model))$coefficients[1
```

```
## Warning in phylolm(LnTTV ~ LnMass, phy = phy, model = model): data names do not match with the tip la

## Warning in phylolm(LnTTV ~ LnMass, phy = phy, model = model): data names do not match with the tip la

## Warning in phylolm(LnTTV ~ LnMass, phy = phy, model = model): data names do not match with the tip la

## Warning in phylolm(LnTTV ~ LnMass, phy = phy, model = model): data names do not match with the tip la

## Warning in phylolm(LnTTV ~ LnMass, phy = phy, model = model): data names do not match with the tip la

## Warning in phylolm(LnTTV ~ LnMass, phy = phy, model = model): data names do not match with the tip la

## Warning in phylolm(LnTTV ~ LnMass, phy = phy, model = model): data names do not match with the tip la

## Warning in phylolm(LnTTV ~ LnMass, phy = phy, model = model): data names do not match with the tip la

## Warning in phylolm(LnTTV ~ LnMass, phy = phy, model = model): data names do not match with the tip la
```

```
sumTableB
```

```
##   Environment        Int     Slope   N      p.slope
## 1         Air  0.2966533 0.1298076  40 4.57081e-01
## 2        Land -1.8053062 0.2035082 271 0.00000e+00
## 3       Water -1.9396616 0.2624683 122 2.77800e-07
```

```r
#C) Acceleration
td <- tds[[2]]
td <- filter(td, !is.na(LnMass), !is.na(TempTraitValue), !is.na(Environment)) %>% mutate(., LnTTV = log
model <- "OUrandomRoot"
sumTableC <- summarise(td, Int=phylolm(LnTTV~LnMass, phy=phy, model=model)$coef[1], Slope=phylolm(LnTTV
                       p.slope=round(summary(phylolm(LnTTV~LnMass, phy=phy, model=model))$coefficients[1
```

```
## Warning in phylolm(LnTTV ~ LnMass, phy = phy, model = model): data names do not match with the tip la

## Warning in phylolm(LnTTV ~ LnMass, phy = phy, model = model): data names do not match with the tip la

## Warning in phylolm(LnTTV ~ LnMass, phy = phy, model = model): data names do not match with the tip la

## Warning in phylolm(LnTTV ~ LnMass, phy = phy, model = model): data names do not match with the tip la

## Warning in phylolm(LnTTV ~ LnMass, phy = phy, model = model): data names do not match with the tip la

## Warning in phylolm(LnTTV ~ LnMass, phy = phy, model = model): data names do not match with the tip la

## Warning in phylolm(LnTTV ~ LnMass, phy = phy, model = model): data names do not match with the tip la

## Warning in phylolm(LnTTV ~ LnMass, phy = phy, model = model): data names do not match with the tip la

## Warning in phylolm(LnTTV ~ LnMass, phy = phy, model = model): data names do not match with the tip la
```

```r
sumTableC
```

```
##   Environment      Int       Slope  N     p.slope
## 1         Air 0.758388 -0.02618402  7 0.166827035
## 2        Land 1.584472 -0.13889878 15 0.005799856
## 3       Water 1.089334  0.08578392 36 0.350860651
```

```r
#D) Min Turning Radius
td <- tds[[4]]
td <- filter(td, !is.na(LnMass), !is.na(TempTraitValue), !is.na(Environment)) %>% mutate(., LnTTV = log
model <- "OUrandomRoot"
sumTableD <- summarise(td, Int=phylolm(LnTTV~LnMass, phy=phy, model=model)$coef[1], Slope=phylolm(LnTTV
                       p.slope=summary(phylolm(LnTTV~LnMass, phy=phy, model=model))$coefficients[1,4])
```

```
## Warning in phylolm(LnTTV ~ LnMass, phy = phy, model = model): data names do not match with the tip la

## Warning in phylolm(LnTTV ~ LnMass, phy = phy, model = model): data names do not match with the tip la

## Warning in phylolm(LnTTV ~ LnMass, phy = phy, model = model): data names do not match with the tip la
```

```r
rownames(sumTableD) <- "Water"
sumTableD
```

```
##             Int     Slope  N      p.slope
## Water -4.769509 0.1557168 29 1.707459e-13
```

```r
#E) Angular Speed
td <- tds[[1]]
td <- filter(td, !is.na(LnMass), !is.na(TempTraitValue), !is.na(Environment)) %>% mutate(., LnTTV = log
model <- "OUrandomRoot"
sumTableE <- summarise(td, Int=phylolm(LnTTV~LnMass, phy=phy, model=model)$coef[1], Slope=phylolm(LnTTV
                       p.slope=summary(phylolm(LnTTV~LnMass, phy=phy, model=model))$coefficients[1,4])
```

```
## Warning in phylolm(LnTTV ~ LnMass, phy = phy, model = model): data names do not match with the tip la

## Warning in phylolm(LnTTV ~ LnMass, phy = phy, model = model): data names do not match with the tip la

## Warning in phylolm(LnTTV ~ LnMass, phy = phy, model = model): data names do not match with the tip la
```

```
rownames(sumTableE) <- "Water"
sumTableE
```

```
##            Int      Slope  N      p.slope
## Water 6.257101 -0.1021807 36 2.928442e-13
```