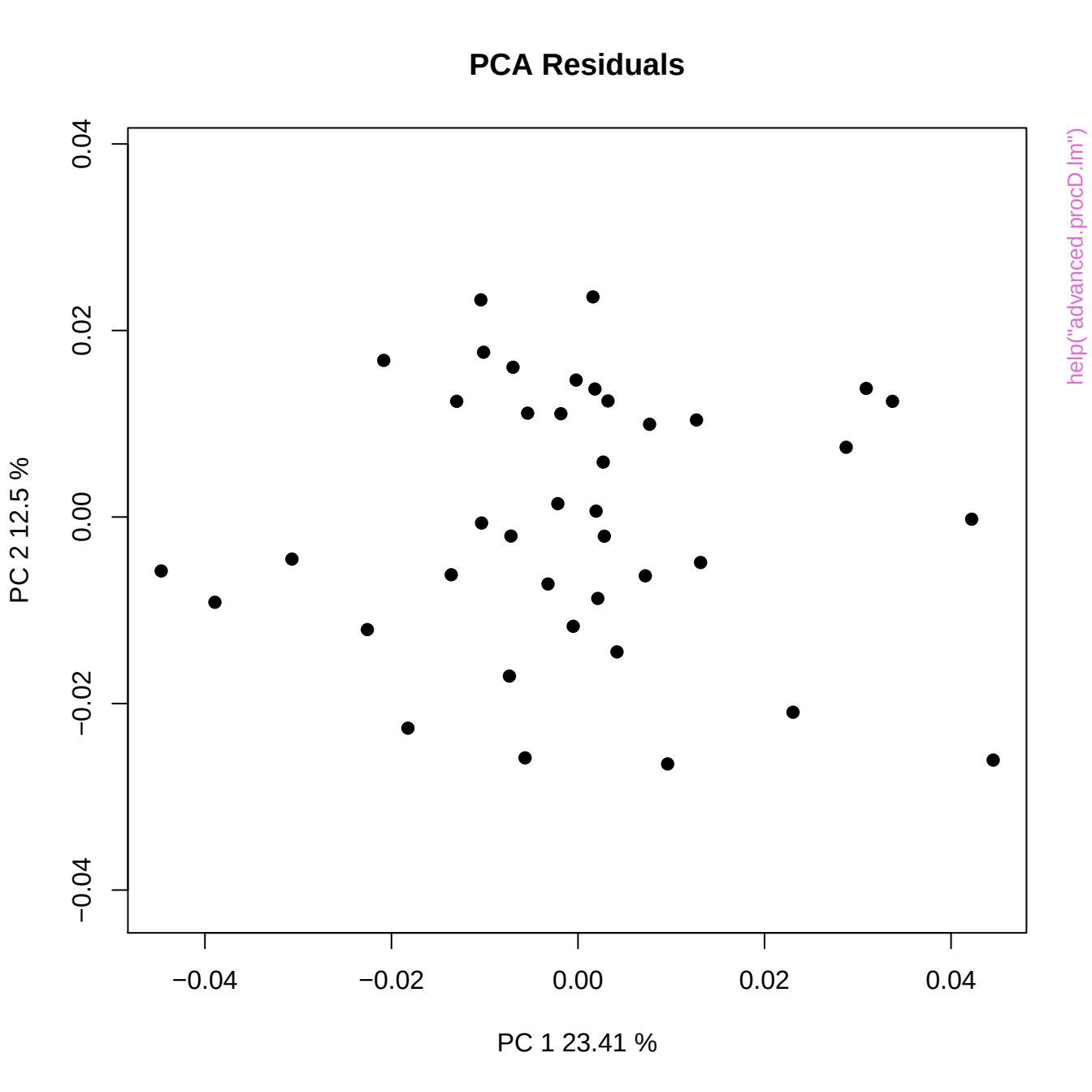
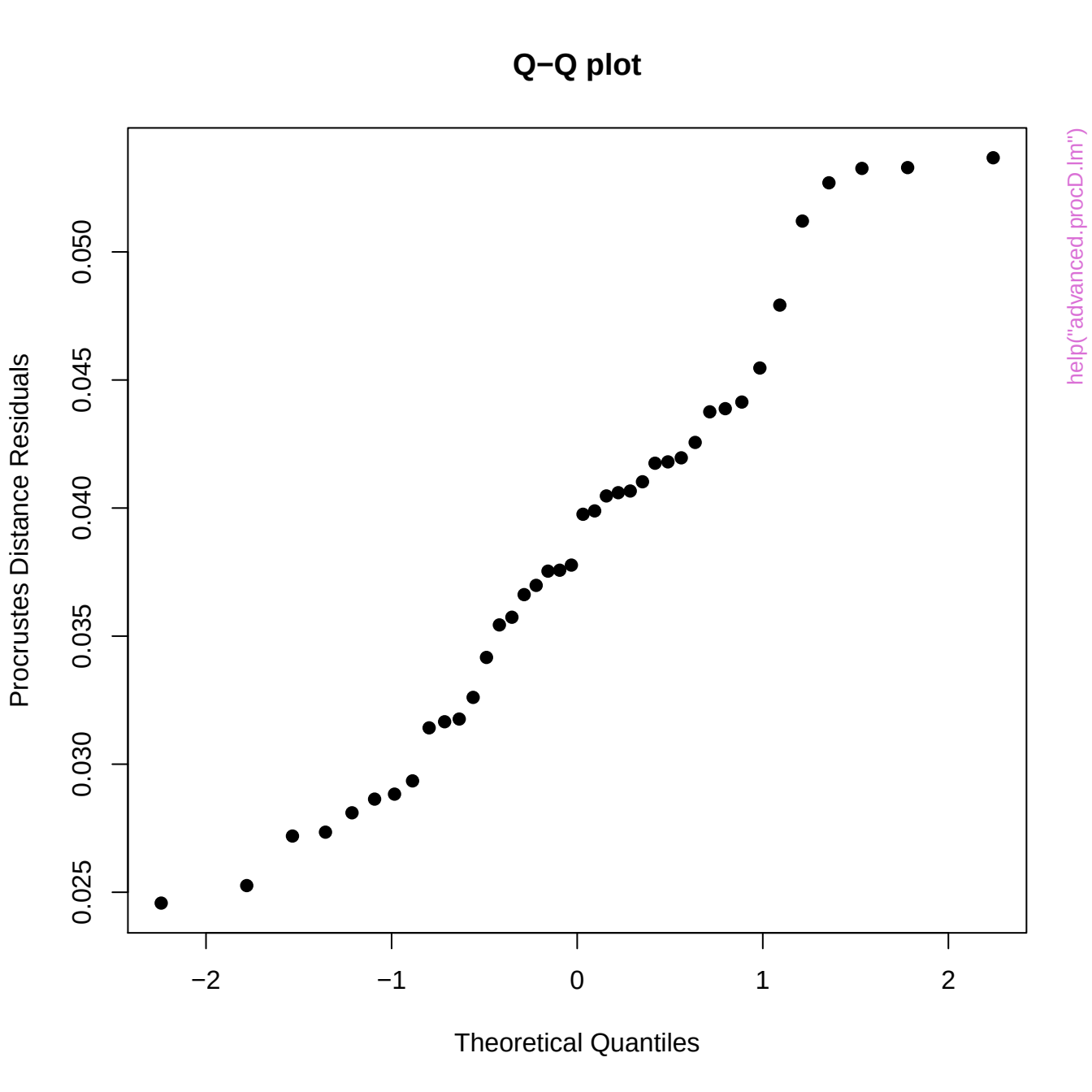
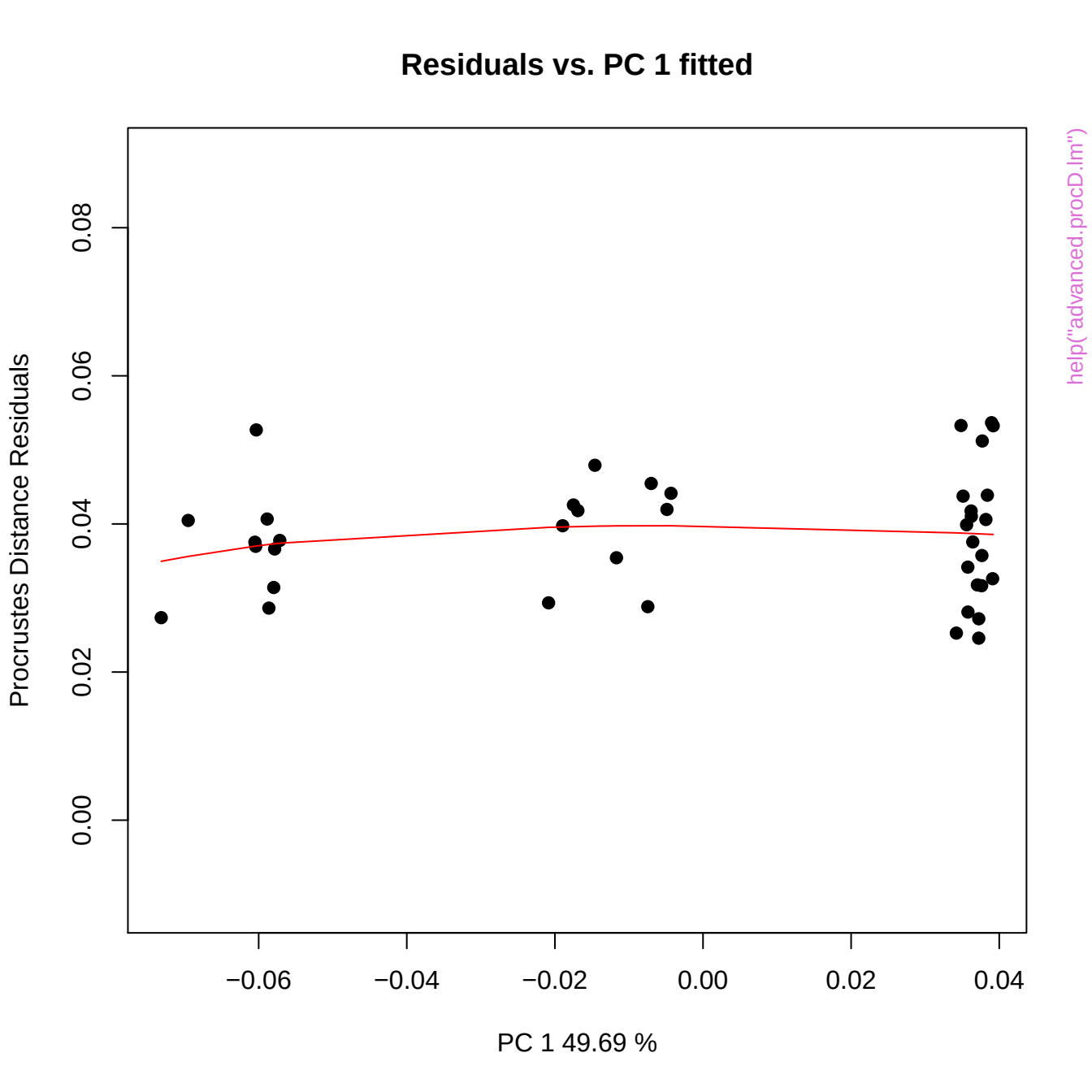
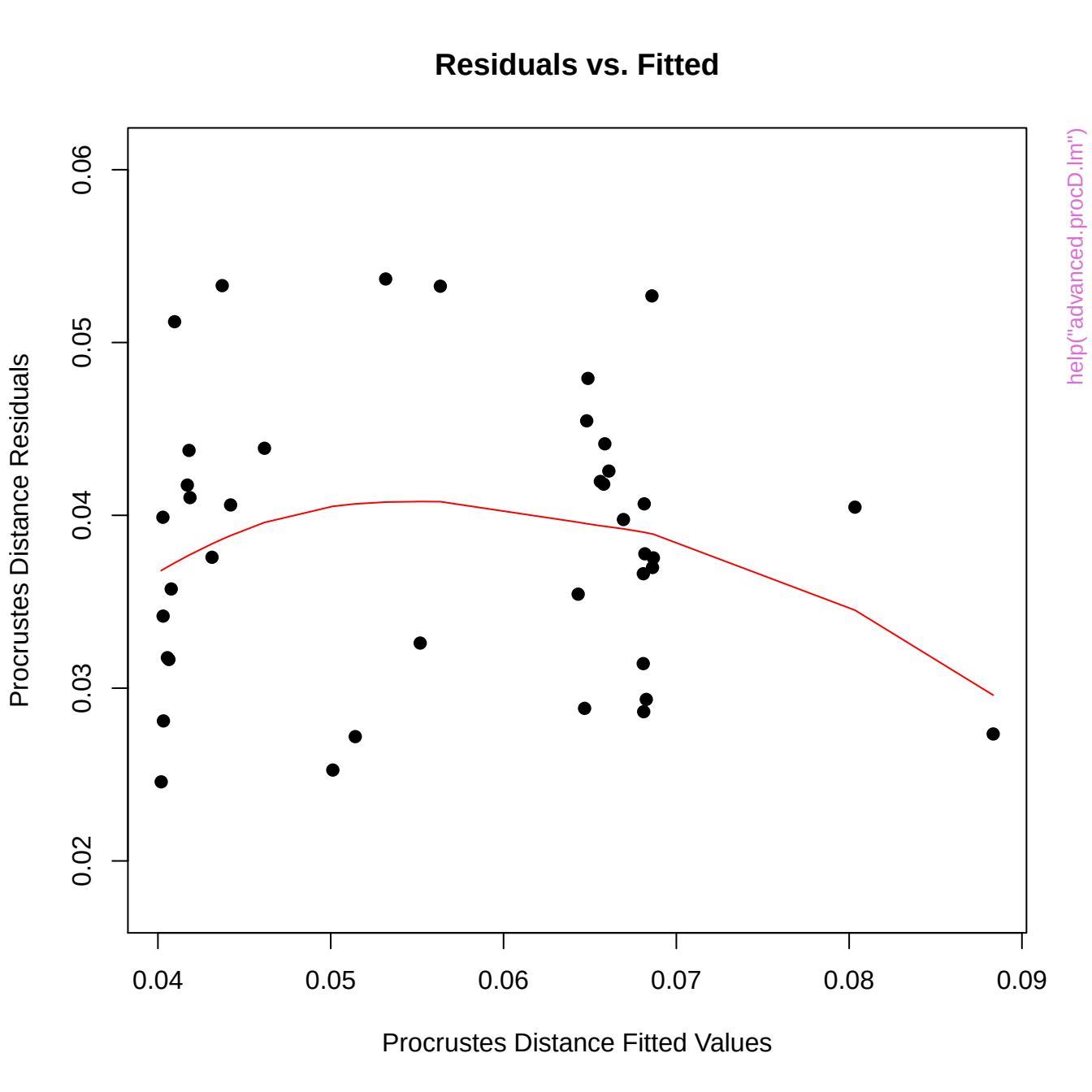
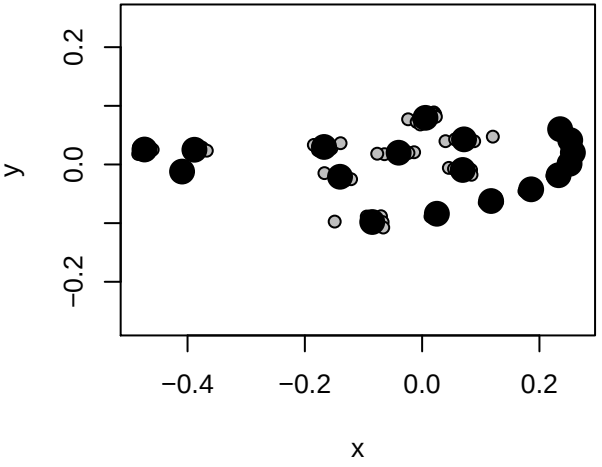

PCA Residuals
PC 2 12.5 %
PC 1 23.41 %
0.04
0.02
0.00
−0.02
−0.04
−0.04
−0.02
0.00
0.02
0.04
help("advanced.procD.lm")

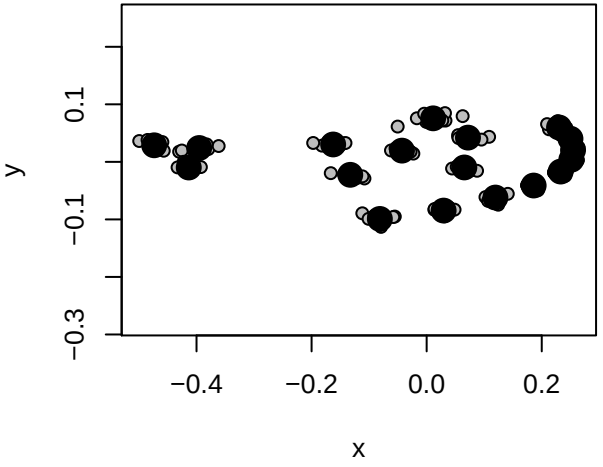

Q−Q plot
Procrustes Distance Residuals
0.025
0.030
0.035
0.040
0.045
0.050
−2
−1
0
1
2
Theoretical Quantiles
help("advanced.procD.lm")


Residuals vs. PC 1 fitted
Procrustes Distance Residuals
0.00
0.02
0.04
0.06
0.08
−0.06
−0.04
−0.02
0.00
0.02
0.04
PC 1 49.69 %
help("advanced.procD.lm")

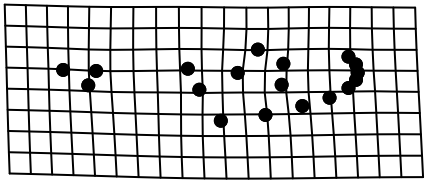

Residuals vs. Fitted
Procrustes Distance Residuals
0.02
0.03
0.04
0.05
0.06
0.04
0.05
0.06
0.07
0.08
0.09
Procrustes Distance Fitted Values
help("advanced.procD.lm")

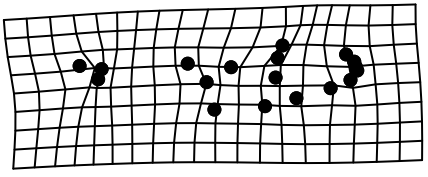
Symmetric Shape Component (left) and Asymmetric Shape Component (right)



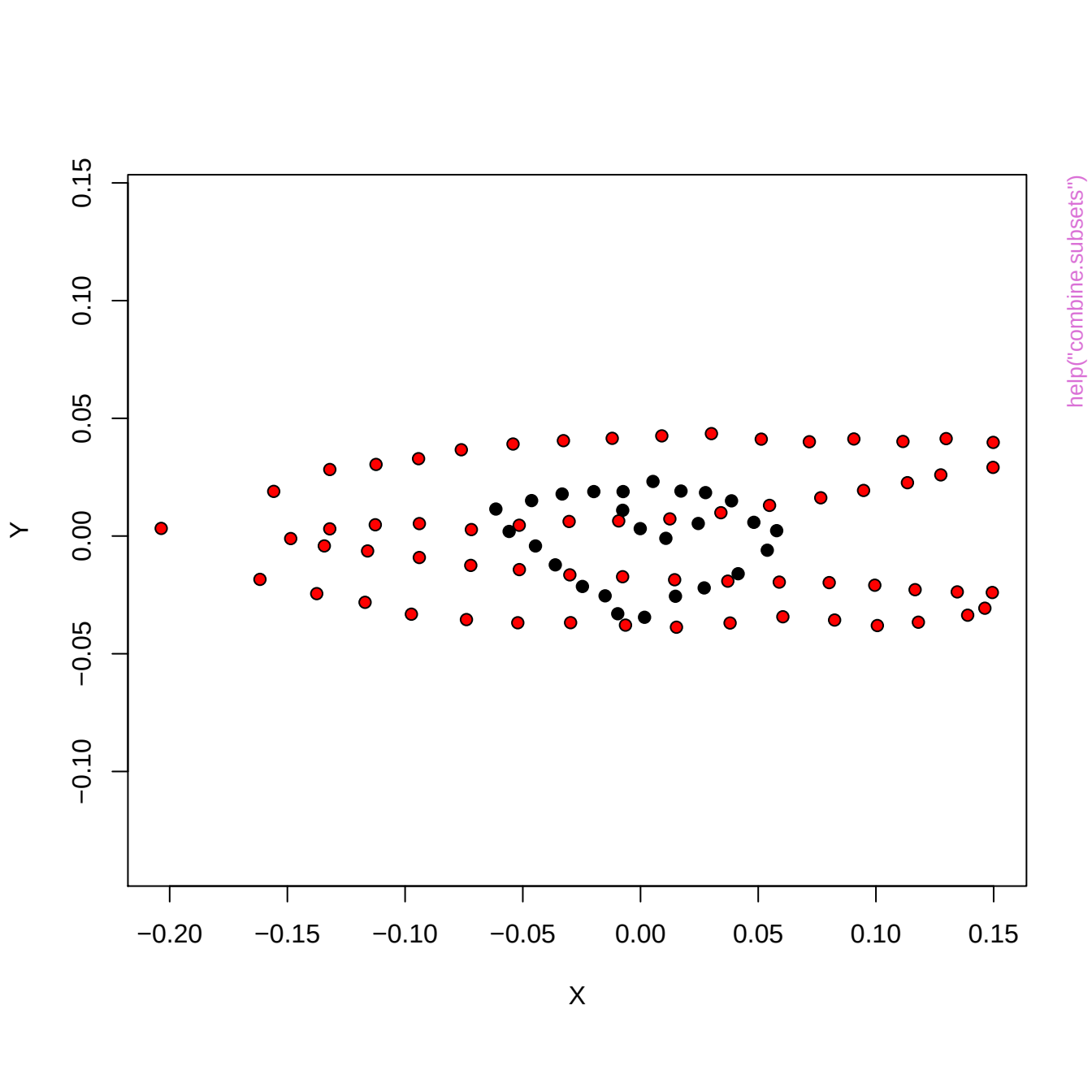


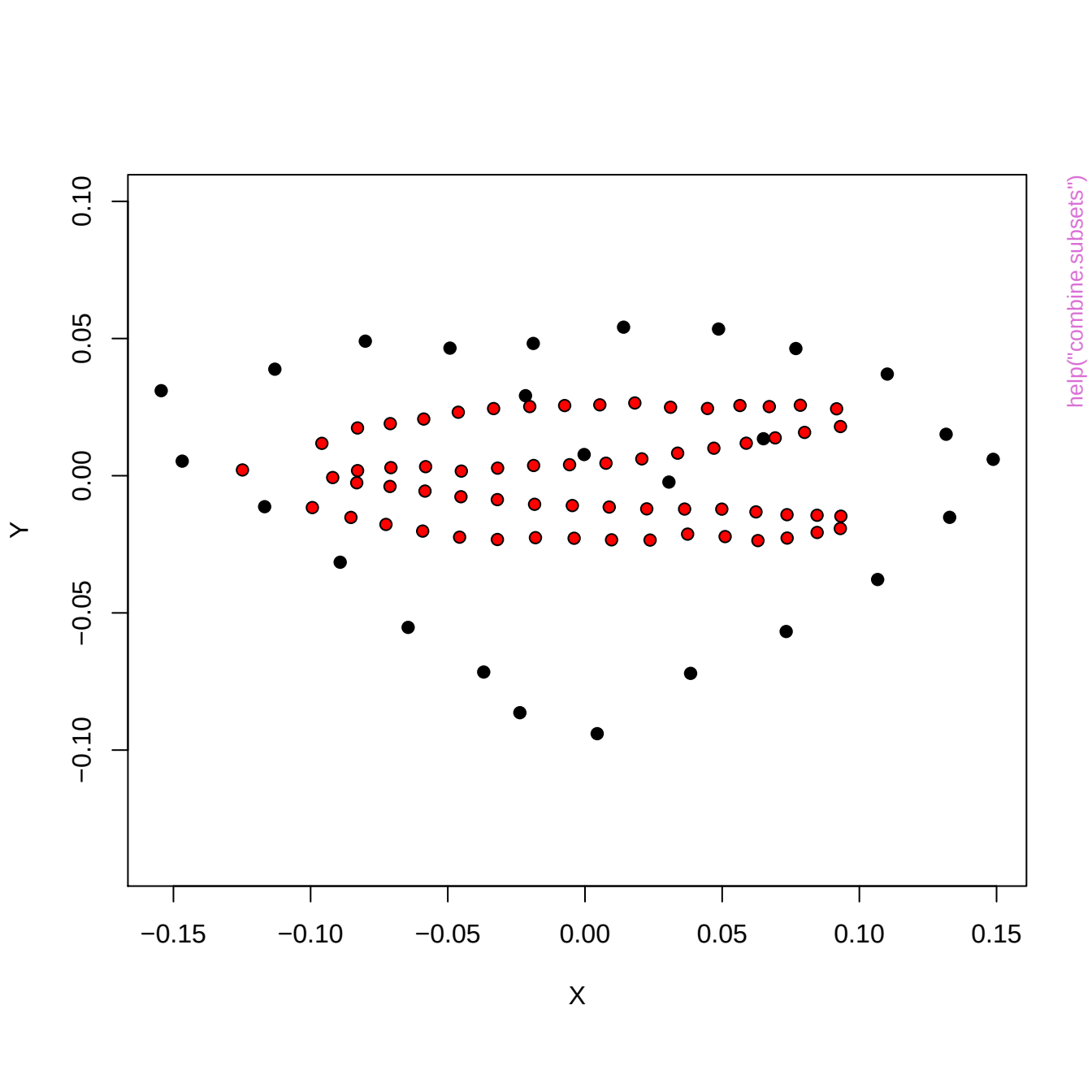
help("bilat.symmetry")

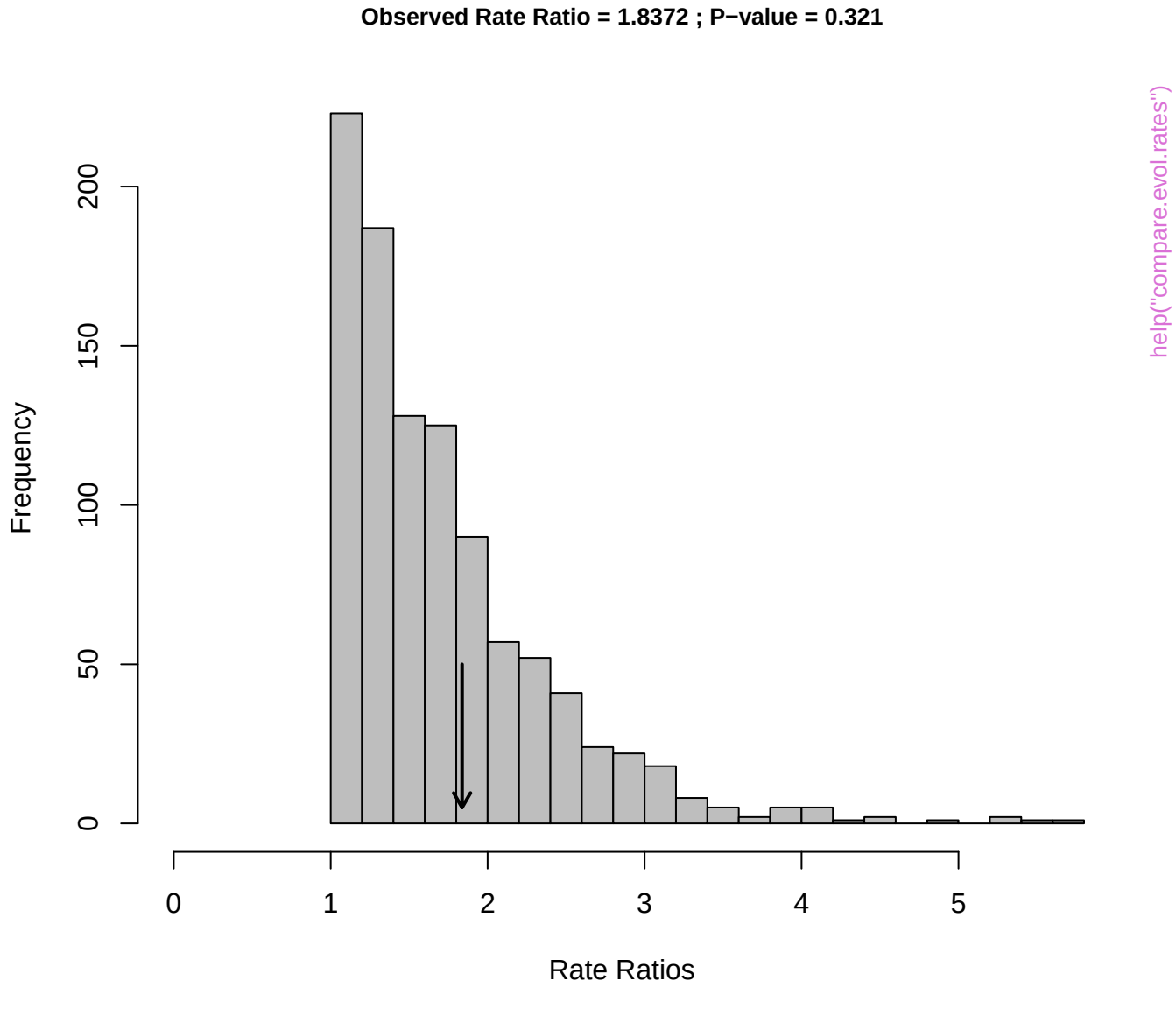


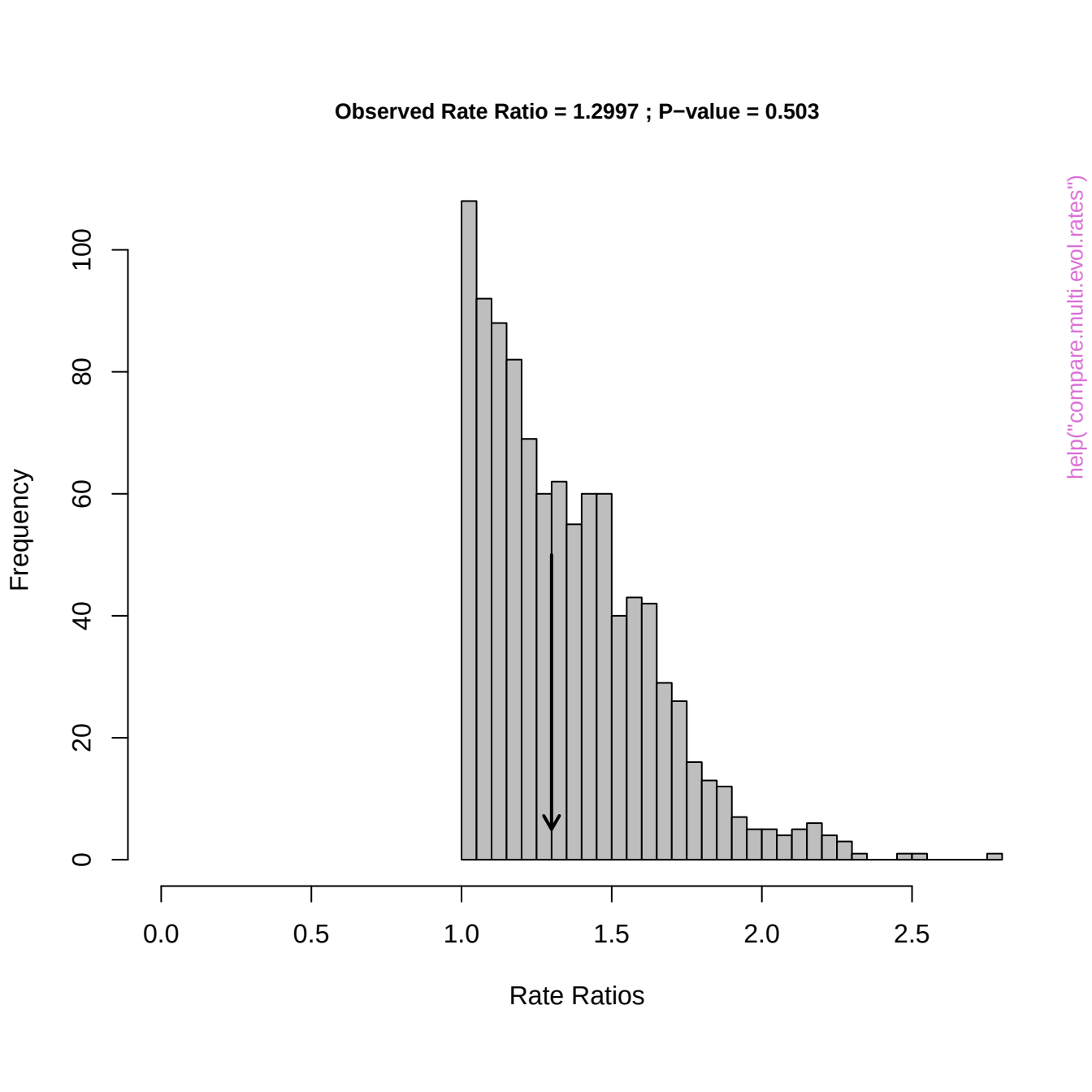


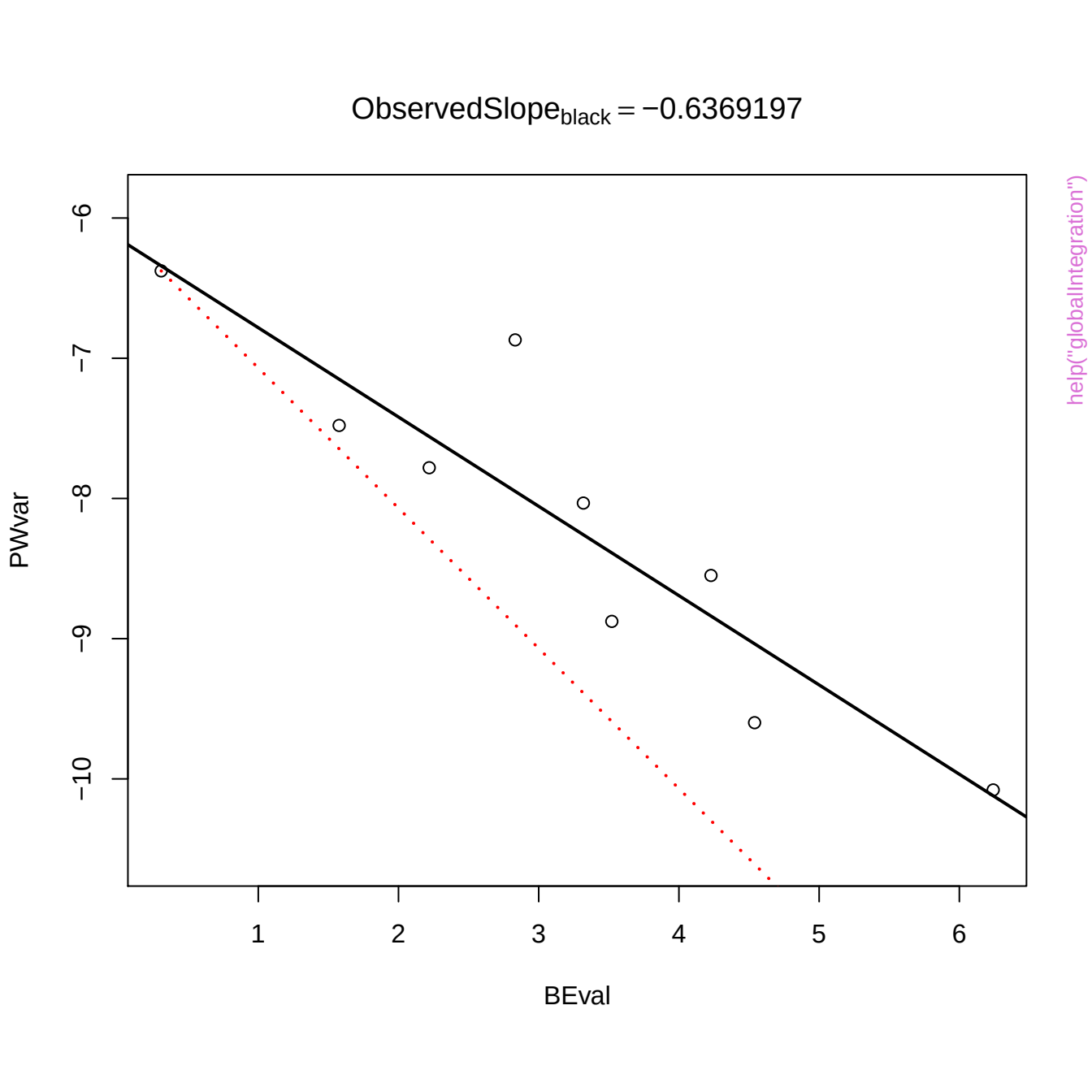
Mean directional (left) and fluctuating (right) asymmetry

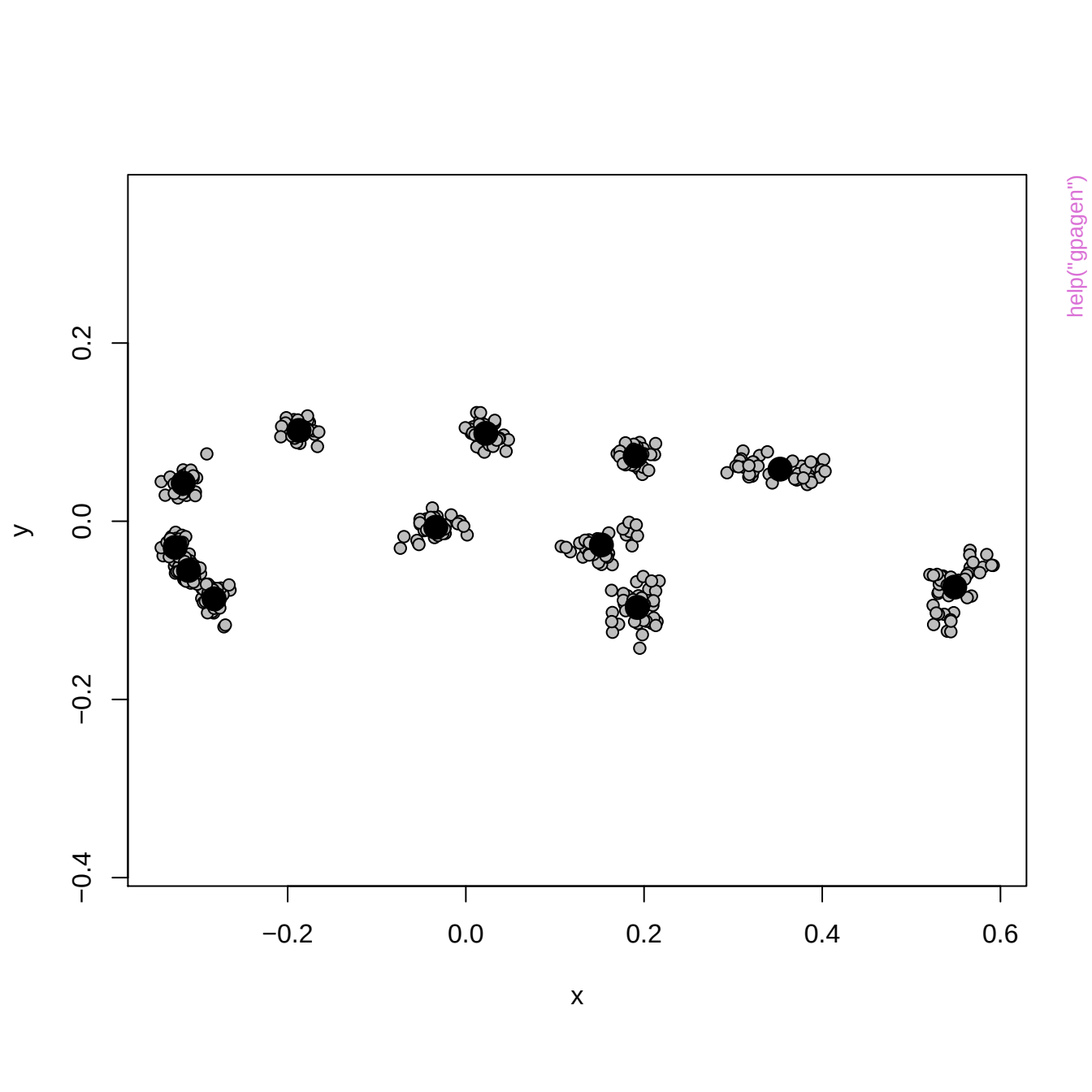

0.15
0.10
0.05
0.00
−0.05
−0.10
Y
−0.20
−0.15
−0.10
−0.05
0.00
0.05
0.10
0.15
X
help("combine.subsets")

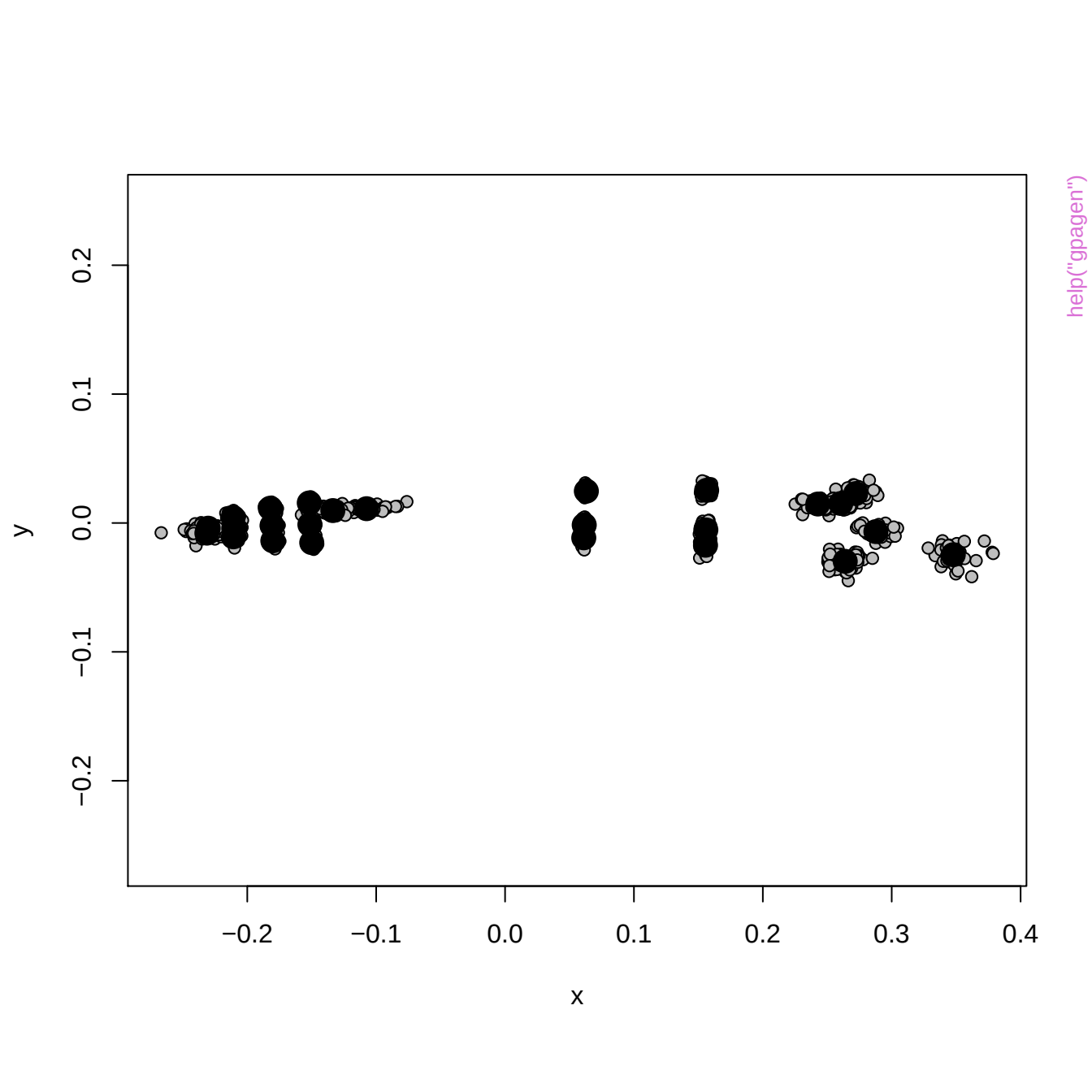

help("combine.subsets")
Y
X
0.10
0.05
0.00
−0.05
−0.10
−0.15
−0.10
−0.05
0.00
0.05
0.10
0.15

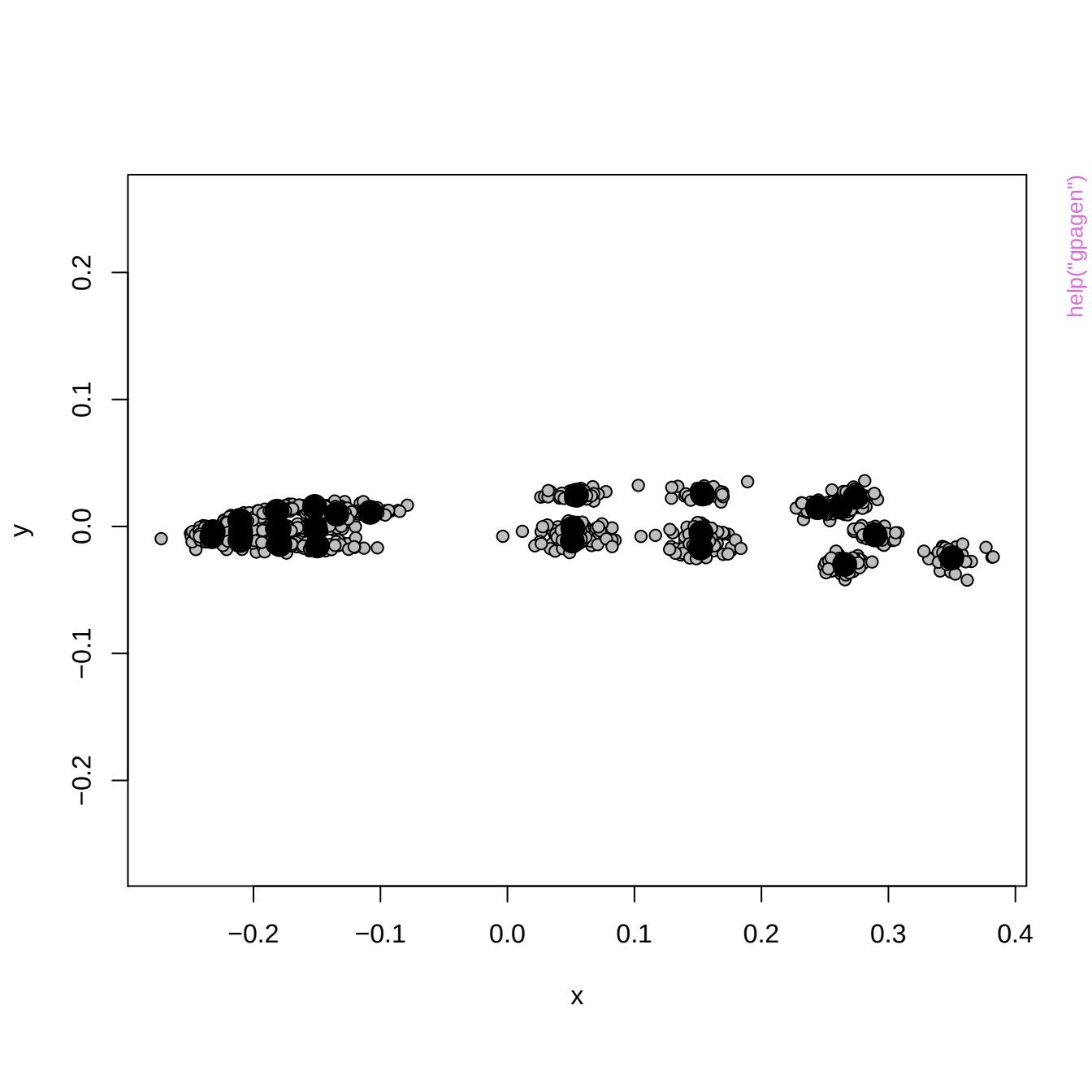

Observed Rate Ratio = 1.8372 ; P−value = 0.321
Frequency
0
50
100
150
200
0
1
2
3
4
5
Rate Ratios
help("compare.evol.rates")

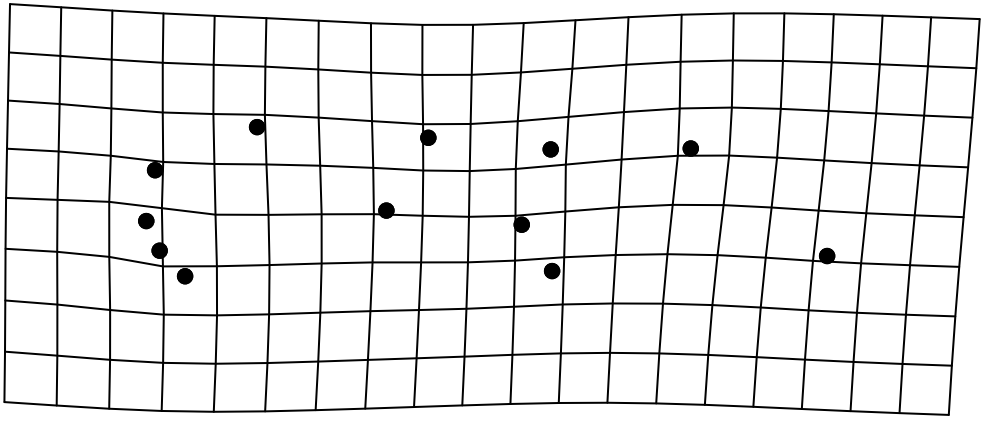

Observed Rate Ratio = 1.2997 ; P−value = 0.503
Frequency
0
20
40
60
80
100
0.0
0.5
1.0
1.5
2.0
2.5
Rate Ratios
help("compare.multi.evol.rates")


ObservedSlope$_{black}$ = −0.6369197
PWvar
−6
−7
−8
−9
−10
1
2
3
4
5
6
BEval
help("globalIntegration")

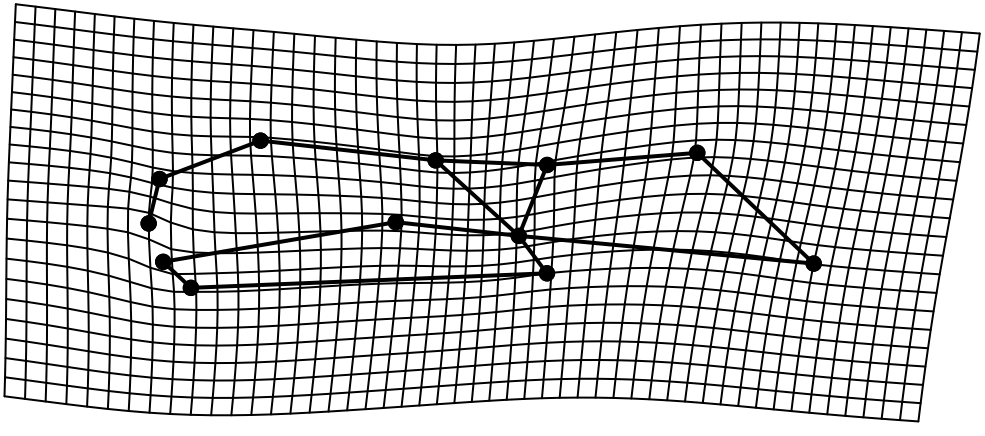

help("gpagen")
y
x
0.2
0.0
−0.2
−0.4
−0.2
0.0
0.2
0.4
0.6


help("gpagen")
y
0.2
0.1
0.0
−0.1
−0.2
−0.2
−0.1
0.0
0.1
0.2
0.3
0.4
x

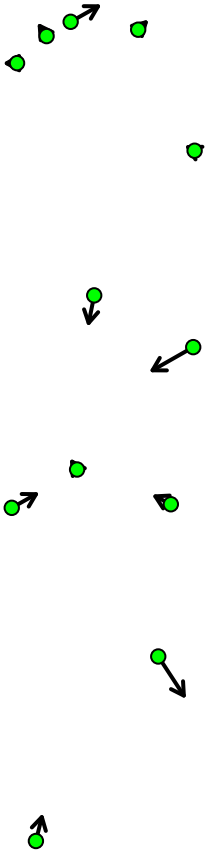

help("gpagen")
y
0.2
0.1
0.0
−0.1
−0.2
−0.2
−0.1
0.0
0.1
0.2
0.3
0.4
x



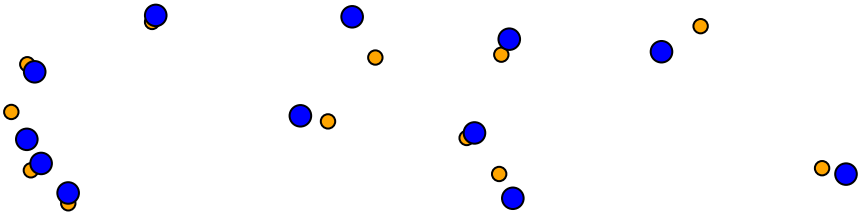
help("gridPar")



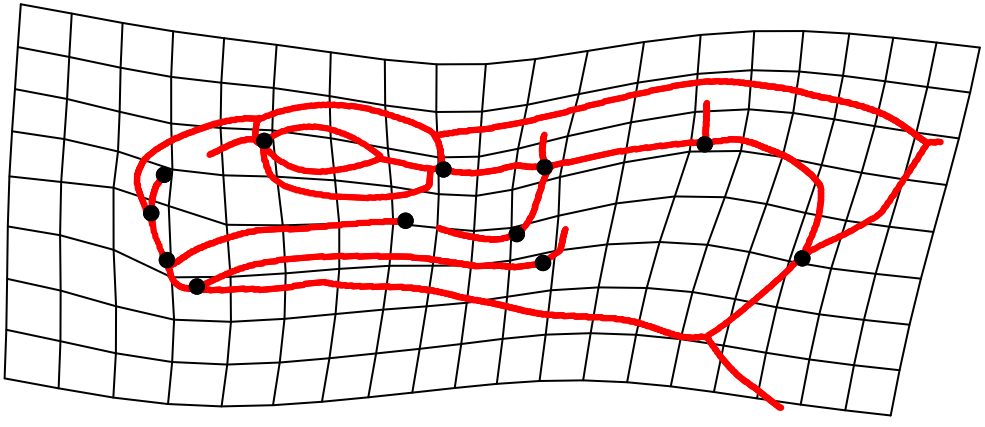
help("gridPar")



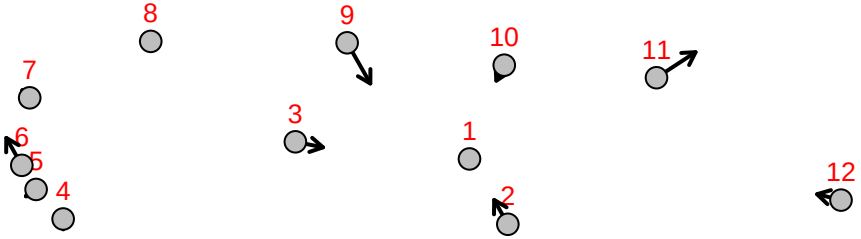
help("gridPar")



help("gridPar")

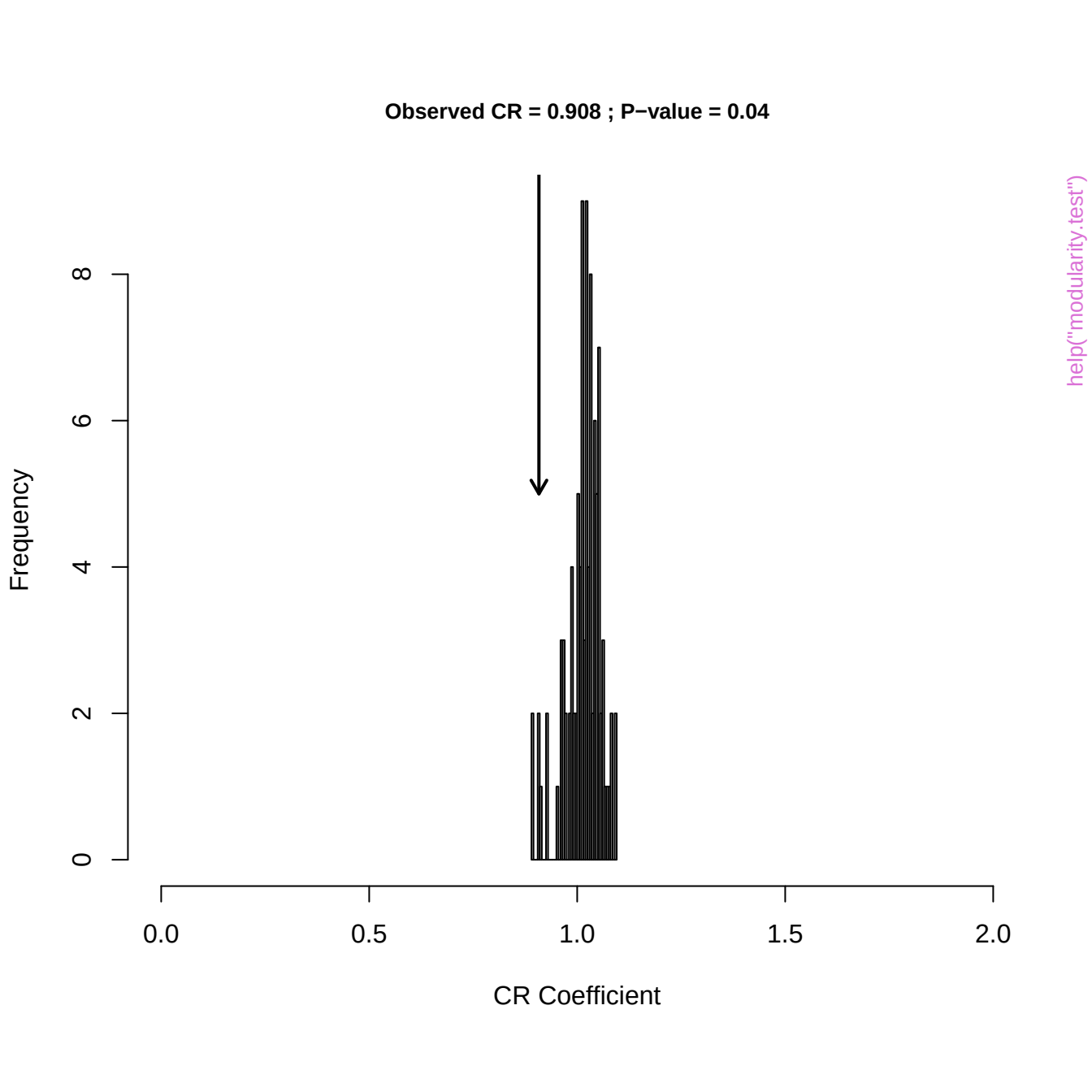


help("gridPar")

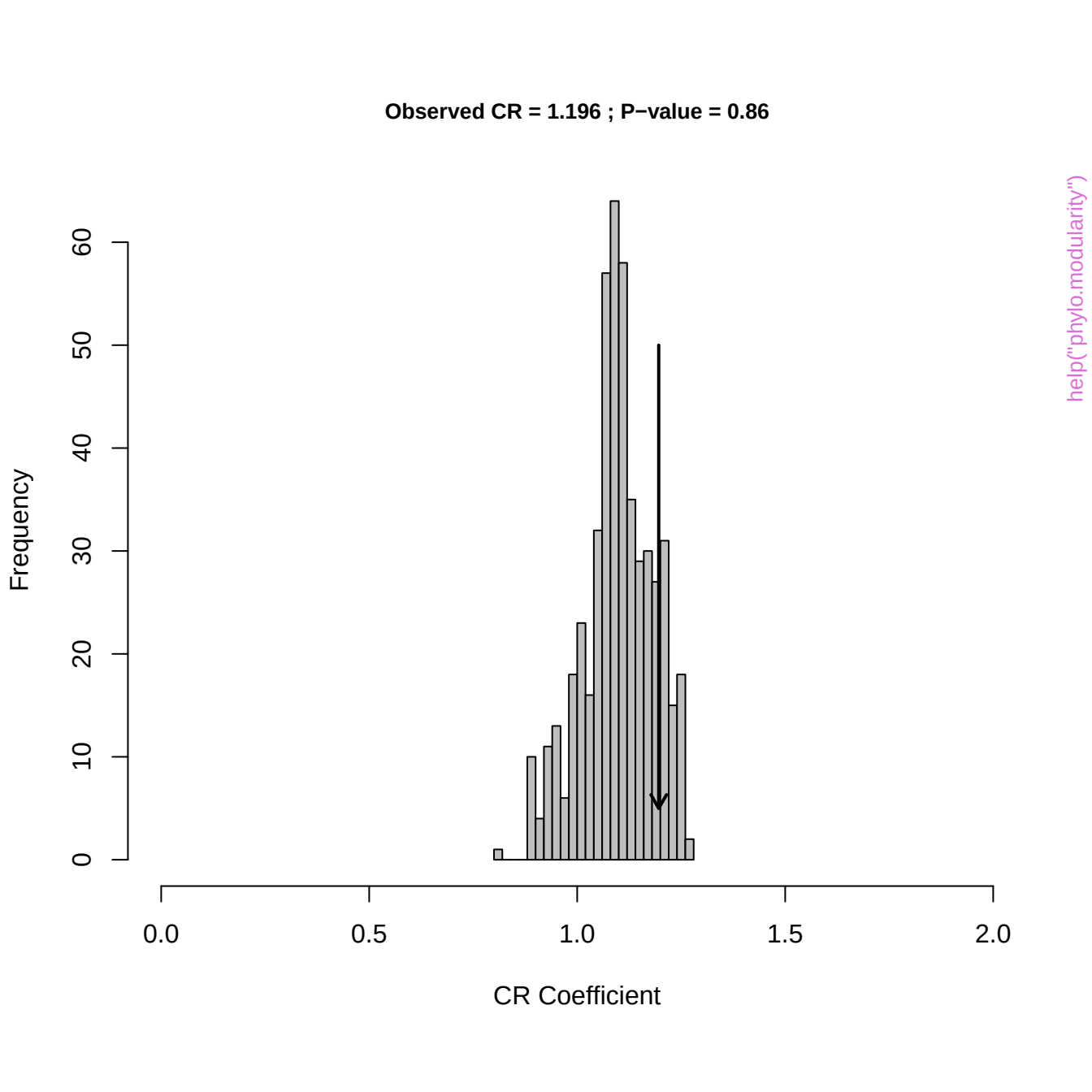


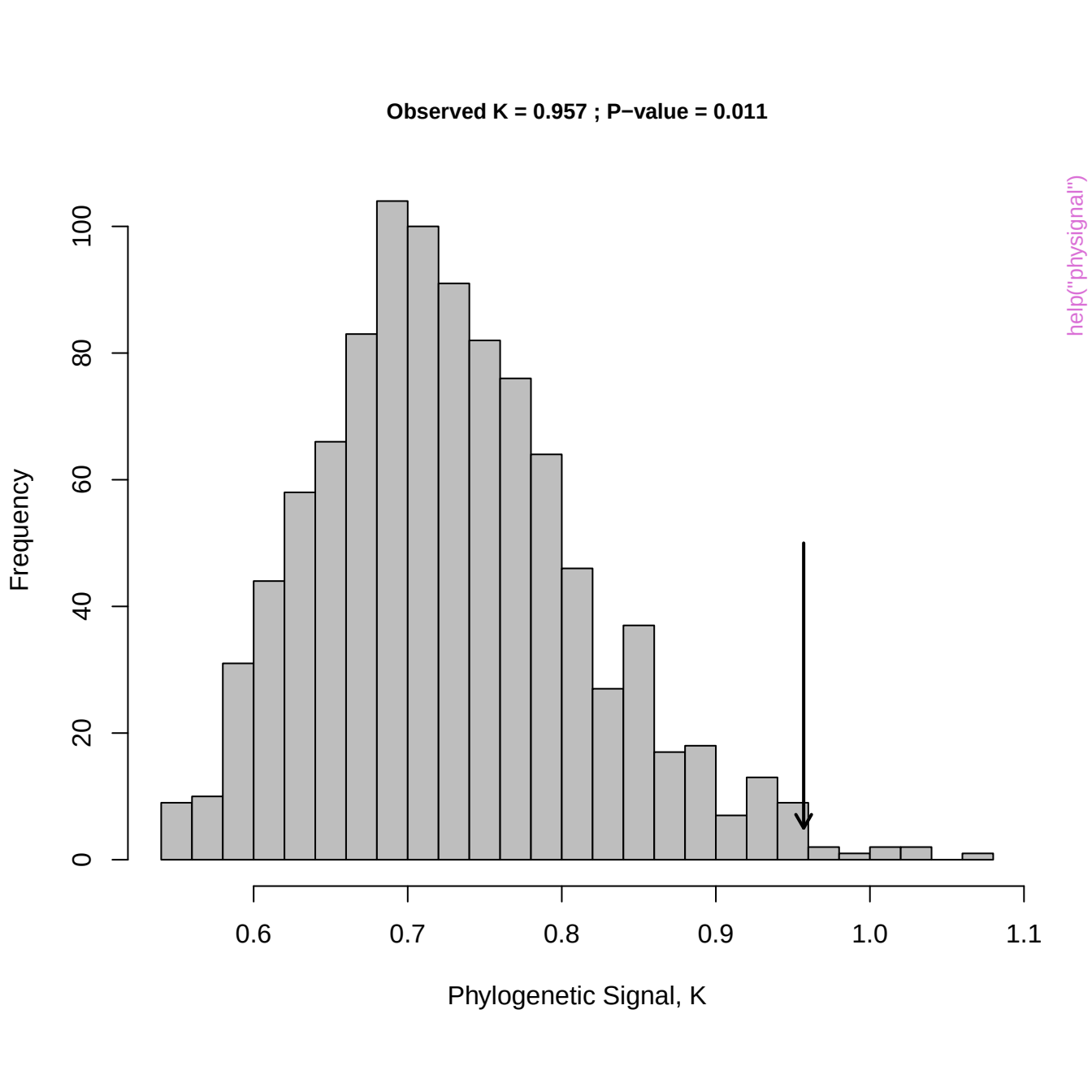
help("gridPar")

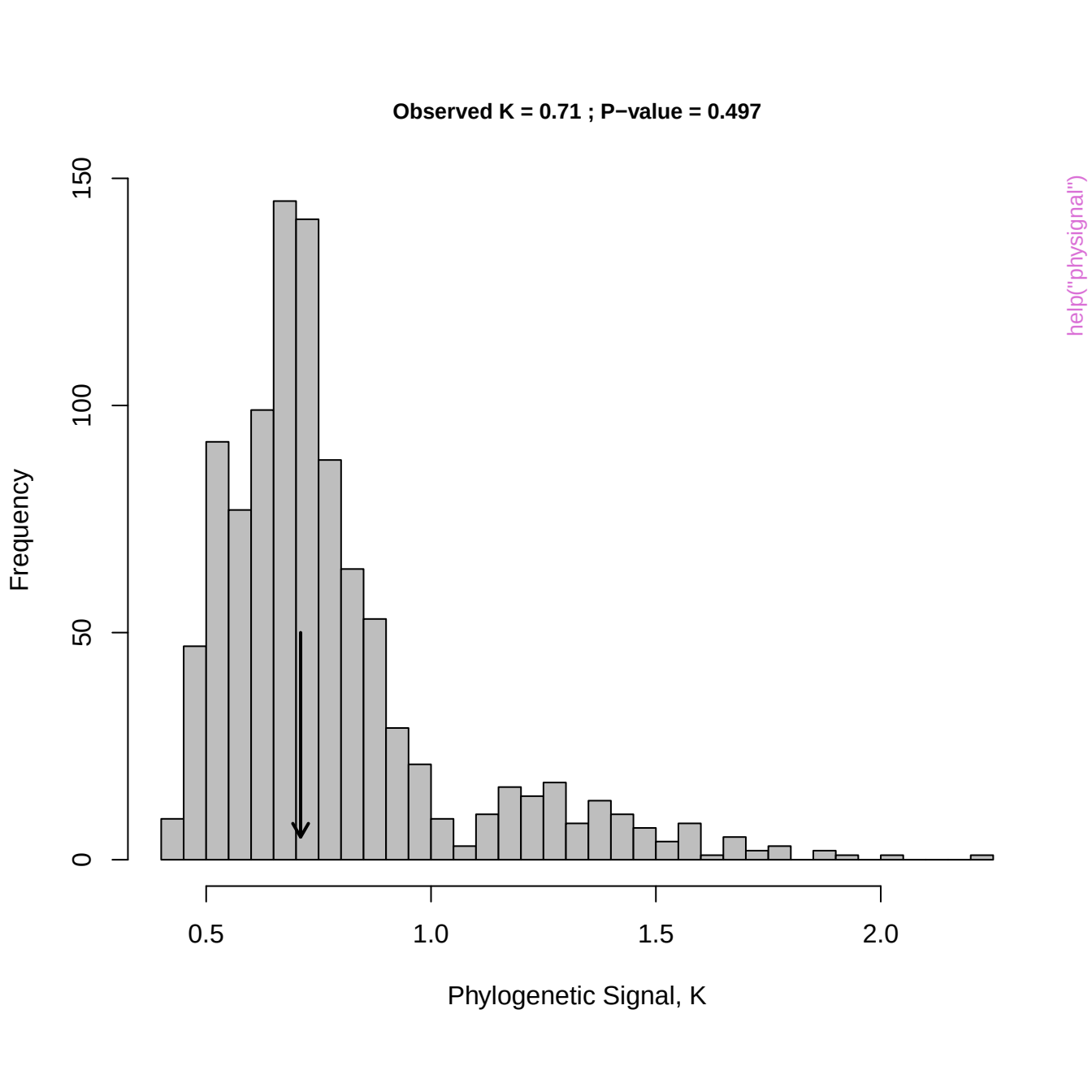
PLS1 Plot: Block 1 (X) vs. Block 2 (Y)
−0.12
−0.14
−0.16
−0.18
−0.20
−0.22
0.12
0.14
0.16
0.18
0.20
0.22

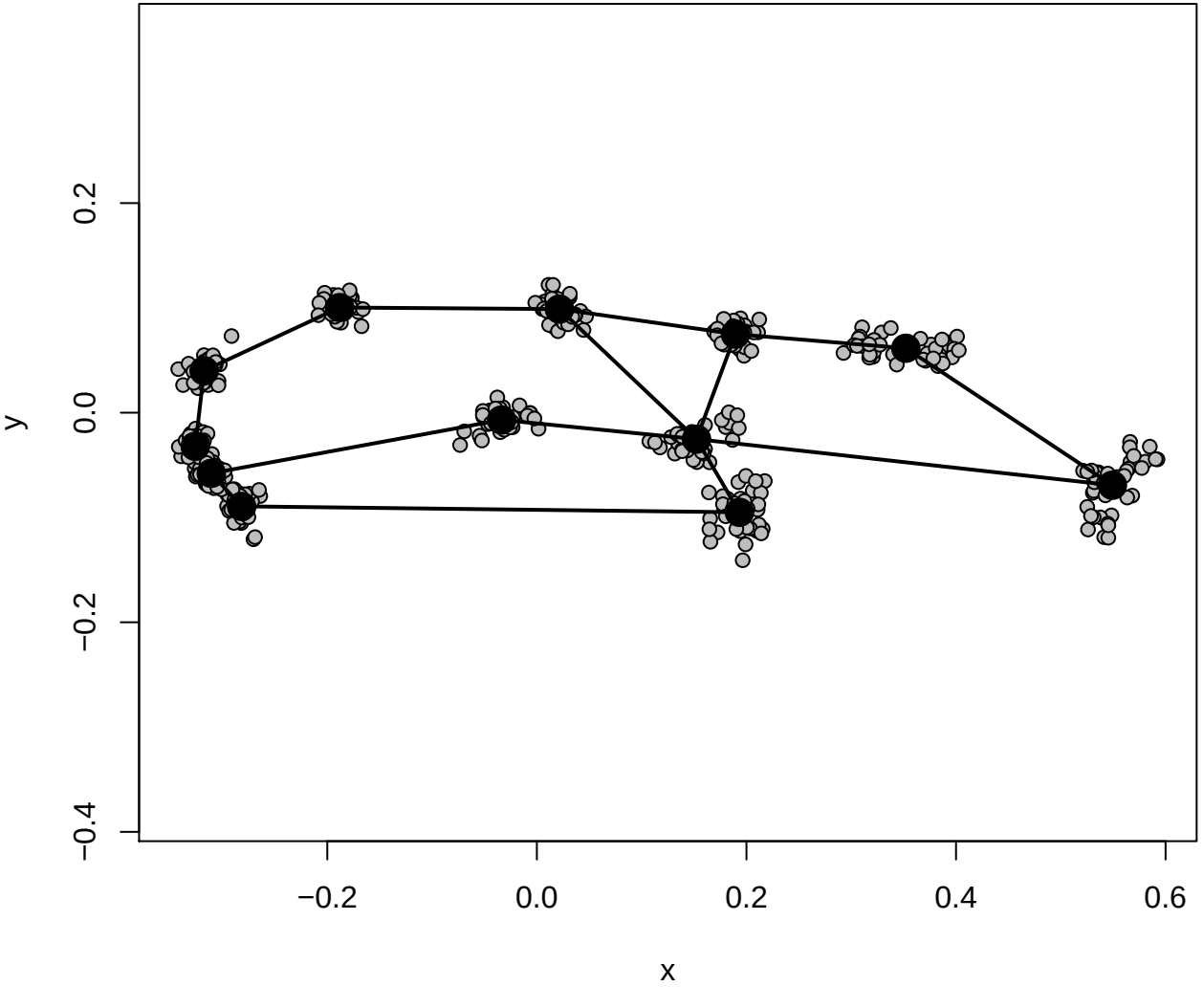

Observed CR = 0.908 ; P−value = 0.04
Frequency
0
2
4
6
8
0.0
0.5
1.0
1.5
2.0
CR Coefficient
help("modularity.test")

PLS1 Plot: Block 1 (X) vs. Block 2 (Y)
0.010
0.005
0.000
−0.005
−0.002
0.000
0.002
0.004
0.006

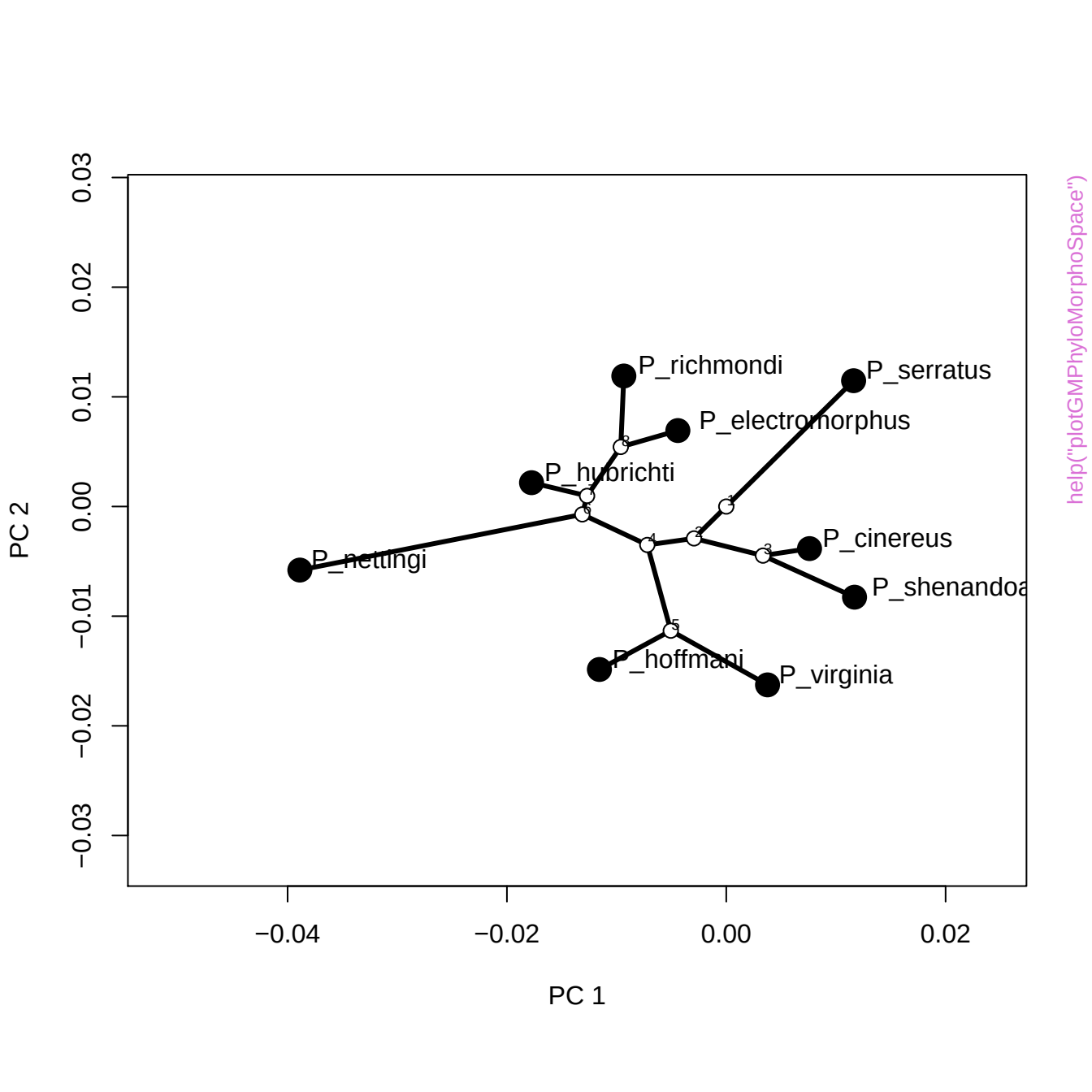

Observed CR = 1.196 ; P−value = 0.86
Frequency
0
10
20
30
40
50
60
0.0
0.5
1.0
1.5
2.0
CR Coefficient
help("phylo.modularity")

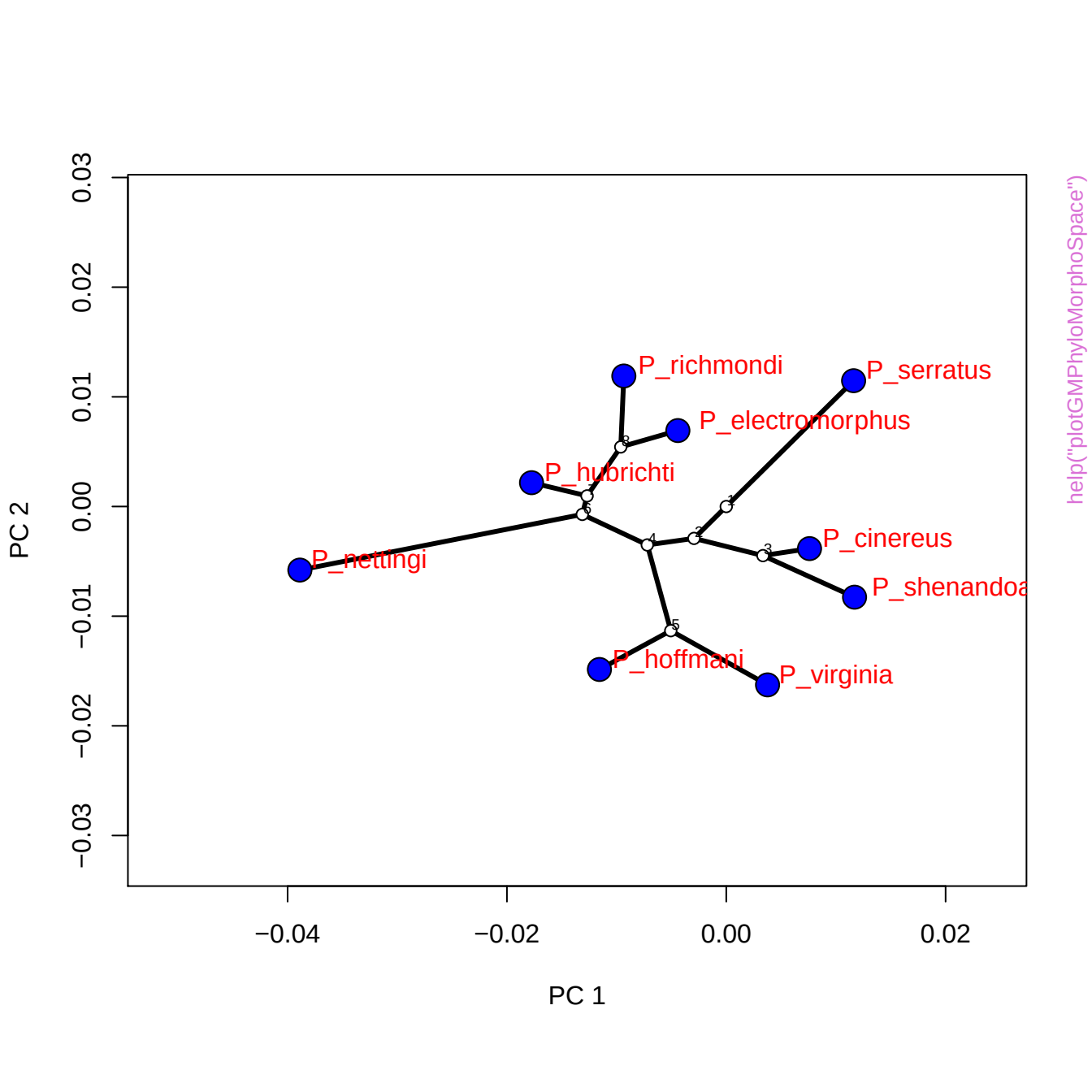

Observed K = 0.957 ; P−value = 0.011
help("physignal")
Frequency
0
20
40
60
80
100
0.6
0.7
0.8
0.9
1.0
1.1
Phylogenetic Signal, K

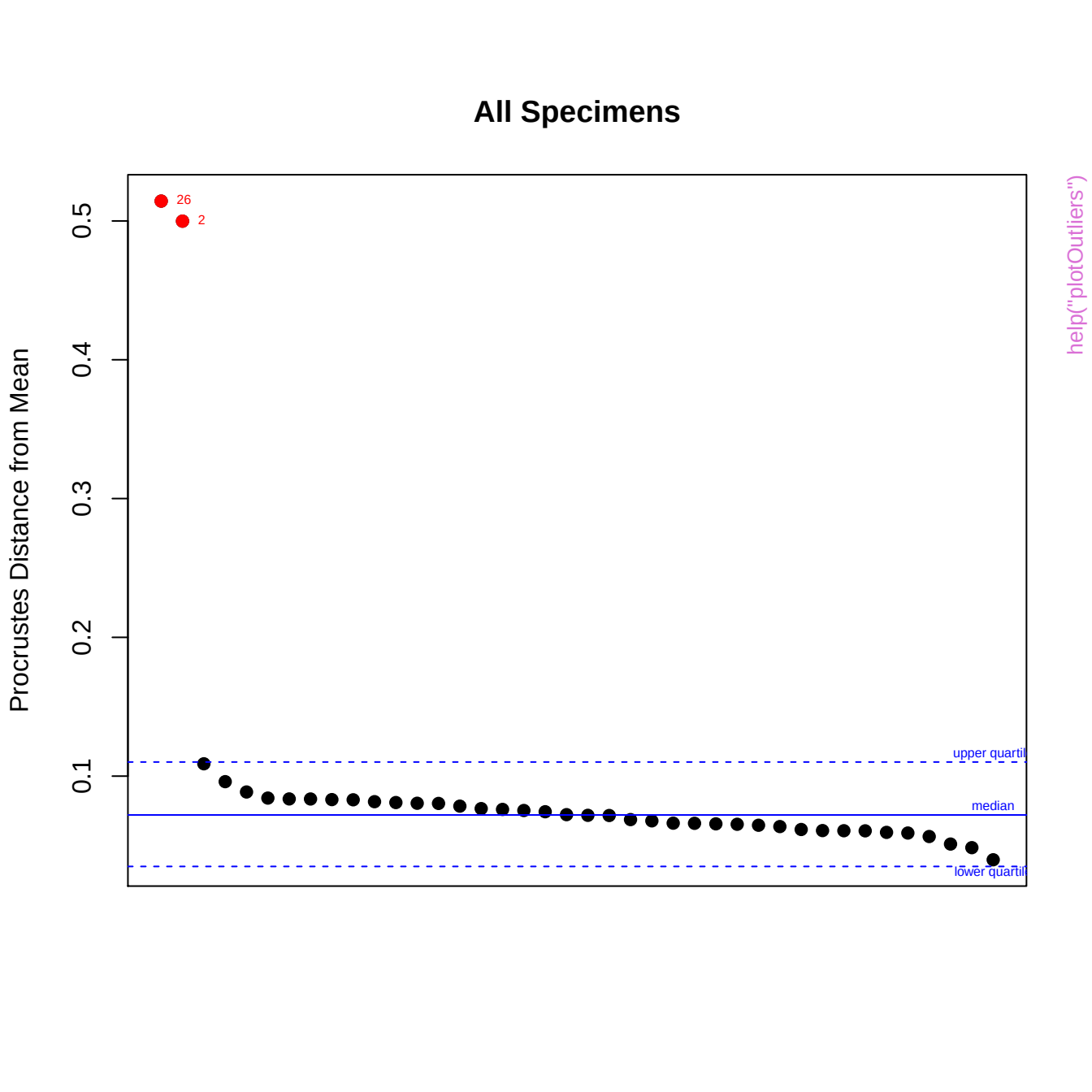

Observed K = 0.71 ; P−value = 0.497
Frequency
0
50
100
150
0.5
1.0
1.5
2.0
Phylogenetic Signal, K
help("physignal")

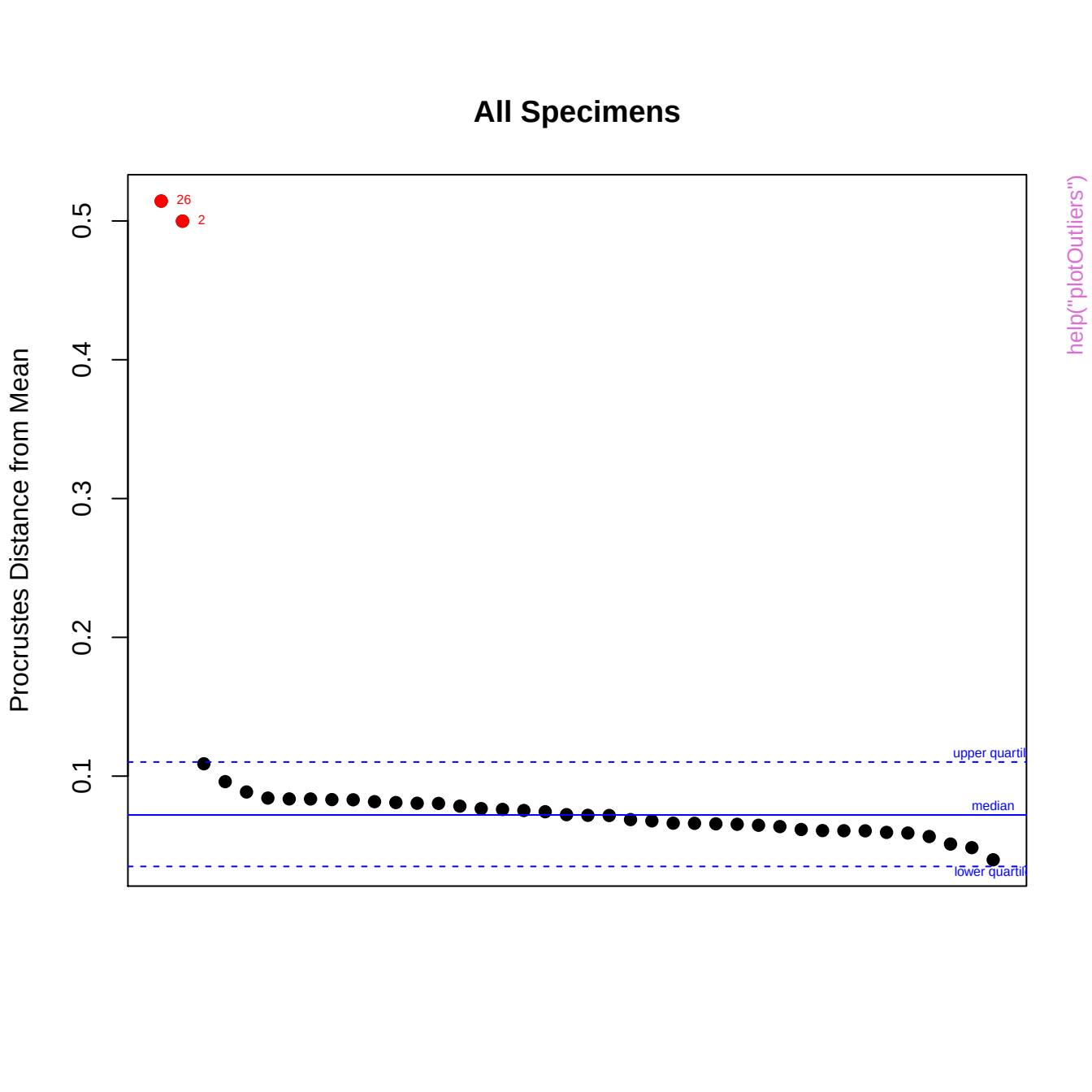


help("plotAllSpecimens")

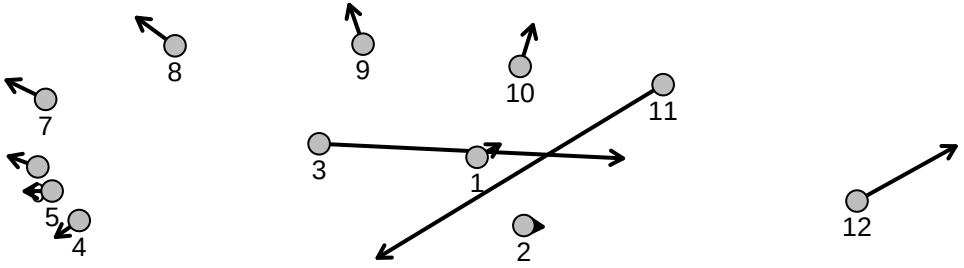

P_richmondi
P_serratus
P_electromorphus
P_hubrichti
P_cinereus
P_nettingi
P_shenandoa
P_hoffmani
P_virginia
1
2
3
4
5
6
7
8
PC 1
PC 2
−0.04
−0.02
0.00
0.02
0.03
0.02
0.01
0.00
−0.01
−0.02
−0.03
help("plotGMPhyloMorphoSpace")


P_richmondi
P_serratus
P_electromorphus
P_hubrichti
P_nettingi
P_cinereus
P_shenandoa
P_hoffmani
P_virginia
1
2
3
4
5
6
7
8
PC 1
PC 2
−0.04
−0.02
0.00
0.02
0.03
0.02
0.01
0.00
−0.01
−0.02
−0.03
help("plotGMPhyloMorphoSpace")


All Specimens
Procrustes Distance from Mean
0.1
0.2
0.3
0.4
0.5
26
2
upper quartil
median
lower quartil
help("plotOutliers")

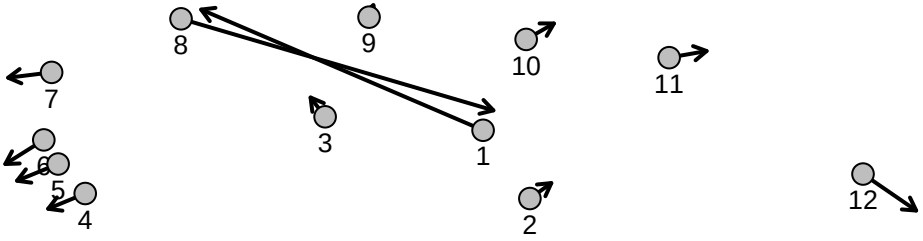

All Specimens
Procrustes Distance from Mean
0.1
0.2
0.3
0.4
0.5
26
2
upper quartil
median
lower quartil
help("plotOutliers")

group: All Specimens, specimen: 26

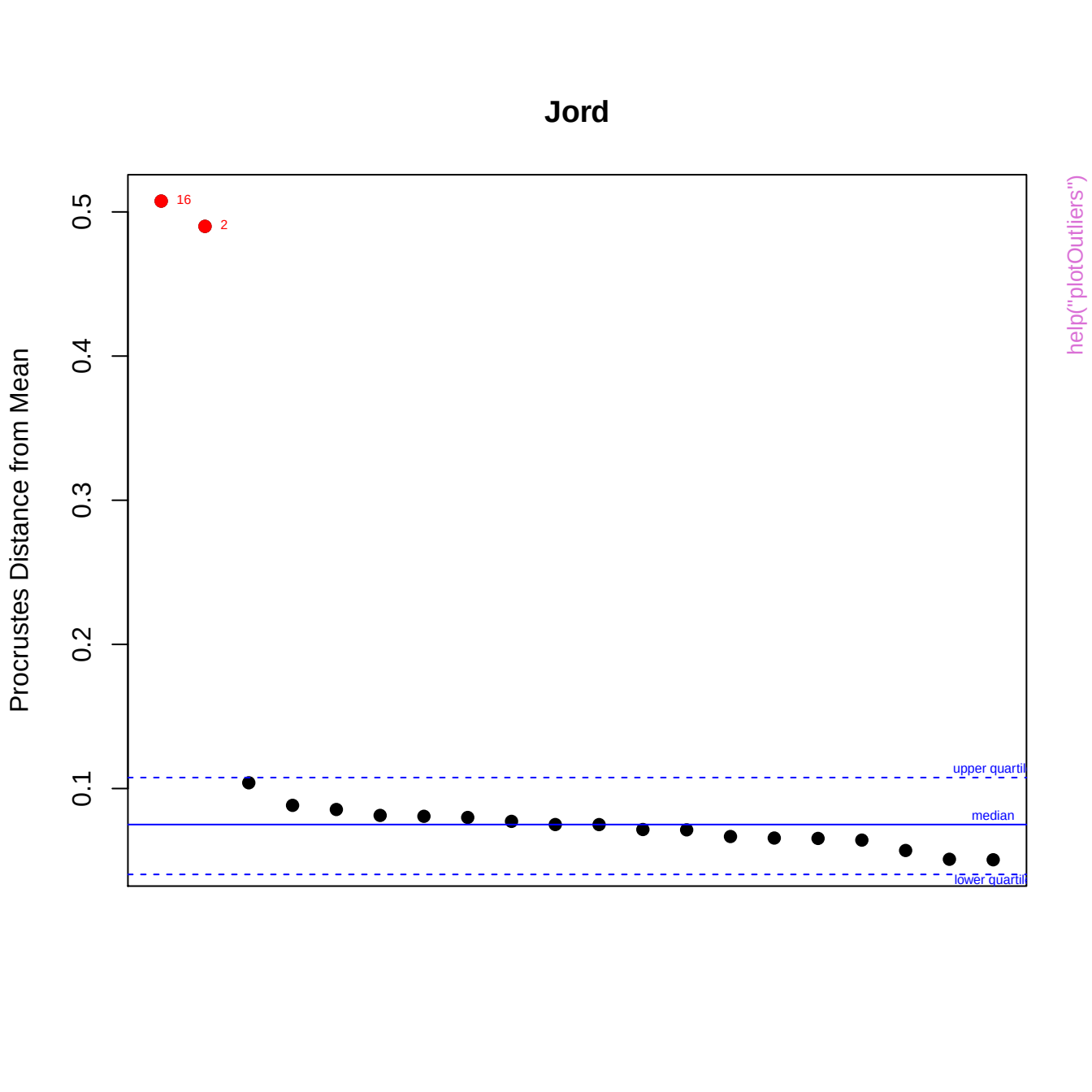


help("plotOutliers")

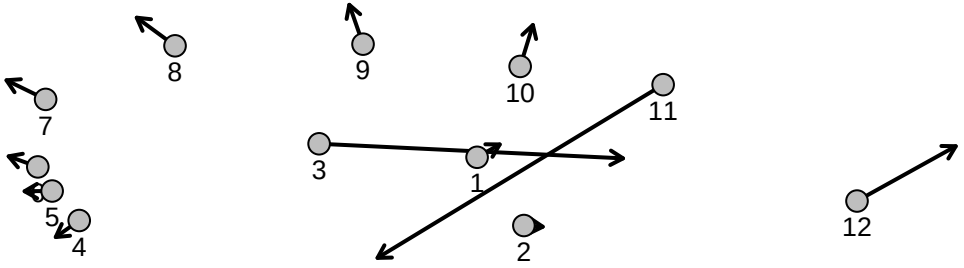
group: All Specimens, specimen: 2



help("plotOutliers")

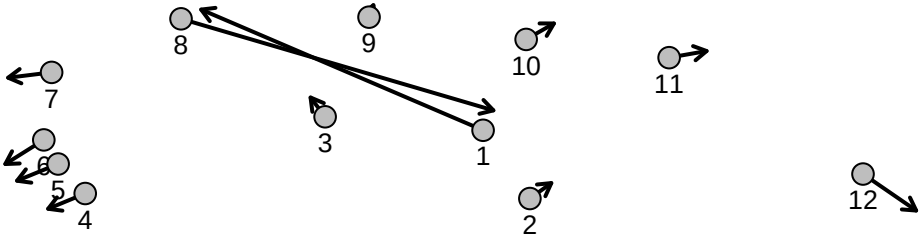

Jord
Procrustes Distance from Mean
0.1
0.2
0.3
0.4
0.5
16
2
upper quartil
median
lower quartil
help("plotOutliers")

group: Jord, specimen: 16

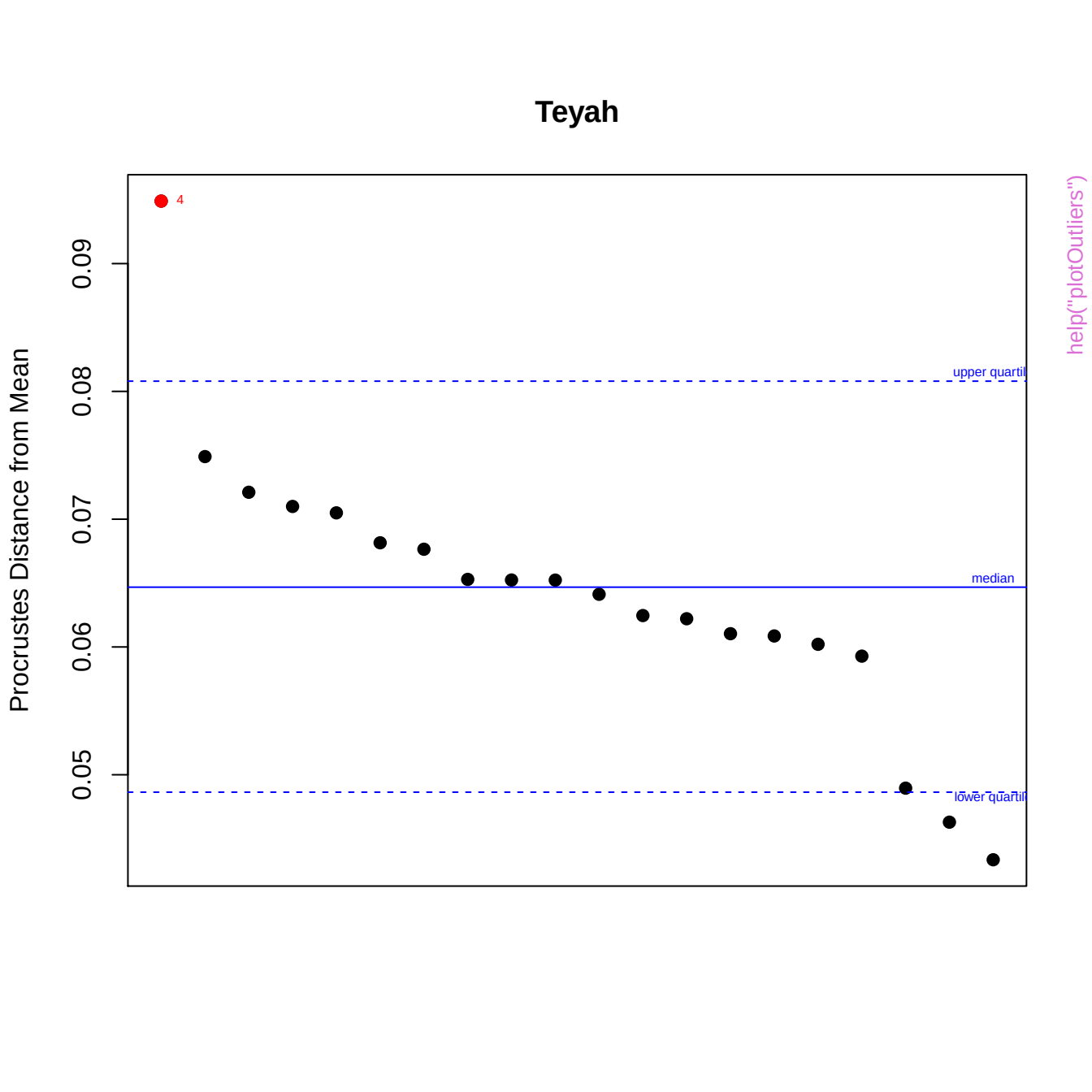


help("plotOutliers")

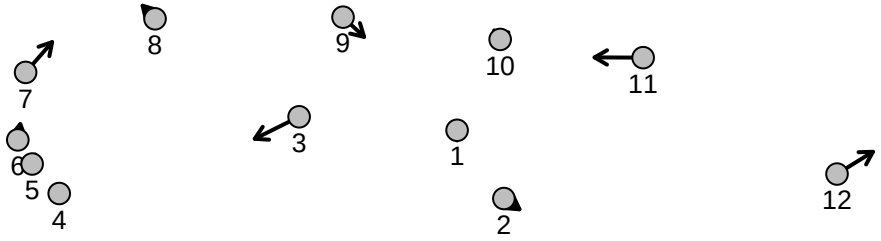
group: Jord, specimen: 2



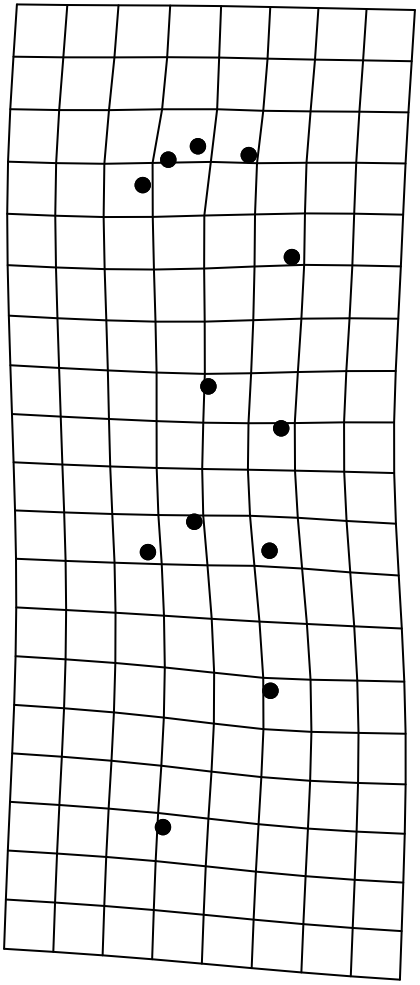
help("plotOutliers")


Teyah
Procrustes Distance from Mean
0.09
0.08
0.07
0.06
0.05
4
upper quartil
median
lower quartil
help("plotOutliers")

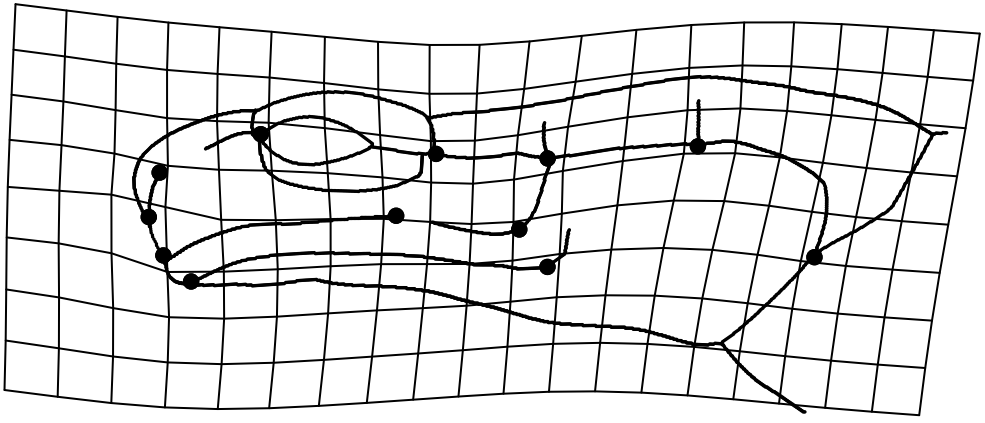
group: Teyah, specimen: 4



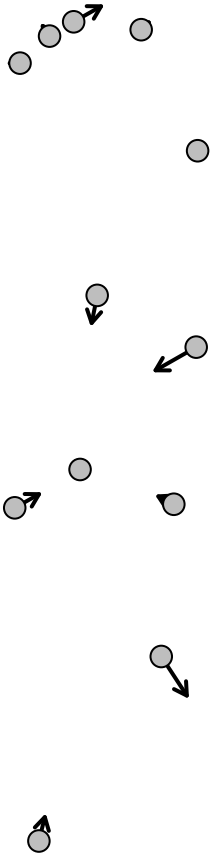
help("plotOutliers")



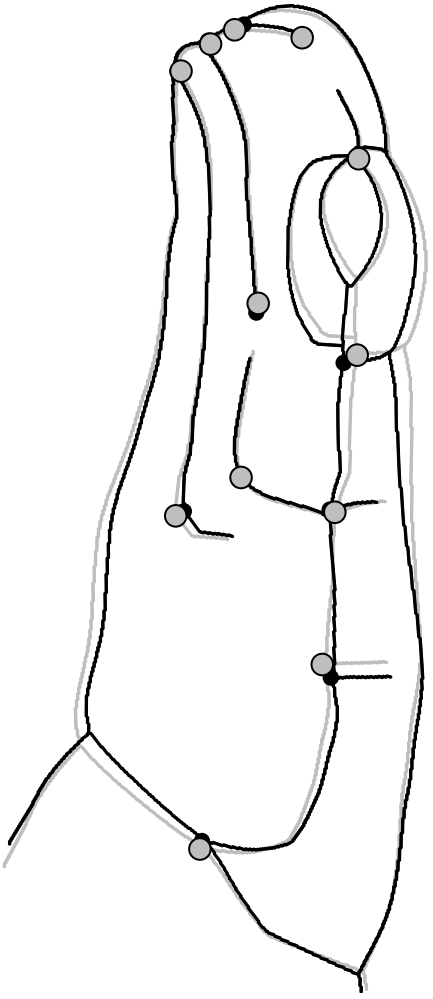
help("plotRefToTarget")



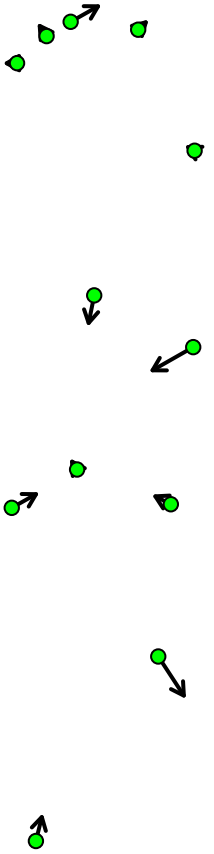
help("plotRefToTarget")



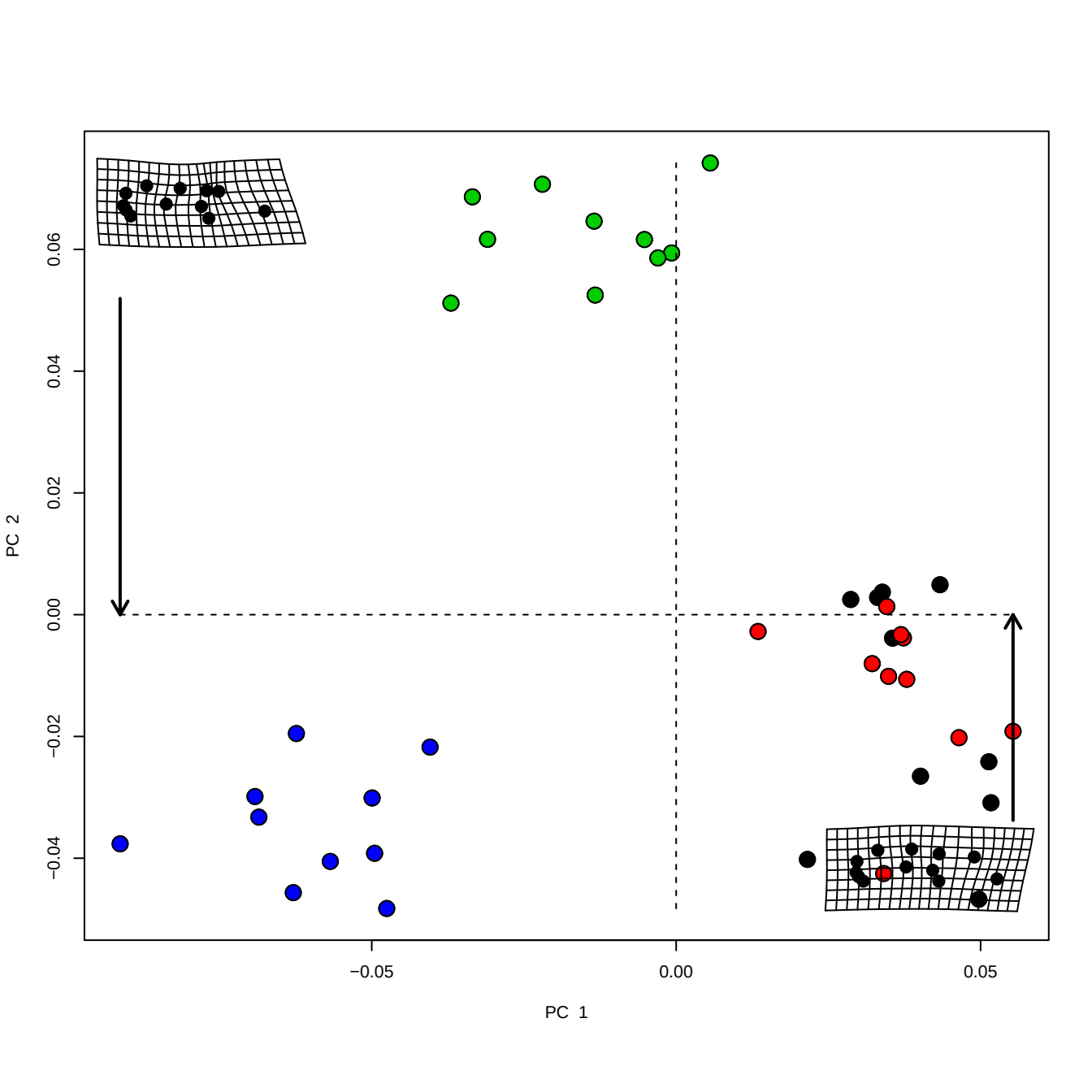
help("plotRefToTarget")

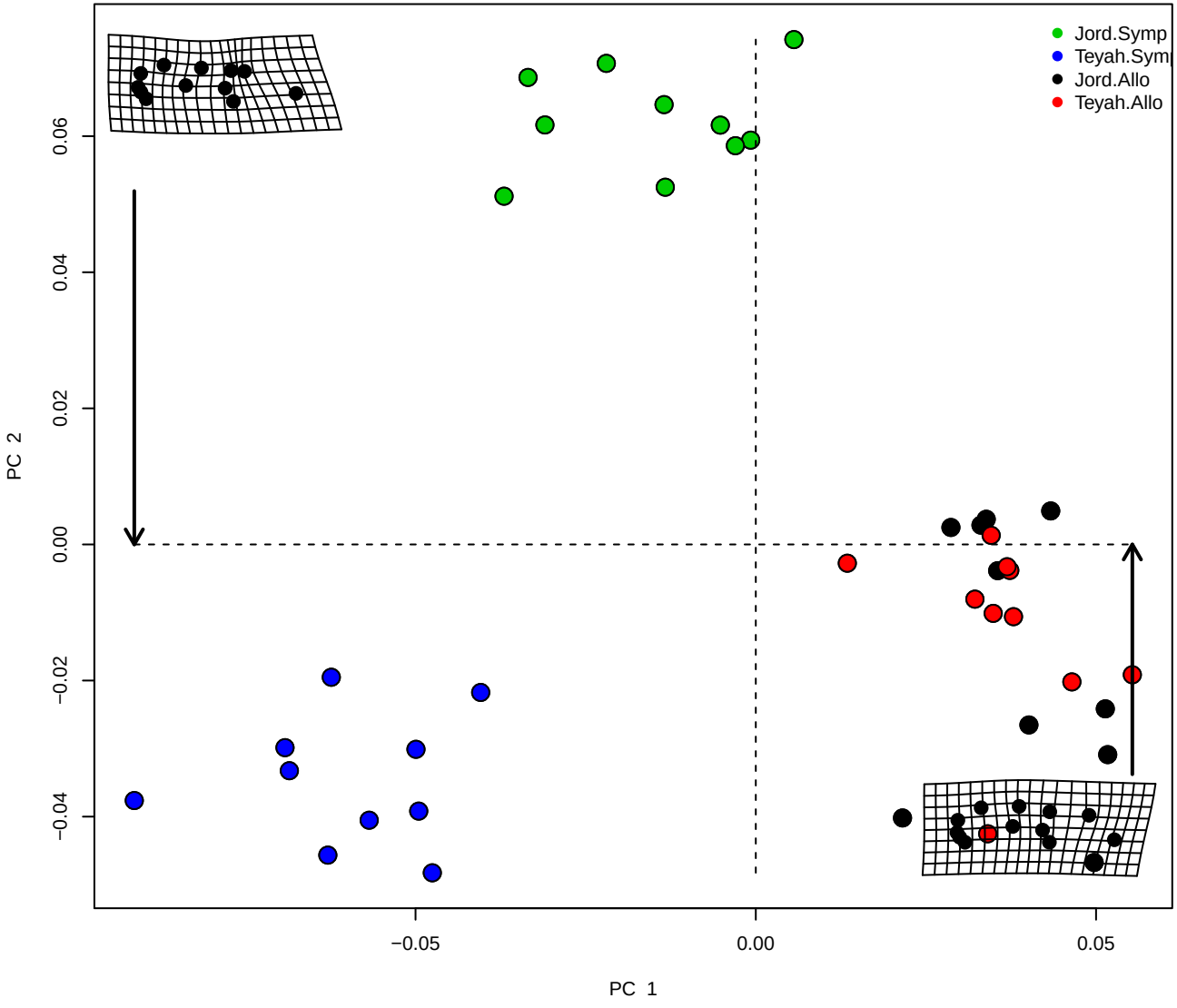


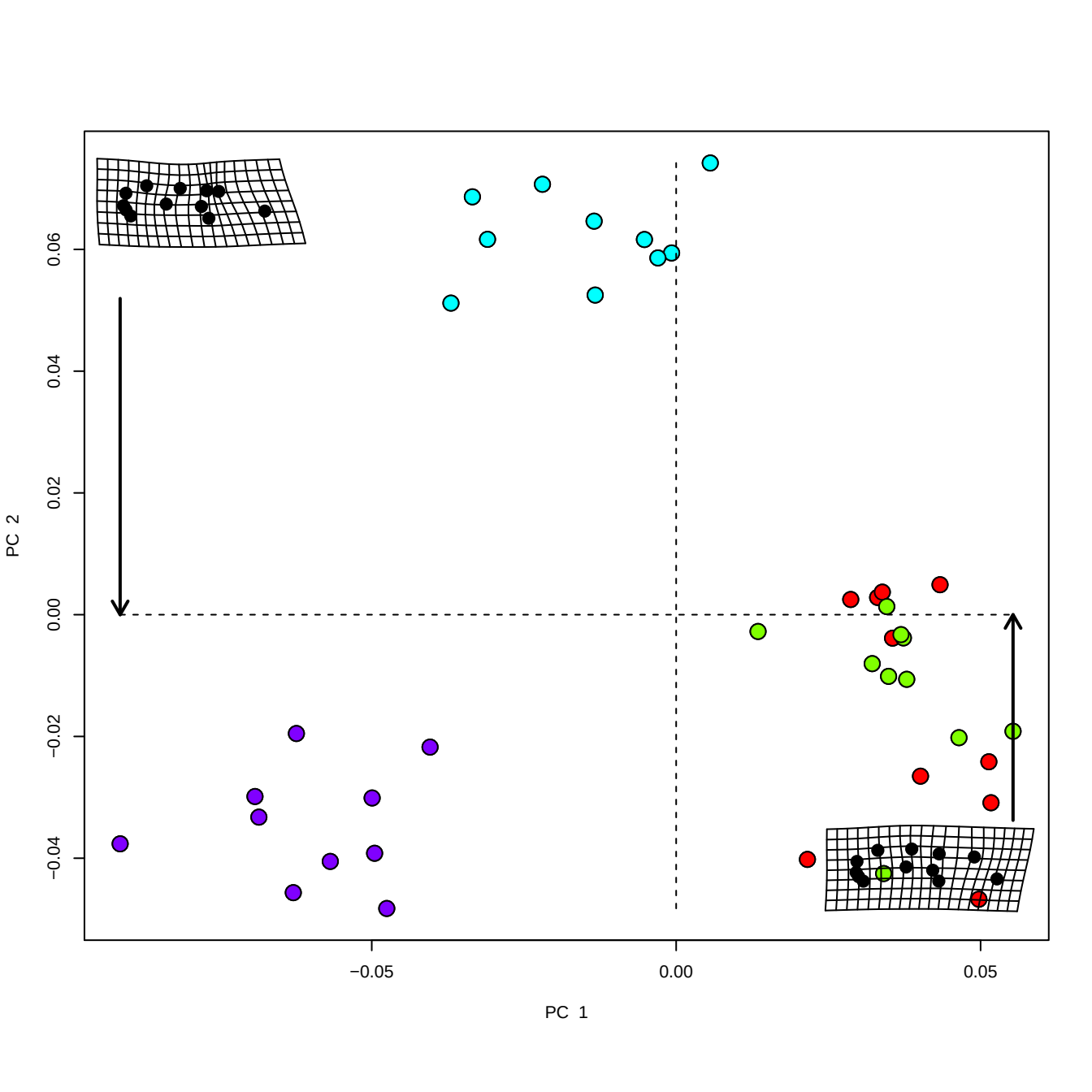
help("plotRefToTarget")

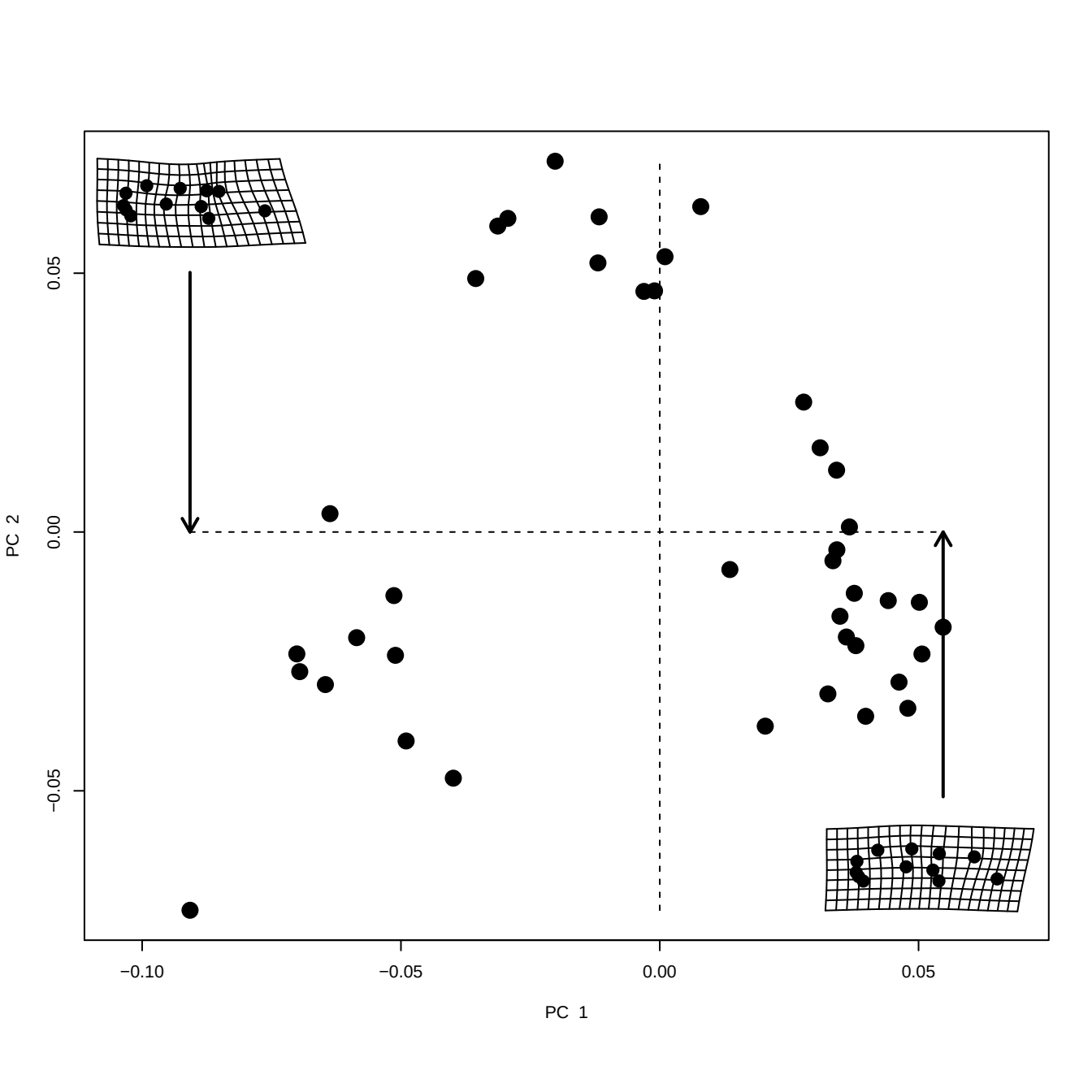


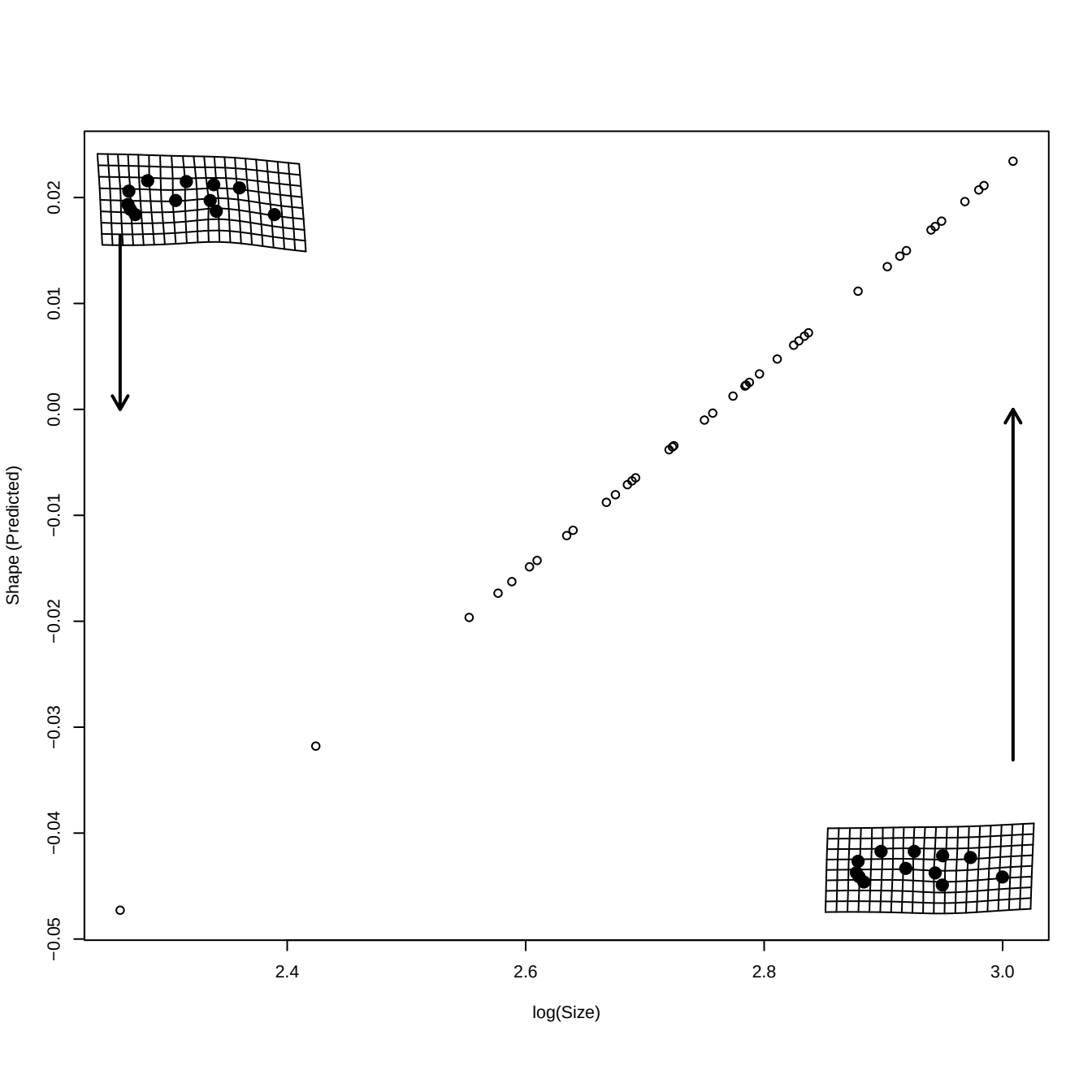
help("plotRefToTarget")

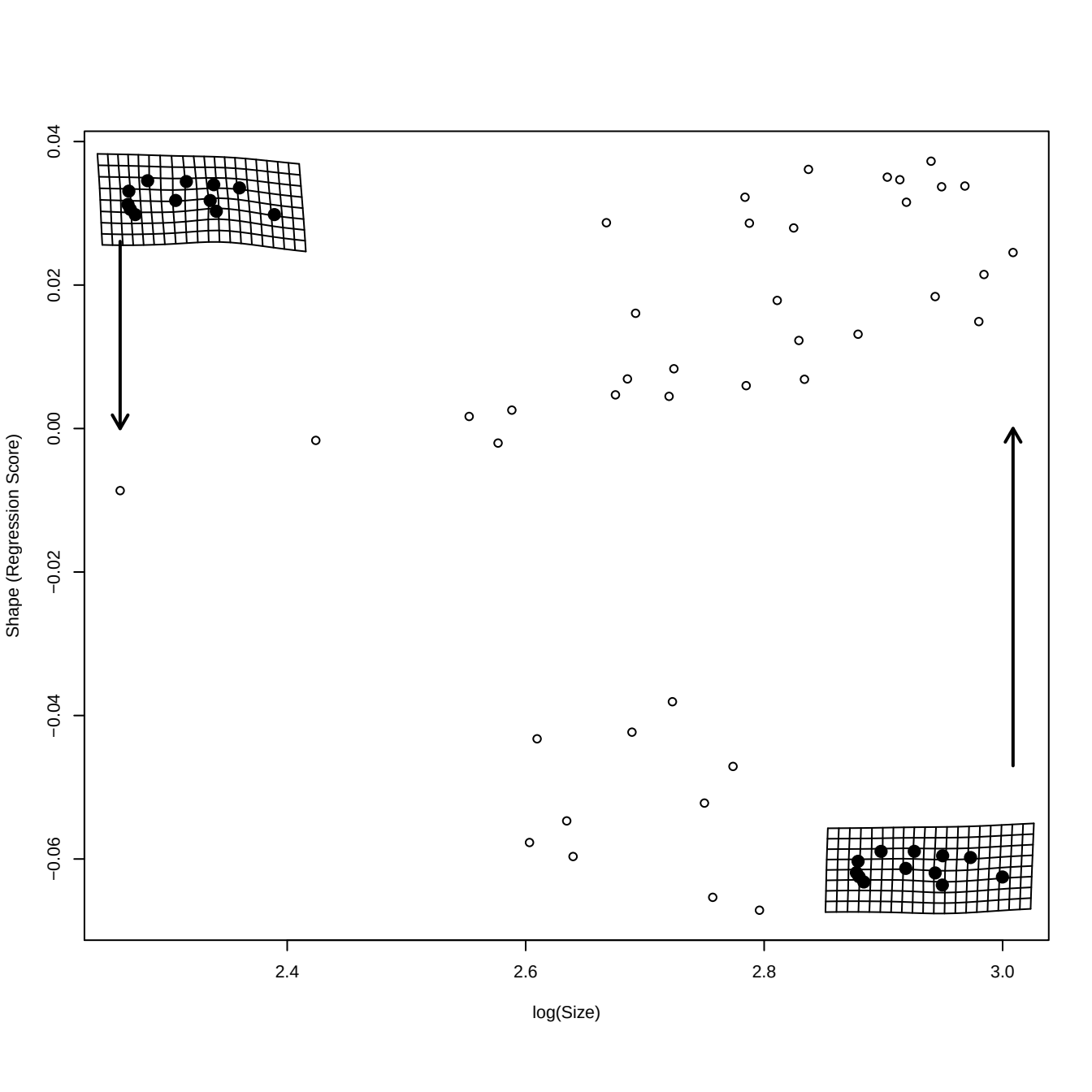

0.06
0.04
0.02
0.00
−0.02
−0.04
PC 2
−0.05
0.00
0.05
PC 1

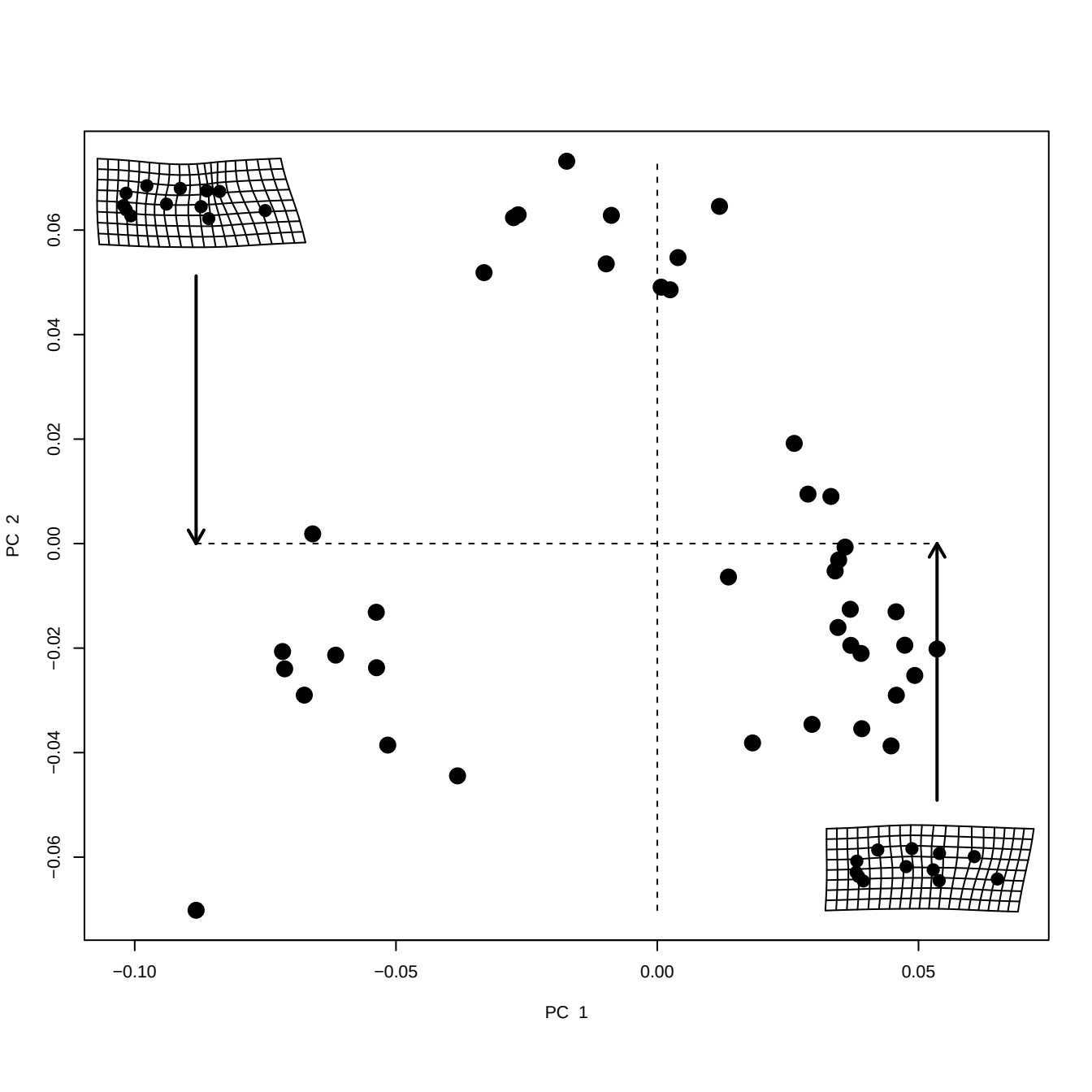

Jord.Symp
Teyah.Sym
Jord.Allo
Teyah.Allo
PC 2
PC 1
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.05
0.00
0.05
help("plotTangentSpace")

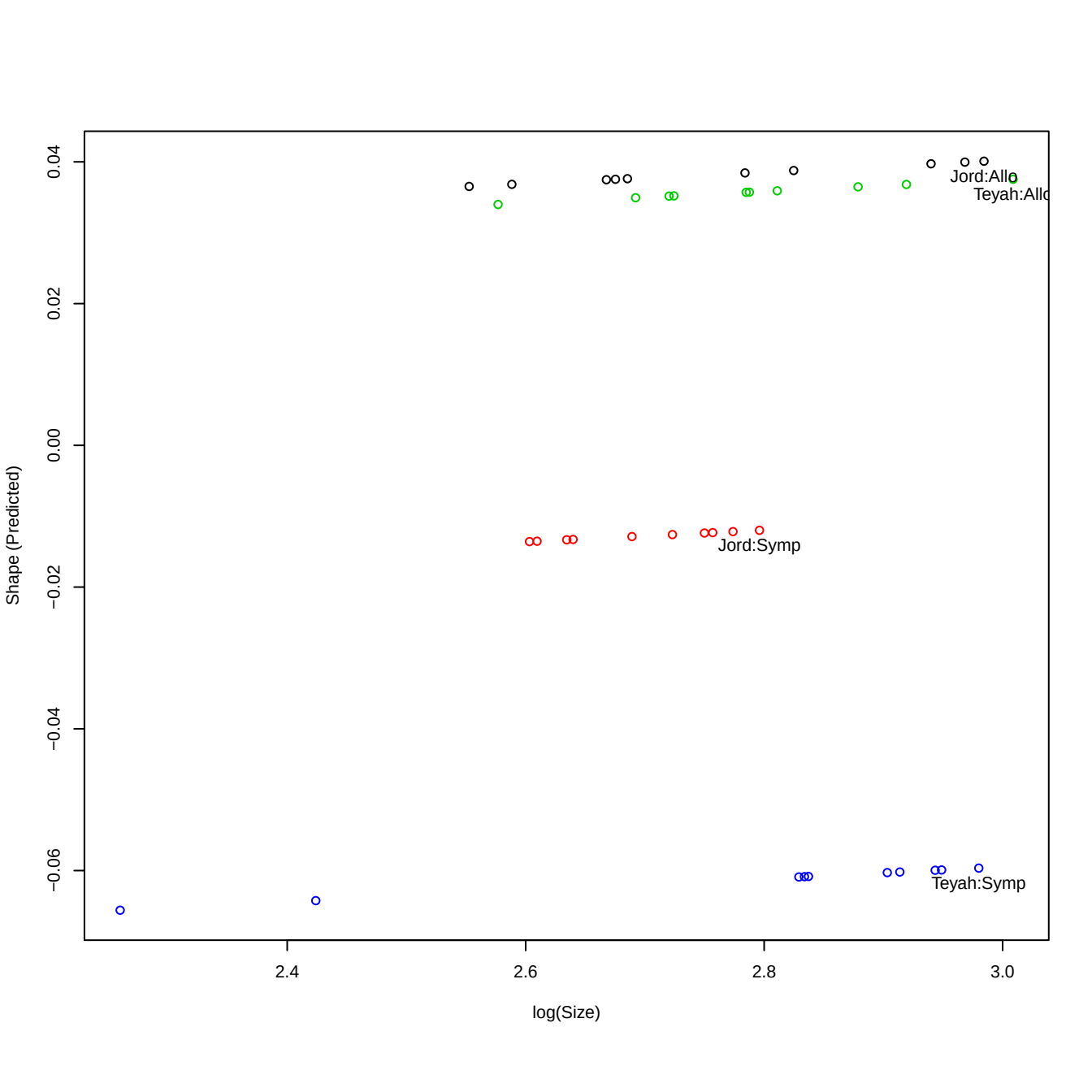

0.06
0.04
0.02
0.00
−0.02
−0.04
PC 2
−0.05
0.00
0.05
PC 1

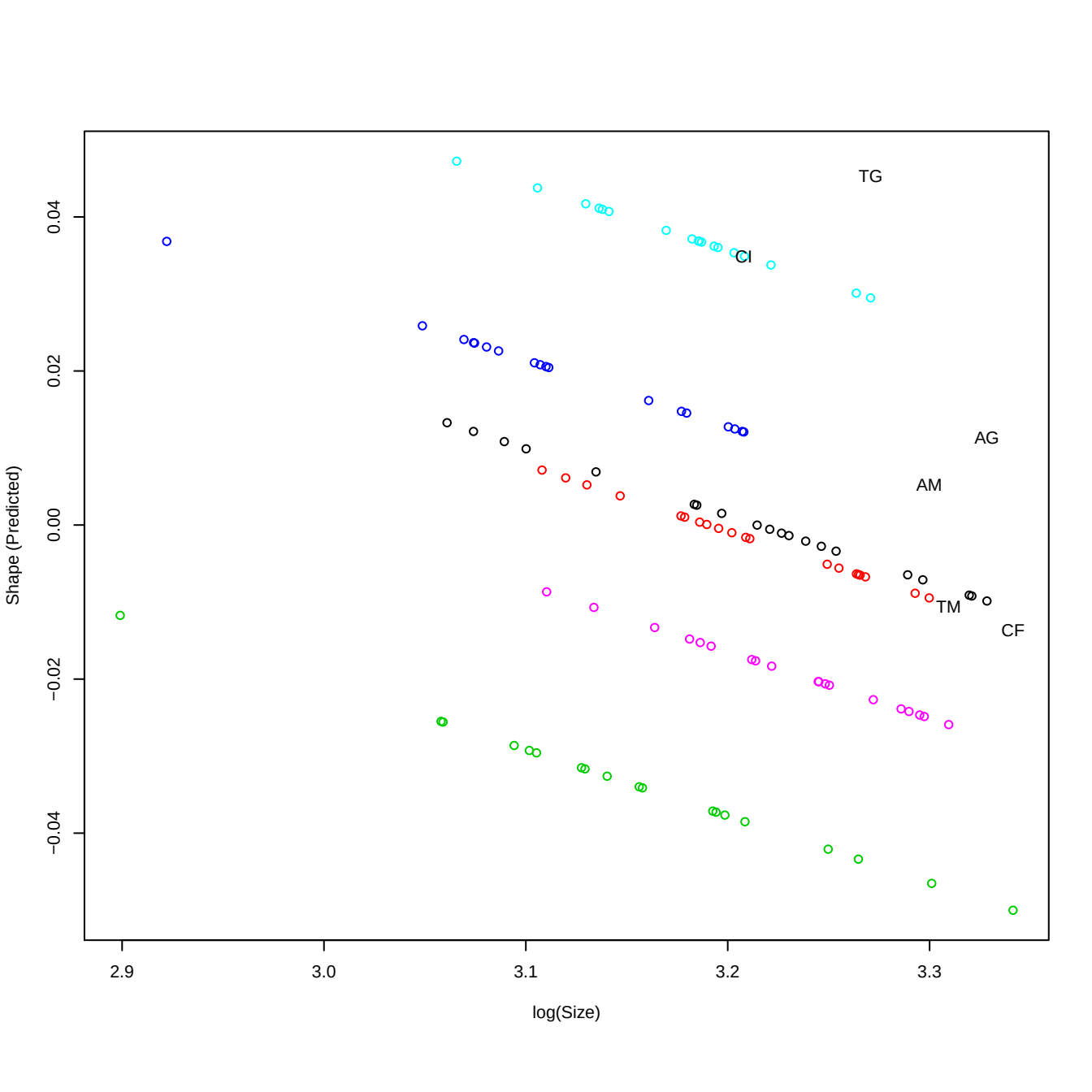

0.05
0.00
−0.05
PC 2
−0.10
−0.05
0.00
0.05
PC 1

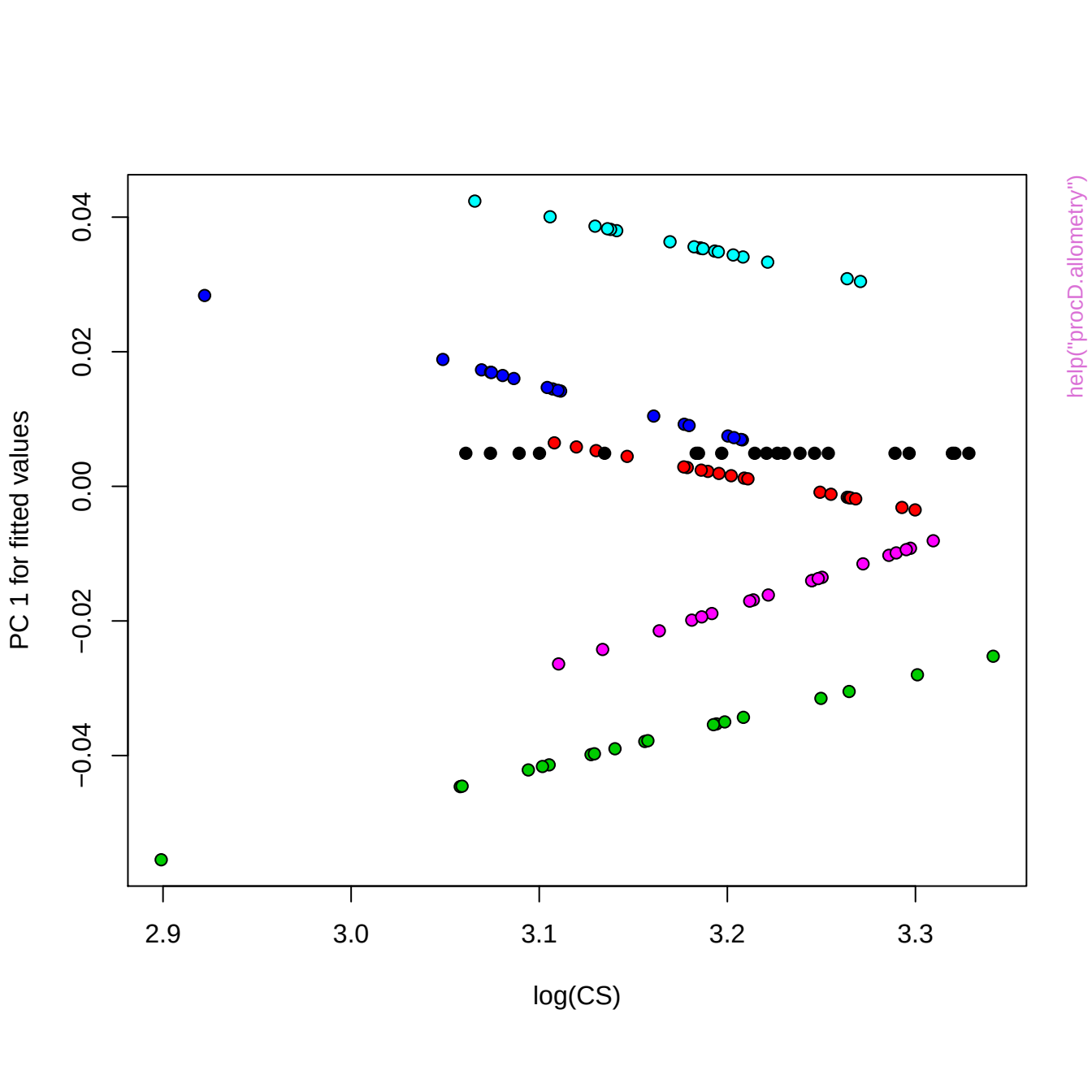

Shape (Predicted)
0.02
0.01
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
2.4
2.6
2.8
3.0
log(Size)

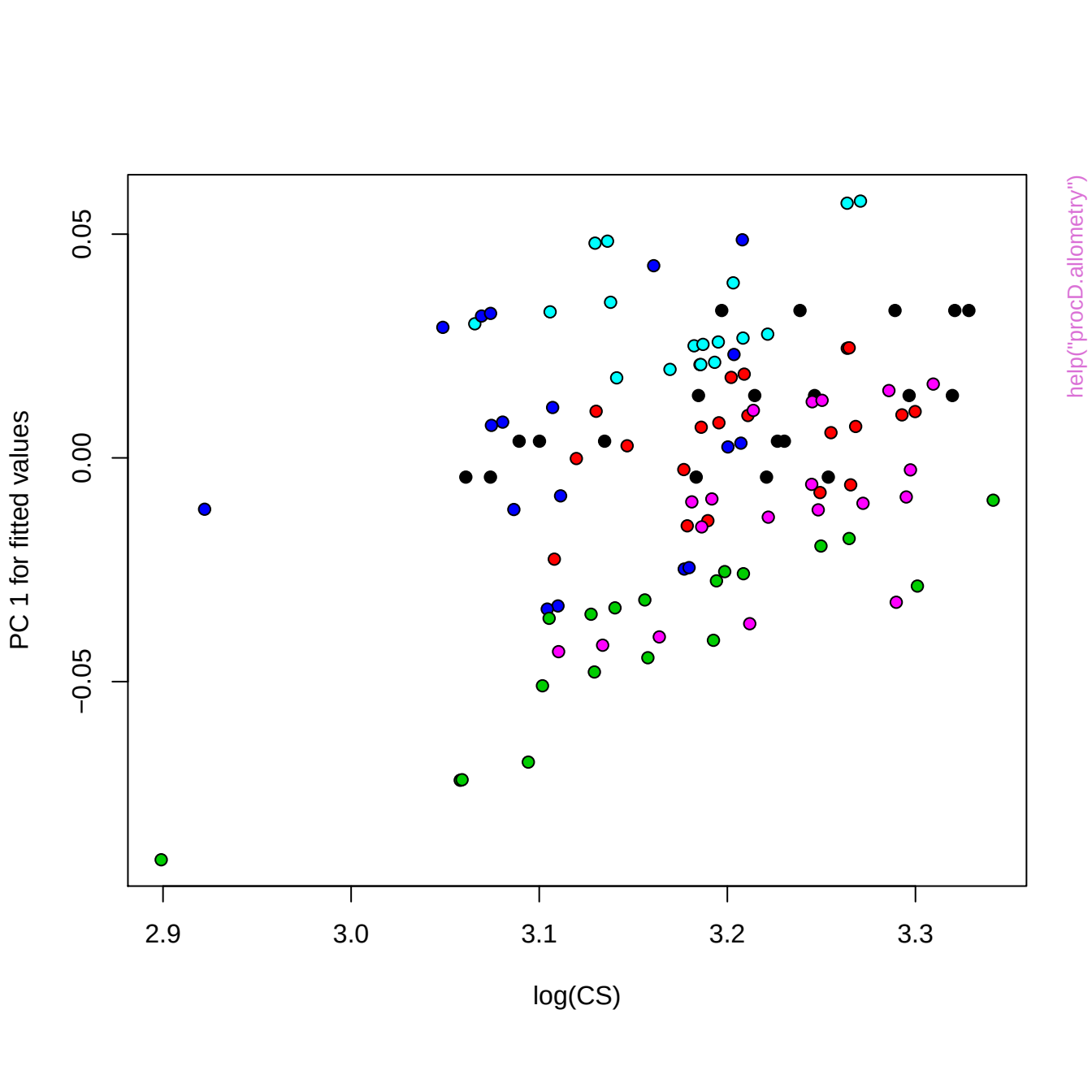

Shape (Regression Score)
0.04
0.02
0.00
−0.02
−0.04
−0.06
2.4
2.6
2.8
3.0
log(Size)

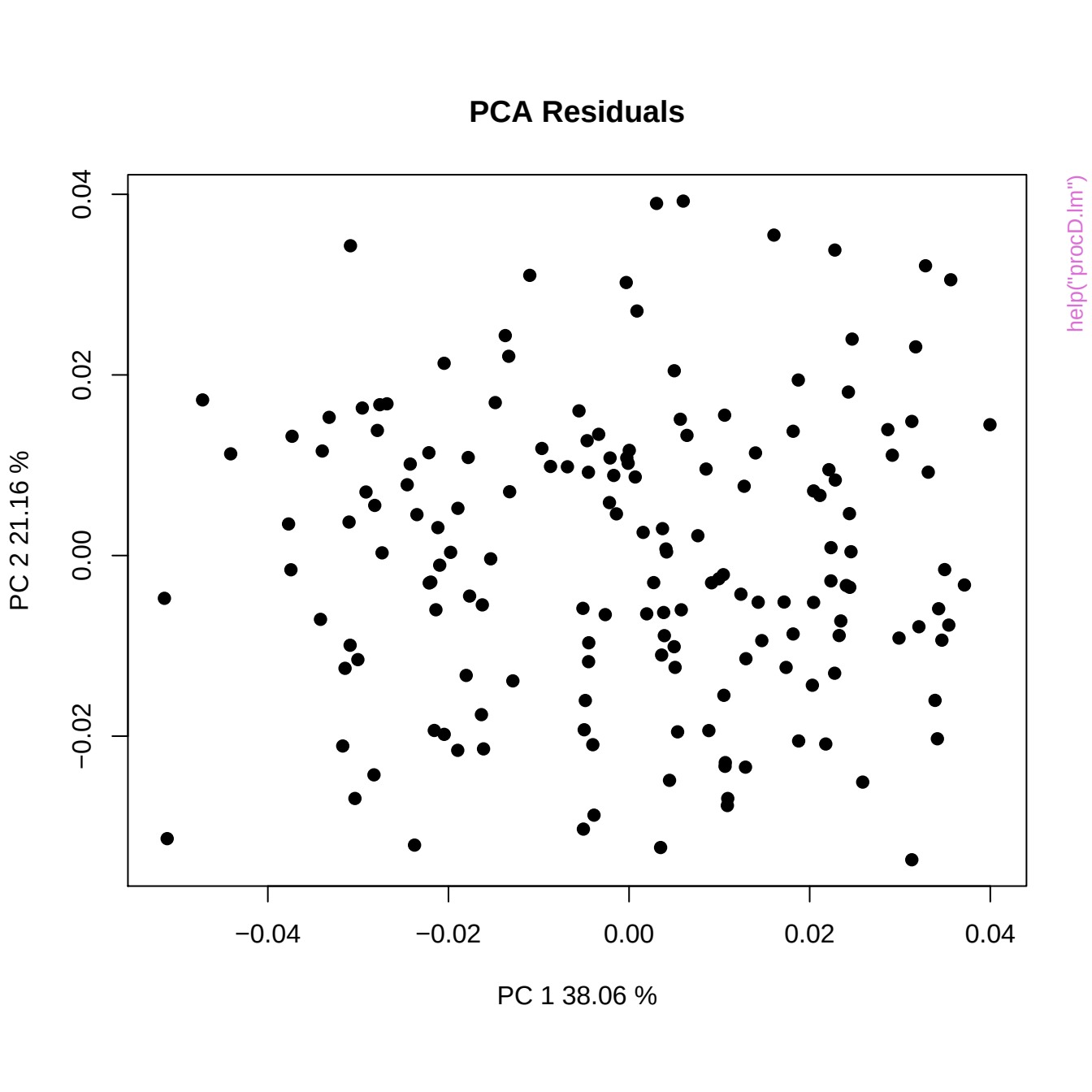

0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
PC 2
−0.10
−0.05
0.00
0.05
PC 1

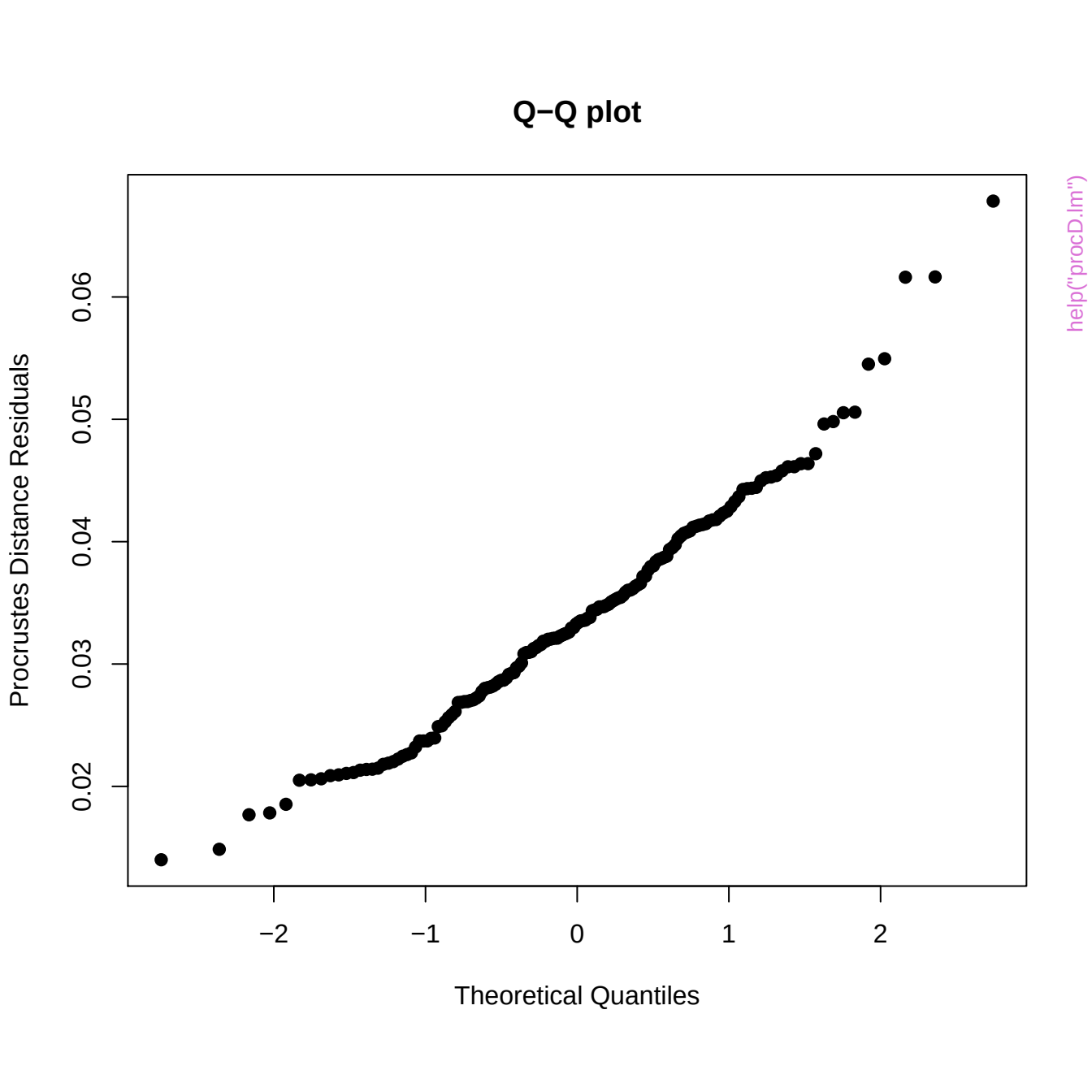

Shape (Predicted)
0.04
0.02
0.00
−0.02
−0.04
−0.06
2.4
2.6
2.8
3.0
log(Size)
Jord:Allo
Teyah:Allo
Jord:Symp
Teyah:Symp

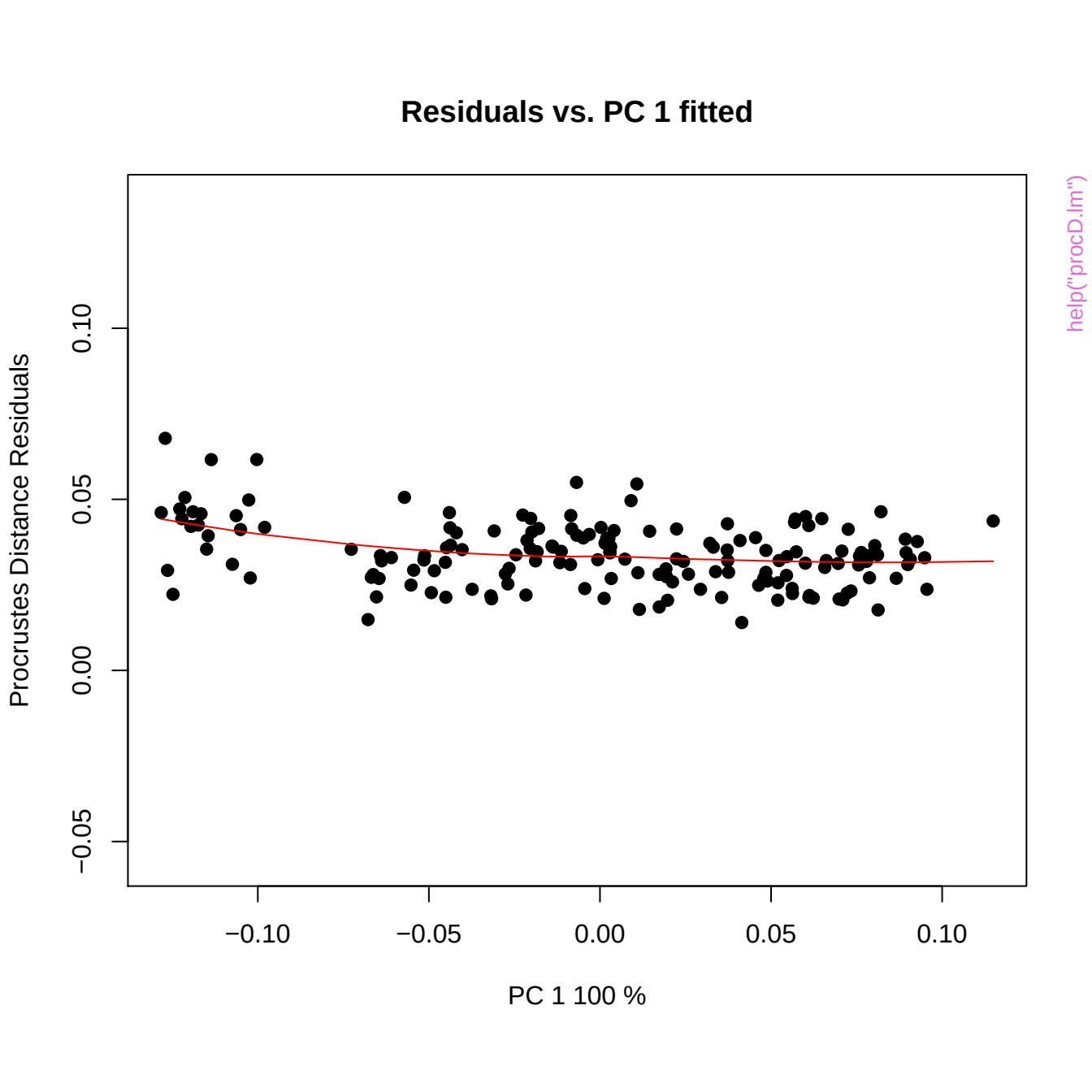

TG
CI
AG
AM
TM
CF
0.04
0.02
0.00
−0.02
−0.04
Shape (Predicted)
2.9
3.0
3.1
3.2
3.3
log(Size)

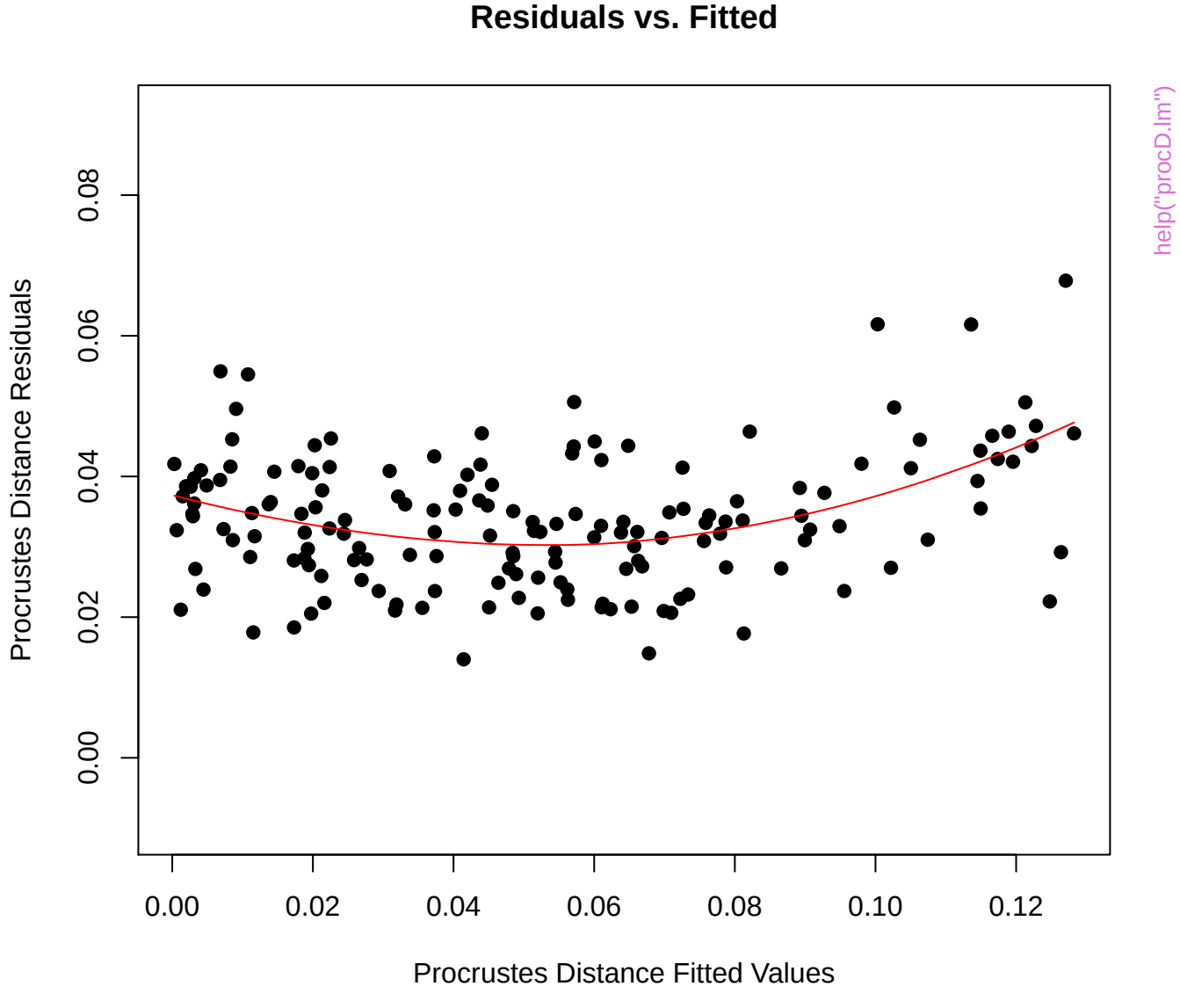

PC 1 for fitted values
0.04
0.02
0.00
−0.02
−0.04
2.9
3.0
3.1
3.2
3.3
log(CS)
help("procD.allometry")

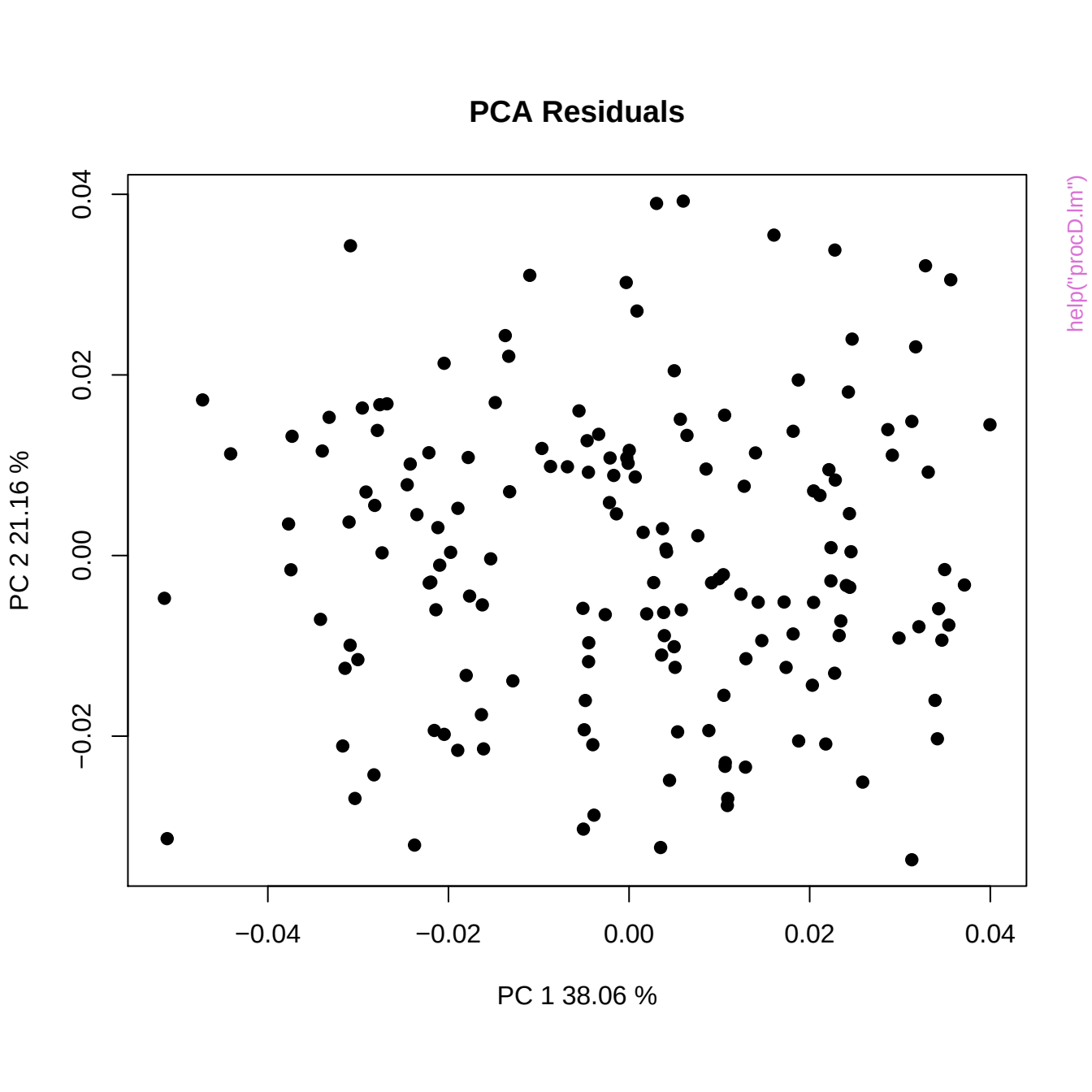

PC 1 for fitted values
0.05
0.00
−0.05
2.9
3.0
3.1
3.2
3.3
log(CS)
help("procD.allometry")

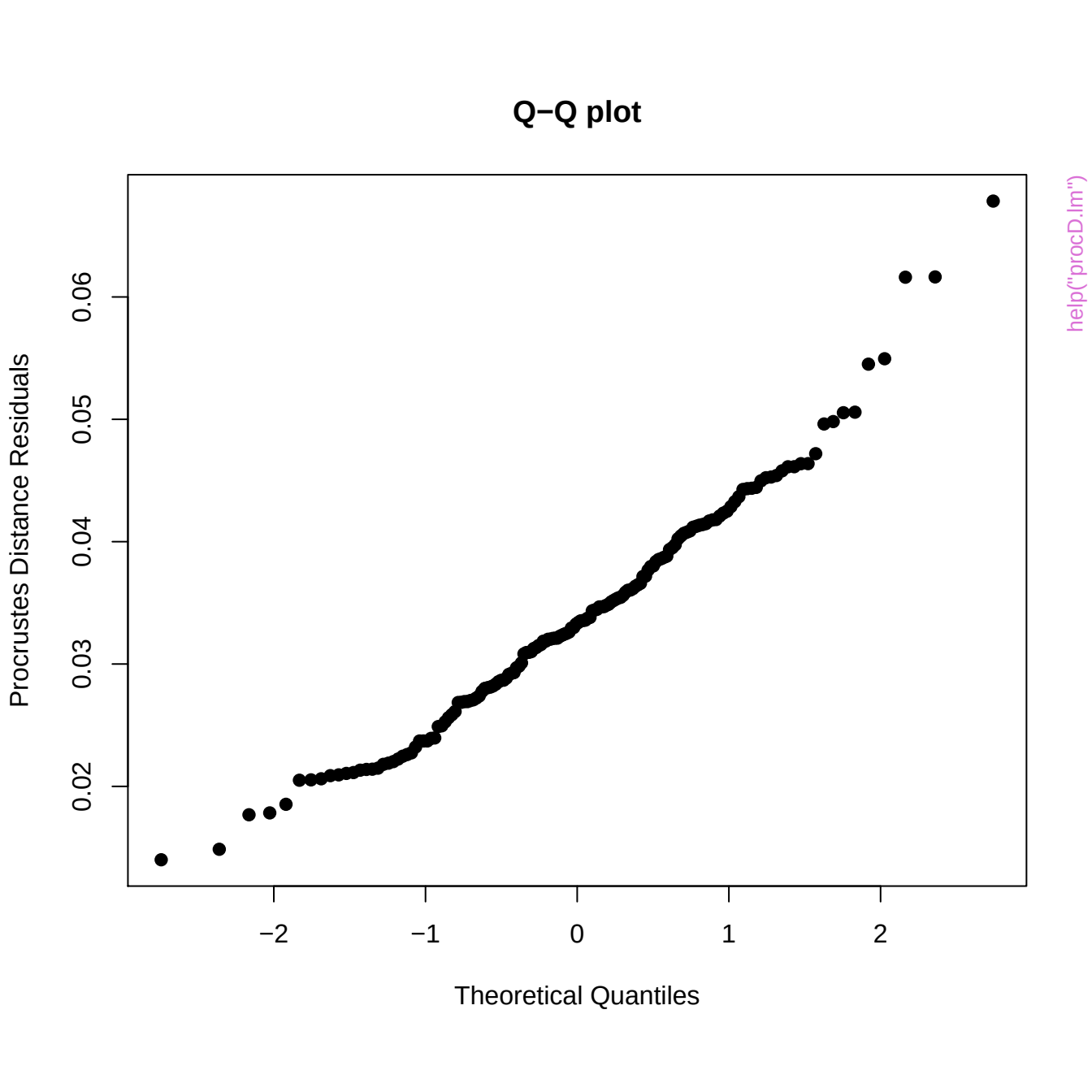

PCA Residuals
PC 2 21.16 %
PC 1 38.06 %
0.04
0.02
0.00
−0.02
−0.04
−0.02
0.00
0.02
0.04
help("procD.lm")

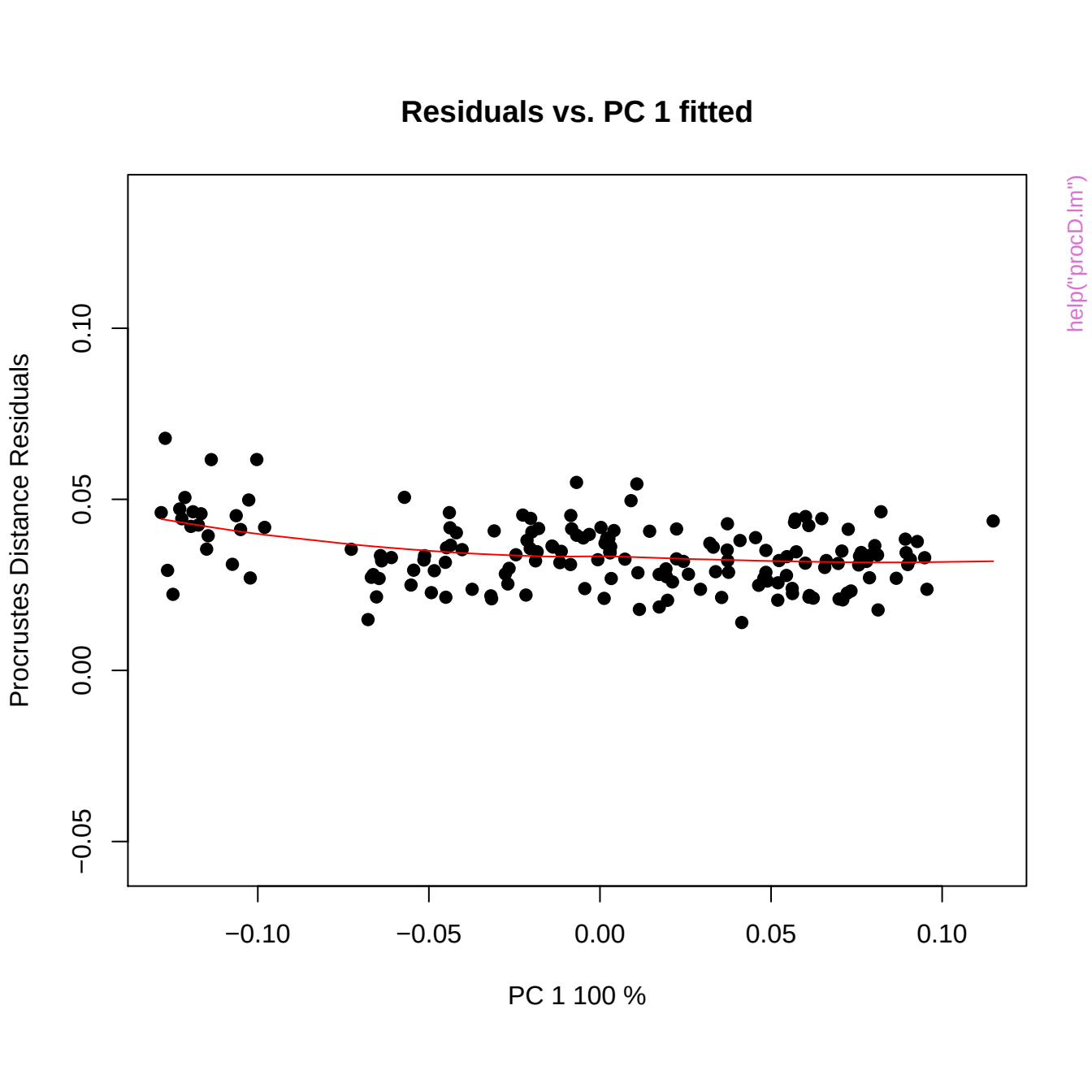

Q−Q plot
Procrustes Distance Residuals
0.02
0.03
0.04
0.05
0.06
−2
−1
0
1
2
Theoretical Quantiles
help("procD.lm")

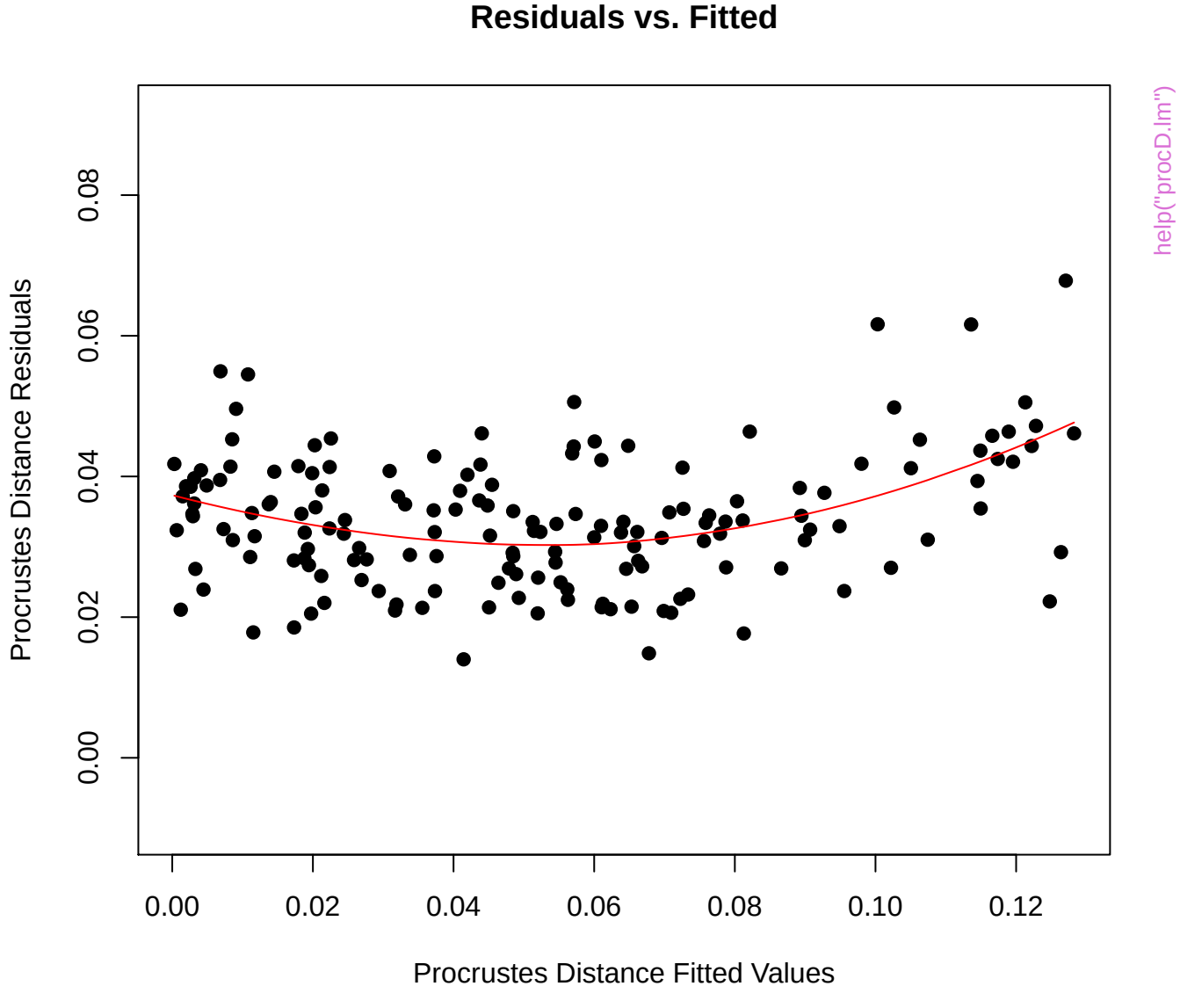

Residuals vs. PC 1 fitted
Procrustes Distance Residuals
0.10
0.05
0.00
−0.05
−0.10
−0.05
0.00
0.05
0.10
PC 1 100 %
help("procD.lm")

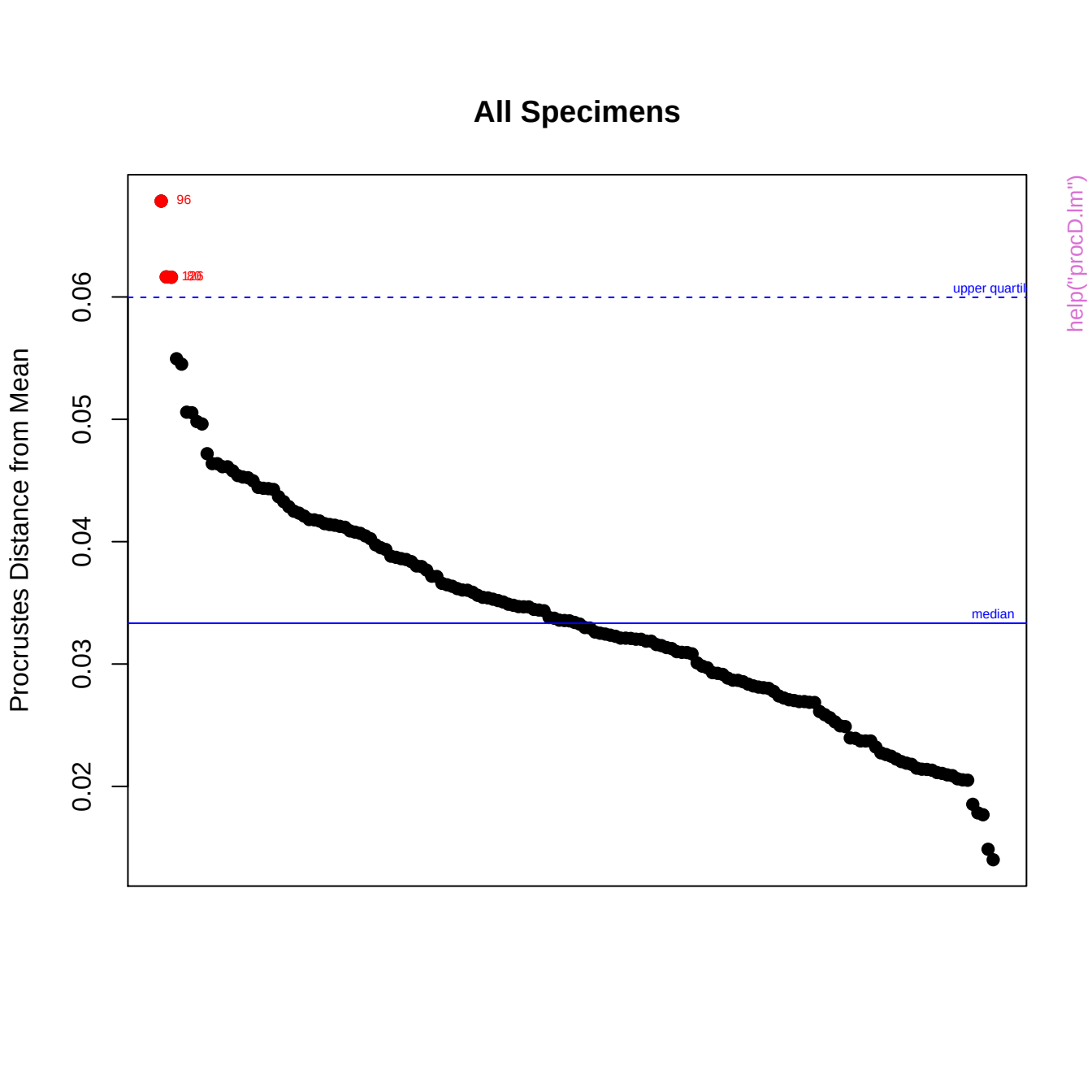

Residuals vs. Fitted
Procrustes Distance Residuals
0.00
0.02
0.04
0.06
0.08
0.00
0.02
0.04
0.06
0.08
0.10
0.12
Procrustes Distance Fitted Values
help("procD.lm")

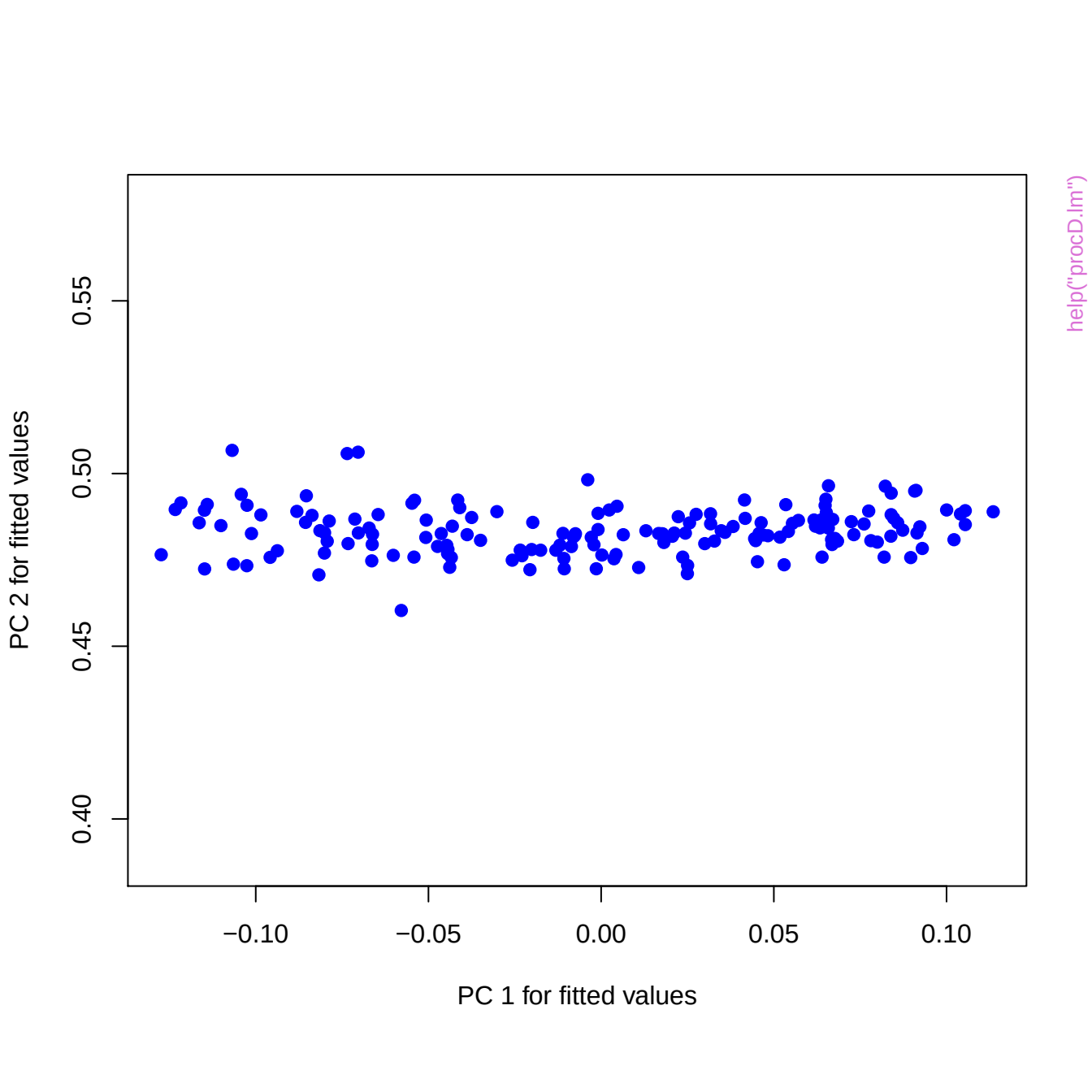

PCA Residuals
PC 2 21.16 %
PC 1 38.06 %
0.04
0.02
0.00
−0.02
−0.04
−0.02
0.00
0.02
0.04
help("procD.lm")

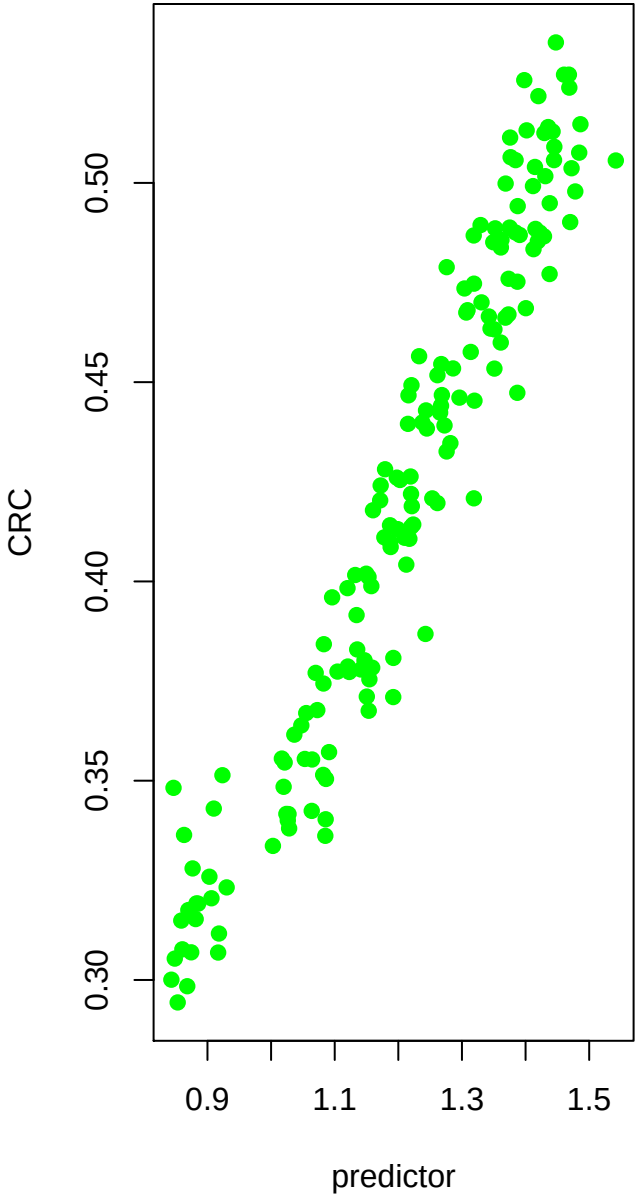

Q−Q plot
Procrustes Distance Residuals
0.02
0.03
0.04
0.05
0.06
−2
−1
0
1
2
Theoretical Quantiles
help("procD.lm")

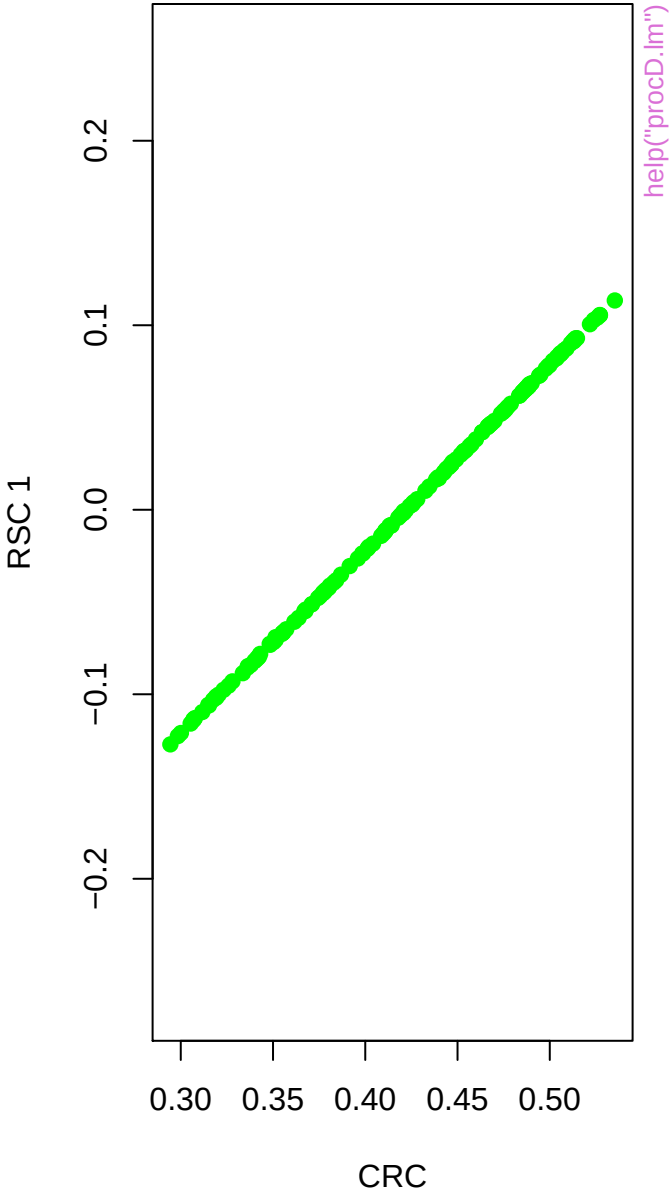

Residuals vs. PC 1 fitted
Procrustes Distance Residuals
0.10
0.05
0.00
−0.05
−0.10
−0.05
0.00
0.05
0.10
PC 1 100 %
help("procD.lm")

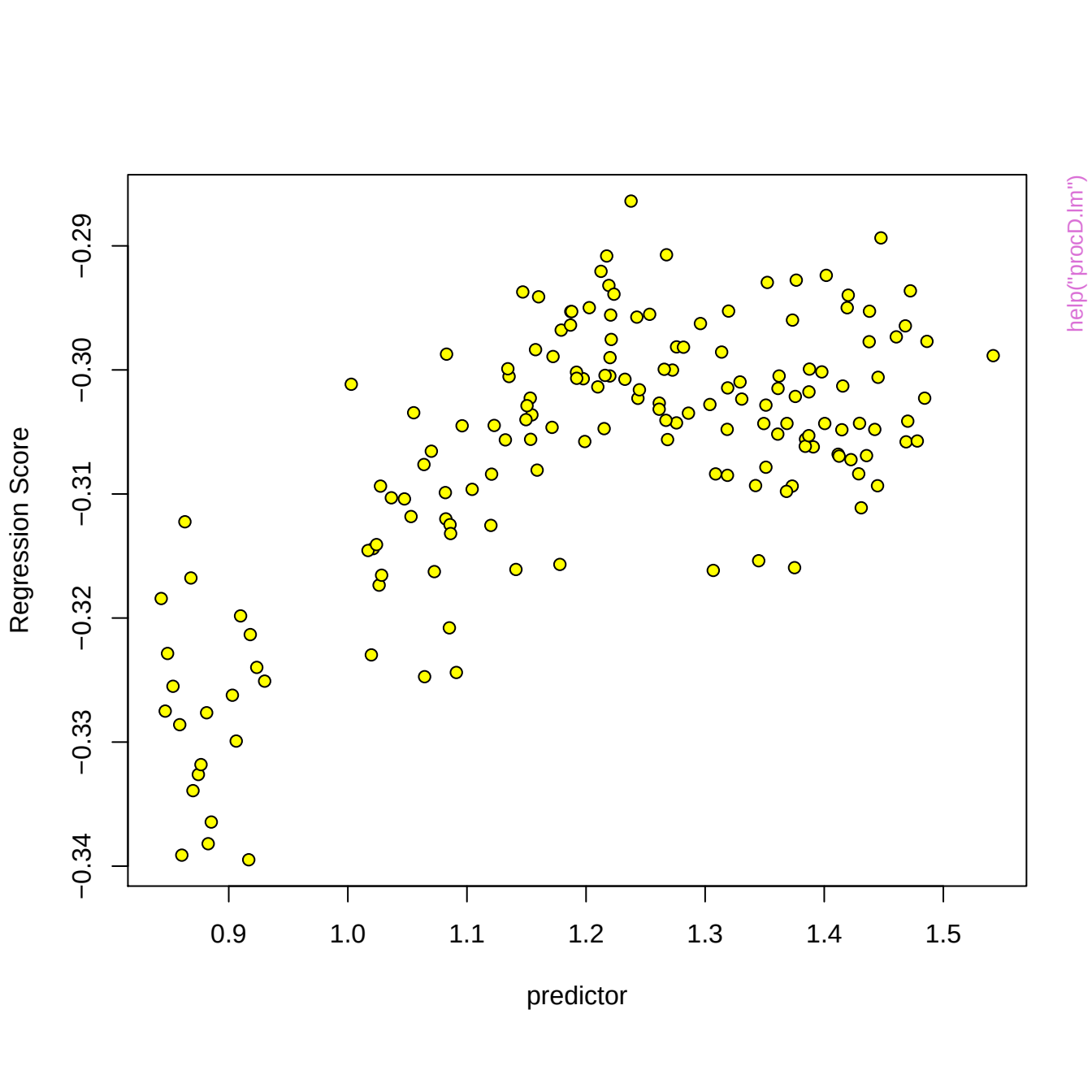

Residuals vs. Fitted
Procrustes Distance Residuals
0.00
0.02
0.04
0.06
0.08
0.00
0.02
0.04
0.06
0.08
0.10
0.12
Procrustes Distance Fitted Values
help("procD.lm")

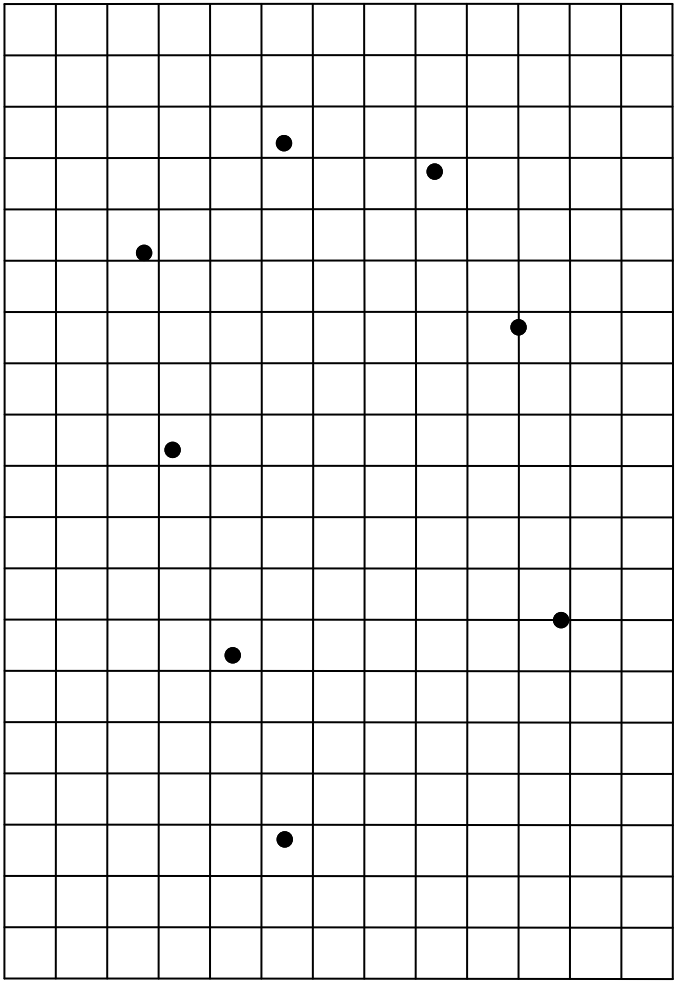

All Specimens
Procrustes Distance from Mean
0.02
0.03
0.04
0.05
0.06
96
upper quartil
median
help("procD.lm")


PC 2 for fitted values
0.40
0.45
0.50
0.55
−0.10
−0.05
0.00
0.05
0.10
PC 1 for fitted values
help("procD.lm")

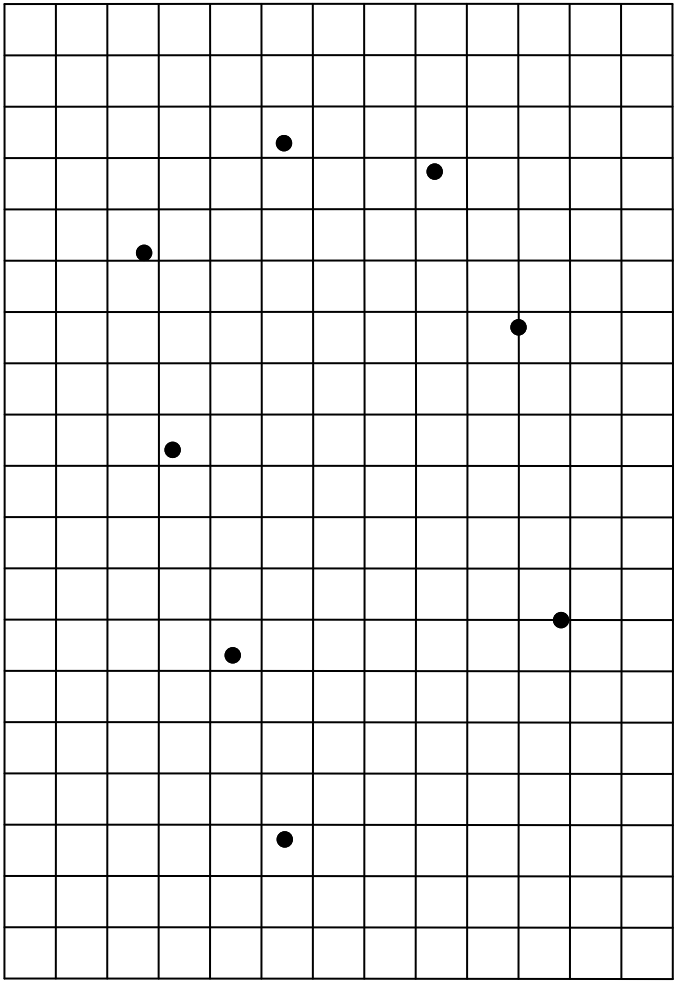

CRC
0.30
0.35
0.40
0.45
0.50
0.9
1.1
1.3
1.5
predictor


RSC 1
−0.2
−0.1
0.0
0.1
0.2
0.30
0.35
0.40
0.45
0.50
CRC
help("procD.lm")

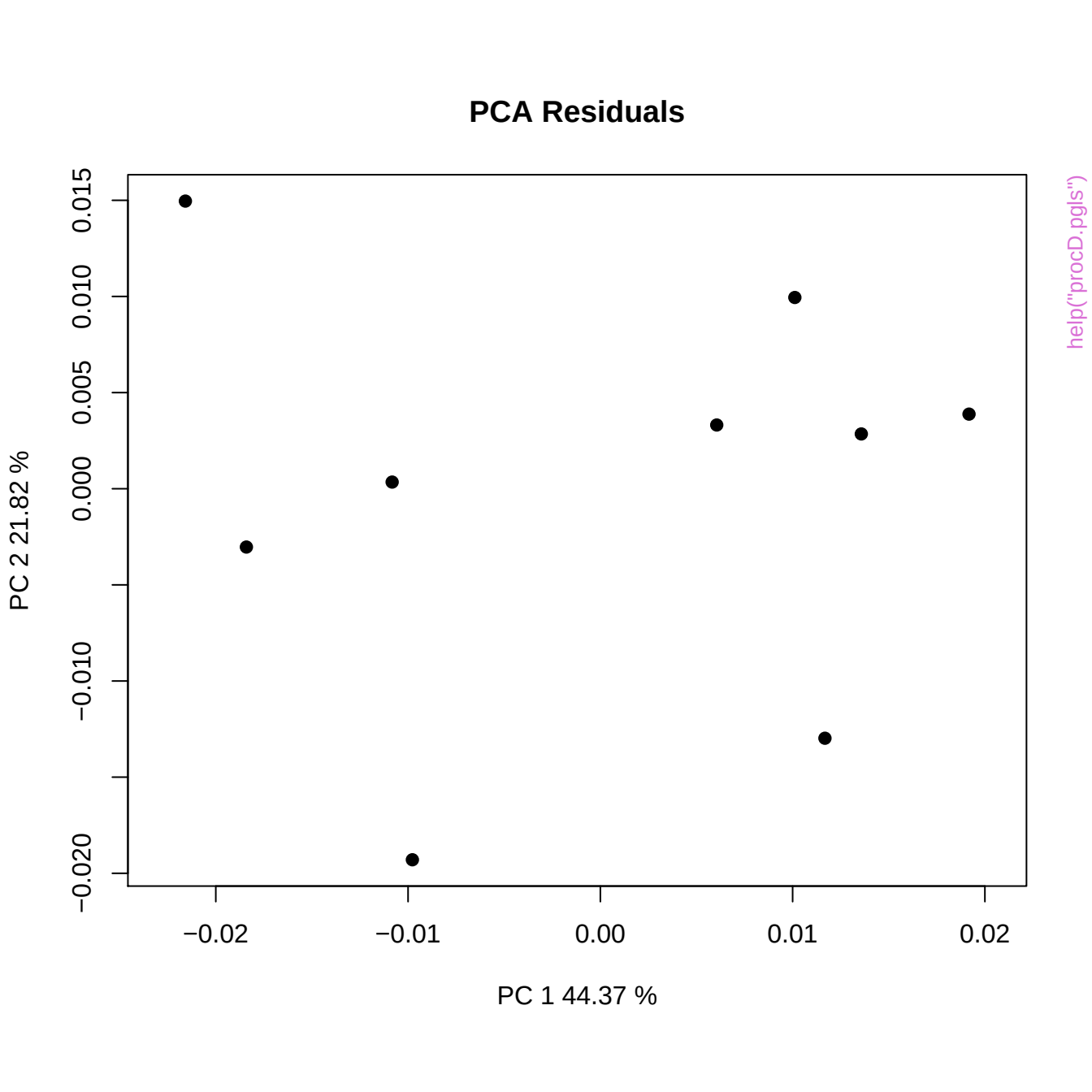

Regression Score
−0.29
−0.30
−0.31
−0.32
−0.33
−0.34
0.9
1.0
1.1
1.2
1.3
1.4
1.5
predictor
help("procD.lm")

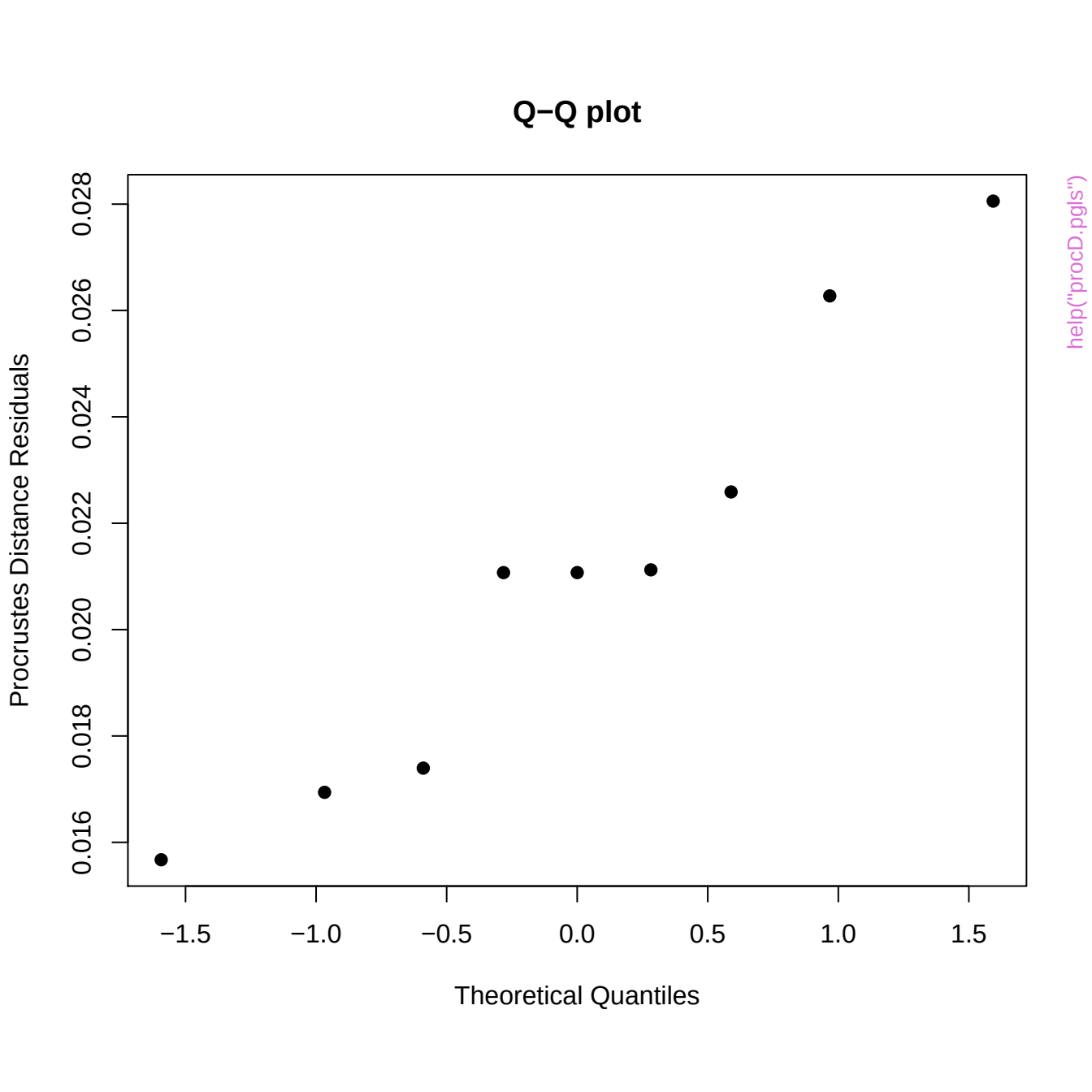


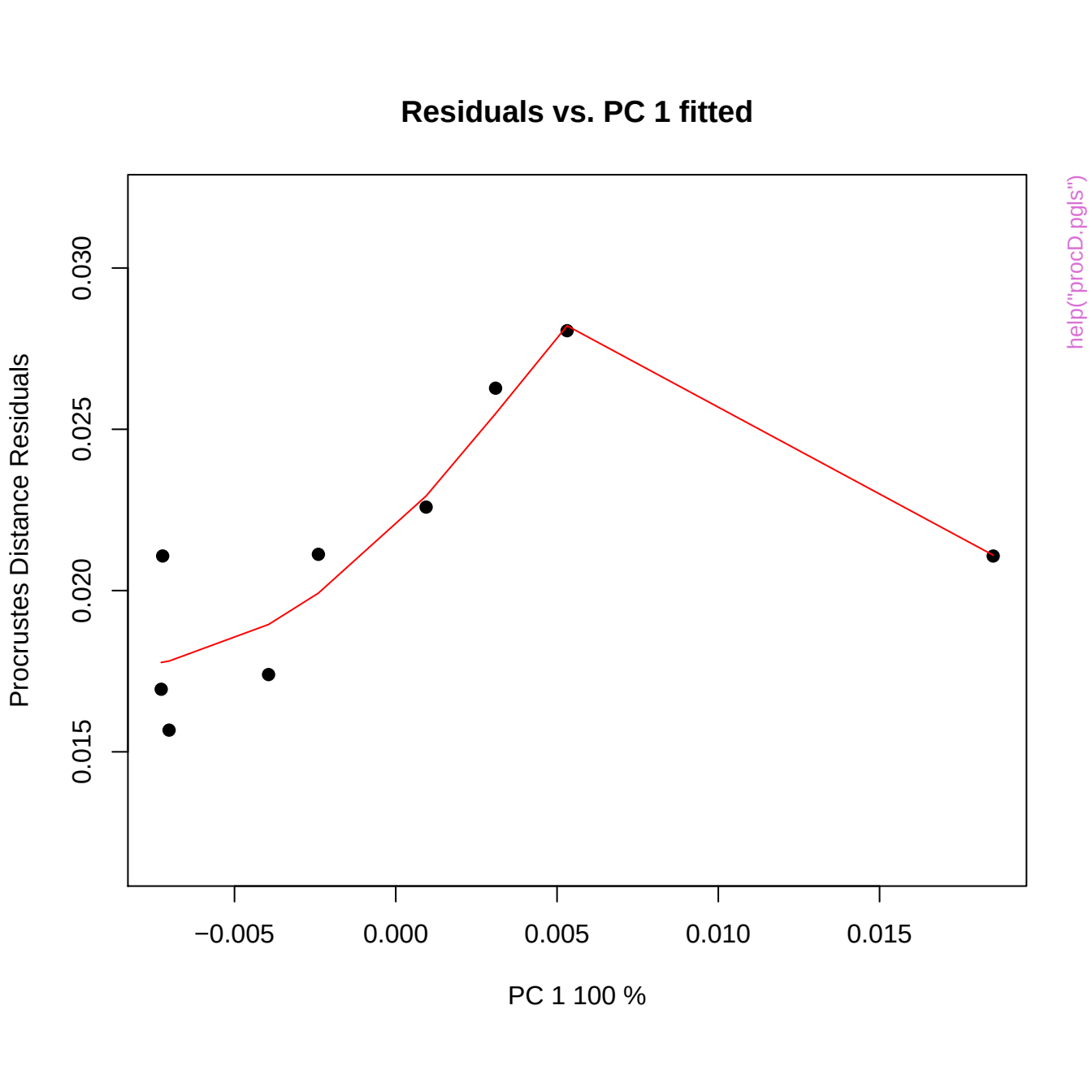
help("procD.lm")

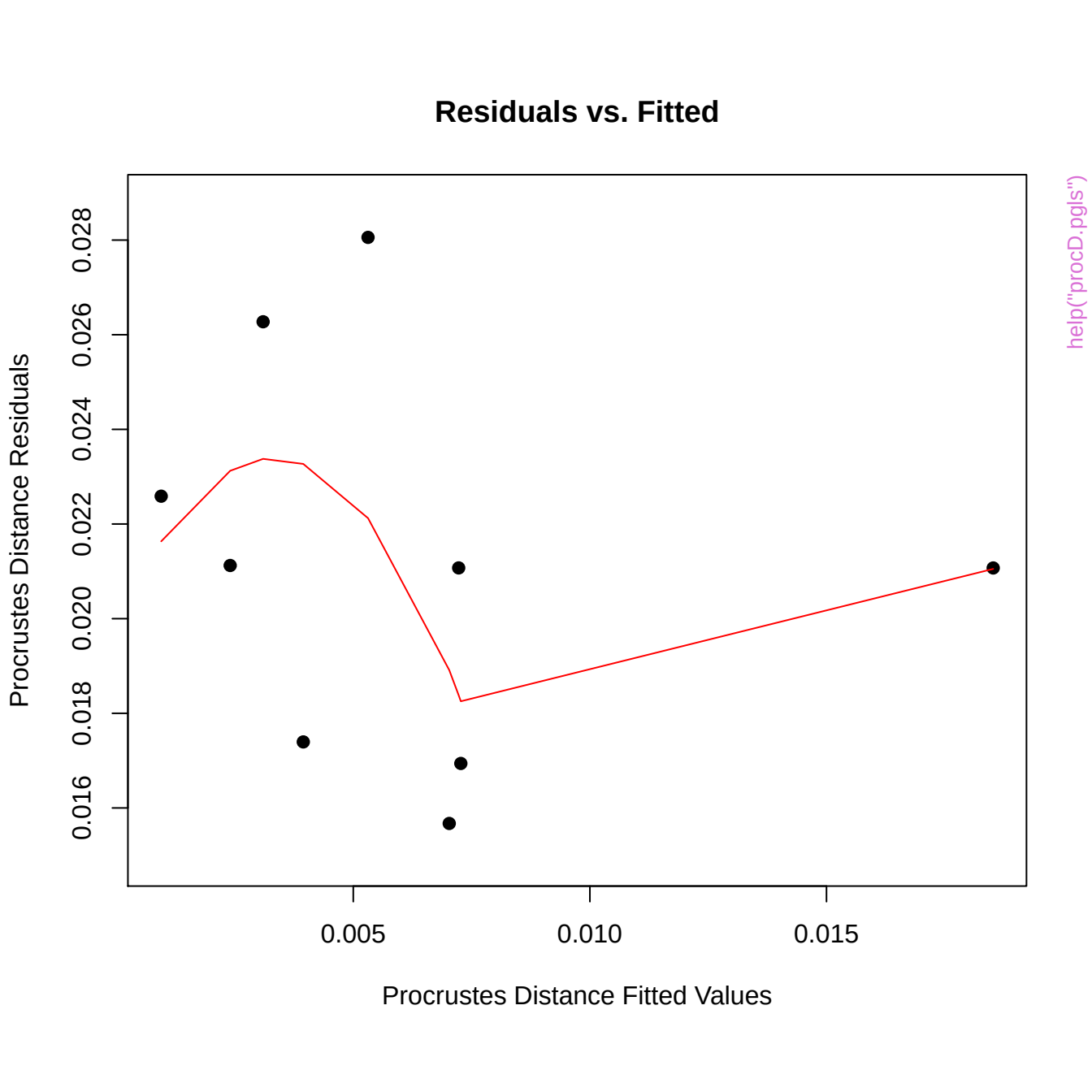


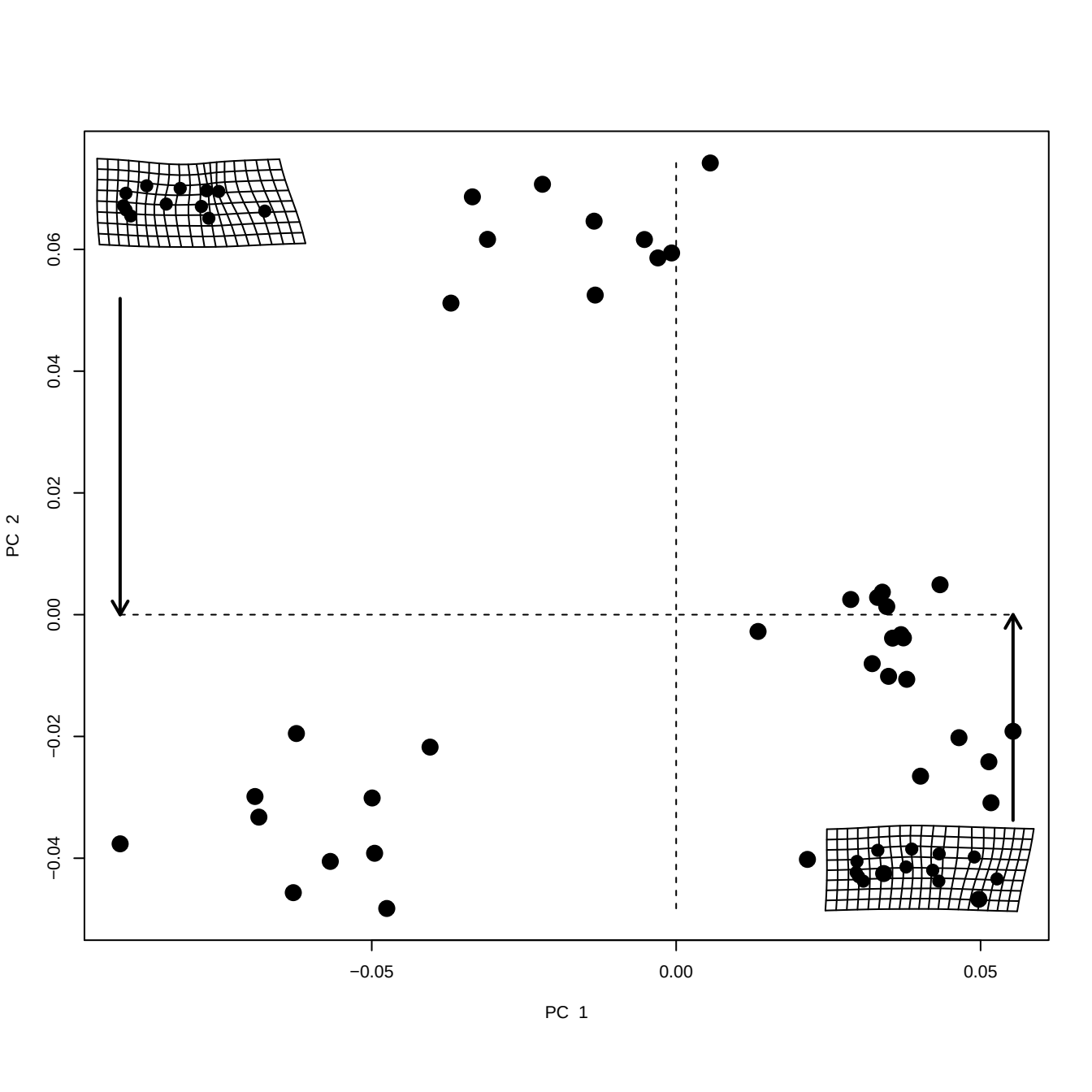
help("procD.lm")

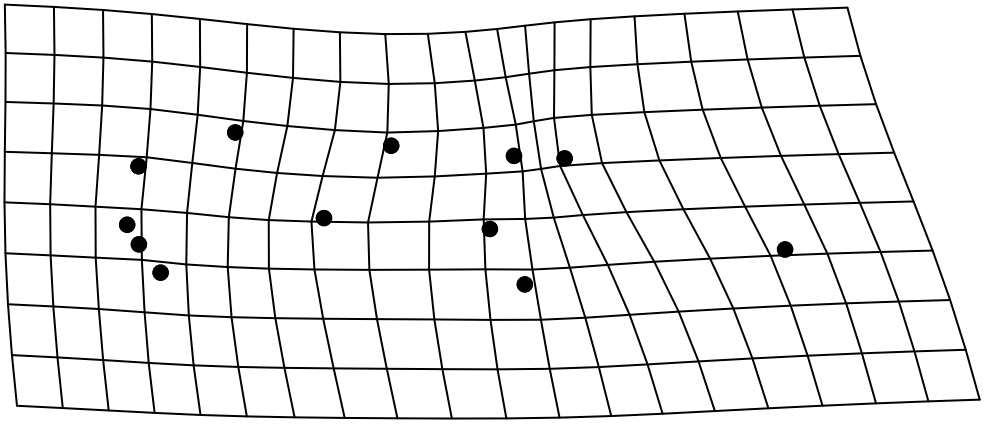

PCA Residuals
PC 2 21.82 %
PC 1 44.37 %
0.015
0.010
0.005
0.000
−0.010
−0.020
−0.02
−0.01
0.00
0.01
0.02
help("procD.pgls")


Q−Q plot
Procrustes Distance Residuals
0.016
0.018
0.020
0.022
0.024
0.026
0.028
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
Theoretical Quantiles
help("procD.pgls")

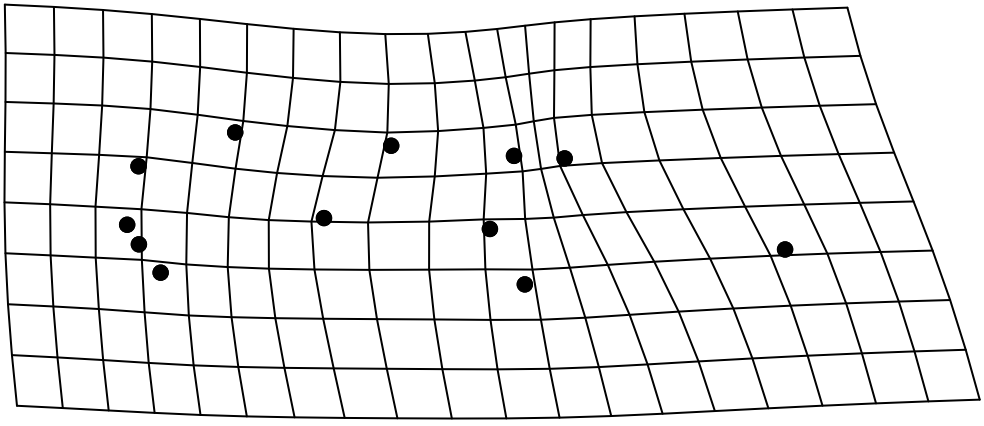

Residuals vs. PC 1 fitted
Procrustes Distance Residuals
0.015
0.020
0.025
0.030
−0.005
0.000
0.005
0.010
0.015
PC 1 100 %
help("procD.pgls")


Residuals vs. Fitted
Procrustes Distance Residuals
0.016
0.018
0.020
0.022
0.024
0.026
0.028
0.005
0.010
0.015
Procrustes Distance Fitted Values
help("procD.pgls")

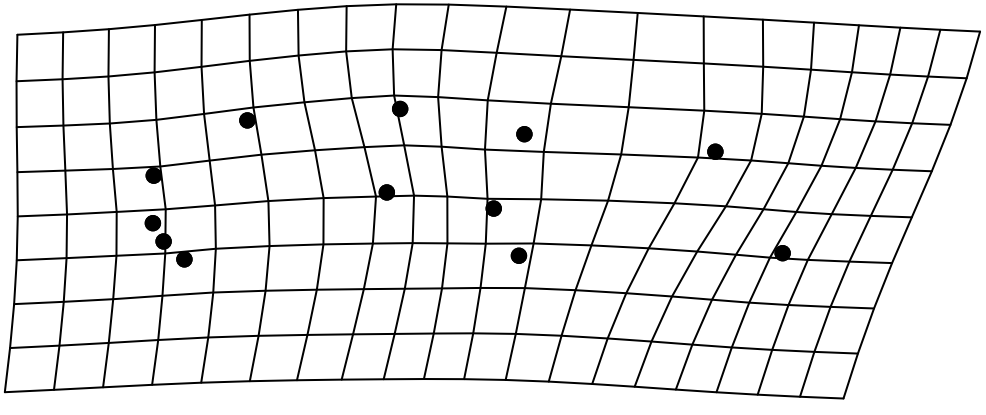

0.06
0.04
0.02
0.00
−0.02
−0.04
PC 2
−0.05
0.00
0.05
PC 1



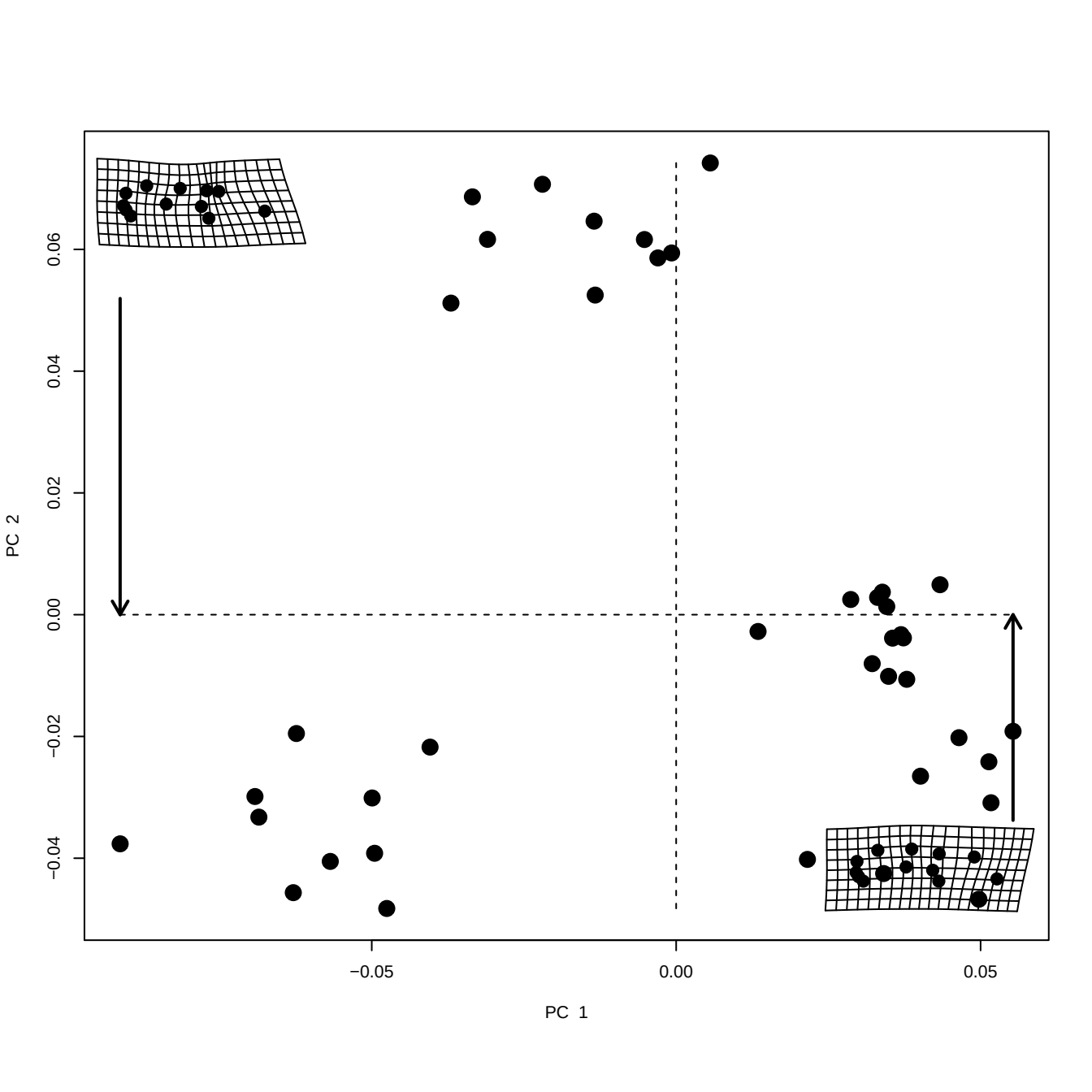
help("shape.predictor")

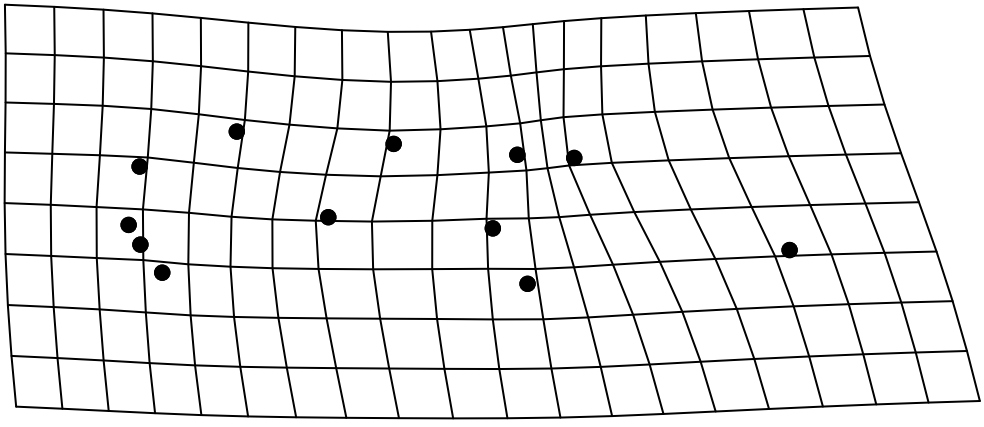


help("shape.predictor")

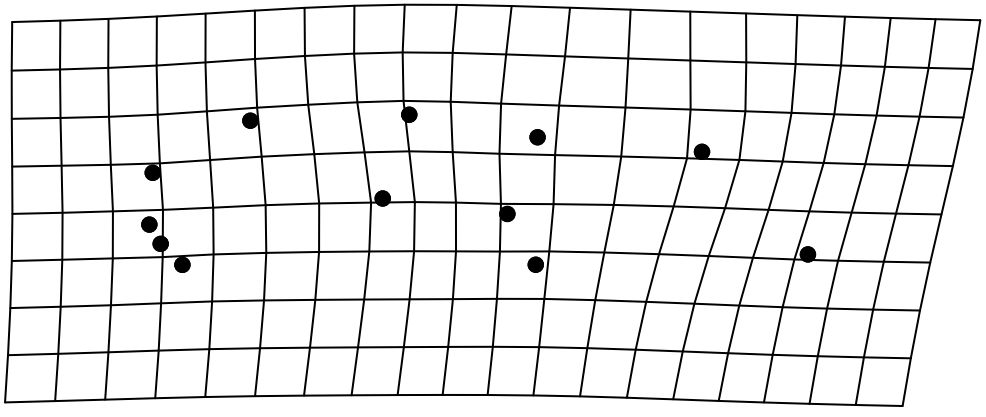


help("shape.predictor")

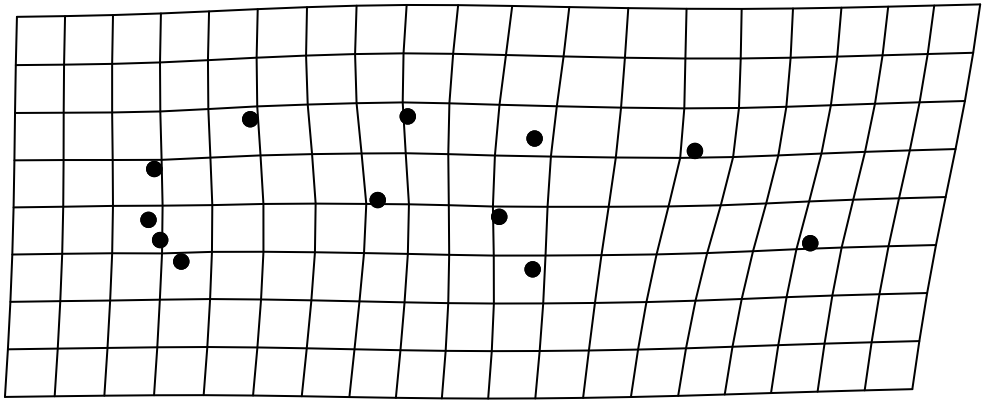

0.06
0.04
0.02
0.00
−0.02
−0.04
PC 2
−0.05
0.00
0.05
PC 1



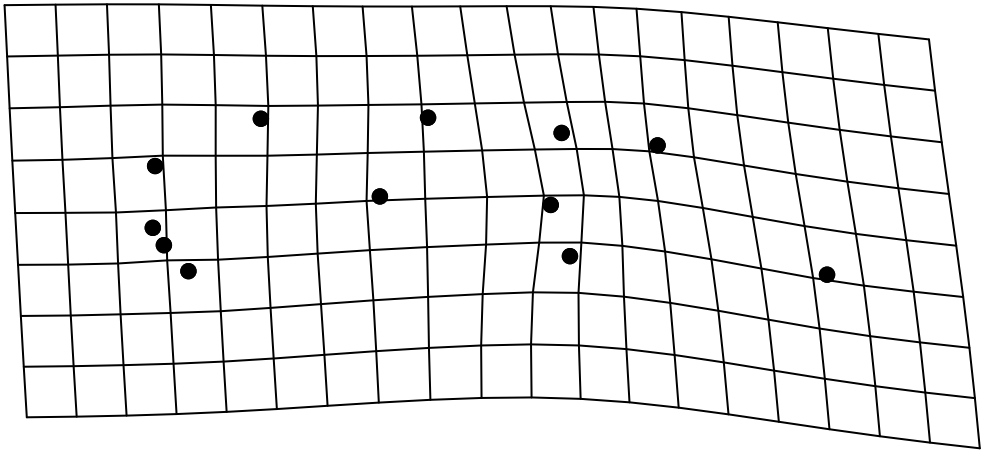
help("shape.predictor")



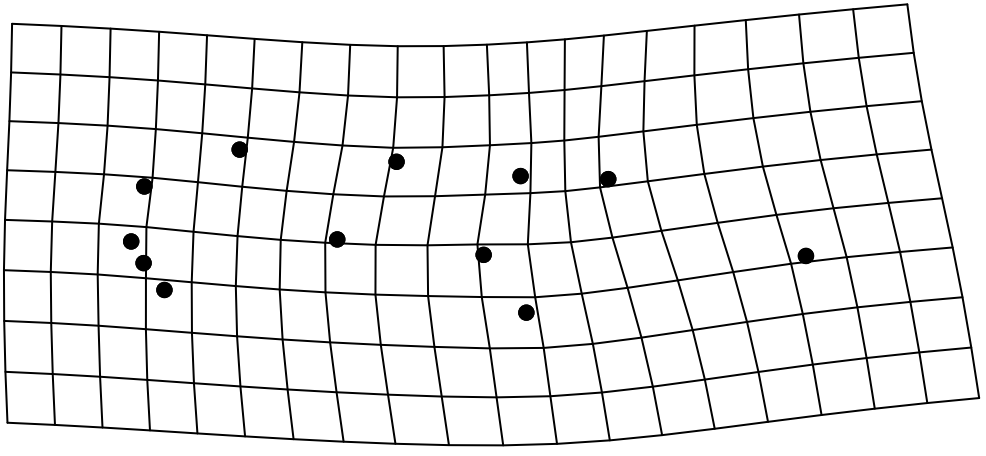
help("shape.predictor")



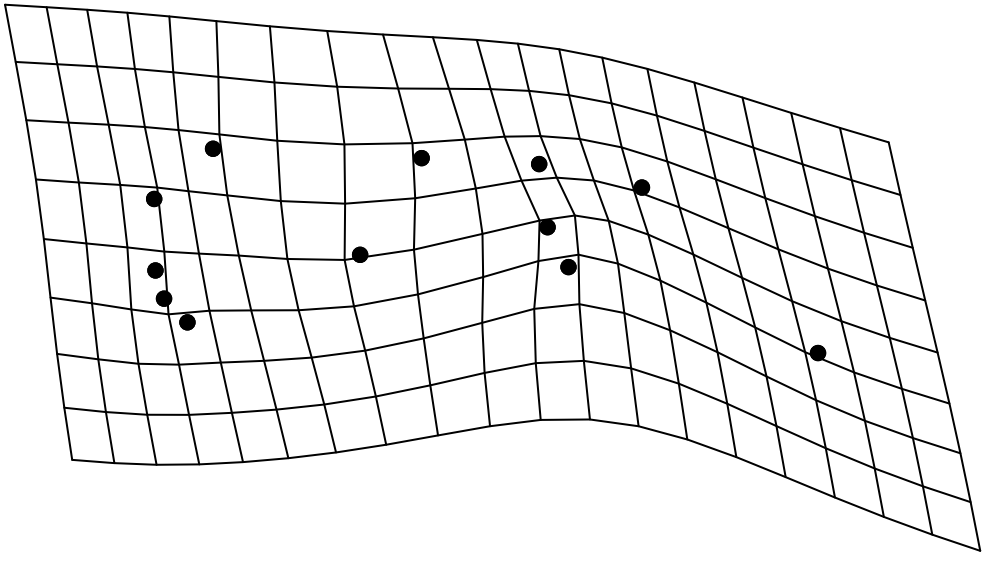
help("shape.predictor")



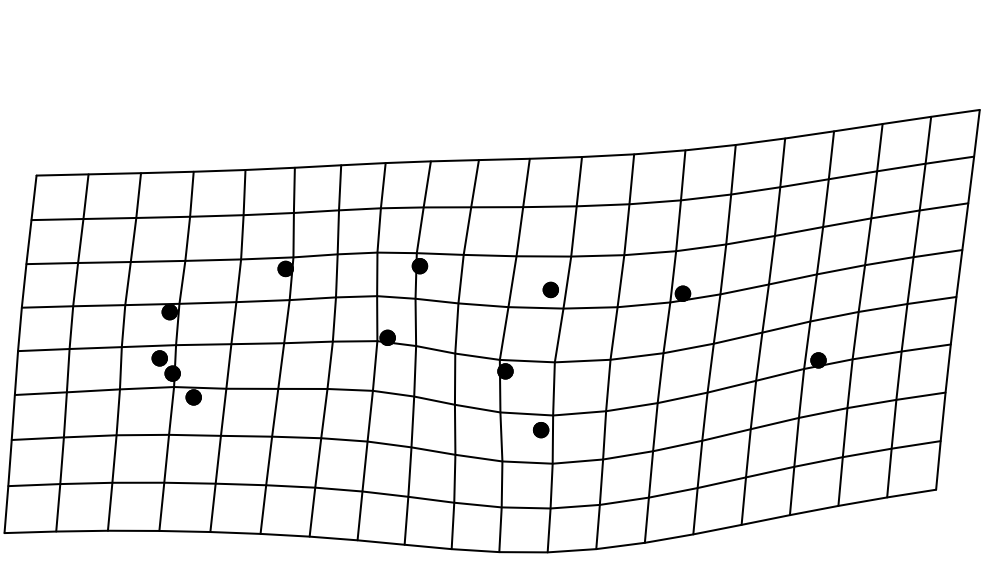
help("shape.predictor")



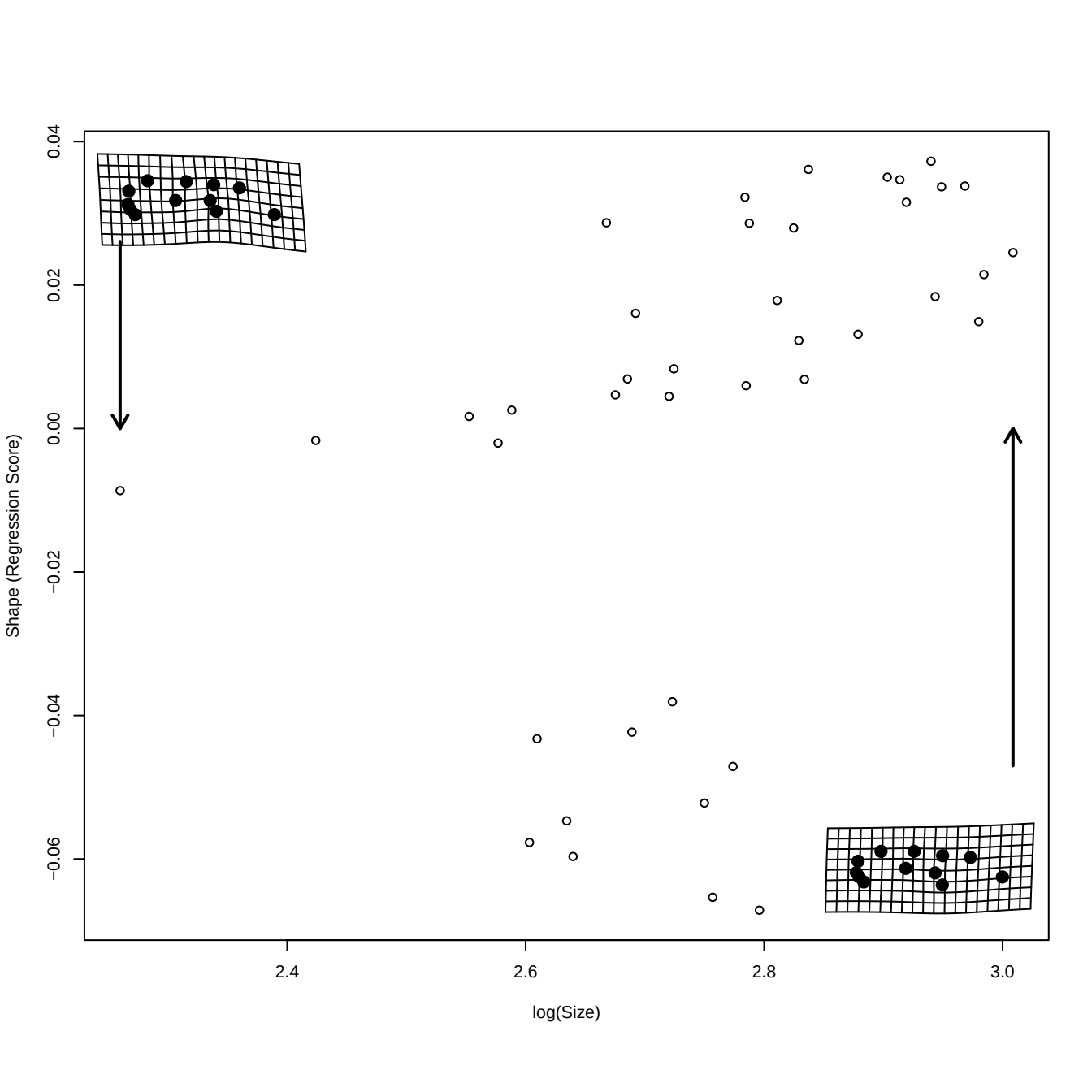
help("shape.predictor")

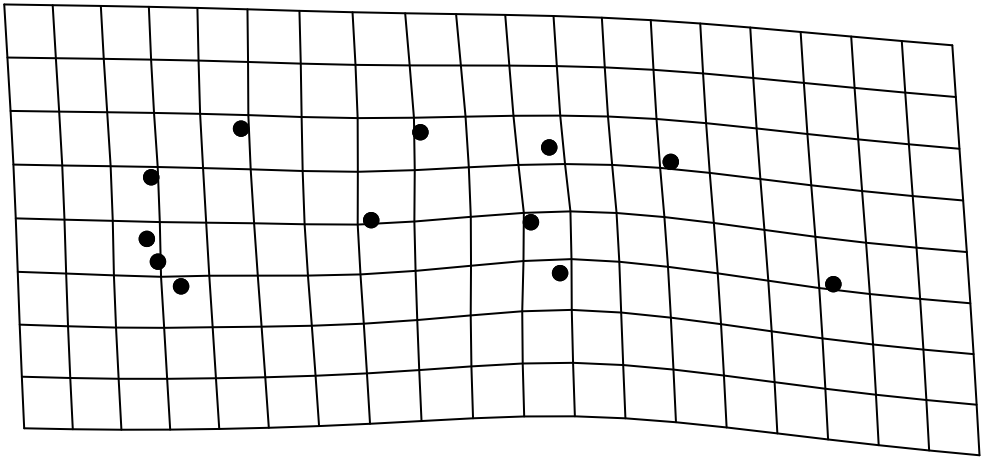


help("shape.predictor")

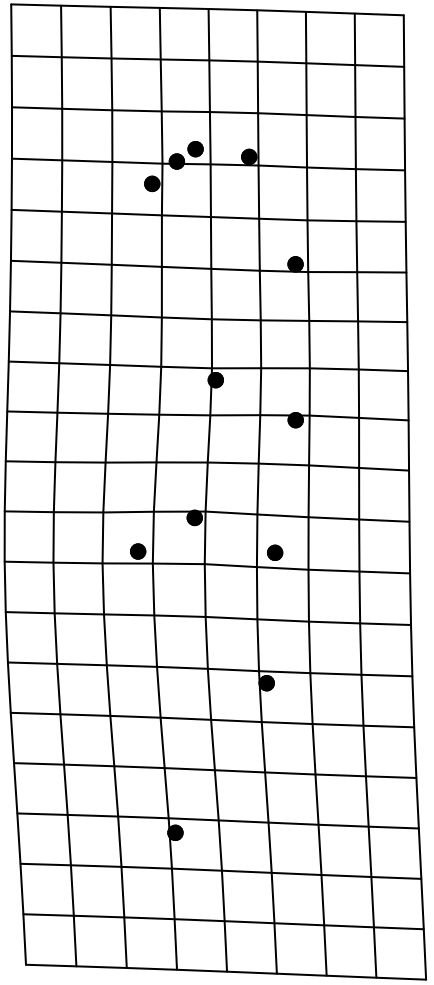


help("shape.predictor")

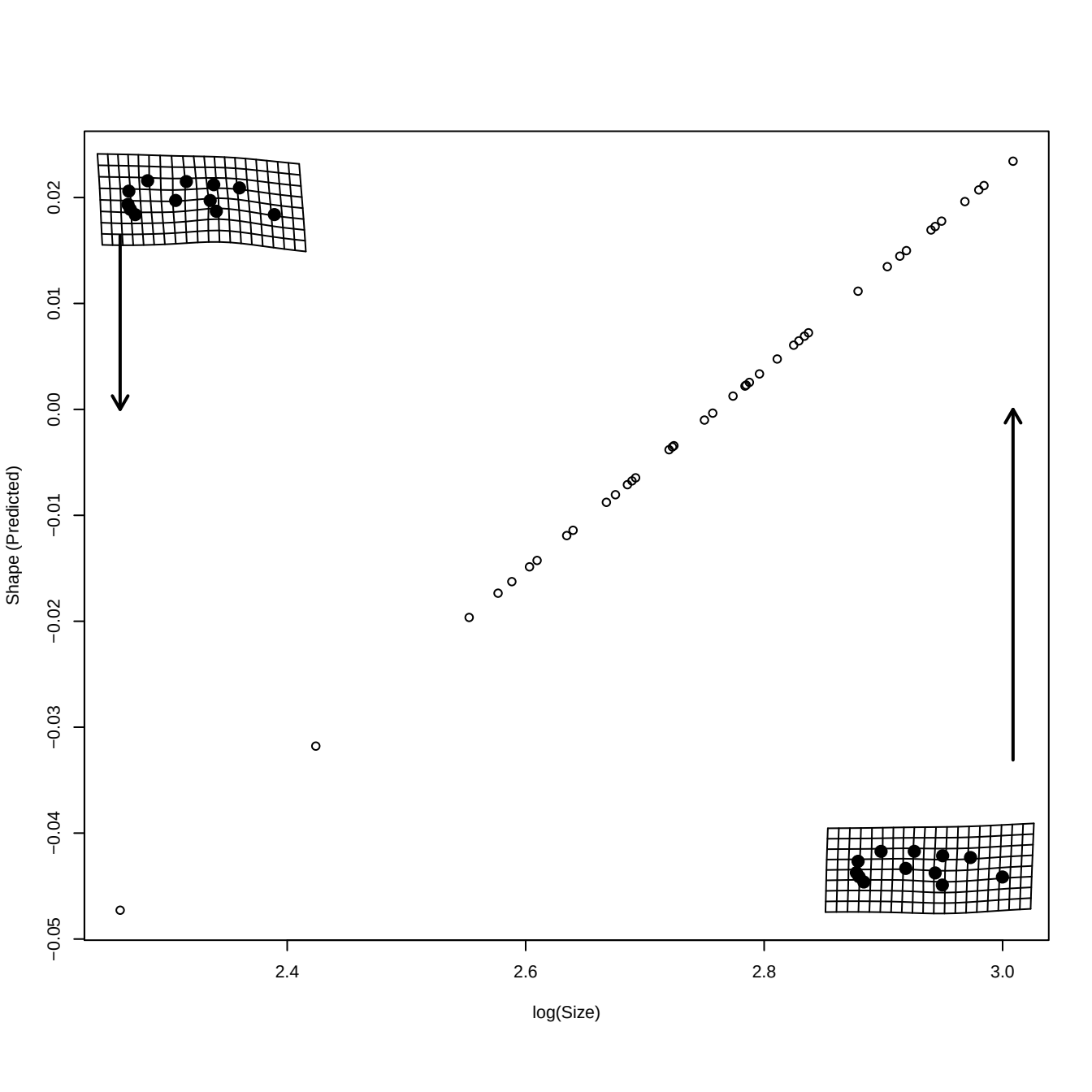

Shape (Regression Score)
0.04
0.02
0.00
−0.02
−0.04
−0.06
2.4
2.6
2.8
3.0
log(Size)

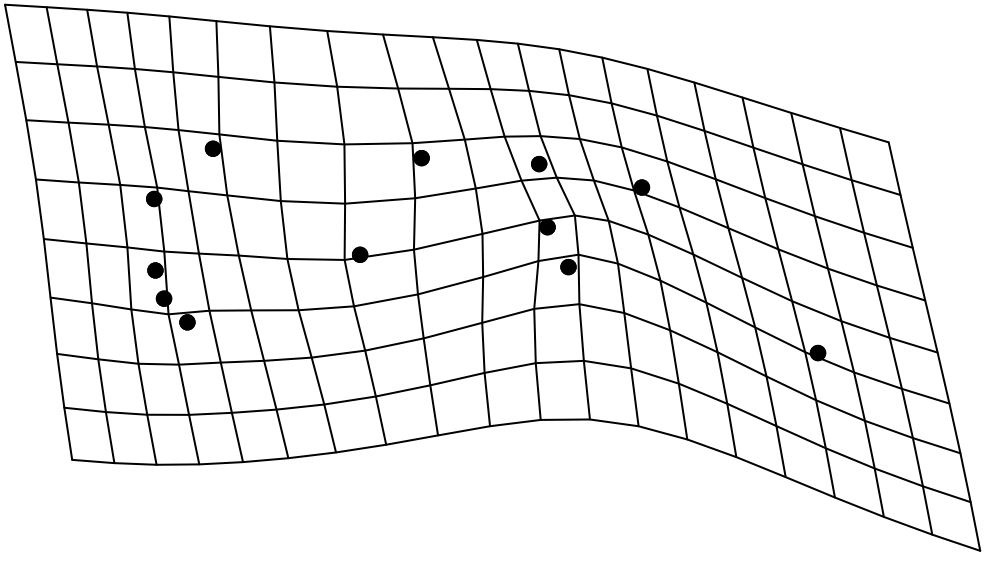


help("shape.predictor")

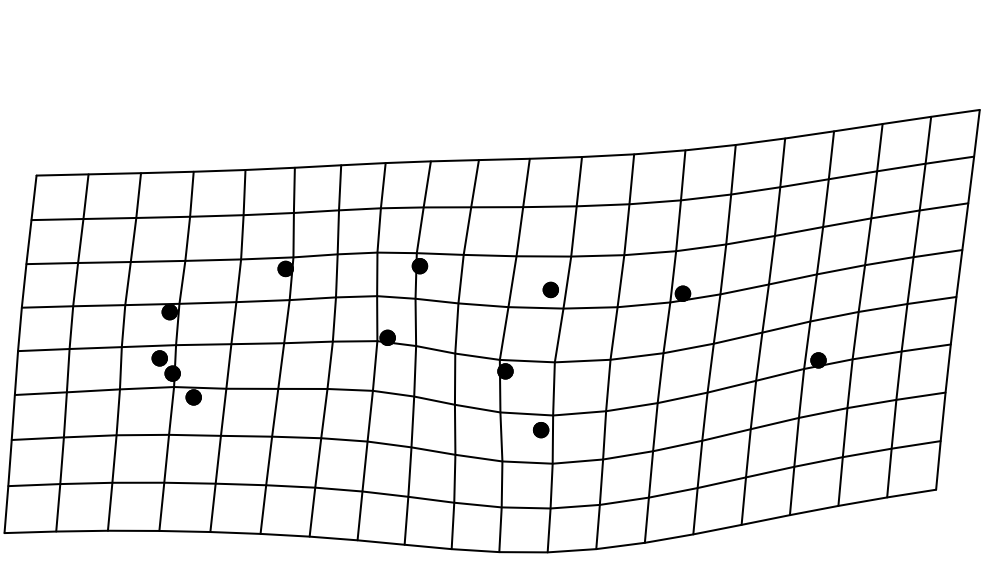


help("shape.predictor")

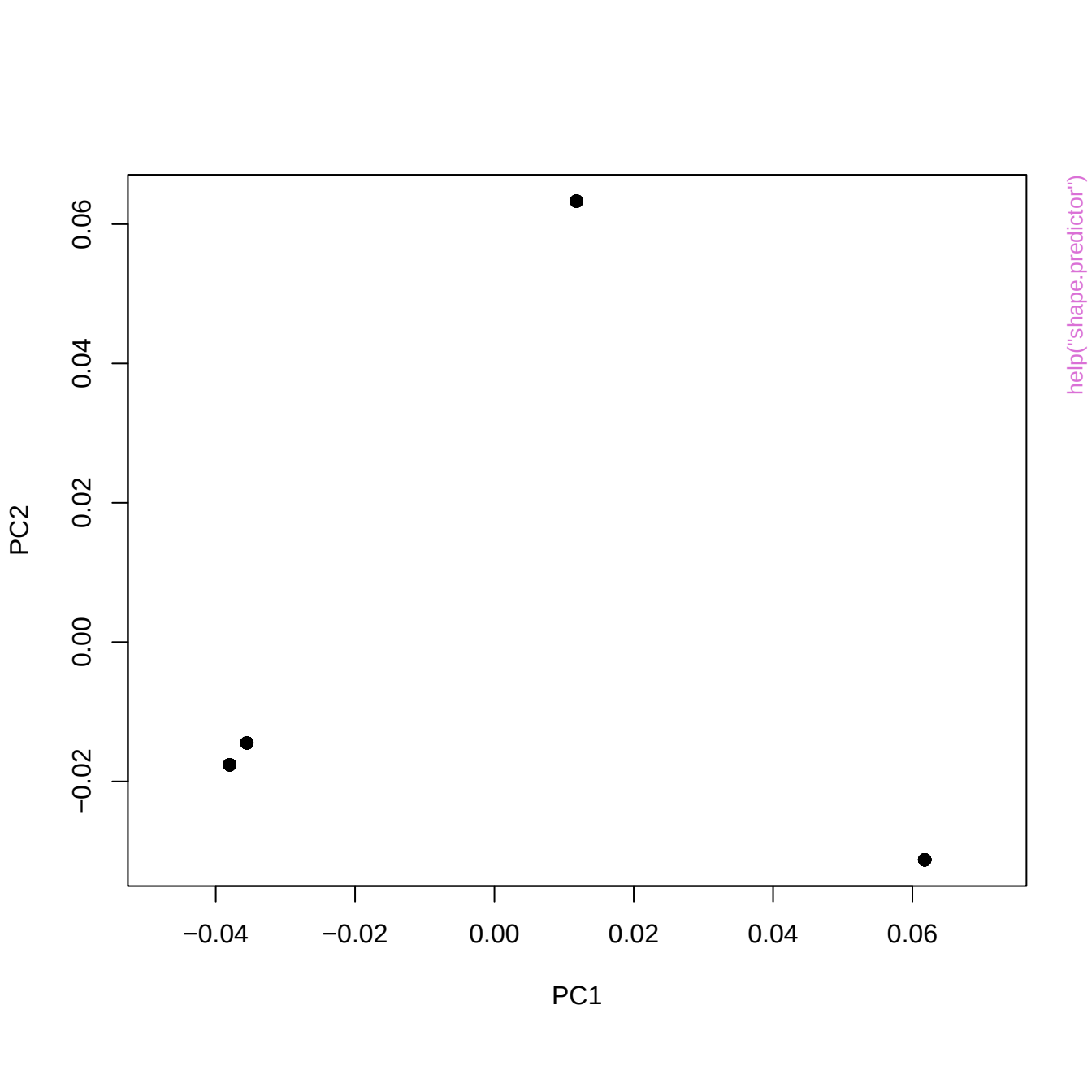

Shape (Predicted)
0.02
0.01
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
2.4
2.6
2.8
3.0
log(Size)

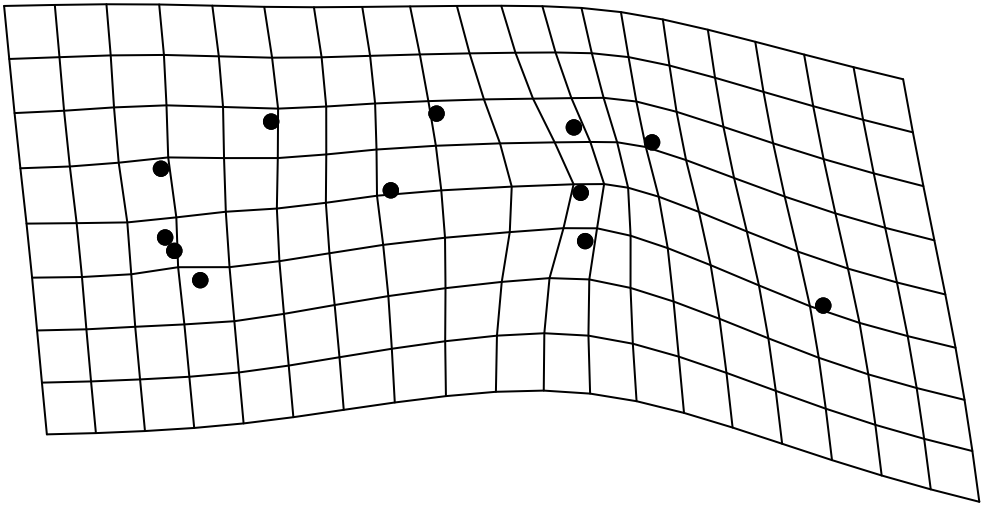


help("shape.predictor")

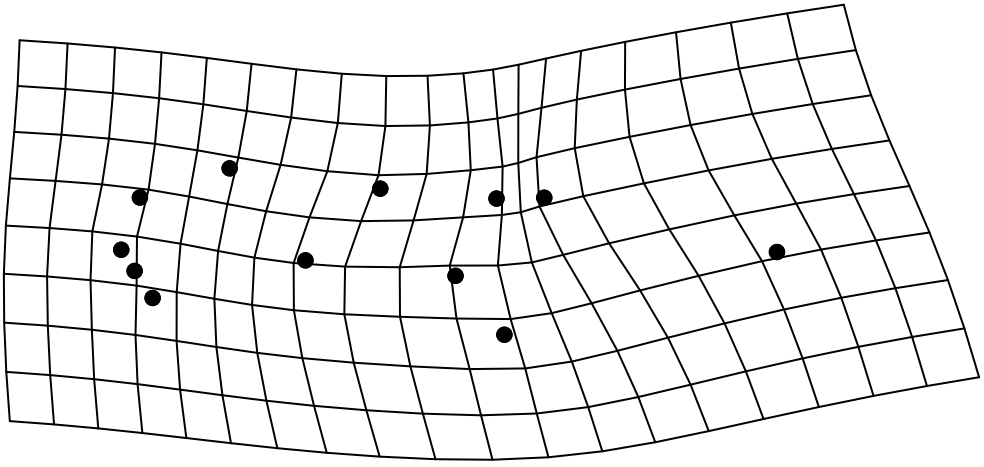


help("shape.predictor")

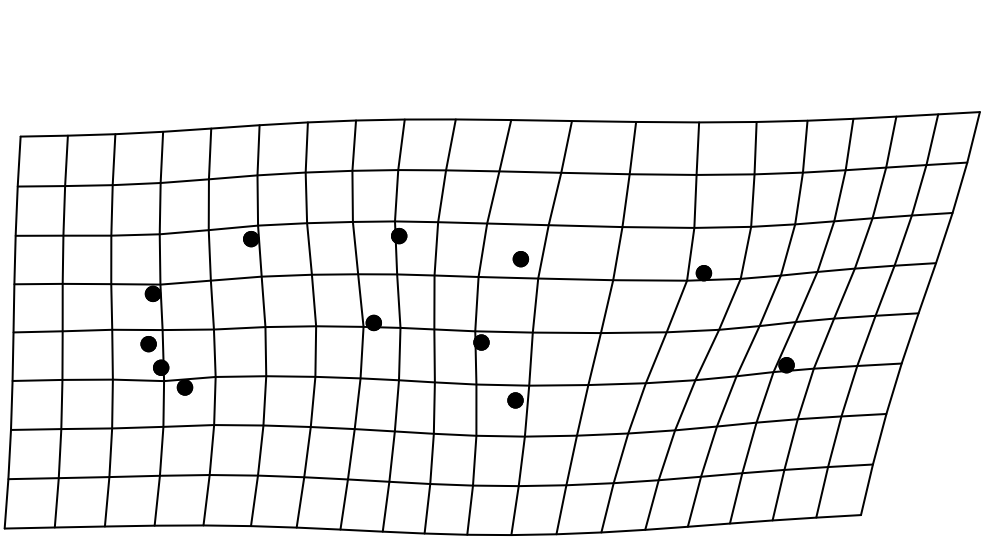

PC2
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.02
0.00
0.02
0.04
0.06
PC1
help("shape.predictor")



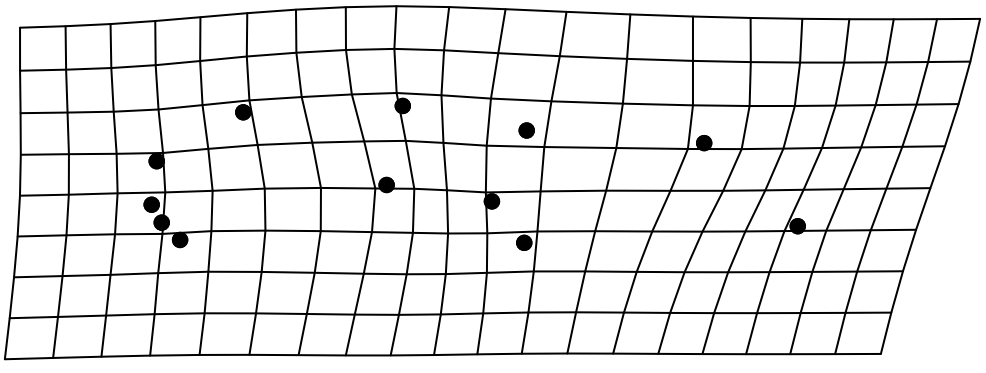
help("shape.predictor")



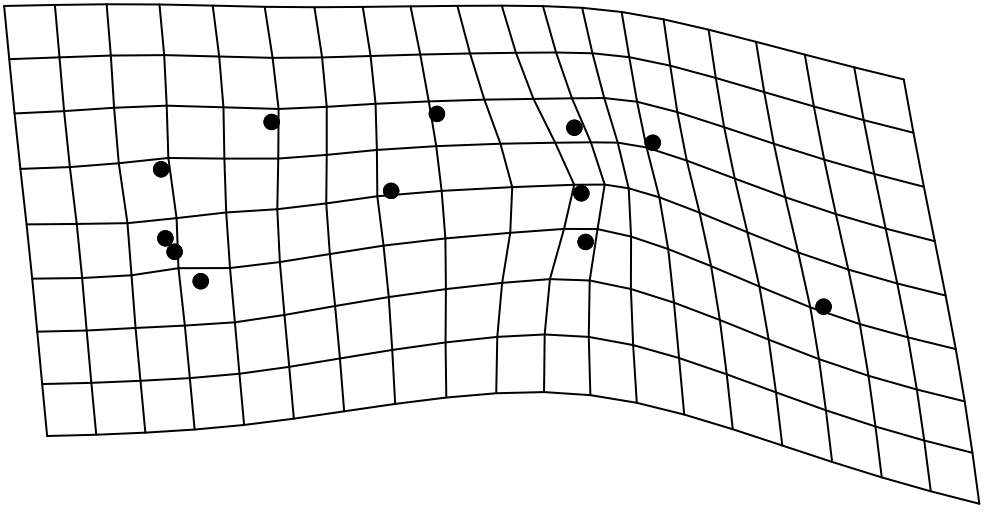
help("shape.predictor")



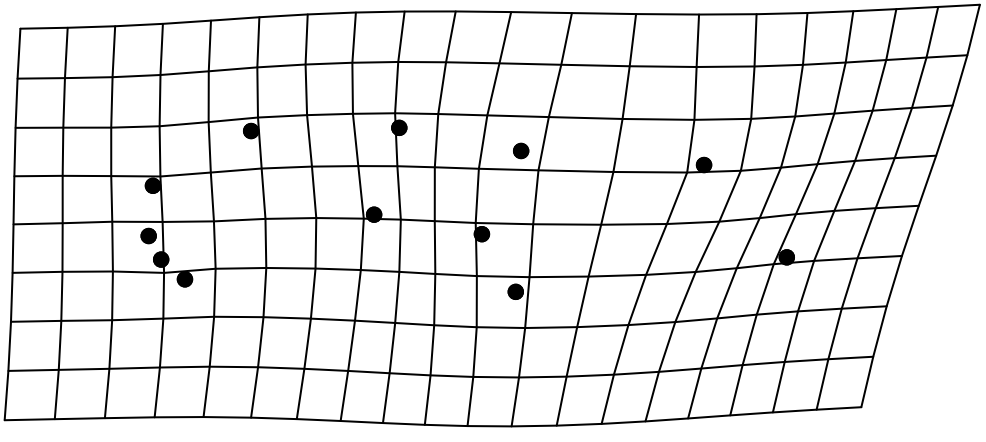
help("shape.predictor")



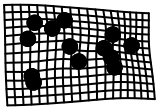
help("shape.predictor")

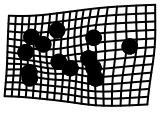


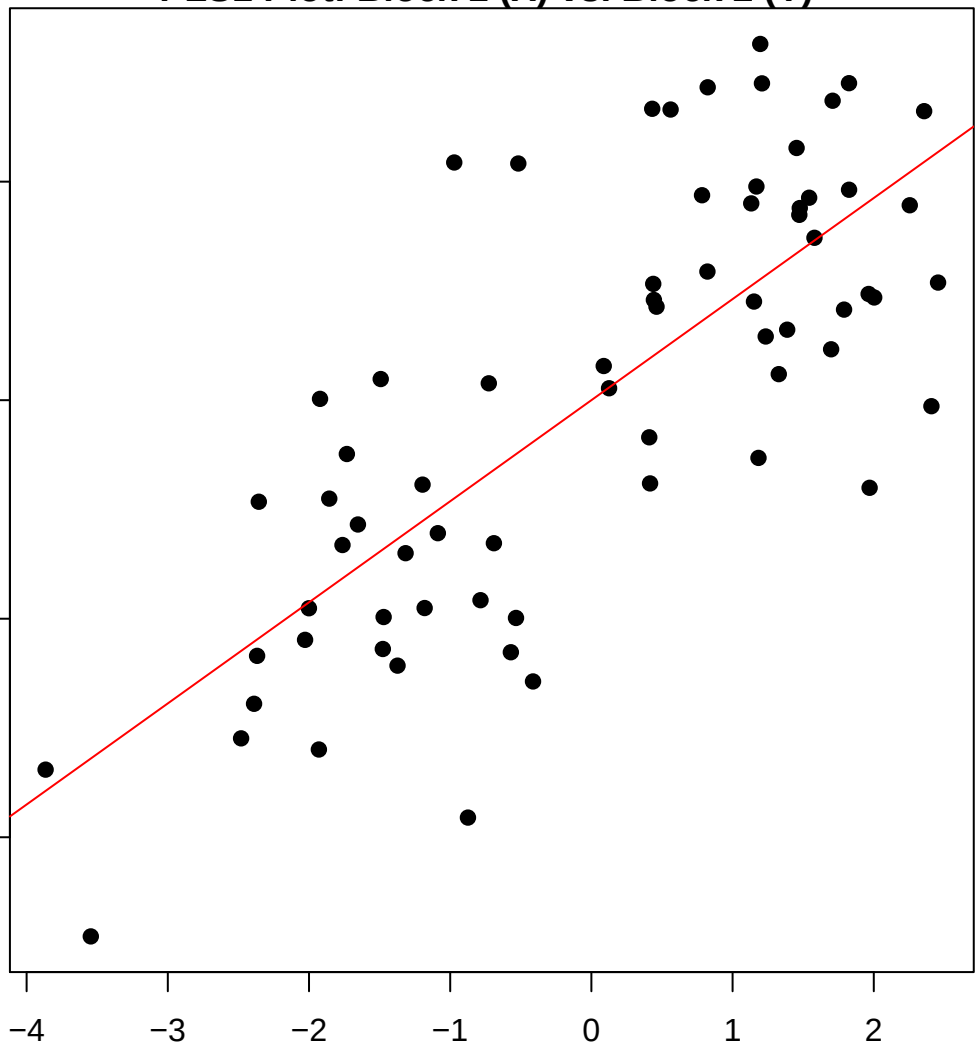
help("shape.predictor")

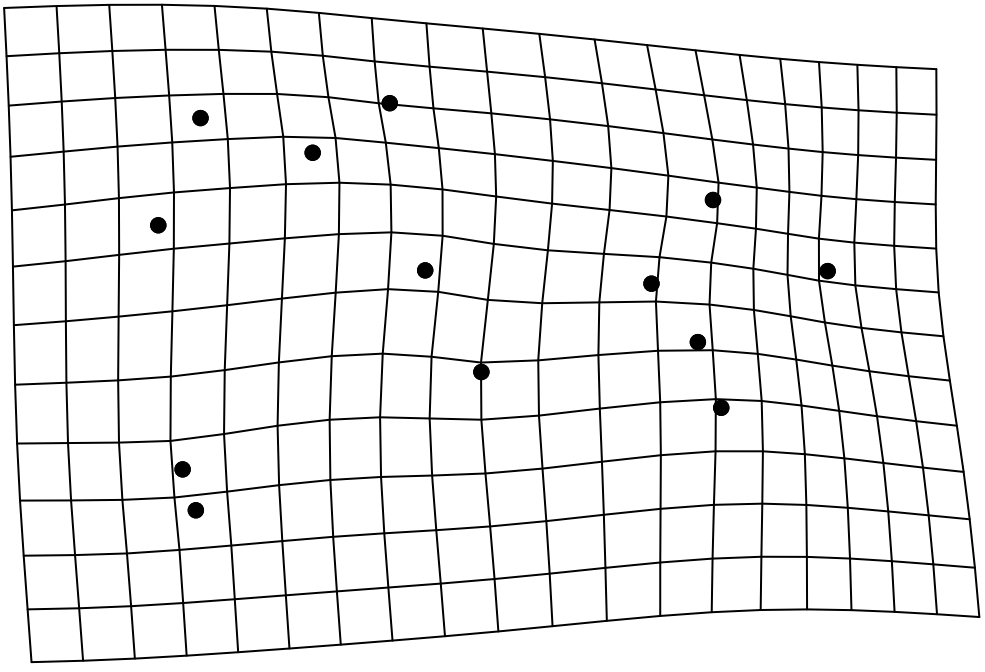


help("shape.predictor")

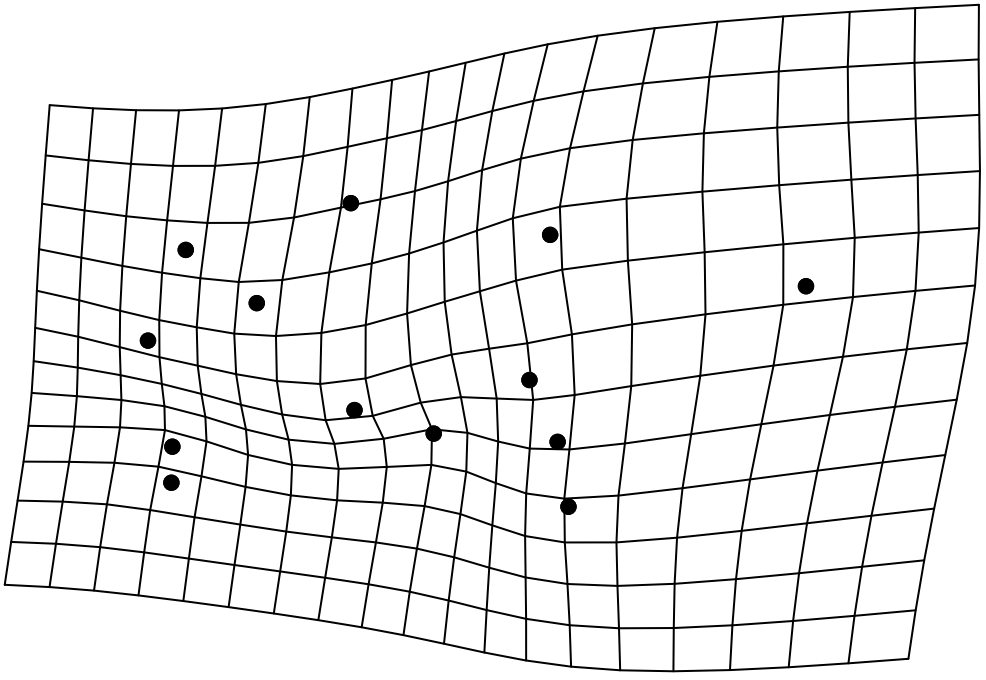




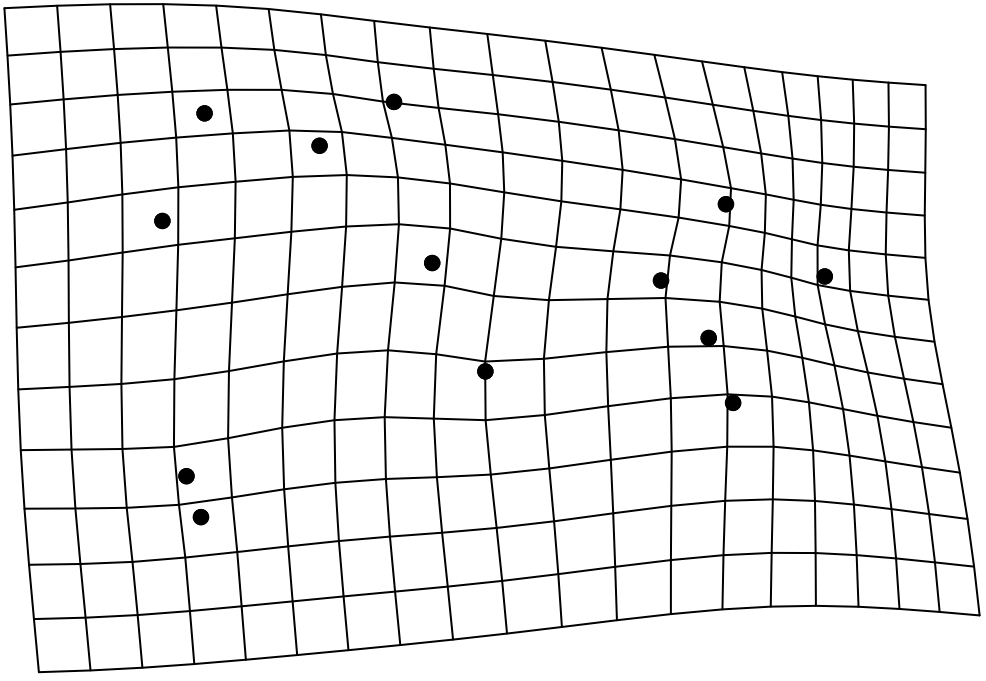

PLS1 Plot: Block 1 (X) vs. Block 2 (Y)
0.05
0.00
−0.05
−0.10
−4
−3
−2
−1
0
1
2



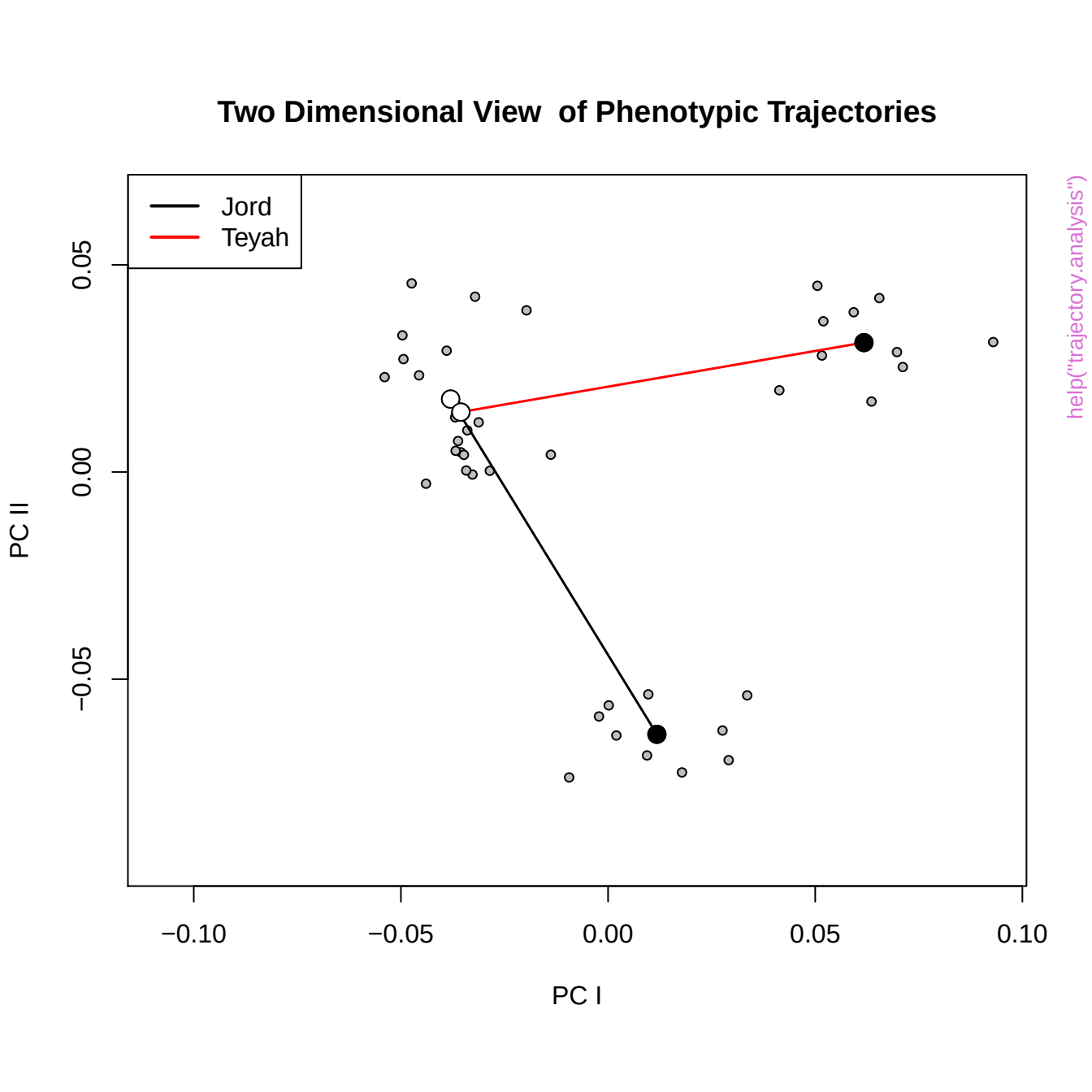
help("shape.predictor")

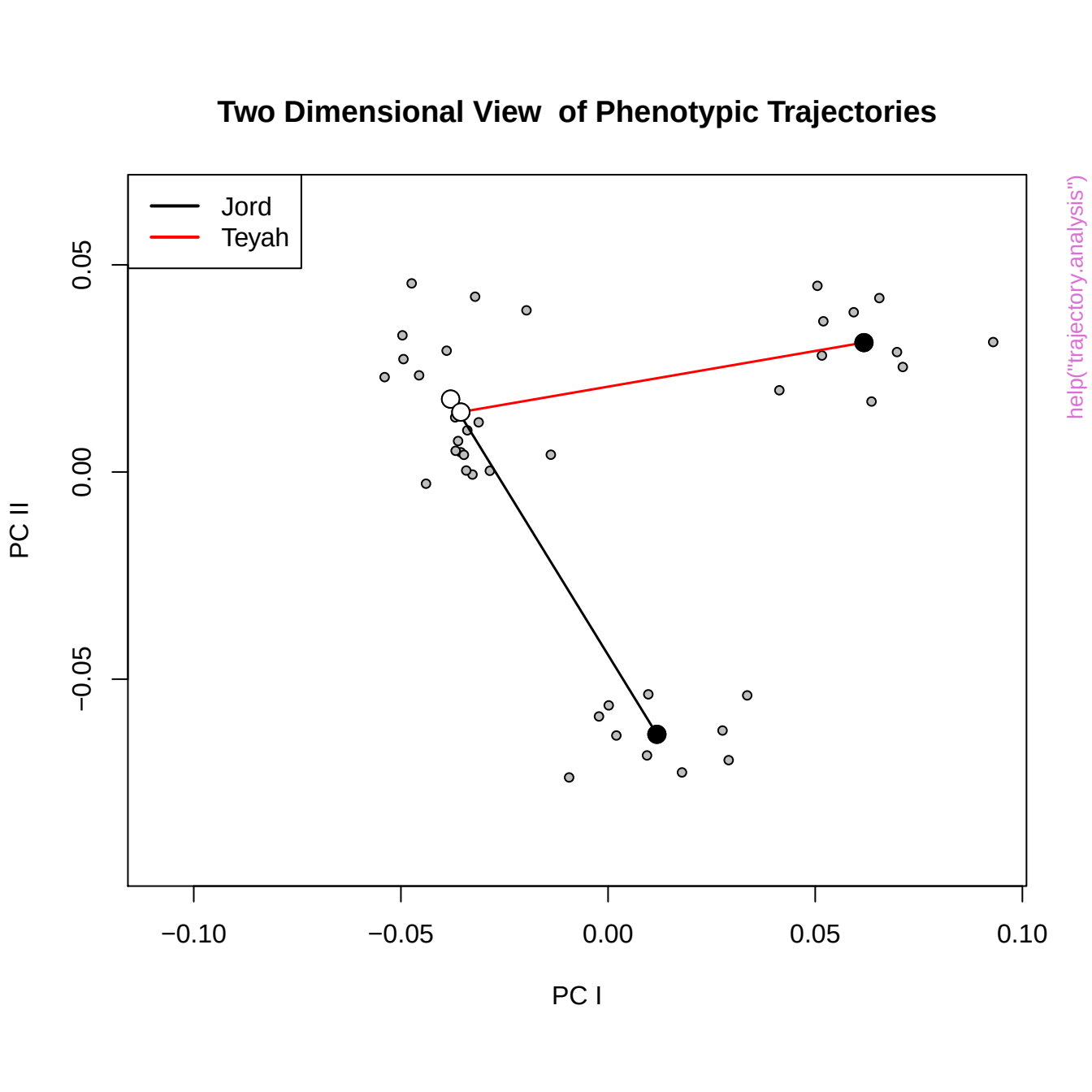


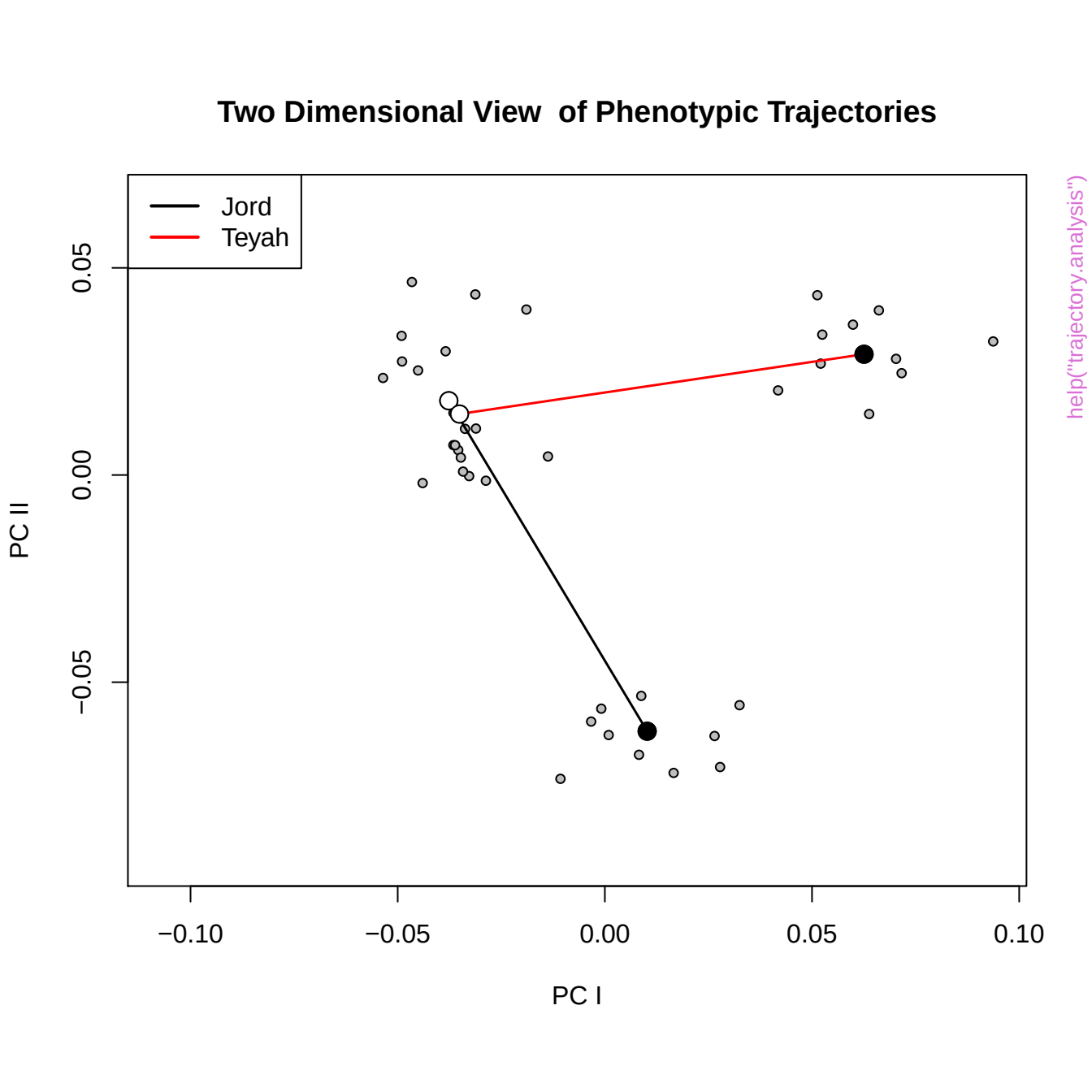
help("shape.predictor")

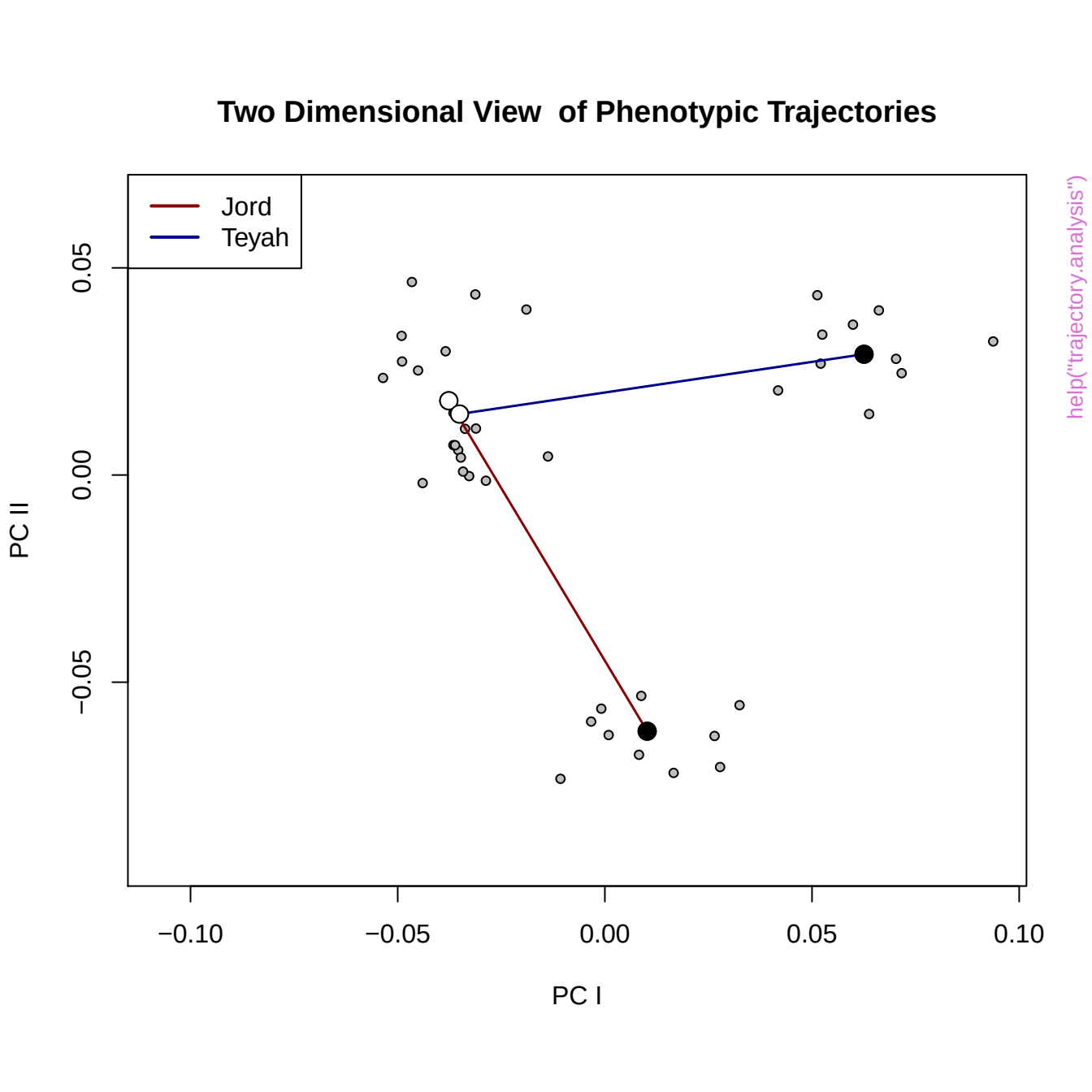


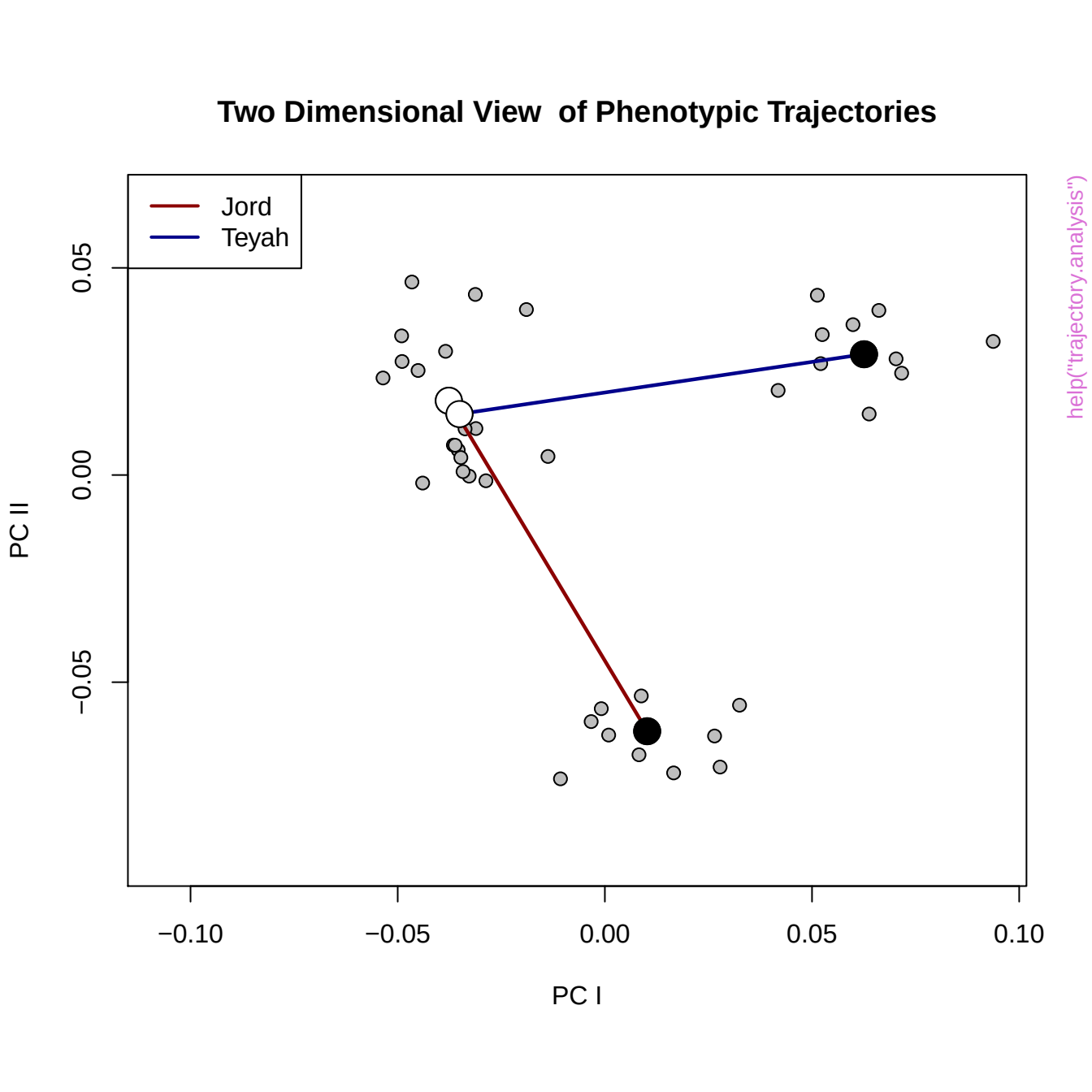
help("shape.predictor")

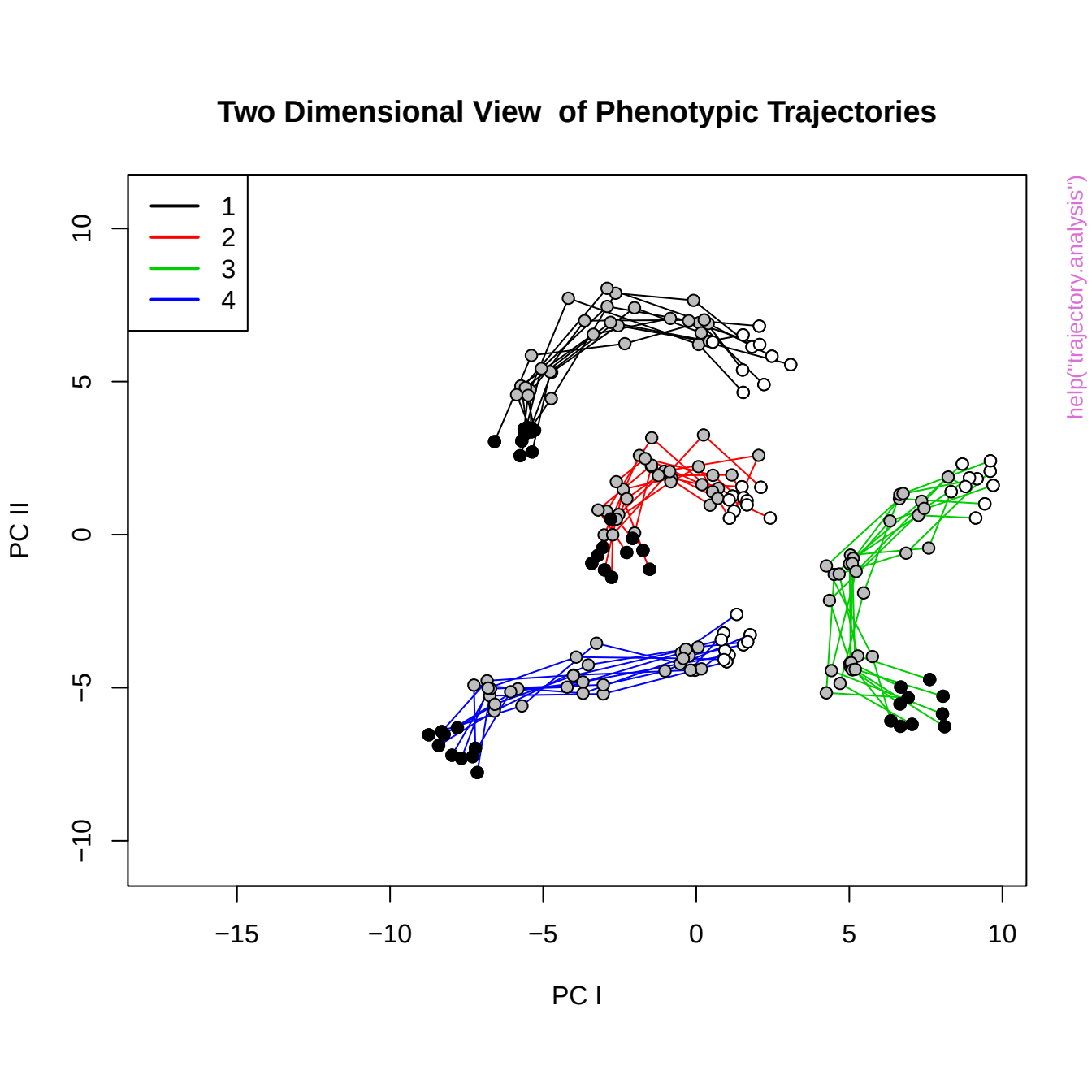

Two Dimensional View of Phenotypic Trajectories
Jord
Teyah
0.05
0.00
−0.05
PC II
−0.10
−0.05
0.00
0.05
0.10
PC I
help("trajectory.analysis")

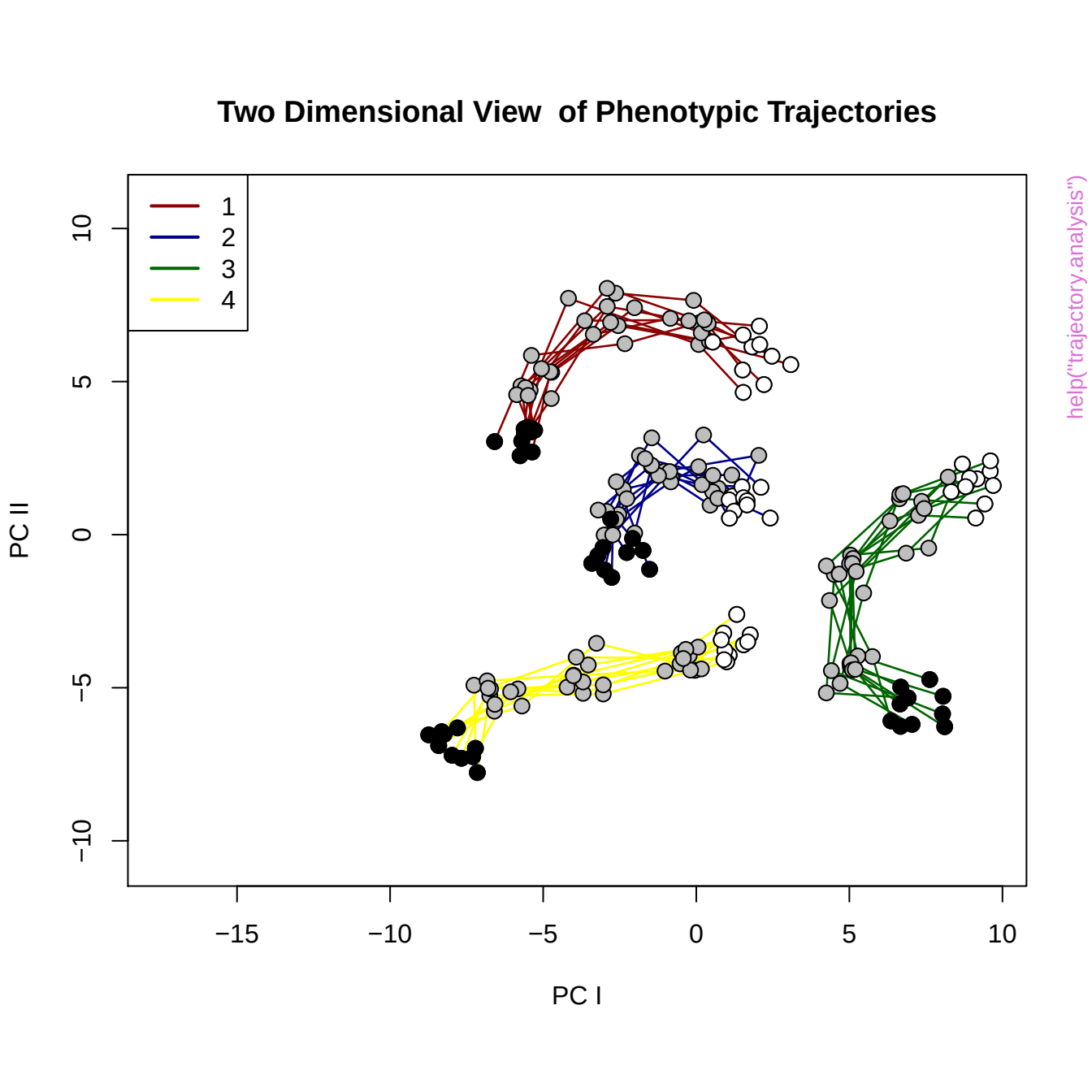

Two Dimensional View of Phenotypic Trajectories
Jord
Teyah
0.05
0.00
−0.05
PC II
−0.10
−0.05
0.00
0.05
0.10
PC I
help("trajectory.analysis")

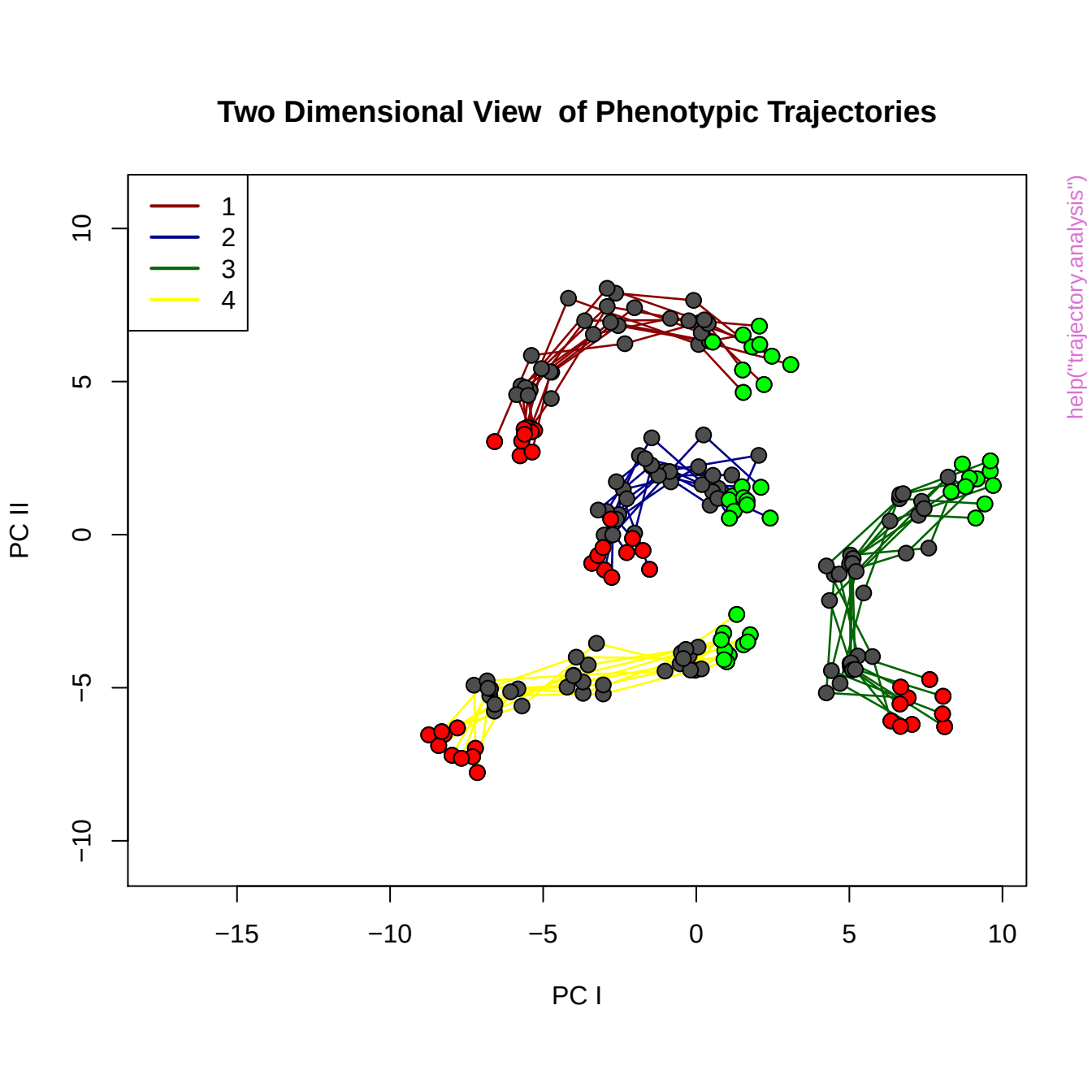

Two Dimensional View of Phenotypic Trajectories
Jord
Teyah
0.05
0.00
−0.05
PC II
−0.10
−0.05
0.00
0.05
0.10
PC I
help("trajectory.analysis")

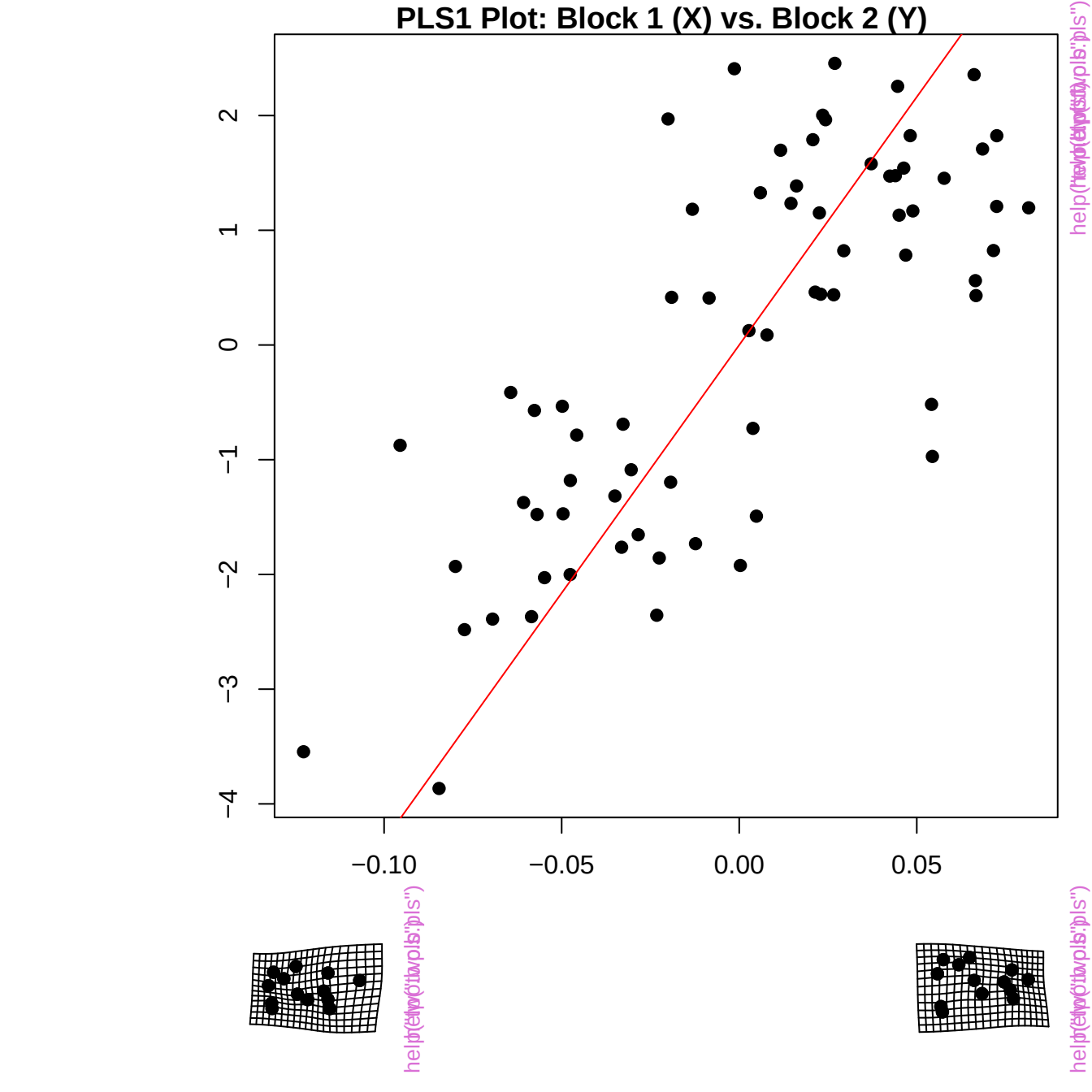

Two Dimensional View of Phenotypic Trajectories
Jord
Teyah
0.05
0.00
−0.05
PC II
−0.10
−0.05
0.00
0.05
0.10
PC I
help("trajectory.analysis")


Two Dimensional View of Phenotypic Trajectories
Jord
Teyah
0.05
0.00
−0.05
PC II
−0.10
−0.05
0.00
0.05
0.10
PC I
help("trajectory.analysis")


Two Dimensional View of Phenotypic Trajectories
1
2
3
4
PC II
PC I
10
5
0
−5
−10
−15
−10
−5
0
5
10
help("trajectory.analysis")


Two Dimensional View of Phenotypic Trajectories
1
2
3
4
PC II
PC I
10
5
0
−5
−10
−15
−10
−5
0
5
10
help("trajectory.analysis")


Two Dimensional View of Phenotypic Trajectories
1
2
3
4
PC II
PC I
10
5
0
−5
−10
−15
−10
−5
0
5
10
help("trajectory.analysis")


PLS1 Plot: Block 1 (X) vs. Block 2 (Y)
2
1
0
−1
−2
−3
−4
−0.10
−0.05
0.00
0.05