Ecological factors influencing primate vocal signaling: a phylogenetic regression workflow for the *mmodely* R-package (Version 0.2.2)

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1 Introduction

The historical relationships between evolved traits of organisms and the ecological settings that shape these traits are complicated systems that can be challenging to untangle [2]. The origins of behavioral traits can particularly difficult to understand as they tend to also be mediated through the behaviors of other organisms, which are themselves constantly in flux and considerably labile [3]. A perfect example of such a trait is that of vocal signal complexity. Animals use complex calls to assert obscured position, unique identity, special status, or emotive state to conspecifics over interference from other calls or distortions from background noise [1]. Here, using the *mmodely* package on a primate vocalization dataset [13], I demonstrate how the origins of complex call structure, such as syllablic diversity [15], can be elucidated from a range of environmental and behavioral covariates from disparate datasets [10]. Model averaging [MA] [6] and model selection [MS] [7] results primarily highlight locomotion [14] and mating system [11] as important factors driving complex calling, as well as the trophic security [16] variables of mass, group size, and arboreality. The *mmodely* package enables implementation of a combination of phylogenetic controlled regression [8] and information theoretic [9] (MA and MS) examination to simultaneously compare (weighted) predictor coefficients across the numerous sub-datasets generated during exploration of all possible model combinations.

2 Licensing

3 Installation

This package largely depends upon the *caper* package, but most functions do not require any particular library. It is recommended that you have *caper*, *ape*, and the *caroline* package installed as a minimum.

```
> # wget https://cran.r-project.org/src/contrib/Archive/caroline/caroline_0.8.0.tar.gz
> # wget https://cran.r-project.org/src/contrib/Archive/caper/caper_0.5.tar.gz
> # wget https://cran.r-project.org/src/contrib/Archive/ape/ape_3.0-5.tar.gz
> # R CMD INSTALL caroline_0.8.0.tar.gz
> # R CMD INSTALL caper_0.5.tar.gz
> # R CMD INSTALL ape_3.0-5.tar.gz
```

Building the *mmodely* package from source requires that you have the proper dependency packages, *caroline*, installed from CRAN. This can typically be accomplished via the following commands from within the R command line environment:

```
install.packages(c('caroline','ape','caper'))
```

After a successful installation the *mmodely* package can be loaded in the normal way: by starting R and invoking the following `library` command:

```
> library(caper)
> library(mmodely)
```

4 Reading in Data

Read in the tree [12] and datasets then merge them together.

```
> data.path <- system.file("extdata","primate-example.data.csv", package="mmodely")
> data <- read.csv(data.path, row.names=1)
> data$gn_sp <- rownames(data)
> #multiply two vocalization metrics together to create "vocal complexity"
> data$VC <- apply(data[,c('syllables_max','rhythm_max')], 1, prod)
> data <- subset(data, !is.na(VC))
> # merge data sets here if applicable
>
> tree.path <- system.file("extdata","primate-springer.2012.tre", package="mmodely")
> phyl <- ape::read.tree(tree.path)[[5]]
> #5. RAxML phylogram based on the 61199 bp concatenation of 69 nuclear and ten mitochondrial genes.
>
> phyl <- trim.phylo(phylo=phyl, gs.vect=data$gn_sp) # prune unused nodes and branches
> comp <- comp.data(phylo=phyl, df=data)
```

Typically there will be some missing data (species) in certain sources that do not occur in others. A merge of these will result in NA values for some cells. The more missing cells and merges there are, the more sub-datasets will be possible, due to case-wise deletion in the process of combinatorics underlying model iteration, averaging, and selection. The above example has little if any missing data, but the examples below introduce some artificially.

5 Basic Reporting

First, for illustration purposes, we perform a simple analysis of a single model using 'pgls' directly from the *caper* package, then show-off the 'pgls.report' functionality of the *mmodely* package. ANOVA, AIC, and one-line model reports can be output via this function.

```
> model <- as.formula('VC ~ mass.Kg + group.size')
> fit <- caper::pgls(formula=model, data=comp)
> summary(fit)

Call:
caper::pgls(formula = model, data = comp)

Residuals:
    Min      1Q  Median      3Q     Max
-7.9014 -0.9478  0.0030  1.2281  8.6394

Branch length transformations:

kappa  [Fix]  : 1.000
lambda [Fix]  : 1.000
delta  [Fix]  : 1.000

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)  2.2345483  1.1333734  1.9716   0.0662 .
mass.Kg     -0.0079678  0.0082070 -0.9709   0.3461
group.size   0.0071381  0.0144792  0.4930   0.6287
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 4.61 on 16 degrees of freedom
Multiple R-squared: 0.1101,        Adjusted R-squared: -0.001146
F-statistic: 0.9897 on 3 and 16 DF,  p-value: 0.4226

> pgls.report(comp, f=model, anova=TRUE, QC.plot=TRUE)
```

```
Call:
pgls(formula = f, data = cd, lambda = l, kappa = k, delta = d,
    bounds = bounds)

Residuals:
    Min      1Q  Median      3Q     Max
-7.9014 -0.9478  0.0030  1.2281  8.6394

Branch length transformations:

kappa  [Fix]  : 1.000
lambda [Fix]  : 1.000
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Coefficients:
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mass.Kg     -0.0079678  0.0082070 -0.9709   0.3461
group.size   0.0071381  0.0144792  0.4930   0.6287
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 4.61 on 16 degrees of freedom
Multiple R-squared: 0.1101,        Adjusted R-squared: -0.001146
F-statistic: 0.9897 on 3 and 16 DF,  p-value: 0.4226
[1] "AIC = 58"
Analysis of Variance Table
Sequential SS for pgls: lambda = 1.00, delta = 1.00, kappa = 1.00

Response: VC
           Df Sum Sq Mean Sq F value Pr(>F)
mass.Kg     1  36.89  36.894  1.7363 0.2062
group.size  1   5.16   5.164  0.2430 0.6287
Residuals  16 339.96  21.248
 group(0.629)  |  mass(0.346)

Call:
pgls(formula = f, data = cd, lambda = l, kappa = k, delta = d,
    bounds = bounds)

Coefficients:
(Intercept)      mass.Kg   group.size
   2.234548    -0.007968     0.007138
```

6 Multivariate Combinatoric Iteration

The *mmodely* package's chief contribution is enabling approaches that utilize multi-model iteration averaging. Using a smaller subset of variables can speed up the (slower) maximum likelihood computation step and still achieve the desired result of fixed tree transformation parameters.

```
> pv0 <- c("mass.Kg","arboreal","home.range","monogamy") #"swing.pct"
> est.mods <- get.model.combos(predictor.vars=pv0, outcome.var='VC', min.q=2)
> ps <- get.phylo.stats(phylo=phyl, data=data, trait.clmn='VC');

$lambda
[1] 0.2903945

$logL
[1] -55.25736

$P
[1] 0.7103404

$K
[1] 0.1886703

$P
[1] 0.409

> lambda <- ps$lambda$lambda ; print(lambda)

[1] 0.2903945

> PGLSi <- pgls.iter(models=est.mods, phylo=phyl, df=data, l=lambda, k='ML', d='ML')

1 VC~mass.Kg+arboreal+home.range+monogamy
2 VC~mass.Kg+arboreal+home.range
3 VC~mass.Kg+arboreal+monogamy
4 VC~mass.Kg+home.range+monogamy
5 VC~arboreal+home.range+monogamy
6 VC~mass.Kg+arboreal
7 VC~mass.Kg+home.range
8 VC~mass.Kg+monogamy
9 VC~arboreal+home.range
10 VC~arboreal+monogamy
11 VC~home.range+monogamy
```

7 Fixed iteration run statistics

We should briefly inspect how this fixed iteration run performed and how many sub-datasets we need to investigate. By default *mmodely* uses 'rwGsm.' This abbreviation stands for 'raw *Genus species* sums.' It represents a sum of the (concatenated) raw character values of all species constituting the underlying dataset (which has all rows with any missing data removed) for a particular combination of model predictor variables. While this default is preferred, the number of species 'n' or number of model variables 'q' can also be used.

```
> pgls.iter.stats(PGLSi) # check run, especially to see how few sub-datasets exist

models: 11
dimensions of sub-datasets:
    q     n   qXn rwGsm
    3     2     5     2
              q        n
Min.    2.000000 22.00000
1st Qu. 2.000000 22.00000
Median  2.000000 22.00000
Mean    2.545455 27.81818
3rd Qu. 3.000000 38.00000
Max.    4.000000 38.00000
tree transformation parameter averages:
        l         k         d
0.2903945 0.5281791 1.2349271
distributions of optimization parameters:
       n              n.1              q             rwGsm          model.no
 Min.   :22.00   Min.   :22.00   Min.   :2.000   Min.   :39841   Min.   : 1.0
 1st Qu.:22.00   1st Qu.:22.00   1st Qu.:2.000   1st Qu.:39841   1st Qu.: 3.5
 Median :22.00   Median :22.00   Median :2.000   Median :39841   Median : 6.0
 Mean   :27.82   Mean   :27.82   Mean   :2.545   Mean   :51216   Mean   : 6.0
 3rd Qu.:38.00   3rd Qu.:38.00   3rd Qu.:3.000   3rd Qu.:71122   3rd Qu.: 8.5
 Max.   :38.00   Max.   :38.00   Max.   :4.000   Max.   :71122   Max.   :11.0
       R2               R2.adj              AIC              AICc             AICw
 Min.   :0.003538   Min.   :-0.12424   Min.   : 57.17   Min.   : 58.50   Min.   :0.00000
 1st Qu.:0.050162   1st Qu.:-0.07481   1st Qu.: 58.62   1st Qu.: 60.46   1st Qu.:0.00000
 Median :0.079980   Median :-0.05753   Median : 59.70   Median : 62.06   Median :0.05586
 Mean   :0.081541   Mean   :-0.02825   Mean   : 78.26   Mean   : 79.91   Mean   :0.09091
 3rd Qu.:0.115393   3rd Qu.: 0.02664   3rd Qu.:110.38   3rd Qu.:111.09   3rd Qu.:0.13947
 Max.   :0.147762   Max.   : 0.09884   Max.   :115.92   Max.   :116.63   Max.   :0.33028
```

8 Tree Transformation Averaging and Re-iteration

After running PGLS on a test-subset of predictor-variable combinations using maximum likelihood, we can average the tree transformation parameters [18]to obtain fixed values going forward. This approach can speed up computations for larger sets of modeling data and variable combinations.

```
> tt.avgs <- apply(PGLSi$params, 2, mean, na.rm=TRUE) # tree transformation averages
> print(tt.avgs)

        l         k         d
0.2903945 0.5281791 1.2349271

>
```

Next we use the full set of variables and our tree transform averages. For demonstration, we sprinkle in some missing values to our dataset so as to artificially boost the number of sub-datasets. The subsequent fixed tree parameter itteration run should now generate more diverse output upon which the *mmodely* can demonstrate it unique model averaging and model selection functionality.

```
> pvs <- c("mass.Kg","group.size","arboreal","monogamy","leap.pct","swing.pct")
> all.mods <- get.model.combos(predictor.vars=pvs, outcome.var='VC', min.q=2)
> # randomly sprinkle in some missing values (for more interesting for model selection)
> missing.value.ct <- 1
> for(pv in pv0){ data[sample(x=1:nrow(data),size=missing.value.ct),pv] <- NA}
> PGLSi <- pgls.iter(models=all.mods, phylo=phyl, df=data, l=lambda, k=tt.avgs['k'], d=tt.avgs['d'])

1 VC~mass.Kg+group.size+arboreal+monogamy+leap.pct+swing.pct
2 VC~mass.Kg+group.size+arboreal+monogamy+leap.pct
3 VC~mass.Kg+group.size+arboreal+monogamy+swing.pct
4 VC~mass.Kg+group.size+arboreal+leap.pct+swing.pct
5 VC~mass.Kg+group.size+monogamy+leap.pct+swing.pct
6 VC~mass.Kg+arboreal+monogamy+leap.pct+swing.pct
7 VC~group.size+arboreal+monogamy+leap.pct+swing.pct
8 VC~mass.Kg+group.size+arboreal+monogamy
9 VC~mass.Kg+group.size+arboreal+leap.pct
10 VC~mass.Kg+group.size+arboreal+swing.pct
11 VC~mass.Kg+group.size+monogamy+leap.pct
12 VC~mass.Kg+group.size+monogamy+swing.pct
13 VC~mass.Kg+group.size+leap.pct+swing.pct
14 VC~mass.Kg+arboreal+monogamy+leap.pct
15 VC~mass.Kg+arboreal+monogamy+swing.pct
16 VC~mass.Kg+arboreal+leap.pct+swing.pct
17 VC~mass.Kg+monogamy+leap.pct+swing.pct
18 VC~group.size+arboreal+monogamy+leap.pct
19 VC~group.size+arboreal+monogamy+swing.pct
20 VC~group.size+arboreal+leap.pct+swing.pct
21 VC~group.size+monogamy+leap.pct+swing.pct
22 VC~arboreal+monogamy+leap.pct+swing.pct
23 VC~mass.Kg+group.size+arboreal
24 VC~mass.Kg+group.size+monogamy
25 VC~mass.Kg+group.size+leap.pct
26 VC~mass.Kg+group.size+swing.pct
27 VC~mass.Kg+arboreal+monogamy
28 VC~mass.Kg+arboreal+leap.pct
29 VC~mass.Kg+arboreal+swing.pct
30 VC~mass.Kg+monogamy+leap.pct
31 VC~mass.Kg+monogamy+swing.pct
32 VC~mass.Kg+leap.pct+swing.pct
33 VC~group.size+arboreal+monogamy
34 VC~group.size+arboreal+leap.pct
35 VC~group.size+arboreal+swing.pct
36 VC~group.size+monogamy+leap.pct
```

```
37 VC~group.size+monogamy+swing.pct
38 VC~group.size+leap.pct+swing.pct
39 VC~arboreal+monogamy+leap.pct
40 VC~arboreal+monogamy+swing.pct
41 VC~arboreal+leap.pct+swing.pct
42 VC~monogamy+leap.pct+swing.pct
43 VC~mass.Kg+group.size
44 VC~mass.Kg+arboreal
45 VC~mass.Kg+monogamy
46 VC~mass.Kg+leap.pct
47 VC~mass.Kg+swing.pct
48 VC~group.size+arboreal
49 VC~group.size+monogamy
50 VC~group.size+leap.pct
51 VC~group.size+swing.pct
52 VC~arboreal+monogamy
53 VC~arboreal+leap.pct
54 VC~arboreal+swing.pct
55 VC~monogamy+leap.pct
56 VC~monogamy+swing.pct
57 VC~leap.pct+swing.pct
```

> pgls.iter.stats(PGLSi)

```
models: 57
dimensions of sub-datasets:
    q     n   qXn rwGsm
    5     4    13     8
                q        n
Min.    2.000000 35.00000
1st Qu. 2.000000 36.00000
Median  3.000000 36.00000
Mean    3.263158 36.36842
3rd Qu. 4.000000 37.00000
Max.    6.000000 38.00000
tree transformation parameter averages:
        l         k         d
0.2903945 0.5281791 1.2349271
distributions of optimization parameters:
       n              n.1              q             rwGsm          model.no
 Min.   :35.00   Min.   :35.00   Min.   :2.000   Min.   :65457   Min.   : 1
 1st Qu.:36.00   1st Qu.:36.00   1st Qu.:2.000   1st Qu.:67242   1st Qu.:15
 Median :36.00   Median :36.00   Median :3.000   Median :67412   Median :29
 Mean   :36.37   Mean   :36.37   Mean   :3.263   Mean   :68041   Mean   :29
 3rd Qu.:37.00   3rd Qu.:37.00   3rd Qu.:4.000   3rd Qu.:69197   3rd Qu.:43
 Max.   :38.00   Max.   :38.00   Max.   :6.000   Max.   :71122   Max.   :57
       R2              R2.adj              AIC             AICc            AICw
 Min.   :0.004977   Min.   :-0.079511   Min.   :104.2   Min.   :105.9   Min.   :0.0005728
 1st Qu.:0.077384   1st Qu.: 0.008698   1st Qu.:106.5   1st Qu.:108.5   1st Qu.:0.0037426
 Median :0.168338   Median : 0.089358   Median :108.0   Median :109.7   Median :0.0120917
 Mean   :0.151979   Mean   : 0.066055   Mean   :108.8   Mean   :110.3   Mean   :0.0175439
 3rd Qu.:0.209148   3rd Qu.: 0.114697   3rd Qu.:111.3   3rd Qu.:112.0   3rd Qu.:0.0213593
 Max.   :0.294926   Max.   : 0.177413   Max.   :114.7   Max.   :115.8   Max.   :0.0804394
```

9 Model Averaging

Now we can estimate the predictor variable parameters by averaging over all possible fixed PGLS runs, using the AICc differences (from the lowest AICc) as weights. By default this AICw weighted average is performed per sub-dataset using 'rwGsm' as mentioned in the preceding section.

```
> w.means.pds <- average.fit.models(vars=pvs, fits=PGLSi$fits, optims=PGLSi$optim, by='rwGsm')
> #
> apply(w.means.pds, 2, mean, na.rm=T) #average of weighted means over all sub-datasets

   mass.Kg group.size   arboreal   monogamy   leap.pct  swing.pct
 0.0047325  0.0151150 -0.0822525  0.9143950  1.4168125  1.5075462

> w.means.pds                                    # weighted means    per   sub-dataset

      mass.Kg group.size arboreal monogamy leap.pct swing.pct
65457 0.00544    0.01897  0.03256  0.93376  0.96050   0.93583
67242 0.00301    0.01019 -0.05364      NaN  1.87357   2.06952
67382     NaN    0.01779 -0.10189  0.83716  0.99948   1.06710
67412 0.00574    0.01975      NaN  0.98870  1.01710   0.96161
69167     NaN    0.01011 -0.20604      NaN  1.84477   2.07283
69197 0.00474    0.01226      NaN      NaN  1.89257   2.03897
69337     NaN    0.01914      NaN  0.89796  0.91820   0.93306
71122     NaN    0.01271      NaN      NaN  1.82831   1.98145
```

10 Model Selection

We can select the best model by sorting each subset (e.g. by AICc) or by using visualization methods.

```
> select.best.models(PGLSi, using='AICc')
```

```
       n n.1 q  qXn rwGsm model.no        R2     R2.adj      AIC     AICc        AICw
67412 36  36 3 3X36 67412       24 0.2346263 0.16287249 104.5954 105.8857 0.080439377
65457 35  35 3 3X35 65457       27 0.1568148 0.07521622 104.7728 106.1062 0.072042586
69337 37  37 2 2X37 69337       49 0.2091481 0.16262736 105.9161 106.6434 0.055071932
67382 36  36 2 2X36 67382       52 0.1360760 0.08371693 105.8954 106.6454 0.055015934
69167 37  37 3 3X37 69167       41 0.1616744 0.08546300 108.6527 109.9027 0.010794015
67242 36  36 4 4X36 67242       16 0.1650392 0.05730236 108.2817 110.2817 0.008930747
69197 37  37 3 3X37 69197       32 0.1683377 0.09273206 109.4537 110.7037 0.007231694
71122 38  38 2 2X38 71122       57 0.1551053 0.10682565 110.2290 110.9348 0.006442551
```

Plotting the coefficients of determination versus the AIC values allows selection of high-performing models for inspection and reporting.

```
> plot.pgls.iters(PGLSi)
```

```
> sdevs.objs <- get.pgls.coefs(PGLSi$fits, est='t value')
> coefs.objs <- get.pgls.coefs(PGLSi$fits, est='Estimate')
```

```
> report.vect <- sapply(1:length(PGLSi$fits), function(i) fit.1ln.rprt(PGLSi$fits[[i]], rtrn.line=FALSE, mn=i),
```

```
1 +monog(0.118) +group(0.123) +leap(0.181) +swing(0.226) mass(0.394)  |  arbore(0.836) R2adj: 0.118 AICc: 109.6
2 ++mono(0.024) +group(0.139) leap(0.434) mass(0.445) arbore(0.875)  |   R2adj: 0.102 AICc: 108.41
3 ++mono(0.016) +group(0.138) mass(0.495) swing(0.597) arbore(0.834)  |   R2adj: 0.092 AICc: 108.81
4 ++leap(0.024) ++swin(0.043) +group(0.274) mass(0.542)  |  arbore(0.641) R2adj: 0.065 AICc: 111.72
5 +group(0.082) +monog(0.093) +leap(0.147) +swing(0.203) +mass(0.288)  |   R2adj: 0.177 AICc: 108.54
6 +leap(0.208) +monog(0.257) +swing(0.266) mass(0.548)  |  arbore(0.649) R2adj: 0.072 AICc: 109.57
7 +group(0.141) +monog(0.152) +leap(0.169) +swing(0.194)  |  arbore(0.561) R2adj: 0.126 AICc: 109.68
8 ++mono(0.009) +group(0.138) mass(0.489) arbore(0.767)  |   R2adj: 0.113 AICc: 106.23
9 +leap(0.145) group(0.519) mass(0.723) arbore(0.835)  |   R2adj: -0.039 AICc: 113.8
10 +swing(0.302) group(0.563) arbore(0.731) mass(0.859)  |   R2adj: -0.076 AICc: 115.04
11 ++mono(0.015) +group(0.105) leap(0.363) mass(0.406)  |   R2adj: 0.159 AICc: 107.62
12 ++mono(0.008) +group(0.105) mass(0.477) swing(0.564)  |   R2adj: 0.145 AICc: 108.2
13 ++leap(0.014) ++swin(0.035) +group(0.194) mass(0.389)  |   R2adj: 0.113 AICc: 111.41
14 +monog(0.064) leap(0.448) mass(0.598)  |  arbore(0.906) R2adj: 0.063 AICc: 108.16
15 ++mono(0.044) swing(0.642) mass(0.655)  |  arbore(0.951) R2adj: 0.051 AICc: 108.58
16 ++leap(0.037) +swing(0.065) mass(0.641)  |  arbore(0.53) R2adj: 0.057 AICc: 110.28
17 +leap(0.197) +monog(0.228) +swing(0.28) mass(0.388)  |   R2adj: 0.118 AICc: 109.34
18 ++mono(0.034) +group(0.157) leap(0.439)  |  arbore(0.882) R2adj: 0.104 AICc: 108.84
19 ++mono(0.022) +group(0.15) swing(0.529)  |  arbore(0.94) R2adj: 0.098 AICc: 109.08
20 ++leap(0.023) ++swin(0.04) +group(0.279)  |  arbore(0.471) R2adj: 0.091 AICc: 111.21
21 +group(0.093) +monog(0.124) +leap(0.179) +swing(0.22)  |   R2adj: 0.17 AICc: 109.28
22 +leap(0.182) +swing(0.219) +monog(0.308)  |  arbore(0.457) R2adj: 0.089 AICc: 109.42
23 arbore(0.579) group(0.654) mass(0.888)  |   R2adj: -0.08 AICc: 113.59
24 +++mon(0.004) +group(0.108) mass(0.495)  |   R2adj: 0.163 AICc: 105.89
25 +leap(0.084) group(0.47) mass(0.726)  |   R2adj: 0.01 AICc: 113.95
26 +swing(0.241) group(0.542) mass(0.952)  |   R2adj: -0.041 AICc: 115.78
27 ++mono(0.027) mass(0.649) arbore(0.989)  |   R2adj: 0.075 AICc: 106.11
28 +leap(0.161) mass(0.774) arbore(0.95)  |   R2adj: -0.021 AICc: 111.58
29 swing(0.328) arbore(0.829) mass(0.903)  |   R2adj: -0.054 AICc: 112.73
30 ++mono(0.048) leap(0.395) mass(0.497)  |   R2adj: 0.112 AICc: 108
31 ++mono(0.027) mass(0.575) swing(0.649)  |   R2adj: 0.097 AICc: 108.59
32 ++leap(0.028) +swing(0.066) mass(0.456)  |   R2adj: 0.093 AICc: 110.7
33 ++mono(0.013) +group(0.152) arbore(0.976)  |   R2adj: 0.115 AICc: 106.84
34 +leap(0.142) group(0.507) arbore(0.939)  |   R2adj: -0.008 AICc: 113.49
35 +swing(0.275) group(0.537) arbore(0.769)  |   R2adj: -0.038 AICc: 114.59
36 ++mono(0.023) +group(0.112) leap(0.4)  |   R2adj: 0.156 AICc: 108.36
```

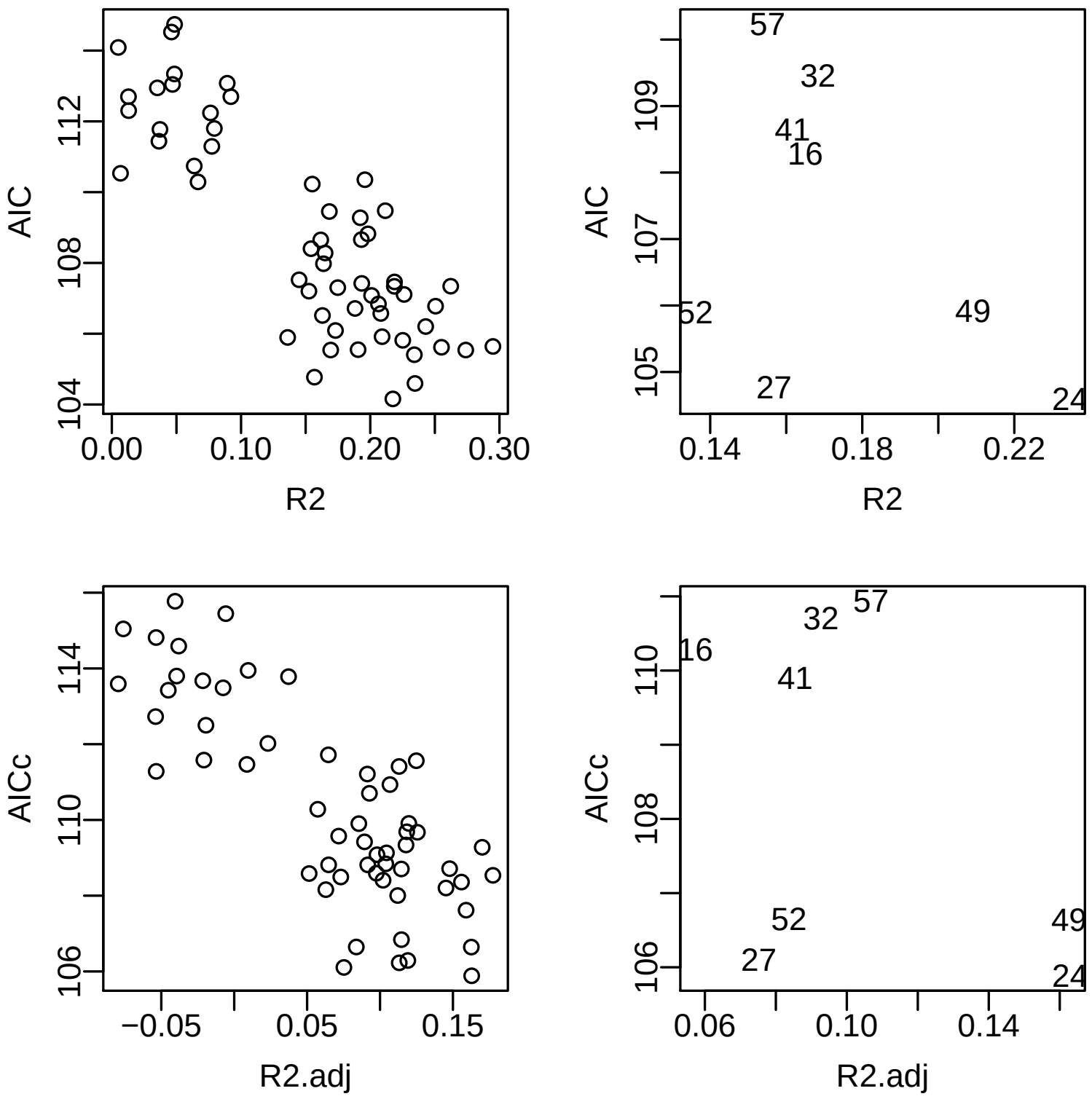

Figure 1: All possible model combinations appear as individual points above. As there is a generally negative association between AIC and the coefficient of determination, the points tend to follow a negative sloping streak to the lower right. The "best" models typically appear in the lower right of each streak. Therefore, minimizing AIC tends to also maximize the coefficient of determination, but not necessarily. This four panel plot looks at correct and adjusted versions of each model assessment measure.

```
37 ++mono(0.012) +group(0.108) swing(0.529)  |   R2adj: 0.148 AICc: 108.71
38 ++leap(0.018) ++swin(0.041) +group(0.198)  |   R2adj: 0.125 AICc: 111.56
39 +monog(0.081) leap(0.436)  |  arbore(0.733) R2adj: 0.073 AICc: 108.49
40 +monog(0.056) swing(0.569)  |  arbore(0.794) R2adj: 0.065 AICc: 108.82
41 ++leap(0.034) +swing(0.058)  |  arbore(0.396) R2adj: 0.085 AICc: 109.9
42 +leap(0.216) +swing(0.282) +monog(0.285)  |   R2adj: 0.12 AICc: 109.91
43 group(0.688)  |  mass(0.93) R2adj: -0.054 AICc: 114.82
44 arbore(0.647) mass(0.92)  |   R2adj: -0.054 AICc: 111.28
45 ++mono(0.014) mass(0.589)  |   R2adj: 0.119 AICc: 106.29
46 +leap(0.101) mass(0.738)  |   R2adj: 0.023 AICc: 112.02
47 +swing(0.274) mass(0.953)  |   R2adj: -0.022 AICc: 113.67
48 arbore(0.579) group(0.626)  |   R2adj: -0.045 AICc: 113.43
49 ++mono(0.006) +group(0.112)  |   R2adj: 0.163 AICc: 106.64
50 +leap(0.081) group(0.442)  |   R2adj: 0.037 AICc: 113.78
51 +swing(0.217) group(0.509)  |   R2adj: -0.006 AICc: 115.45
52 ++mono(0.034)  |  arbore(0.867) R2adj: 0.084 AICc: 106.65
53 +leap(0.156)  |  arbore(0.951) R2adj: 0.009 AICc: 111.47
54 +swing(0.3) arbore(0.87)  |   R2adj: -0.019 AICc: 112.5
55 +monog(0.069) leap(0.418)  |   R2adj: 0.115 AICc: 108.71
56 ++mono(0.038) swing(0.602)  |   R2adj: 0.104 AICc: 109.13
57 ++leap(0.033) +swing(0.075)  |   R2adj: 0.107 AICc: 110.93
```

```
> par(mar=c(5,5,3,3))
> plot.pgls.R2AIC(PGLSi$optim)
```

11 Coefficient Plotting

Finally, the resulting model fits from the PGLS runs can be be plotted out horizontally as distributions so the influence of each ecological predictor variable can be compared.

```
> par.old <- par(mar=c(5,8,1,4),mfrow=c(2,1))
> distro.dots.modsel(sdevs.objs, R2x=7, xlab='t value')
> distro.dots.modsel(coefs.objs, R2x=7, xlab='Estimate')
```

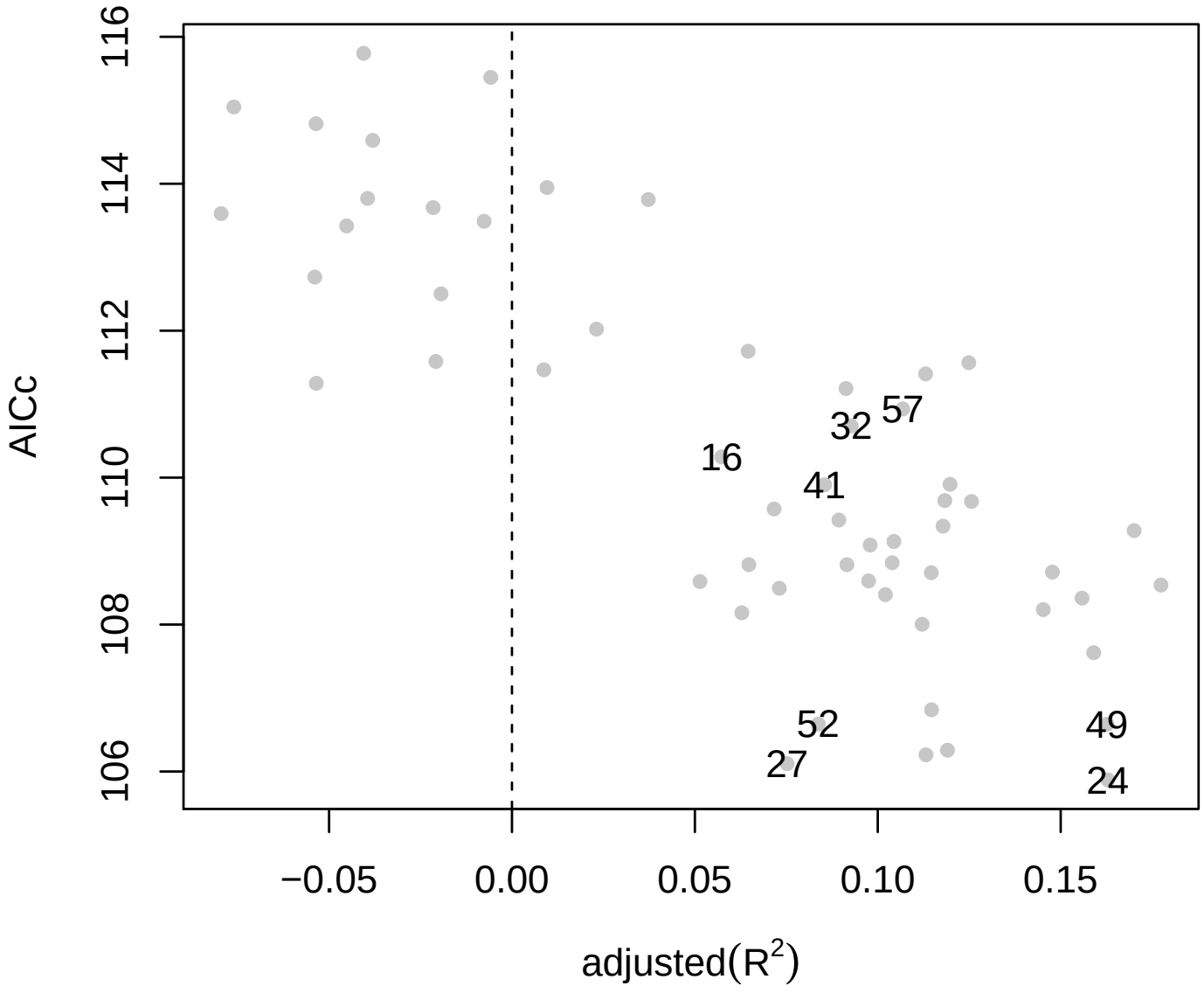

Figure 2: This is a one panel verison of the previous model selection plot. The numbered points in the lower right corner of each streak of possible models represent the best model within a sub-dataset. Since these AICc values should not strictly be compared, it is not a bad idea that all "best" models selected from each sub-dataset should get reported, such as in the form of the 'distro dots' plot below.

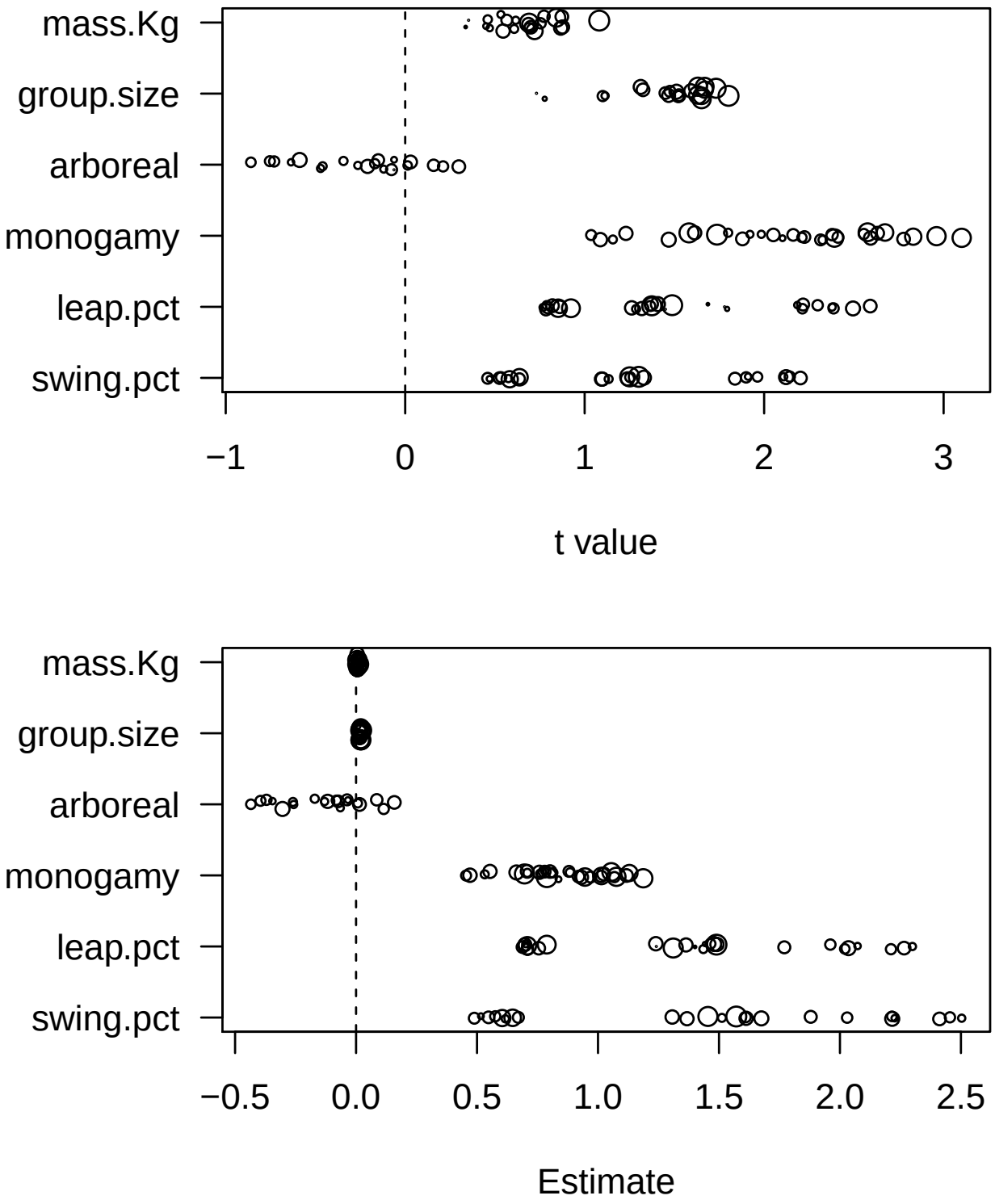

Figure 3: These horizontal parameter distribution dot-plots demonstrate how the (t-values of) coefficients from models can be simultaneously plot in order to verify consistency of estimates across the various (often missing-data driven) sub-datasets. Note that mate choice, locomotion, and statural factors drive complex (here rhythmically syllabic) calling in primates.

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