

Ecological factors influencing primate vision conformation: a phylogenetic regression workflow for the *mmodely* R-package (Version 0.2.0)

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1 Introduction

Perform multivariate modeling of evolved traits, with special attention to understanding the interplay of the multifactorial determinants of their origins in complex ecological settings (Stephens, 2007 <doi:10.1016/j.tree.2006.12.003>). This software primarily concentrates on phylogenetic regression analysis, enabling implementation of tree transformation averaging and visualization functionality. Functions additionally support information theoretic approaches (Grueber, 2011 <doi:10.1111/j.1420-9101.2010.02210.x>; Garamszegi, 2011 <doi:10.1007/s00265-010-1028-7>) such as model averaging and selection of phylogenetic models. There are other numerous functions for visualizing confounded variables, plotting phylogenetic trees, as well as reporting and exporting modeling results. Lastly, as challenges to ecology are inherently multifarious, and therefore often multi-dataset, this package features several functions to support the identification, interpolation, merging, and updating of missing data and outdated nomenclature.

2 Licensing

The *mmodely* package is licensed under the Apache License v2.0: it is therefore free to use and redistribute, however, we, the copyright holders, wish to maintain primary control over any further development. Please be sure to cite *mmodely* if you use the package in presentations or work leading to publication.

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 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$gn_sp <- rownames(data)
> # merge data sets here if applicable
>
> tree.path <- system.file("extdata", "primate-springer.2012.tre", package="mmodely")
> phyl <- ape::read.tree(tree.path)[[5]]
> #5. RAxML phylogram based on the 61199 bp concatenation of 69 nuclear and ten mitochondrial genes.
>
> phyl <- trim.phylo(phylo=phyl, gs.vect=data$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 appear 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

```
> model <- as.formula('OC ~ 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
-30.495	-5.996	17.023	34.907	54.965

Branch length transformations:

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

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	66.037399	8.409402	7.8528	7.05e-07 ***
mass.Kg	0.153139	0.060894	2.5148	0.02298 *
group.size	-0.030092	0.107433	-0.2801	0.78299

Signif. codes:

0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 34.2 on 16 degrees of freedom

Multiple R-squared: 0.3513, Adjusted R-squared: 0.2702

F-statistic: 4.332 on 3 and 16 DF, p-value: 0.02045

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

Call:

```
pgls(formula = f, data = cd, lambda = 1, kappa = k, delta = d,
      bounds = bounds)
```

Residuals:

Min	1Q	Median	3Q	Max
-----	----	--------	----	-----

-30.495 -5.996 17.023 34.907 54.965

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kappa [Fix] : 1.000
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Residual standard error: 34.2 on 16 degrees of freedom

Multiple R-squared: 0.3513, Adjusted R-squared: 0.2702

F-statistic: 4.332 on 3 and 16 DF, p-value: 0.02045

[1] "AIC = 134.2"

Analysis of Variance Table

Sequential SS for pglis: lambda = 1.00, delta = 1.00, kappa = 1.00

Response: OC

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
mass.Kg	1	10043.9	10043.9	8.5862	0.009806 **
group.size	1	91.8	91.8	0.0785	0.782991
Residuals	16	18716.2	1169.8		

Signif. codes:

0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

++mass(0.023) | group(0.783)

Call:

pgls(formula = f, data = cd, lambda = 1, kappa = k, delta = d,
 bounds = bounds)

Coefficients:

(Intercept)	mass.Kg	group.size
66.03740	0.15314	-0.03009

6 Multivariate Combinatoric Iteration

The *mmodely* package's chief contribution is in 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", "group.size", "arboreal", "nocturnal") #"swing.pct"
> est.mods <- get.model.combos(predictor.vars=pv0, outcome.var='OC', min.q=2)
> ps <- get.phylo.stats(phylo=phyl, data=data, trait.clmn='OC');

$lambda
[1] 0.8133958

$logL
[1] -204.9656

$P
[1] 0

$K
[1] 0.7251836

$P
[1] 0.001

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

[1] 0.8133958

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

1 OC~mass.Kg+group.size+arboreal+nocturnal
2 OC~mass.Kg+group.size+arboreal
3 OC~mass.Kg+group.size+nocturnal
4 OC~mass.Kg+arboreal+nocturnal
5 OC~group.size+arboreal+nocturnal
6 OC~mass.Kg+group.size
7 OC~mass.Kg+arboreal
8 OC~mass.Kg+nocturnal
9 OC~group.size+arboreal
10 OC~group.size+nocturnal
11 OC~arboreal+nocturnal
```

7 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 to obtain fixed values going forward. This approach can speed up computations for larger sets of modeling data and variable combinations. But in order to show off the model selection functionality we will only artificially sprinkle in some missing values to this small dataset for illustration purposes.

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

      l      k      d
0.8133958 1.4591898 1.2008103

> pvs <- c("mass.Kg", "group.size", "infant.carry", "arboreal", "DPL.km", "swing.pct", "nocturnal")
> all.mods <- get.model.combos(predictor.vars=pvs, outcome.var='OC', min.q=2)
> data <- subset(data, !grepl(rownames(data), pattern='gorilla')) # remove an outlier
> # randomly sprinkle in some missing values (to keep things interesting for model selection)
> missing.value.ct <- 1
> for(pv in pvs){ data[sample(x=1:nrow(data), size=missing.value.ct), pv] <- NA}
> PGLSi <- pglis.iter(models=all.mods, phylo=phyl, df=data, l=lambda, k=tt.avgs['k'], d=tt.avgs['d'])
```

- 1 OC~mass.Kg+group.size+infant.carry+arboreal+DPL.km+swing.pct+nocturnal
- 2 OC~mass.Kg+group.size+infant.carry+arboreal+DPL.km+swing.pct
- 3 OC~mass.Kg+group.size+infant.carry+arboreal+DPL.km+nocturnal
- 4 OC~mass.Kg+group.size+infant.carry+arboreal+swing.pct+nocturnal
- 5 OC~mass.Kg+group.size+infant.carry+DPL.km+swing.pct+nocturnal
- 6 OC~mass.Kg+group.size+arboreal+DPL.km+swing.pct+nocturnal
- 7 OC~mass.Kg+infant.carry+arboreal+DPL.km+swing.pct+nocturnal
- 8 OC~group.size+infant.carry+arboreal+DPL.km+swing.pct+nocturnal
- 9 OC~mass.Kg+group.size+infant.carry+arboreal+DPL.km
- 10 OC~mass.Kg+group.size+infant.carry+arboreal+swing.pct
- 11 OC~mass.Kg+group.size+infant.carry+arboreal+nocturnal
- 12 OC~mass.Kg+group.size+infant.carry+DPL.km+swing.pct
- 13 OC~mass.Kg+group.size+infant.carry+DPL.km+nocturnal
- 14 OC~mass.Kg+group.size+infant.carry+swing.pct+nocturnal
- 15 OC~mass.Kg+group.size+arboreal+DPL.km+swing.pct
- 16 OC~mass.Kg+group.size+arboreal+DPL.km+nocturnal
- 17 OC~mass.Kg+group.size+arboreal+swing.pct+nocturnal
- 18 OC~mass.Kg+group.size+DPL.km+swing.pct+nocturnal
- 19 OC~mass.Kg+infant.carry+arboreal+DPL.km+swing.pct
- 20 OC~mass.Kg+infant.carry+arboreal+DPL.km+nocturnal
- 21 OC~mass.Kg+infant.carry+arboreal+swing.pct+nocturnal
- 22 OC~mass.Kg+infant.carry+DPL.km+swing.pct+nocturnal
- 23 OC~mass.Kg+arboreal+DPL.km+swing.pct+nocturnal
- 24 OC~group.size+infant.carry+arboreal+DPL.km+swing.pct
- 25 OC~group.size+infant.carry+arboreal+DPL.km+nocturnal
- 26 OC~group.size+infant.carry+arboreal+swing.pct+nocturnal
- 27 OC~group.size+infant.carry+DPL.km+swing.pct+nocturnal
- 28 OC~group.size+arboreal+DPL.km+swing.pct+nocturnal
- 29 OC~infant.carry+arboreal+DPL.km+swing.pct+nocturnal
- 30 OC~mass.Kg+group.size+infant.carry+arboreal
- 31 OC~mass.Kg+group.size+infant.carry+DPL.km
- 32 OC~mass.Kg+group.size+infant.carry+swing.pct
- 33 OC~mass.Kg+group.size+infant.carry+nocturnal
- 34 OC~mass.Kg+group.size+arboreal+DPL.km
- 35 OC~mass.Kg+group.size+arboreal+swing.pct
- 36 OC~mass.Kg+group.size+arboreal+nocturnal
- 37 OC~mass.Kg+group.size+DPL.km+swing.pct
- 38 OC~mass.Kg+group.size+DPL.km+nocturnal
- 39 OC~mass.Kg+group.size+swing.pct+nocturnal
- 40 OC~mass.Kg+infant.carry+arboreal+DPL.km
- 41 OC~mass.Kg+infant.carry+arboreal+swing.pct
- 42 OC~mass.Kg+infant.carry+arboreal+nocturnal
- 43 OC~mass.Kg+infant.carry+DPL.km+swing.pct
- 44 OC~mass.Kg+infant.carry+DPL.km+nocturnal
- 45 OC~mass.Kg+infant.carry+swing.pct+nocturnal
- 46 OC~mass.Kg+arboreal+DPL.km+swing.pct
- 47 OC~mass.Kg+arboreal+DPL.km+nocturnal
- 48 OC~mass.Kg+arboreal+swing.pct+nocturnal
- 49 OC~mass.Kg+DPL.km+swing.pct+nocturnal
- 50 OC~group.size+infant.carry+arboreal+DPL.km
- 51 OC~group.size+infant.carry+arboreal+swing.pct
- 52 OC~group.size+infant.carry+arboreal+nocturnal
- 53 OC~group.size+infant.carry+DPL.km+swing.pct
- 54 OC~group.size+infant.carry+DPL.km+nocturnal
- 55 OC~group.size+infant.carry+swing.pct+nocturnal
- 56 OC~group.size+arboreal+DPL.km+swing.pct
- 57 OC~group.size+arboreal+DPL.km+nocturnal
- 58 OC~group.size+arboreal+swing.pct+nocturnal
- 59 OC~group.size+DPL.km+swing.pct+nocturnal
- 60 OC~infant.carry+arboreal+DPL.km+swing.pct

61 OC~infant.carry+arboreal+DPL.km+nocturnal
 62 OC~infant.carry+arboreal+swing.pct+nocturnal
 63 OC~infant.carry+DPL.km+swing.pct+nocturnal
 64 OC~arboreal+DPL.km+swing.pct+nocturnal
 65 OC~mass.Kg+group.size+infant.carry
 66 OC~mass.Kg+group.size+arboreal
 67 OC~mass.Kg+group.size+DPL.km
 68 OC~mass.Kg+group.size+swing.pct
 69 OC~mass.Kg+group.size+nocturnal
 70 OC~mass.Kg+infant.carry+arboreal
 71 OC~mass.Kg+infant.carry+DPL.km
 72 OC~mass.Kg+infant.carry+swing.pct
 73 OC~mass.Kg+infant.carry+nocturnal
 74 OC~mass.Kg+arboreal+DPL.km
 75 OC~mass.Kg+arboreal+swing.pct
 76 OC~mass.Kg+arboreal+nocturnal
 77 OC~mass.Kg+DPL.km+swing.pct
 78 OC~mass.Kg+DPL.km+nocturnal
 79 OC~mass.Kg+swing.pct+nocturnal
 80 OC~group.size+infant.carry+arboreal
 81 OC~group.size+infant.carry+DPL.km
 82 OC~group.size+infant.carry+swing.pct
 83 OC~group.size+infant.carry+nocturnal
 84 OC~group.size+arboreal+DPL.km
 85 OC~group.size+arboreal+swing.pct
 86 OC~group.size+arboreal+nocturnal
 87 OC~group.size+DPL.km+swing.pct
 88 OC~group.size+DPL.km+nocturnal
 89 OC~group.size+swing.pct+nocturnal
 90 OC~infant.carry+arboreal+DPL.km
 91 OC~infant.carry+arboreal+swing.pct
 92 OC~infant.carry+arboreal+nocturnal
 93 OC~infant.carry+DPL.km+swing.pct
 94 OC~infant.carry+DPL.km+nocturnal
 95 OC~infant.carry+swing.pct+nocturnal
 96 OC~arboreal+DPL.km+swing.pct
 97 OC~arboreal+DPL.km+nocturnal
 98 OC~arboreal+swing.pct+nocturnal
 99 OC~DPL.km+swing.pct+nocturnal
 100 OC~mass.Kg+group.size
 101 OC~mass.Kg+infant.carry
 102 OC~mass.Kg+arboreal
 103 OC~mass.Kg+DPL.km
 104 OC~mass.Kg+swing.pct
 105 OC~mass.Kg+nocturnal
 106 OC~group.size+infant.carry
 107 OC~group.size+arboreal
 108 OC~group.size+DPL.km
 109 OC~group.size+swing.pct
 110 OC~group.size+nocturnal
 111 OC~infant.carry+arboreal
 112 OC~infant.carry+DPL.km
 113 OC~infant.carry+swing.pct
 114 OC~infant.carry+nocturnal
 115 OC~arboreal+DPL.km
 116 OC~arboreal+swing.pct
 117 OC~arboreal+nocturnal
 118 OC~DPL.km+swing.pct
 119 OC~DPL.km+nocturnal
 120 OC~swing.pct+nocturnal

8 Model Averaging

Now we can estimate the predictor variable parameters by averaging over all possible fixed PGLS runs.

```
> calculate.weighted.means(vars=pvs, fits=PGLSi$fits, optims=PGLSi$optim)
```

mass.Kg	group.size	infant.carry	arboreal
0.15716	0.11684	5.47869	2.35591
DPL.km	swing.pct	nocturnal	
-0.13352	4.84748	-3.16960	

9 Model Selection

Plotting the coefficients of determination versus the AIC values allows selection of certain models for 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]], rtn.line=FALSE, mn=i))
```

```
1 +group(0.073) +mass(0.092) +infan(0.196) arbore(0.353) swing(0.359) | DPL(0.757) noctur(0.342) R2adj: 0.092 AICc: 344.08
2 +group(0.059) +mass(0.075) +infan(0.144) swing(0.332) arbore(0.334) | DPL(0.799) R2adj: 0.1 AICc: 344.08
3 +group(0.088) +mass(0.115) +infan(0.174) +arbor(0.27) | DPL(0.861) -noctu(0.301) R2adj: 0.095 AICc: 339.09
4 +mass(0.085) +group(0.106) +infan(0.208) arbore(0.33) swing(0.334) | noctur(0.683) R2adj: 0.062 AICc: 348.3
5 +group(0.067) +mass(0.113) +infan(0.25) +swing(0.268) | DPL(0.444) noctur(0.364) R2adj: 0.106 AICc: 344.02
6 ++grou(0.041) +mass(0.074) +swing(0.299) arbore(0.491) | DPL(0.502) -noctu(0.314) R2adj: 0.079 AICc: 370.78
7 +mass(0.068) +infan(0.117) arbore(0.422) swing(0.49) DPL(0.726) | -noctu(0.27) R2adj: 0.044 AICc: 341.93
8 +group(0.054) +infan(0.207) swing(0.508) arbore(0.553) | DPL(0.722) -noctu(0.309) R2adj: 0.052 AICc: 341.48
9 +group(0.072) +mass(0.096) +infan(0.127) +arbor(0.254) | DPL(0.905) R2adj: 0.101 AICc: 342.52
10 +mass(0.071) +group(0.089) +infan(0.161) +arbor(0.309) swing(0.327) | R2adj: 0.085 AICc: 350.98
11 +mass(0.109) +group(0.12) +infan(0.204) +arbor(0.274) | noctur(0.629) R2adj: 0.063 AICc: 346.8
12 +group(0.056) +mass(0.094) +infan(0.187) +swing(0.247) | DPL(0.469) R2adj: 0.113 AICc: 347.39
13 +group(0.089) +mass(0.16) +infan(0.238) | DPL(0.499) -noctu(0.318) R2adj: 0.101 AICc: 342.79
14 +mass(0.11) +group(0.122) +infan(0.226) +swing(0.27) | noctur(0.698) R2adj: 0.076 AICc: 351.69
15 ++grou(0.031) +mass(0.059) +swing(0.273) arbore(0.488) | DPL(0.508) R2adj: 0.079 AICc: 374.64
16 +group(0.056) +mass(0.147) arbore(0.699) | DPL(0.384) -noctu(0.276) R2adj: 0.062 AICc: 376.33
17 +mass(0.068) +group(0.077) +swing(0.298) arbore(0.383) | noctur(0.612) R2adj: 0.058 AICc: 378.04
18 ++grou(0.036) +mass(0.082) +swing(0.236) | noctur(0.332) -DPL(0.318) R2adj: 0.099 AICc: 373.67
19 +mass(0.054) +infan(0.081) arbore(0.414) swing(0.455) DPL(0.661) | R2adj: 0.047 AICc: 345.56
20 +mass(0.08) +infan(0.107) arbore(0.343) DPL(0.664) | -noctu(0.244) R2adj: 0.054 AICc: 339.81
21 +mass(0.065) +infan(0.19) swing(0.406) arbore(0.58) | noctur(0.551) R2adj: 0.027 AICc: 348.76
22 +mass(0.077) +infan(0.136) swing(0.393) DPL(0.883) | -noctu(0.287) R2adj: 0.058 AICc: 345.26
23 +mass(0.055) swing(0.437) arbore(0.638) | DPL(0.944) -noctu(0.233) R2adj: 0.017 AICc: 372.99
24 ++grou(0.043) +infan(0.149) swing(0.485) arbore(0.54) | DPL(0.767) R2adj: 0.055 AICc: 345.13
25 +group(0.062) +infan(0.188) arbore(0.452) | DPL(0.796) -noctu(0.28) R2adj: 0.063 AICc: 339.32
26 +group(0.081) +infan(0.214) swing(0.485) arbore(0.541) | noctur(0.634) R2adj: 0.02 AICc: 349.18
27 ++grou(0.046) +infan(0.227) swing(0.415) | DPL(0.536) noctur(0.323) R2adj: 0.075 AICc: 344.28
28 ++grou(0.03) swing(0.444) arbore(0.744) | DPL(0.494) -noctu(0.279) R2adj: 0.037 AICc: 371.84
29 +infan(0.13) arbore(0.658) DPL(0.694) swing(0.712) | -noctu(0.104) R2adj: 0.011 AICc: 347.83
30 +mass(0.093) +group(0.101) +infan(0.157) +arbor(0.257) | R2adj: 0.085 AICc: 349.54
31 +group(0.075) +mass(0.137) +infan(0.178) | DPL(0.526) R2adj: 0.106 AICc: 346.38
32 +mass(0.095) +group(0.106) +infan(0.176) +swing(0.264) | R2adj: 0.096 AICc: 354.49
33 +group(0.15) +mass(0.153) +infan(0.226) | noctur(0.639) R2adj: 0.071 AICc: 350.54
34 ++grou(0.043) +mass(0.122) arbore(0.701) | DPL(0.39) R2adj: 0.06 AICc: 380.45
35 +mass(0.056) +group(0.062) +swing(0.292) arbore(0.365) | R2adj: 0.073 AICc: 381.2
36 +group(0.118) +mass(0.14) arbore(0.565) | noctur(0.554) R2adj: 0.037 AICc: 383.97
37 ++grou(0.028) +mass(0.066) +swing(0.217) | -DPL(0.32) R2adj: 0.099 AICc: 377.62
38 ++grou(0.046) +mass(0.145) | -DPL(0.305) -noctu(0.281) R2adj: 0.086 AICc: 378.99
39 +group(0.083) +mass(0.085) +swing(0.243) | noctur(0.628) R2adj: 0.075 AICc: 381.28
```

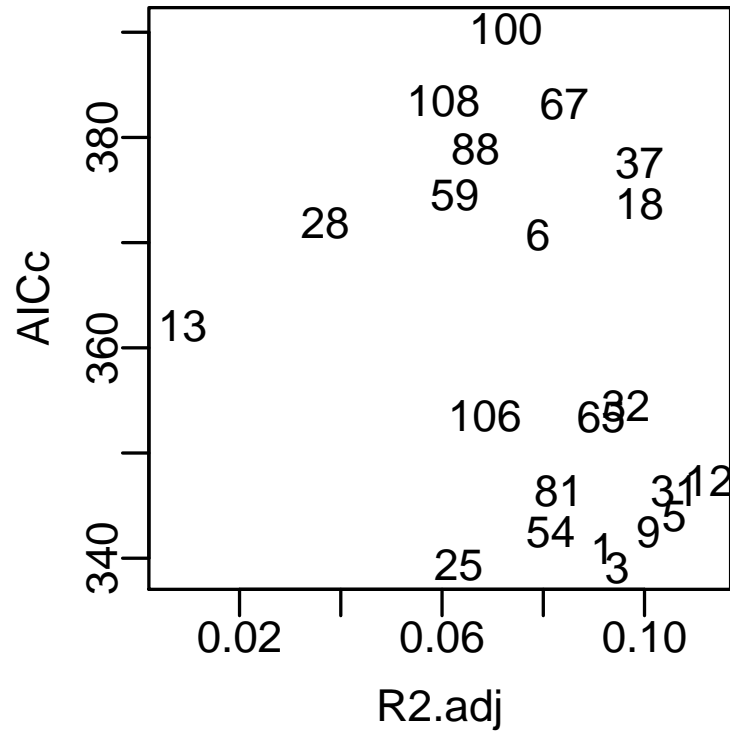
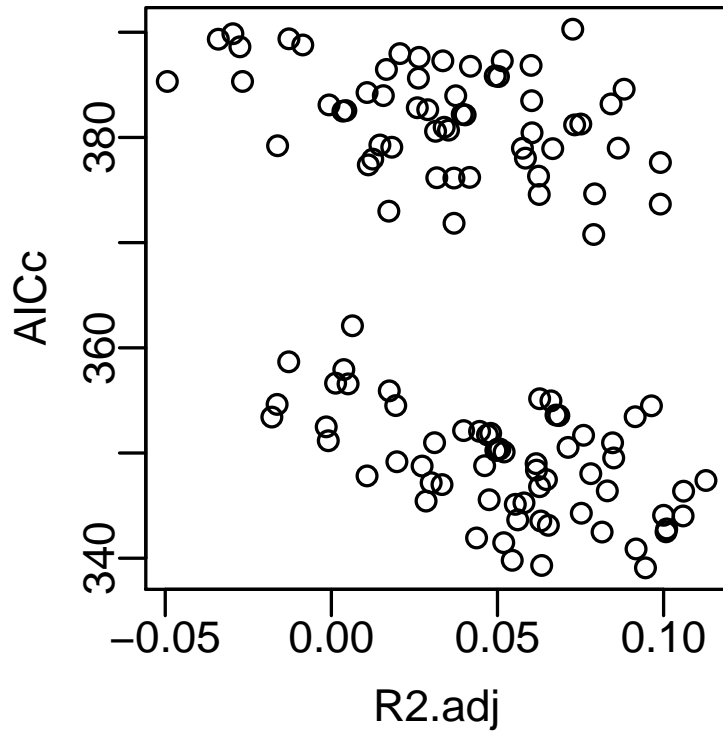
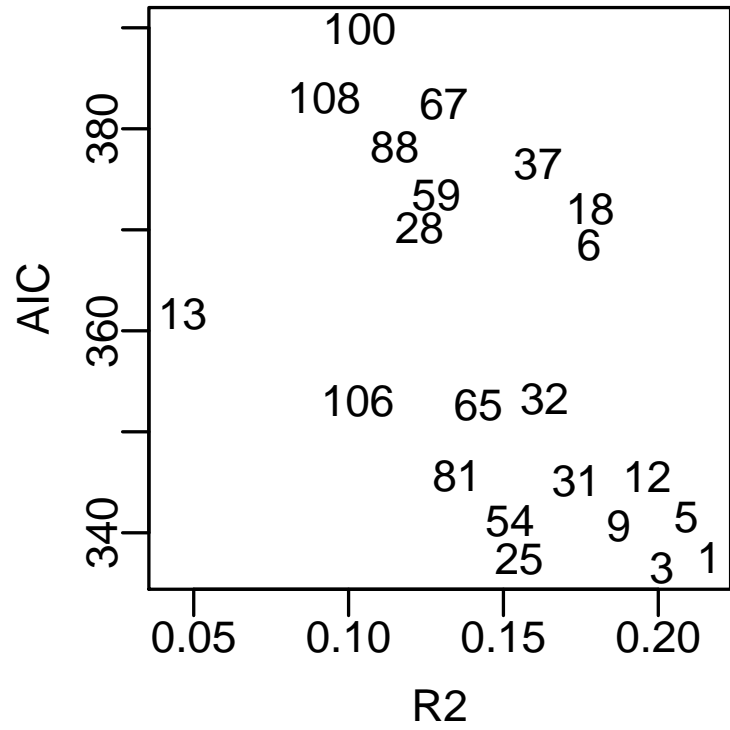
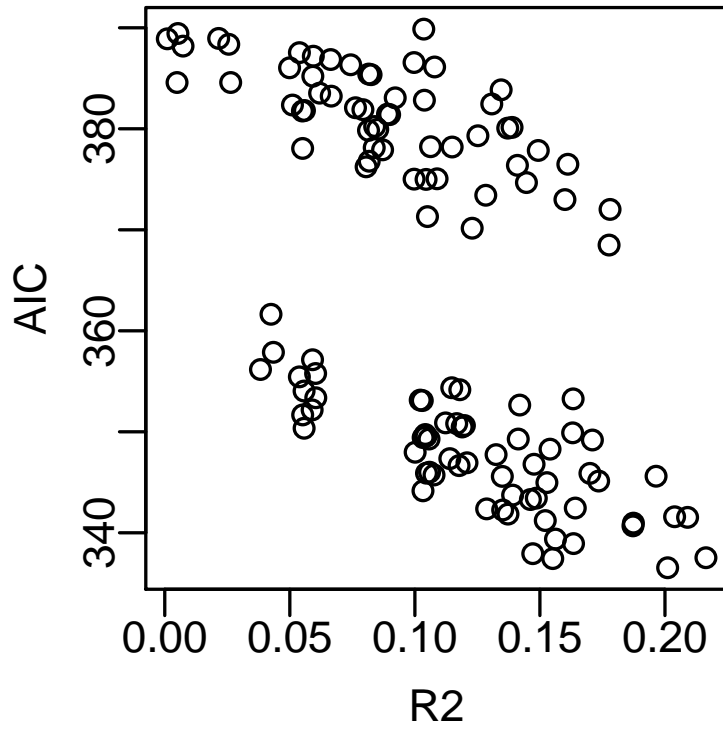


Figure 1: All possible model combinations appear as individual points above. As there is a generally negative association between AIC and the coefficient of determination, the points tend to follow a negative sloping streak to the lower right. The "best" models appear in the lower right of each streak. 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.

40 +mass(0.065) +infan(0.073) arbore(0.335) DPL(0.599) | R2adj: 0.056 AICc: 343.65
 41 +mass(0.053) +infan(0.141) swing(0.395) arbore(0.571) | R2adj: 0.047 AICc: 351.73
 42 +mass(0.081) +infan(0.186) arbore(0.497) | noctur(0.512) R2adj: 0.033 AICc: 347
 43 +mass(0.061) +infan(0.094) swing(0.365) DPL(0.814) | R2adj: 0.062 AICc: 348.99
 44 +mass(0.101) +infan(0.134) DPL(0.869) | -noctu(0.259) R2adj: 0.063 AICc: 343.54
 45 +mass(0.06) +infan(0.197) swing(0.352) | noctur(0.567) R2adj: 0.048 AICc: 351.88
 46 ++mass(0.042) swing(0.403) arbore(0.656) | DPL(0.976) R2adj: 0.011 AICc: 377.39
 47 +mass(0.101) arbore(0.885) | DPL(0.751) -noctu(0.213) R2adj: 0.012 AICc: 377.94
 48 +mass(0.052) swing(0.385) arbore(0.666) | noctur(0.476) R2adj: 0.018 AICc: 379.07
 49 +mass(0.051) swing(0.379) | DPL(0.91) -noctu(0.243) R2adj: 0.037 AICc: 376.15
 50 ++grou(0.049) +infan(0.135) arbore(0.441) | DPL(0.844) R2adj: 0.065 AICc: 343.13
 51 +group(0.066) +infan(0.162) swing(0.485) arbore(0.524) | R2adj: 0.04 AICc: 352.14
 52 +group(0.09) +infan(0.209) arbore(0.466) | noctur(0.596) R2adj: 0.03 AICc: 347.18
 53 ++grou(0.037) +infan(0.165) swing(0.397) | DPL(0.572) R2adj: 0.078 AICc: 348.04
 54 +group(0.056) +infan(0.219) | DPL(0.57) -noctu(0.293) R2adj: 0.081 AICc: 342.49
 55 +group(0.066) +infan(0.222) swing(0.414) | noctur(0.649) R2adj: 0.045 AICc: 352.07
 56 ++grou(0.022) swing(0.42) arbore(0.759) | DPL(0.503) R2adj: 0.032 AICc: 376.17
 57 ++grou(0.039) arbore(0.908) | DPL(0.391) -noctu(0.254) R2adj: 0.042 AICc: 376.21
 58 +group(0.058) swing(0.448) arbore(0.636) | noctur(0.56) R2adj: 0.015 AICc: 379.28
 59 ++grou(0.022) swing(0.389) | DPL(0.413) -noctu(0.287) R2adj: 0.063 AICc: 374.58
 60 +infan(0.099) DPL(0.566) arbore(0.678) swing(0.685) | R2adj: -0.018 AICc: 353.42
 61 +infan(0.121) arbore(0.587) DPL(0.659) | -noctu(0.097) R2adj: 0.029 AICc: 345.44
 62 +infan(0.203) swing(0.603) arbore(0.925) | -noctu(0.312) R2adj: -0.016 AICc: 354.62
 63 +infan(0.122) DPL(0.627) swing(0.639) | -noctu(0.11) R2adj: 0.031 AICc: 350.99
 64 swing(0.654) arbore(0.938) | DPL(0.997) -noctu(0.102) R2adj: -0.016 AICc: 379.21
 65 +group(0.13) +mass(0.134) +infan(0.176) | R2adj: 0.091 AICc: 353.45
 66 +group(0.097) +mass(0.119) arbore(0.55) | R2adj: 0.051 AICc: 387.29
 67 ++grou(0.036) +mass(0.12) | -DPL(0.307) R2adj: 0.084 AICc: 383.19
 68 +group(0.069) +mass(0.072) +swing(0.238) | R2adj: 0.088 AICc: 384.59
 69 +group(0.112) +mass(0.152) | noctur(0.559) R2adj: 0.06 AICc: 386.85
 70 +mass(0.067) +infan(0.138) arbore(0.49) | R2adj: 0.052 AICc: 350.11
 71 +mass(0.083) +infan(0.093) DPL(0.798) | R2adj: 0.065 AICc: 347.47
 72 ++mass(0.048) +infan(0.147) swing(0.343) | R2adj: 0.066 AICc: 354.97
 73 +mass(0.082) +infan(0.198) | noctur(0.527) R2adj: 0.05 AICc: 350.41
 74 +mass(0.08) arbore(0.907) | DPL(0.785) R2adj: 0.004 AICc: 382.56
 75 ++mass(0.04) swing(0.374) arbore(0.666) | R2adj: 0.029 AICc: 382.64
 76 +mass(0.099) arbore(0.855) | noctur(0.444) R2adj: 0.011 AICc: 384.27
 77 ++mass(0.038) swing(0.352) | DPL(0.952) R2adj: 0.031 AICc: 380.59
 78 +mass(0.083) | DPL(0.836) -noctu(0.213) R2adj: 0.034 AICc: 380.97
 79 ++mass(0.043) swing(0.341) | noctur(0.488) R2adj: 0.039 AICc: 382.2
 80 +group(0.072) +infan(0.158) arbore(0.451) | R2adj: 0.05 AICc: 350.25
 81 ++grou(0.046) +infan(0.159) | DPL(0.607) R2adj: 0.083 AICc: 346.41
 82 +group(0.054) +infan(0.169) swing(0.414) | R2adj: 0.063 AICc: 355.17
 83 +group(0.08) +infan(0.221) | noctur(0.608) R2adj: 0.051 AICc: 350.38
 84 ++grou(0.029) arbore(0.925) | DPL(0.4) R2adj: 0.035 AICc: 380.7
 85 ++grou(0.045) swing(0.447) arbore(0.627) | R2adj: 0.026 AICc: 382.83
 86 +group(0.084) arbore(0.783) | noctur(0.523) R2adj: 0.016 AICc: 383.98
 87 ++grou(0.016) swing(0.371) | DPL(0.423) R2adj: 0.058 AICc: 378.97
 88 ++grou(0.027) | DPL(0.377) -noctu(0.254) R2adj: 0.067 AICc: 378.94
 89 ++grou(0.042) swing(0.389) | noctur(0.574) R2adj: 0.04 AICc: 382.15
 90 +infan(0.093) DPL(0.531) arbore(0.604) | R2adj: -0.001 AICc: 351.17
 91 +infan(0.16) swing(0.602) arbore(0.966) | R2adj: -0.013 AICc: 358.68
 92 +infan(0.198) arbore(0.844) | -noctu(0.297) R2adj: -0.002 AICc: 352.49
 93 +infan(0.092) DPL(0.484) swing(0.619) | R2adj: 0.005 AICc: 356.57
 94 +infan(0.12) DPL(0.63) | -noctu(0.102) R2adj: 0.046 AICc: 348.8
 95 +infan(0.198) swing(0.596) | -noctu(0.307) R2adj: 0.004 AICc: 357.94
 96 swing(0.63) DPL(0.888) arbore(0.984) | R2adj: -0.049 AICc: 385.33
 97 | arbore(0.856) DPL(0.83) -noctu(0.095) R2adj: -0.001 AICc: 383.1
 98 swing(0.584) | arbore(0.951) -noctu(0.294) R2adj: -0.027 AICc: 385.33
 99 swing(0.643) DPL(0.804) | -noctu(0.103) R2adj: 0.003 AICc: 382.5

```

100 +group(0.093) +mass(0.131) | R2adj: 0.073 AICc: 390.29
101 +mass(0.067) +infan(0.148) | R2adj: 0.068 AICc: 353.62
102 +mass(0.08) arbore(0.861) | R2adj: 0.021 AICc: 387.97
103 +mass(0.065) | DPL(0.878) R2adj: 0.026 AICc: 385.64
104 ++mass(0.033) swing(0.333) | R2adj: 0.049 AICc: 385.85
105 +mass(0.076) | noctur(0.444) R2adj: 0.034 AICc: 387.29
106 +group(0.065) +infan(0.168) | R2adj: 0.068 AICc: 353.56
107 +group(0.065) arbore(0.778) | R2adj: 0.026 AICc: 387.62
108 ++grou(0.02) | DPL(0.386) R2adj: 0.06 AICc: 383.5
109 ++grou(0.032) swing(0.39) | R2adj: 0.05 AICc: 385.79
110 +group(0.057) | noctur(0.527) R2adj: 0.042 AICc: 386.77
111 +infan(0.156) arbore(0.887) | R2adj: 0.001 AICc: 356.64
112 +infan(0.091) DPL(0.486) | R2adj: 0.019 AICc: 354.51
113 +infan(0.154) swing(0.601) | R2adj: 0.006 AICc: 362.1
114 +infan(0.195) | -noctu(0.295) R2adj: 0.017 AICc: 355.92
115 | DPL(0.954) arbore(0.813) R2adj: -0.034 AICc: 389.34
116 swing(0.585) | arbore(0.902) R2adj: -0.03 AICc: 389.87
117 | arbore(0.82) -noctu(0.286) R2adj: -0.013 AICc: 389.38
118 swing(0.626) DPL(0.666) | R2adj: -0.028 AICc: 388.62
119 DPL(0.894) | -noctu(0.094) R2adj: 0.017 AICc: 386.47
120 swing(0.597) | -noctu(0.283) R2adj: -0.009 AICc: 388.79

```

```
> plot.pgls.R2AIC(PGLSi$optim)
```

10 Coefficient Plotting

```

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

```

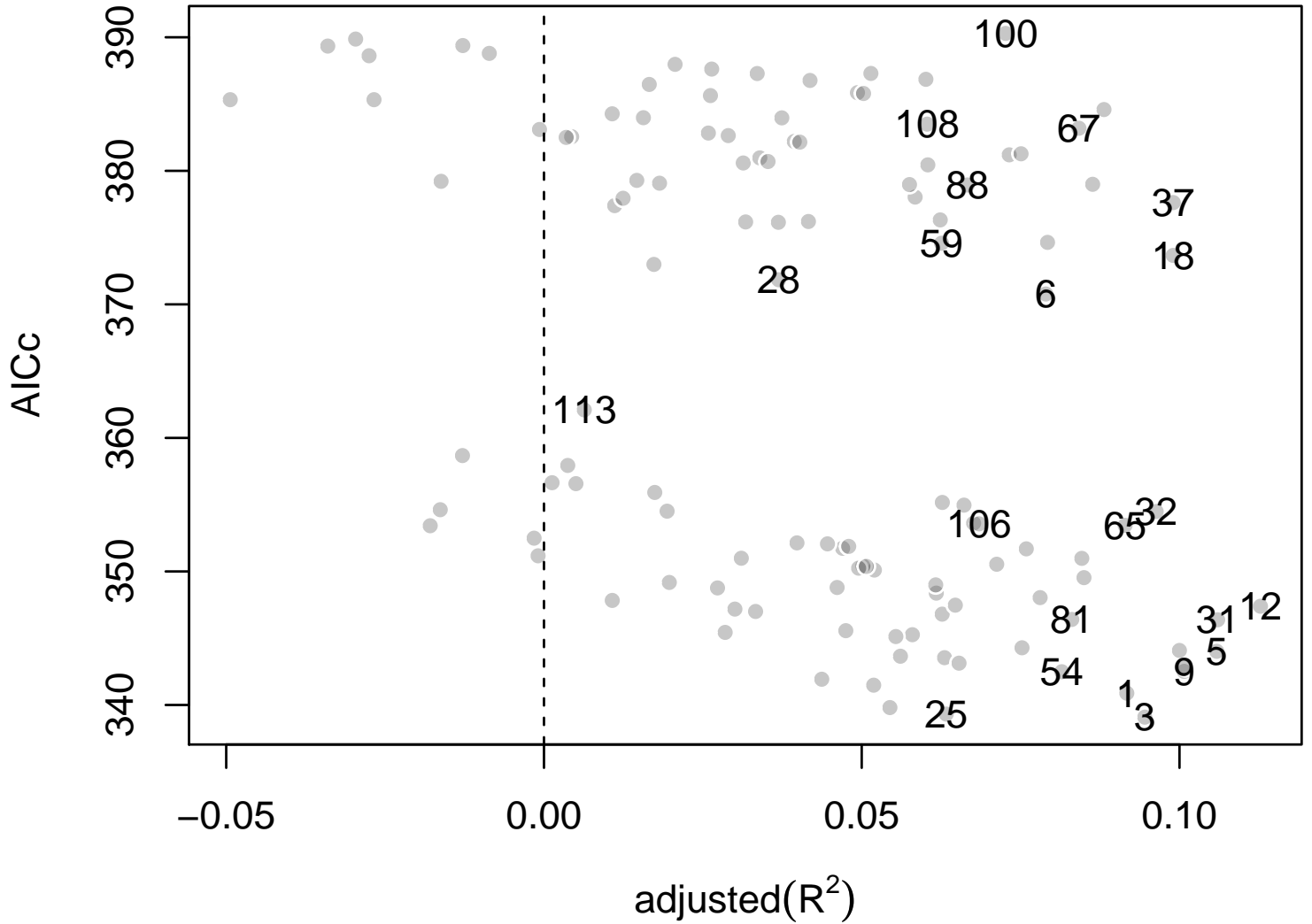


Figure 2: This is a one panel version of the previous model selection plot. The numbered points in the lower right corner of each streak of possible models represent the best model within a sub-dataset. Since these AICc values should not strictly be compared, it is recommended that all "best" models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

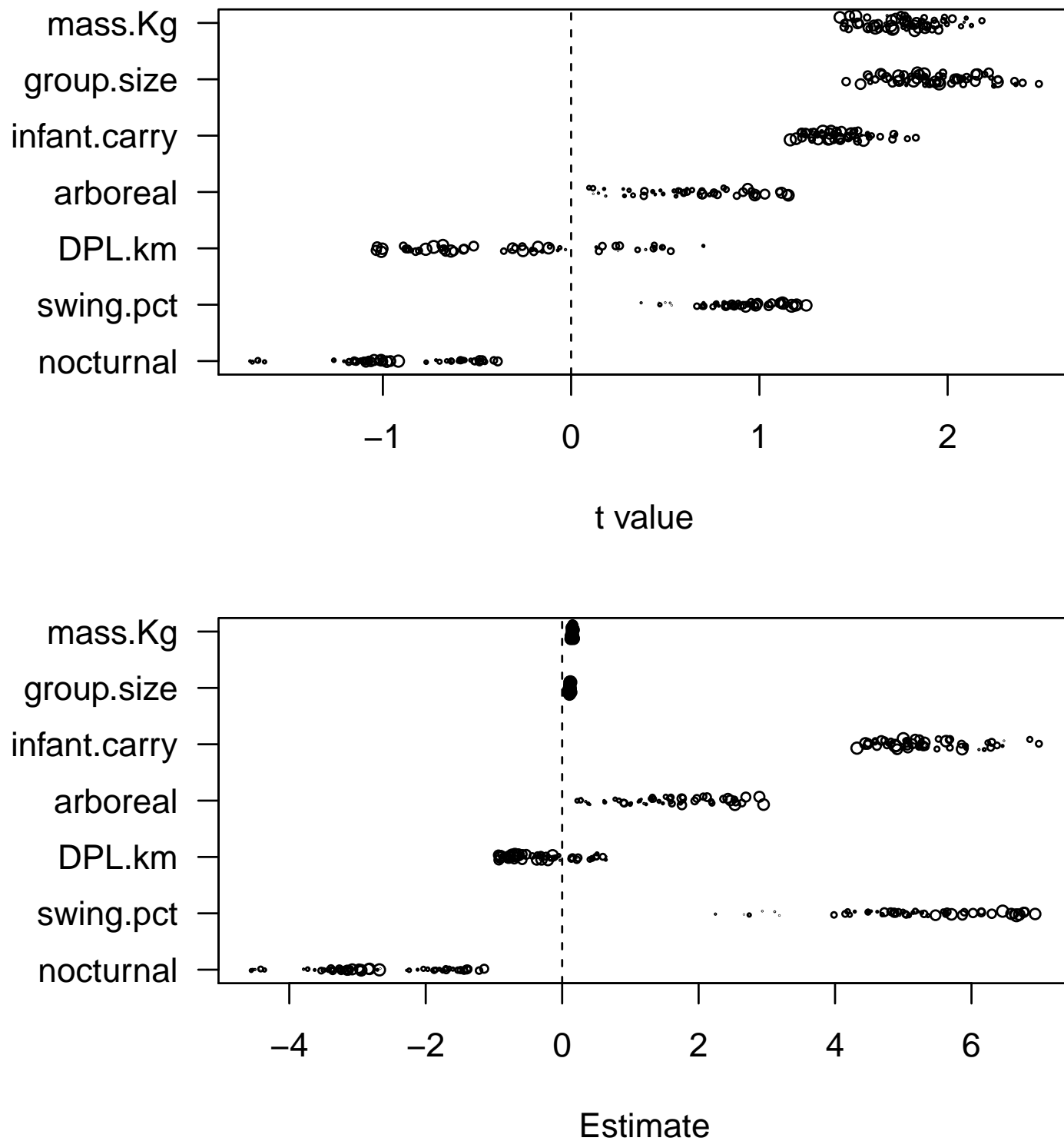


Figure 3: These 'distro dots' plots demonstrate how the (t-values of) coefficients from all "best" selected models can be simultaneously plot in order to verify consistency of estimates across the various (missing data driven) sub-datasets.

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