

R Notebook

```
#1
myPCA <- principal(mydata[,c('tas_breadth', 'tas_position', 'pcp_breadth',
                             'pcp_position', 'mtn_mass2', 'wtr_mass2', "npamcells",
                             'dispersal_ability', 'pair_age', "pd0", "pd25", 'meanEle')], nfactors = 11,
myPCA$loadings # this looks solid so far!
```

```
##
## Loadings:
##          PC1    PC2    PC3    PC4    PC5    PC6    PC7    PC8
## tas_breadth    0.750  0.371 -0.386
## tas_position  -0.239 -0.769  0.328  0.198 -0.107 -0.136      0.360
## pcp_breadth   -0.662  0.371  0.521
## pcp_position  -0.743  0.125  0.497      0.112  0.112 -0.296
## mtn_mass2     -0.177  0.751      0.261  0.378  0.414
## wtr_mass2     -0.343 -0.563 -0.289      0.335  0.437  0.342 -0.121
## npamcells      0.543      0.361  0.394 -0.512  0.147  0.218 -0.169
## dispersal_ability      0.149  0.109  0.801  0.380  0.255 -0.322
## pair_age       0.302 -0.336  0.378 -0.461 -0.193  0.518 -0.342  0.106
## pd0            0.557      0.485 -0.249  0.537 -0.156  0.113
## pd25           0.695      0.594      0.162      0.159
## meanEle       -0.122  0.841      -0.215  0.106      -0.232
##          PC9    PC10    PC11
## tas_breadth   -0.257  0.162
## tas_position   -0.167  0.301
## pcp_breadth    -0.125 -0.158
## pcp_position    -0.109
## mtn_mass2       0.127  0.144
## wtr_mass2       0.176  0.105 -0.128
## npamcells
## dispersal_ability
## pair_age
## pd0            0.106 -0.225
## pd25           -0.134  0.287
## meanEle        0.377
##
##          PC1    PC2    PC3    PC4    PC5    PC6    PC7    PC8    PC9    PC10
## SS loadings    2.958 2.611 1.737 1.171 0.905 0.690 0.642 0.455 0.321 0.227
## Proportion Var 0.247 0.218 0.145 0.098 0.075 0.058 0.053 0.038 0.027 0.019
## Cumulative Var 0.247 0.464 0.609 0.706 0.782 0.839 0.893 0.931 0.957 0.976
##          PC11
## SS loadings    0.184
## Proportion Var 0.015
## Cumulative Var 0.992
```

```
mydata$PC1 <- myPCA$scores[, 'PC1']
mydata$PC2 <- myPCA$scores[, 'PC2']
mydata$PC3 <- myPCA$scores[, 'PC3']
```

```

mydata$PC4 <- myPCA$scores[, 'PC4']
mytree <- drop.tip(trees[[i]], CHK$tree_not_data)
mymod <- phylolm(I(log(cost)) ~ PC1 + PC2 + PC3 + PC4,
  phy = mytree, model = 'lambda', data = mydata)
summary(mymod)

```

```

##
## Call:
## phylolm(formula = I(log(cost)) ~ PC1 + PC2 + PC3 + PC4, data = mydata,
##   phy = mytree, model = "lambda")
##
##   AIC logLik
## 622.6 -304.3
##
## Raw residuals:
##      Min      1Q   Median      3Q      Max
## -2.29603 -0.53320  0.00801  0.57202  2.31148
##
## Mean tip height: 100.4834
## Parameter estimate(s) using ML:
## lambda : 1e-07
## sigma2: 0.007765104
##
## Coefficients:
##              Estimate      StdErr  t.value  p.value
## (Intercept) 18.550271  0.058245 318.4869 < 2.2e-16 ***
## PC1          0.414327  0.058369   7.0984 1.555e-11 ***
## PC2          0.441935  0.058369   7.5714 8.893e-13 ***
## PC3          0.535117  0.058369   9.1678 < 2.2e-16 ***
## PC4         -0.148371  0.058369  -2.5420  0.01168 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-squared: 0.4629    Adjusted R-squared: 0.4536
##
## Note: p-values and R-squared are conditional on lambda=1e-07.

```

```

#2
myPCA <- principal(mydata[,c('tas_breadth', 'tas_position', 'pcp_breadth',
  'pcp_position', 'mtn_mass2', 'wtr_mass2', "npamcells",
  'dispersal_ability', 'pair_age', "pd25", 'meanEle')], nfactors = 10, rotate = "varimax")
myPCA$loadings # this looks solid so far!

```

```

##
## Loadings:
##
##      PC1    PC2    PC3    PC4    PC5    PC6    PC7    PC8
## tas_breadth -0.843  0.260 -0.268          0.125
## tas_position 0.371 -0.724  0.341  0.137 -0.178          0.223  0.280
## pcp_breadth  0.680  0.469  0.406
## pcp_position 0.791  0.235  0.362          0.101  0.126 -0.221 -0.200
## mtn_mass2    0.769          0.457  0.256  0.315
## wtr_mass2    0.387 -0.522 -0.389          0.420  0.422 -0.153
## npamcells   -0.540          0.604  0.165 -0.167  0.345  0.135 -0.340
## dispersal_ability 0.140  0.193  0.837  0.406 -0.235

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## pair_age      -0.196 -0.357  0.395 -0.578  0.499 -0.112  0.270
## pd25          -0.563      0.615      0.104      -0.449  0.295
## meanEle              0.854      -0.178  0.175 -0.212
##              PC9      PC10
## tas_breadth      -0.256  0.181
## tas_position              0.103
## pcp_breadth      -0.165  0.313
## pcp_position      -0.125 -0.170
## mtn_mass2              -0.110
## wtr_mass2          0.126  0.162
## npamcells          0.183
## dispersal_ability
## pair_age
## pd25
## meanEle          0.377
##
##              PC1  PC2  PC3  PC4  PC5  PC6  PC7  PC8  PC9  PC10
## SS loadings    2.75 2.607 1.574 1.137 0.721 0.653 0.488 0.428 0.321 0.220
## Proportion Var 0.25 0.237 0.143 0.103 0.066 0.059 0.044 0.039 0.029 0.020
## Cumulative Var 0.25 0.487 0.630 0.733 0.799 0.858 0.903 0.942 0.971 0.991

mydata$PC1 <- -myPCA$scores[, 'PC1']
mydata$PC2 <- myPCA$scores[, 'PC2']
mydata$PC3 <- myPCA$scores[, 'PC3']
mydata$PC4 <- myPCA$scores[, 'PC4']
mytree <- drop.tip(trees[[i]], CHK$tree_not_data)
mymod <- phylolm(I(log(cost)) ~ PC1 + PC2 + PC3 + PC4,
                phy = mytree, model = 'lambda', data = mydata)
summary(mymod)

##
## Call:
## phylolm(formula = I(log(cost)) ~ PC1 + PC2 + PC3 + PC4, data = mydata,
##        phy = mytree, model = "lambda")
##
##      AIC logLik
##      678   -332
##
## Raw residuals:
##      Min      1Q   Median      3Q      Max
## -2.57853 -0.63905 -0.08202  0.63507  2.85060
##
## Mean tip height: 100.4834
## Parameter estimate(s) using ML:
## lambda : 1e-07
## sigma2: 0.009830174
##
## Coefficients:
##              Estimate      StdErr  t.value  p.value
## (Intercept) 18.550271  0.065534 283.0640 < 2.2e-16 ***
## PC1          0.317304  0.065673  4.8315 2.475e-06 ***
## PC2          0.421771  0.065673  6.4222 7.617e-10 ***
## PC3          0.423013  0.065673  6.4412 6.854e-10 ***
## PC4         -0.097119  0.065673 -1.4788  0.1406
## ---

```

```

## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-squared:  0.3201    Adjusted R-squared:  0.3082
##
## Note: p-values and R-squared are conditional on lambda=1e-07.

# 4
myPCA <- principal(mydata[,c('tas_breadth', 'tas_position', 'pcp_breadth',
                             'pcp_position', 'mtn_mass2', 'wtr_mass2', "boundary_length",
                             'dispersal_ability', 'pair_age', "pd25", 'meanEle')], nfactors = 10, rotate = "none")
myPCA$loadings # this looks solid so far!

##
## Loadings:
##
##          PC1    PC2    PC3    PC4    PC5    PC6    PC7    PC8
## tas_breadth    0.840          -0.368          0.106          -0.261
## tas_position  -0.455 -0.633    0.413    0.133 -0.186          0.328    0.154
## pcp_breadth   -0.546    0.596    0.434 -0.102          0.128    0.110 -0.256 -0.160
## pcp_position  -0.690    0.386    0.433          0.128    0.110 -0.256 -0.190
## mtn_mass2           0.775          0.200    0.395    0.430
## wtr_mass2     -0.508 -0.450 -0.312          0.514    0.326 -0.150    0.112
## boundary_length 0.652          0.631    0.116          0.182
## dispersal_ability 0.139    0.128    0.204    0.843    0.326 -0.310
## pair_age        0.164 -0.382    0.371 -0.580    0.467 -0.294    0.198
## pd25            0.635 -0.125    0.600          0.222 -0.229    0.140
## meanEle         0.131    0.840          -0.168    0.126 -0.238          0.381
##
##          PC9    PC10
## tas_breadth           0.189
## tas_position          0.106
## pcp_breadth          0.164    0.276
## pcp_position        -0.120 -0.132
## mtn_mass2            -0.119
## wtr_mass2            0.169
## boundary_length    -0.326    0.123
## dispersal_ability
## pair_age
## pd25                0.298
## meanEle              0.108
##
##          PC1    PC2    PC3    PC4    PC5    PC6    PC7    PC8    PC9    PC10
## SS loadings    2.840 2.602 1.721 1.135 0.713 0.611 0.481 0.345 0.245 0.217
## Proportion Var 0.258 0.237 0.156 0.103 0.065 0.056 0.044 0.031 0.022 0.020
## Cumulative Var 0.258 0.495 0.651 0.754 0.819 0.875 0.918 0.950 0.972 0.992

mydata$PC1 <- myPCA$scores[, 'PC1']
mydata$PC2 <- myPCA$scores[, 'PC2']
mydata$PC3 <- myPCA$scores[, 'PC3']
mydata$PC4 <- myPCA$scores[, 'PC4']
mytree <- drop.tip(trees[[i]], CHK$tree_not_data)
mymod <- phylolm(I(log(cost)) ~ PC1 + PC2 + PC3 + PC4,
                phy = mytree, model = 'lambda', data = mydata)
summary(mymod)

##
## Call:

```

```
## phylolm(formula = I(log(cost)) ~ PC1 + PC2 + PC3 + PC4, data = mydata,
##       phy = mytree, model = "lambda")
##
##      AIC logLik
##      668   -327
##
## Raw residuals:
##      Min      1Q  Median      3Q      Max
## -2.4657 -0.5386 -0.0063  0.6957  2.5825
##
## Mean tip height: 100.4834
## Parameter estimate(s) using ML:
## lambda : 1e-07
## sigma2: 0.009418626
##
## Coefficients:
##              Estimate      StdErr  t.value  p.value
## (Intercept) 18.550271  0.064147 289.1822 < 2.2e-16 ***
## PC1          0.451557  0.064284   7.0244 2.408e-11 ***
## PC2          0.361903  0.064284   5.6297 5.233e-08 ***
## PC3          0.406806  0.064284   6.3283 1.283e-09 ***
## PC4         -0.090044  0.064284  -1.4007  0.1626
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-squared: 0.3485      Adjusted R-squared: 0.3372
##
## Note: p-values and R-squared are conditional on lambda=1e-07.
```

```
# 5
```

```
myPCA <- principal(mydata[,c('tas_breadth', 'tas_position', 'pcp_breadth',
                              'pcp_position', 'mtn_mass2', 'wtr_mass2', "boundary_length",
                              'dispersal_ability', 'pair_age', "pd0", 'meanEle')], nfactors = 10, rotate
myPCA$loadings # this looks solid so far!
```

```
##
## Loadings:
##           PC1    PC2    PC3    PC4    PC5    PC6    PC7    PC8
## tas_breadth -0.895      -0.217      0.127 -0.102
## tas_position  0.595 -0.555  0.327  0.185 -0.169      0.151  0.309
## pcp_breadth  0.528  0.671  0.342
## pcp_position  0.706  0.484  0.283      -0.337
## mtn_mass2    -0.143  0.764      0.107  0.187  0.498  0.293
## wtr_mass2     0.509 -0.396 -0.422      0.463  0.253  0.232 -0.151
## boundary_length -0.497      0.648  0.256 -0.230  0.146  0.251 -0.263
## dispersal_ability -0.114  0.124  0.170  0.848  0.329  0.199 -0.244
## pair_age      -0.394  0.494 -0.499      0.531 -0.171  0.128
## pd0           -0.360 -0.219  0.508 -0.192  0.567 -0.443
## meanEle       -0.256  0.807      -0.193  0.132      -0.264
##           PC9    PC10
## tas_breadth -0.228  0.189
## tas_position      0.108
## pcp_breadth  -0.194  0.302
## pcp_position      -0.157
## mtn_mass2      -0.114
```

```
## wtr_mass2          0.149  0.166
## boundary_length    0.223
## dispersal_ability -0.104
## pair_age
## pd0
## meanEle            0.361
##
##              PC1   PC2   PC3   PC4   PC5   PC6   PC7   PC8   PC9  PC10
## SS loadings    2.672 2.611 1.480 1.158 0.777 0.665 0.573 0.428 0.328 0.218
## Proportion Var 0.243 0.237 0.135 0.105 0.071 0.060 0.052 0.039 0.030 0.020
## Cumulative Var 0.243 0.480 0.615 0.720 0.791 0.851 0.903 0.942 0.972 0.992
```

```
mydata$PC1 <- -myPCA$scores[, 'PC1']
mydata$PC2 <- myPCA$scores[, 'PC2']
mydata$PC3 <- myPCA$scores[, 'PC3']
mydata$PC4 <- myPCA$scores[, 'PC4']
mytree <- drop.tip(trees[[i]], CHK$tree_not_data)
mymod <- phylolm(I(log(cost)) ~ PC1 + PC2 + PC3 + PC4,
                 phy = mytree, model = 'lambda', data = mydata)
summary(mymod)
```

```
##
## Call:
## phylolm(formula = I(log(cost)) ~ PC1 + PC2 + PC3 + PC4, data = mydata,
##         phy = mytree, model = "lambda")
##
##      AIC logLik
## 656.5 -321.3
##
## Raw residuals:
##      Min      1Q   Median      3Q      Max
## -2.57154 -0.60480  0.02421  0.64680  2.33406
##
## Mean tip height: 100.4834
## Parameter estimate(s) using ML:
## lambda : 1e-07
## sigma2: 0.008970898
##
## Coefficients:
##              Estimate   StdErr  t.value  p.value
## (Intercept) 18.550271  0.062604 296.3107 < 2.2e-16 ***
## PC1          0.430699  0.062738   6.8651 6.120e-11 ***
## PC2          0.298225  0.062738   4.7535 3.525e-06 ***
## PC3          0.513809  0.062738   8.1898 1.807e-14 ***
## PC4         -0.123359  0.062738  -1.9663  0.05047 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-squared: 0.3795    Adjusted R-squared: 0.3687
##
## Note: p-values and R-squared are conditional on lambda=1e-07.
```

```
#7
myPCA <- principal(mydata[,c('tas_breadth', 'tas_position', 'pcp_breadth',
                             'pcp_position', 'mtn_mass2', 'wtr_mass2',
```

```

                                'dispersal_ability', 'pair_age', "pd0", "pd25")], nfactors = 9, rotate = "
myPCA$loadings # this looks solid so far!

```

```

##
## Loadings:
##          PC1    PC2    PC3    PC4    PC5    PC6    PC7    PC8
## tas_breadth -0.809 -0.380 -0.241 -0.123
## tas_position 0.354 0.738 0.144 0.216 -0.226      0.419
## pcp_breadth 0.688 -0.347 0.507 -0.112
## pcp_position 0.786 -0.123 0.438      0.174      -0.243 0.165
## mtn_mass2 0.140 -0.774 0.161      0.298 0.118 0.485
## wtr_mass2 0.332 0.504 -0.382      0.681
## dispersal_ability      -0.197      0.904      0.352
## pair_age -0.249 0.499 0.354 -0.388      0.639
## pd0 -0.552 0.200 0.614      0.282 -0.294      -0.318
## pd25 -0.617 0.102 0.656 0.128      -0.108      0.362
##          PC9
## tas_breadth      0.287
## tas_position      0.115
## pcp_breadth      0.311
## pcp_position
## mtn_mass2
## wtr_mass2      0.129
## dispersal_ability
## pair_age
## pd0
## pd25
##
##          PC1    PC2    PC3    PC4    PC5    PC6    PC7    PC8    PC9
## SS loadings  2.749 2.016 1.639 1.078 0.734 0.658 0.483 0.285 0.228
## Proportion Var 0.275 0.202 0.164 0.108 0.073 0.066 0.048 0.029 0.023
## Cumulative Var 0.275 0.476 0.640 0.748 0.822 0.887 0.936 0.964 0.987

```

```

mydata$PC1 <- -myPCA$scores[, 'PC1']
mydata$PC2 <- -myPCA$scores[, 'PC2']
mydata$PC3 <- myPCA$scores[, 'PC3']
mydata$PC4 <- myPCA$scores[, 'PC4']
mytree <- drop.tip(trees[[i]], CHK$tree_not_data)
mymod <- phylolm(I(log(cost)) ~ PC1 + PC2 + PC3 + PC4,
                phy = mytree, model = 'lambda', data = mydata)
summary(mymod)

```

```

##
## Call:
## phylolm(formula = I(log(cost)) ~ PC1 + PC2 + PC3 + PC4, data = mydata,
##         phy = mytree, model = "lambda")
##
##      AIC logLik
## 628.1 -307.1
##
## Raw residuals:
##      Min      1Q   Median      3Q      Max
## -2.63450 -0.59152  0.00074  0.57895  2.50822
##

```

```
## Mean tip height: 100.4834
## Parameter estimate(s) using ML:
## lambda : 1e-07
## sigma2: 0.007949422
##
## Coefficients:
##           Estimate      StdErr  t.value   p.value
## (Intercept) 18.550271  0.058932 314.7730 < 2.2e-16 ***
## PC1          0.408229  0.059058   6.9124 4.647e-11 ***
## PC2          0.233501  0.059058   3.9538 0.0001024 ***
## PC3          0.657685  0.059058  11.1363 < 2.2e-16 ***
## PC4          0.054905  0.059058   0.9297 0.3535142
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-squared: 0.4501      Adjusted R-squared: 0.4406
##
## Note: p-values and R-squared are conditional on lambda=1e-07.
```

```
#8
myPCA <- principal(mydata[,c('tas_breadth', 'tas_position', 'pcp_breadth',
                             'pcp_position', 'mtn_mass2', 'wtr_mass2',
                             'dispersal_ability', 'pair_age', "pd25")], nfactors = 8, rotate = "none")
myPCA$loadings # this looks solid so far!
```

```
##
## Loadings:
##           PC1    PC2    PC3    PC4    PC5    PC6    PC7    PC8
## tas_breadth  -0.883  0.263          -0.126  0.102          0.274
## tas_position  0.454 -0.672  0.184  0.247 -0.208  0.160  0.384  0.107
## pcp_breadth   0.730  0.484  0.304          0.165          -0.281
## pcp_position  0.842  0.263  0.215          0.312  0.200  0.442
## mtn_mass2     0.329 -0.523 -0.493          0.540  0.237          0.127
## wtr_mass2     0.206          0.918  0.235 -0.241
## dispersal_ability -0.137 -0.459  0.610 -0.295  0.408 -0.359  0.128
## pair_age      -0.447          0.714  0.213          0.453 -0.170
##
##           PC1    PC2    PC3    PC4    PC5    PC6    PC7    PC8
## SS loadings  2.561 1.994 1.306 1.072 0.703 0.519 0.476 0.229
## Proportion Var 0.285 0.222 0.145 0.119 0.078 0.058 0.053 0.025
## Cumulative Var 0.285 0.506 0.651 0.770 0.848 0.906 0.959 0.985
```

```
mydata$PC1 <- -myPCA$scores[, 'PC1']
mydata$PC2 <- myPCA$scores[, 'PC2']
mydata$PC3 <- myPCA$scores[, 'PC3']
mydata$PC4 <- myPCA$scores[, 'PC4']
mytree <- drop.tip(trees[[i]], CHK$tree_not_data)
mymod <- phylolm(I(log(cost)) ~ PC1 + PC2 + PC3 + PC4,
                phy = mytree, model = 'lambda', data = mydata)
summary(mymod)
```

```
##
## Call:
## phylolm(formula = I(log(cost)) ~ PC1 + PC2 + PC3 + PC4, data = mydata,
```



```
##      phy = mytree, model = "lambda")
##
##      AIC logLik
##      680.4 -333.2
##
## Raw residuals:
##      Min      1Q   Median      3Q      Max
## -2.84249 -0.63706 -0.01418  0.65484  2.86572
##
## Mean tip height: 100.4834
## Parameter estimate(s) using ML:
## lambda : 1e-07
## sigma2: 0.009930412
##
## Coefficients:
##      Estimate   StdErr  t.value  p.value
## (Intercept) 18.550271  0.065867 281.6317 < 2.2e-16 ***
## PC1         0.256080  0.066007   3.8796 0.0001367 ***
## PC2         0.327906  0.066007   4.9677 1.322e-06 ***
## PC3         0.524068  0.066007   7.9395 8.922e-14 ***
## PC4         0.095305  0.066007   1.4439 0.1501401
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-squared: 0.3131      Adjusted R-squared: 0.3012
##
## Note: p-values and R-squared are conditional on lambda=1e-07.
```

```
#9
```

```
myPCA <- principal(mydata[,c('tas_breadth', 'tas_position', 'pcp_breadth',
                             'pcp_position', 'mtn_mass2', 'wtr_mass2',
                             'dispersal_ability', 'pair_age', "pd0")], nfactors = 8, rotate = "none") #
myPCA$loadings # this looks solid so far!
```

```
##
## Loadings:
##      PC1    PC2    PC3    PC4    PC5    PC6    PC7    PC8
## tas_breadth -0.871  0.313      -0.113      0.274
## tas_position  0.441 -0.700      0.231 -0.228      0.419 0.107
## pcp_breadth  0.763  0.427  0.321      0.174      -0.249 0.327
## pcp_position  0.867  0.206  0.194      0.304      0.485
## mtn_mass2    0.121  0.793      0.635      0.125
## wtr_mass2    0.266 -0.520 -0.446 -0.195  0.635
## dispersal_ability      0.208 -0.302  0.876  0.120  0.278
## pair_age    -0.132 -0.478  0.631      0.141  0.574
## pd0         -0.349 -0.164  0.624  0.376  0.321 -0.465
##
##      PC1    PC2    PC3    PC4    PC5    PC6    PC7    PC8
## SS loadings  2.511 2.010 1.223 1.025 0.727 0.641 0.482 0.229
## Proportion Var 0.279 0.223 0.136 0.114 0.081 0.071 0.054 0.025
## Cumulative Var 0.279 0.502 0.638 0.752 0.833 0.904 0.958 0.983
```

```
mydata$PC1 <- -myPCA$scores[, 'PC1']
mydata$PC2 <- myPCA$scores[, 'PC2']
mydata$PC3 <- myPCA$scores[, 'PC3']
```

```

mydata$PC4 <- myPCA$scores[, 'PC4']
mytree <- drop.tip(trees[[i]], CHK$tree_not_data)
mymod <- phylolm(I(log(cost)) ~ PC1 + PC2 + PC3 + PC4,
                 phy = mytree, model = 'lambda', data = mydata)
summary(mymod)

##
## Call:
## phylolm(formula = I(log(cost)) ~ PC1 + PC2 + PC3 + PC4, data = mydata,
##         phy = mytree, model = "lambda")
##
##      AIC logLik
## 664.1 -325.0
##
## Raw residuals:
##      Min      1Q   Median      3Q      Max
## -3.06536 -0.58953  0.02061  0.65700  2.89571
##
## Mean tip height: 100.4834
## Parameter estimate(s) using ML:
## lambda : 1e-07
## sigma2: 0.009263628
##
## Coefficients:
##              Estimate   StdErr  t.value  p.value
## (Intercept) 18.550271  0.063617 291.5914 < 2.2e-16 ***
## PC1          0.216092  0.063753   3.3895 0.0008238 ***
## PC2          0.281363  0.063753   4.4133 1.565e-05 ***
## PC3          0.551880  0.063753   8.6565 8.601e-16 ***
## PC4          0.306079  0.063753   4.8010 2.844e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-squared: 0.3592    Adjusted R-squared: 0.3481
##
## Note: p-values and R-squared are conditional on lambda=1e-07.

```