Field Chlorophyll Analysis of Old and Young Leaves

Kenia E. Segura Aba

5/2/2020

This tutorial uses R version 4.0.0, `RRPP` version 0.5.2, `tidyverse` version 1.3.0, and `kableExtra` version 1.1.0.

1. load necessary packages

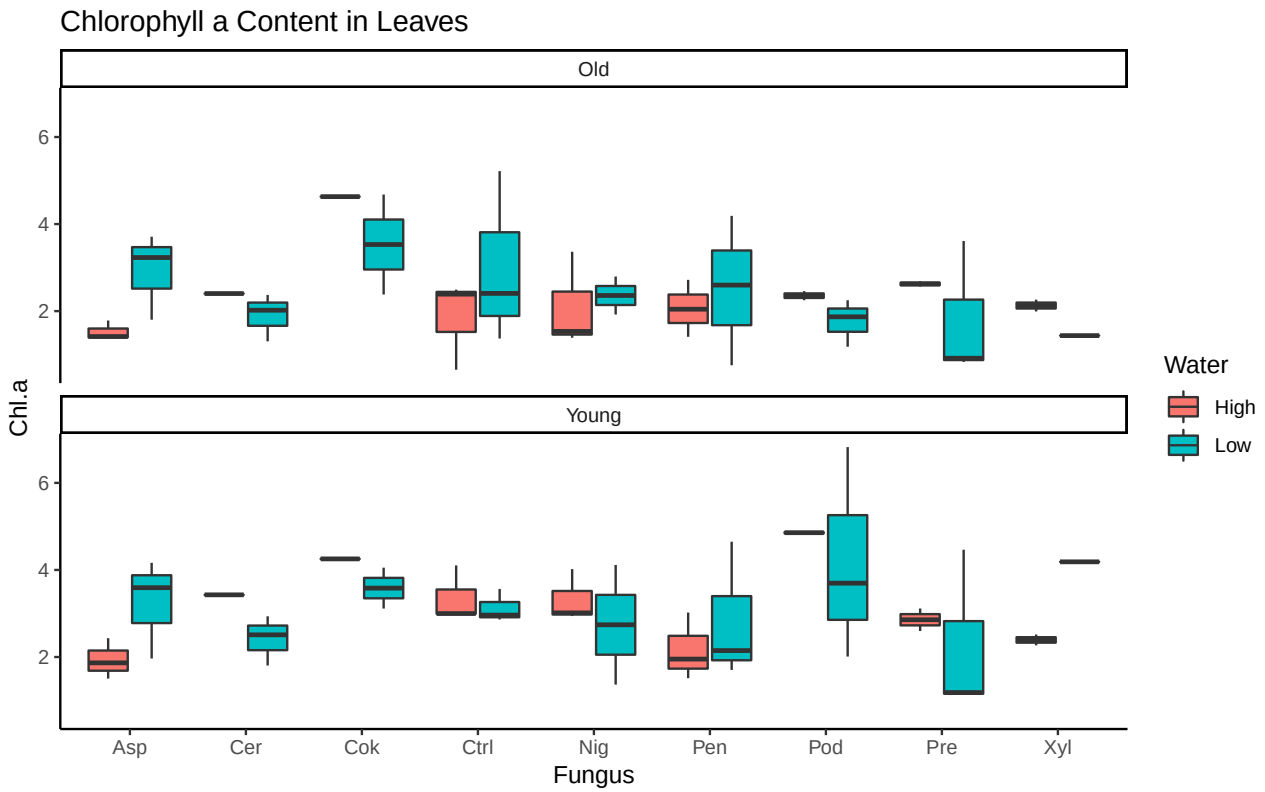
```
library(RRPP)
library(tidyverse)
library(kableExtra)
```

2. Upload data

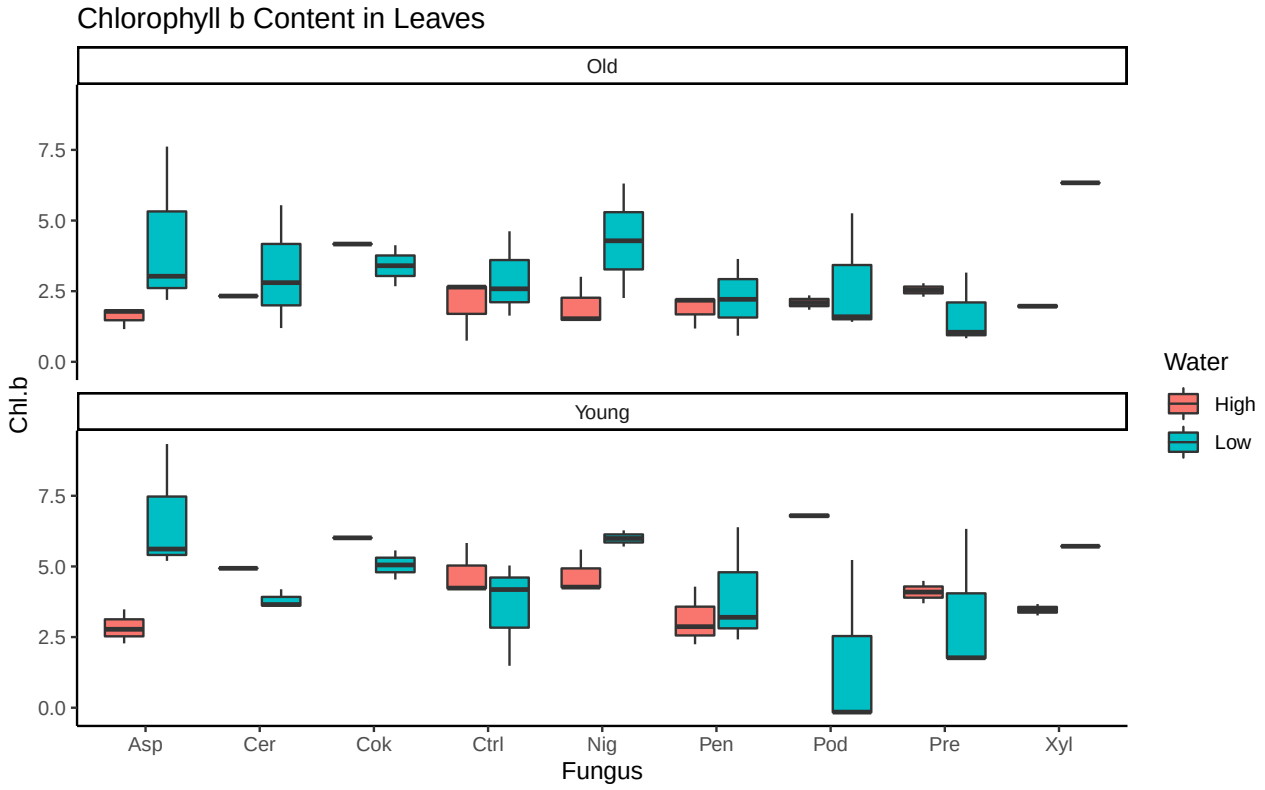
```
path <- "~/Box/Summer 2018 TX Endo Field Samples and Analysis/Statistics/Old + Young Chlorophyll/"

chldata <- read.csv(paste(path, "chlorophyll_data.csv", sep = ""),
    header = T, row.names = 1)

# create a total chlorophyll column (a + b)
chldata$Total <- chldata$Chl.a + chldata$Chl.b
```

3. Calculate total chlorophyll content, summary statistics, and visualize data.

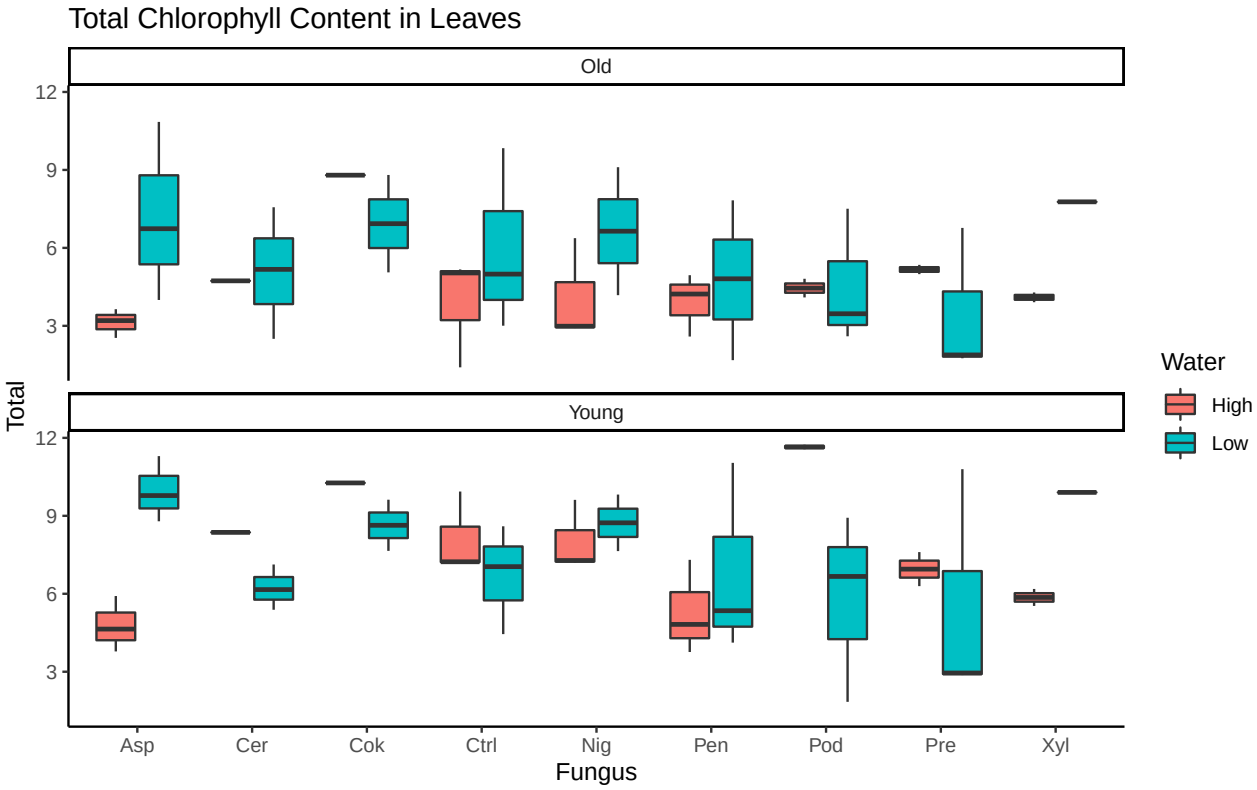
```
# plot chl a
chla <- chldata %>% ggplot(aes(x = Fungus, y = Chl.a, fill = Water)) +
    geom_boxplot() + theme_classic() + facet_wrap(~Age, dir = "v")
print(chla + labs(title = "Chlorophyll a Content in Leaves"))
```



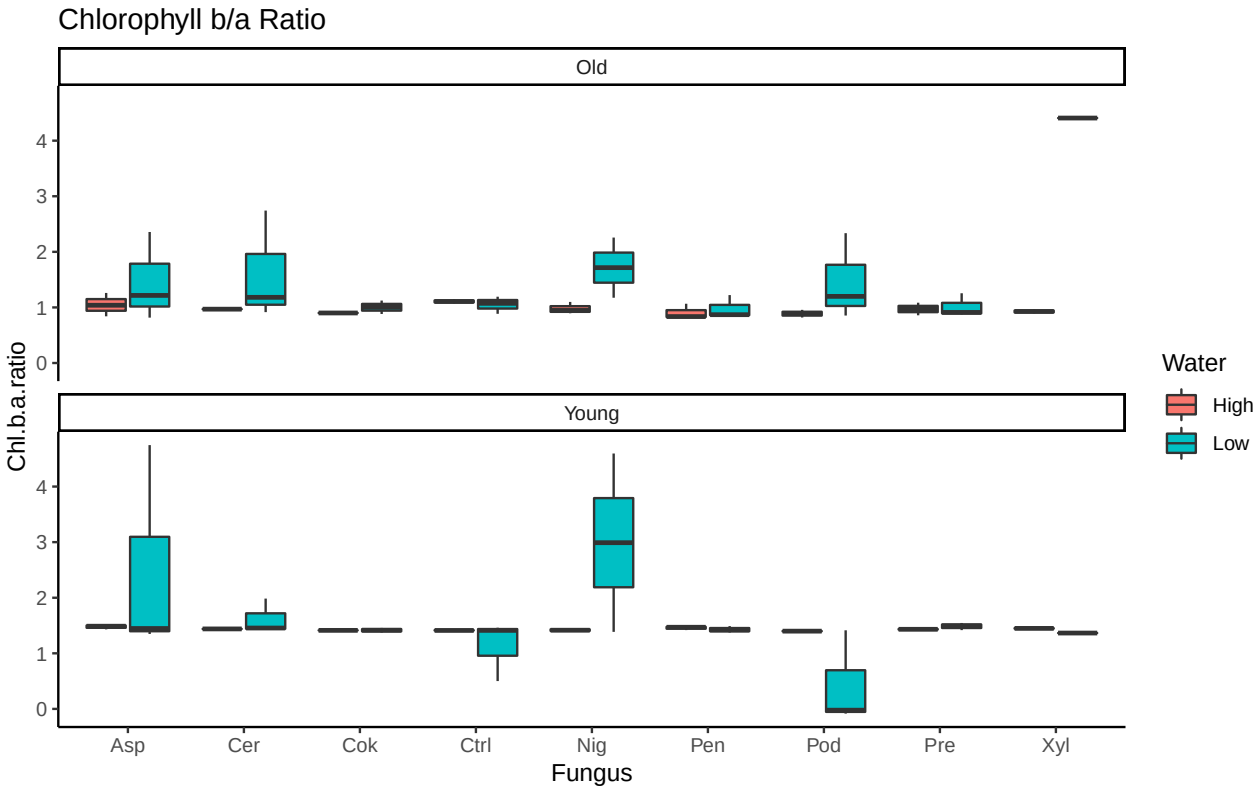

```
# plot chl b
chlb <- chldata %>% ggplot(aes(x = Fungus, y = Chl.b, fill = Water)) +
    geom_boxplot() + theme_classic() + facet_wrap(~Age, dir = "v")
print(chlb + labs(title = "Chlorophyll b Content in Leaves"))
```



```
# plot total chlorophyll
tot <- chldata %>% ggplot(aes(x = Fungus, y = Total, fill = Water)) +
    geom_boxplot() + theme_classic() + facet_wrap(~Age, dir = "v")
print(tot + labs(title = "Total Chlorophyll Content in Leaves"))
```




```
# plot chl b/a ratio
chlb.a <- chldata %>% ggplot(aes(x = Fungus, y = Chl.b.a.ratio,
    fill = Water)) + geom_boxplot() + theme_classic() + facet_wrap(~Age,
    dir = "v")
print(chlb.a + labs(title = "Chlorophyll b/a Ratio"))
```




```
# summary statistics
stats <- chldata %>% group_by(Water, Fungus) %>% select(Chl.a) %>%
    summarise_each(funs(Min = min, Q1 = quantile(., 0.25), Median = median,
        Q3 = quantile(., 0.75), Max = max, Mean = mean, SD = sd))

stats2 <- chldata %>% group_by(Water, Fungus) %>% select(Chl.b) %>%
    summarise_each(funs(Min = min, Q1 = quantile(., 0.25), Median = median,
        Q3 = quantile(., 0.75), Max = max, Mean = mean, SD = sd))

stats3 <- chldata %>% group_by(Water, Fungus) %>% select(Chl.b.a.ratio) %>%
    summarise_each(funs(Min = min, Q1 = quantile(., 0.25), Median = median,
        Q3 = quantile(., 0.75), Max = max, Mean = mean, SD = sd))

stats4 <- chldata %>% group_by(Water, Fungus) %>% select(Total) %>%
    summarise_each(funs(Min = min, Q1 = quantile(., 0.25), Median = median,
        Q3 = quantile(., 0.75), Max = max, Mean = mean, SD = sd))


stats %>% kable() %>% kable_styling(full_width = F) %>% add_header_above(c(` ` = 2,
    `Chl a` = 7)) %>% collapse_rows()
```

		Chl a						
Water	Fungus	Min	Q1	Median	Q3	Max	Mean	SD
High	Asp	1.3785	1.438375	1.64465	1.845525	2.4325	1.730400	0.3969141
	Cer	2.4034	2.659700	2.91600	3.172300	3.4286	2.916000	0.7249259
	Cok	4.2542	4.348175	4.44215	4.536125	4.6301	4.442150	0.2658014
	Ctrl	0.6543	2.416075	2.74235	2.996475	4.1046	2.605350	1.1327896
	Nig	1.3885	1.886175	2.97785	3.276550	4.0201	2.710450	1.0410501
	Pen	1.4103	1.623000	1.99855	2.549825	3.0217	2.110083	0.6443822
	Pod	2.2508	2.407100	3.64395	4.842250	4.8829	3.605400	1.4465113
	Pre	2.5646	2.589350	2.64125	2.792350	3.1147	2.740450	0.2546096
	Xyl	1.9925	2.196050	2.26565	2.330000	2.5178	2.260400	0.2145433
Low	Asp	1.8032	2.282550	3.41230	3.680150	4.1644	3.077933	0.9724927
	Cer	1.3056	1.858450	2.19620	2.475375	2.9348	2.157850	0.5733045
	Cok	2.3816	2.930825	3.58330	4.209275	4.6790	3.556800	1.0136576
	Ctrl	1.3706	2.521075	2.91315	3.413525	5.2171	3.064117	1.2833496
	Nig	1.3661	1.783475	2.35900	3.125225	4.1147	2.549700	1.1977419
	Pen	0.7559	1.814325	2.37305	3.791275	4.6496	2.673950	1.4901283
	Pod	1.1815	1.904725	2.13075	3.335300	6.8223	2.971917	2.0599131
	Pre	0.8341	0.970475	1.15580	3.003875	4.4658	2.023350	1.5892062
	Xyl	1.4374	2.124750	2.81210	3.499450	4.1868	2.812100	1.9441194

```
stats2 %>% kable() %>% kable_styling(full_width = F) %>% add_header_above(c(` ` = 2,
    `Chl b` = 7)) %>% collapse_rows()
```

		Chl b						
Water	Fungus	Min	Q1	Median	Q3	Max	Mean	SD
High	Asp	1.1578	1.802800	2.06590	2.651275	3.4807	2.221967	0.8188023
	Cer	2.3279	2.979350	3.63080	4.282250	4.9337	3.630800	1.8425789
	Cok	4.1675	4.628375	5.08925	5.550125	6.0110	5.089250	1.3035514
	Ctrl	0.7493	2.652775	3.44605	4.228750	5.8297	3.391517	1.7540252
	Nig	1.4517	1.897100	3.63340	4.264575	5.5941	3.350983	1.6580124
	Pen	1.1784	2.192475	2.23820	2.712925	4.2843	2.497917	1.0301252
	Pod	1.8431	2.224775	4.54235	6.762600	6.8523	4.445025	2.7190193
	Pre	2.3051	2.662850	3.23910	3.894375	4.4892	3.318125	0.9708800
	Xyl	1.9172	1.994675	2.64285	3.366050	3.6686	2.717875	0.8814486
Low	Asp	2.1927	3.570600	5.40600	7.116375	9.3309	5.496817	2.6947445
	Cer	1.1950	2.996500	3.61605	4.056800	5.5423	3.493850	1.4477185
	Cok	2.6757	3.764025	4.33190	4.794500	5.5670	4.226625	1.1983699
	Ctrl	1.4843	1.872325	3.38255	4.510275	5.0331	3.256267	1.5551574
	Nig	2.2579	4.842175	5.99005	6.284650	6.3091	5.136775	1.9392895
	Pen	0.9236	2.263875	2.80870	3.530525	6.3876	3.130333	1.8490598
	Pod	-0.1698	0.237575	1.50615	4.320025	5.2567	2.195317	2.4760652
	Pre	0.8355	1.220800	1.75545	2.810150	6.3290	2.479950	2.0534522
	Xyl	5.7141	5.869250	6.02440	6.179550	6.3347	6.024400	0.4388305

```
stats3 %>% kable() %>% kable_styling(full_width = F) %>% add_header_above(c(` ` = 2,
    `Chl b/a` = 7)) %>% collapse_rows()
```

Water	Fungus	Chl b/a						
		Min	Q1	Median	Q3	Max	Mean	SD
High	Asp	0.8399000	1.0947000	1.345747	1.473605	1.513249	1.261981	0.2721681
	Cer	0.9686000	1.0861968	1.203794	1.321390	1.438987	1.203794	0.3326139
	Cok	0.9001000	1.0283148	1.156530	1.284744	1.412959	1.156530	0.3626463
	Ctrl	1.0730000	1.1162250	1.277402	1.411244	1.420294	1.261076	0.1690156
	Nig	0.8948000	0.9843500	1.245312	1.409754	1.446971	1.199054	0.2498186
	Pen	0.8204000	0.8932000	1.242076	1.456214	1.484446	1.182250	0.3142204
	Pod	0.8189000	0.9220250	1.175364	1.396577	1.403323	1.143238	0.3004410
	Pre	0.8585000	1.0282250	1.253842	1.427493	1.441321	1.201876	0.2815388
	Xyl	0.8925000	0.9447750	1.201136	1.444321	1.457067	1.187960	0.3023483
Low	Asp	0.8165000	1.2490922	1.397398	2.129357	4.745607	1.988317	1.4430095
	Cer	0.9153000	1.2432041	1.441539	1.852052	2.742500	1.617810	0.6550962
	Cok	0.8820000	1.0631250	1.248568	1.394481	1.457018	1.209038	0.2600366
	Ctrl	0.5008402	0.9324500	1.133150	1.357552	1.460632	1.087613	0.3580767
	Nig	1.1744000	1.3332090	1.821573	2.841354	4.594418	2.352991	1.5660008
	Pen	0.8517000	0.9573000	1.297849	1.408012	1.489756	1.204278	0.2805299
	Pod	-0.0844468	0.1964067	1.026300	1.360309	2.335800	0.949229	0.9190565
	Pre	0.8746000	0.9963500	1.335999	1.474218	1.545791	1.249302	0.2936034
	Xyl	1.3647763	2.1253072	2.885838	3.646369	4.406900	2.885838	2.1511063

```
stats4 %>% kable() %>% kable_styling(full_width = F, ) %>% add_header_above(c(` ` = 2,
    `Total Chlorophyll` = 7)) %>% collapse_rows()
```

Water	Fungus	Total Chlorophyll						
		Min	Q1	Median	Q3	Max	Mean	SD
High	Asp	2.5363	3.311200	3.71055	4.426775	5.9132	3.952367	1.184572
	Cer	4.7313	5.639050	6.54680	7.454550	8.3623	6.546800	2.567505
	Cok	8.7976	9.164500	9.53140	9.898300	10.2652	9.531400	1.037750
	Ctrl	1.4036	5.068850	6.18840	7.225225	9.9343	5.996867	2.870463
	Nig	2.9146	3.833050	6.78635	7.260450	9.6142	6.061433	2.640505
	Pen	2.5887	3.875550	4.52275	4.916675	7.3060	4.608000	1.573892
	Pod	4.0939	4.631875	8.18630	11.604850	11.7352	8.050425	4.165380
	Pre	4.9900	5.257525	5.82020	6.621250	7.6039	6.058575	1.167894
	Xyl	3.9097	4.190725	4.90850	5.696050	6.1864	4.978275	1.063039
Low	Asp	3.9959	7.250750	9.28470	10.581175	11.2971	8.574750	2.771967
	Cer	2.5006	5.226200	5.77320	6.885400	7.5632	5.651700	1.806590
	Cok	5.0573	7.002500	8.22835	9.009275	9.6197	7.783425	1.988842
	Ctrl	3.0058	4.583650	6.01750	8.208475	9.8370	6.320383	2.620370
	Nig	4.1805	6.777075	8.37355	9.282950	9.8183	7.686475	2.506609
	Pen	1.6795	4.293075	5.07940	7.209275	11.0372	5.804283	3.241293
	Pod	1.8412	2.814625	5.06620	7.297150	8.9249	5.167233	2.912251
	Pre	1.7535	2.128350	2.91125	5.814025	10.7948	4.503300	3.583994
	Xyl	7.7721	8.304300	8.83650	9.368700	9.9009	8.836500	1.505289

4. Run Linear models in RRPP for each fungal treatment and estimate model coefficients. "d" is the amount of change in a variable for the coefficient indicated.

```
high <- chldata %>% filter(Water == "High") %>% droplevels.data.frame()
low <- chldata %>% filter(Water == "Low") %>% droplevels.data.frame()

# chl b/a ratio linear models and coefficient tests
highLM <- lm.rrpp(Chl.b.a.ratio ~ Block * Fungus * Age, data = high,
```

```
    SS.type = "III", print.progress = F)
```

```
##
## Warning: Because variables in the linear model are redundant,
## the linear model design has been truncated (via QR decomposition).
## Original X columns: 36
## Final X columns (rank): 32
## Check coefficients or degrees of freedom in ANOVA to see changes.
```

```
summary(highLM)
```

```
##
## Warning: Because variables in the linear model are redundant,
## the linear model design has been truncated (via QR decomposition).
## Original X columns: 36
## Final X columns (rank): 32
## Check coefficients or degrees of freedom in ANOVA to see changes.
```

```
##
## Linear Model fit with lm.rrpp
##
## Number of observations: 40
## Number of dependent variables: 1
## Data space dimensions: 1
## Sums of Squares and Cross-products: Type III
## Number of permutations: 1000
##
## Full Model Analysis of Variance
##
##                       Df Residual Df       SS Residual SS       Rsq        F
## Block * Fungus * Age 31           8 2.392622  0.01395011 0.9942033 44.26136
##                       Z (from F) Pr(>F)
## Block * Fungus * Age   7.565094  0.001
##
##
## Redundancy Analysis (PCA on fitted values and residuals)
##
##                Trace Proportion Rank
## Fitted    0.06134928  0.9942034    1
## Residuals 0.00035770  0.0057968    1
## Total     0.06170697  1.0000000    1
##
## Eigenvalues
##
##                   PC1
## Fitted    0.06134928
## Residuals 0.00035770
## Total     0.06170697
```

```
coef(highLM, test = T)
```

```
##
## Linear Model fit with lm.rrpp
##
## Number of observations: 40
## Number of dependent variables: 1
```

```
## Data space dimensions: 1
## Sums of Squares and Cross-products: Type III
## Number of permutations: 1000
##
## Statistics (distances) of coefficients with 95 percent confidence intervals,
## effect sizes, and probabilities of exceeding observed values based on
## 1000 random permutations using RRPP
##
##                                 d.obs  UCL (95%)          Zd Pr(>d)
## (Intercept)                 0.62593333 0.78240545 -1.61026300  0.940
## Block                       0.21035000 0.10644294  6.17690316  0.001
## FungusCer                   0.13231667 0.13025502  2.03270522  0.047
## FungusCok                   0.06381667 0.13567589  0.34866901  0.309
## FungusCtrl                  0.44870000 0.21121828  5.32948001  0.001
## FungusNig                   0.14976667 0.20847996  1.03705091  0.159
## FungusPen                   0.03556667 0.20911076 -0.69398103  0.694
## FungusPod                   0.46796667 0.25391620  4.60884320  0.001
## FungusPre                   0.11941667 0.20343556  0.59221237  0.251
## FungusXyl                   0.19686667 0.26144524  1.21008749  0.124
## AgeYoung                    0.76904060 0.28815474  7.38986713  0.001
## Block:FungusCtrl            0.19355000 0.09351292  5.20915960  0.001
## Block:FungusNig             0.10820000 0.09778119  2.32840271  0.032
## Block:FungusPen             0.08740000 0.08993824  1.86990070  0.055
## Block:FungusPod             0.34785000 0.14343138  6.07693157  0.001
## Block:FungusPre             0.09720000 0.08836244  2.13479907  0.033
## Block:FungusXyl             0.14065000 0.14044561  1.90008510  0.050
## Block:AgeYoung              0.16917263 0.06077501  7.02633383  0.001
## FungusCer:AgeYoung          0.12948086 0.13349893  1.77002306  0.058
## FungusCok:AgeYoung          0.08700861 0.13480982  0.75017254  0.219
## FungusCtrl:AgeYoung         0.41916536 0.21472050  5.08899738  0.001
## FungusNig:AgeYoung          0.09549141 0.21626233  0.08565683  0.394
## FungusPen:AgeYoung          0.02459043 0.21354610 -0.97526937  0.823
## FungusPod:AgeYoung          0.47760590 0.26753430  4.38983017  0.001
## FungusPre:AgeYoung          0.10072544 0.20879287  0.18385219  0.382
## FungusXyl:AgeYoung          0.16876311 0.26846199  0.66919439  0.251
## Block:FungusCtrl:AgeYoung 0.14707756 0.08723097  4.09145843  0.003
## Block:FungusNig:AgeYoung  0.05145228 0.08926494  0.54736940  0.269
## Block:FungusPen:AgeYoung  0.07179740 0.08828676  1.28525319  0.118
## Block:FungusPod:AgeYoung  0.31566678 0.14426725  5.85033910  0.001
## Block:FungusPre:AgeYoung  0.06524132 0.08845217  1.07151266  0.153
## Block:FungusXyl:AgeYoung  0.11646746 0.14196521  1.32866227  0.117
```

```
lowLM <- lm.rrpp(Chl.b.a.ratio ~ Block * Fungus * Age, data = low,
    SS.type = "III", print.progress = F)
```

```
##
## Warning: Because variables in the linear model are redundant,
## the linear model design has been truncated (via QR decomposition).
## Original X columns: 36
## Final X columns (rank): 34
## Check coefficients or degrees of freedom in ANOVA to see changes.
```

```
summary(lowLM)
```

```
##
```

```
## Warning: Because variables in the linear model are redundant,
## the linear model design has been truncated (via QR decomposition).
## Original X columns: 36
## Final X columns (rank): 34
## Check coefficients or degrees of freedom in ANOVA to see changes.
```

```
##
## Linear Model fit with lm.rrpp
##
## Number of observations: 46
## Number of dependent variables: 1
## Data space dimensions: 1
## Sums of Squares and Cross-products: Type III
## Number of permutations: 1000
##
## Full Model Analysis of Variance
##
##                       Df Residual Df       SS Residual SS       Rsq        F
## Block * Fungus * Age 33          12 38.48417    4.291964 0.8996645 3.260568
##                       Z (from F) Pr(>F)
## Block * Fungus * Age   1.596751  0.058
##
##
## Redundancy Analysis (PCA on fitted values and residuals)
##
##               Trace Proportion Rank
## Fitted    0.8552037  0.8996645    1
## Residuals 0.0953770  0.1003355    1
## Total     0.9505807  1.0000000    1
##
## Eigenvalues
##
##                 PC1
## Fitted    0.8552037
## Residuals 0.0953770
## Total     0.9505807
```

```
coef(lowLM, test = T)
```

```
##
## Linear Model fit with lm.rrpp
##
## Number of observations: 46
## Number of dependent variables: 1
## Data space dimensions: 1
## Sums of Squares and Cross-products: Type III
## Number of permutations: 1000
##
## Statistics (distances) of coefficients with 95 percent confidence intervals,
## effect sizes, and probabilities of exceeding observed values based on
## 1000 random permutations using RRPP
##
##                                d.obs UCL (95%)          Zd Pr(>d)
## (Intercept)              2.604166667 2.3812771  2.20410896  0.033
## Block                    0.570500000 0.5182633  2.39472974  0.023
```

```
## FungusCer                 0.569933333 2.5153066 -0.43813451  0.582
## FungusCok                 1.963666667 3.1369098  0.75802946  0.163
## FungusCtrl                1.861066667 2.4327801  1.17769678  0.102
## FungusNig                 0.194133333 2.6074282 -0.88687596  0.863
## FungusPen                 1.976066667 2.5036802  1.27796647  0.104
## FungusPod                 0.004266667 2.5230863 -1.14346043  0.998
## FungusPre                 1.971166667 2.4519874  1.32155944  0.094
## FungusXyl                 2.373233333 1.5507146  3.30853828  0.025
## AgeYoung                  3.487937297 1.8351196  4.70526110  0.001
## Block:FungusCer           0.210000000 0.7316576 -0.42391780  0.590
## Block:FungusCok           0.812000000 1.1892988  0.92705073  0.173
## Block:FungusCtrl          0.724250000 0.7455906  1.81465289  0.057
## Block:FungusNig           0.029200000 0.7266514 -1.20670602  0.932
## Block:FungusPen           0.746900000 0.7732649  1.79272389  0.060
## Block:FungusPod           0.001950000 0.7500426 -1.37779019  0.998
## Block:FungusPre           0.760600000 0.7510175  2.00685659  0.046
## Block:AgeYoung            2.269119123 0.9889150  5.82392308  0.001
## FungusCer:AgeYoung        1.380191764 3.2901755  0.02929035  0.408
## FungusCok:AgeYoung        4.137690011 4.1991110  1.85918413  0.054
## FungusCtrl:AgeYoung       4.781024939 3.3113151  3.27755878  0.008
## FungusNig:AgeYoung        0.471646460 3.2815666 -0.89368918  0.799
## FungusPen:AgeYoung        4.241875805 3.4237166  2.69264946  0.018
## FungusPod:AgeYoung        2.760631578 3.3447833  1.37856771  0.109
## FungusPre:AgeYoung        4.264315316 3.4016271  2.88634671  0.018
## FungusXyl:AgeYoung        1.823305527 2.0418265  1.51061262  0.083
## Block:FungusCer:AgeYoung  1.210536461 1.5631762  1.25734412  0.122
## Block:FungusCok:AgeYoung  2.427236353 2.3633451  2.01267211  0.044
## Block:FungusCtrl:AgeYoung 2.878650458 1.5046734  4.79128042  0.001
## Block:FungusNig:AgeYoung  0.123682936 1.4894862 -1.08974218  0.884
## Block:FungusPen:AgeYoung  2.422709974 1.5582108  3.76434507  0.002
## Block:FungusPod:AgeYoung  2.419037276 1.5234606  3.83380075  0.002
## Block:FungusPre:AgeYoung  2.421205917 1.5330067  3.91195236  0.001
```

5. Run ANOVA in RRPP for each linear model.

```
# chl b/a ratio anovas
highANOVA <- anova(highLM, effect.type = "F", error = c("Residuals",
    "Block:Fungus", "Block:Fungus:Age", "Residuals", "Block:Fungus:Age",
    "Block:Fungus:Age", "Residuals"))
summary(highANOVA)
```

```
##
## Analysis of Variance, using Residual Randomization
## Permutation procedure: Randomization of null model residuals
## Number of permutations: 1000
## Estimation method: Ordinary Least Squares
## Sums of Squares and Cross-products: Type III
## Effect sizes (Z) based on F distributions
##
##                  Df      SS       MS      Rsq       F        Z Pr(>F)
## Block             1 0.08849 0.088494 0.036772 50.7490           0.002 **
## Fungus            8 0.07465 0.009331 0.031019  0.8201 -0.47624  0.671
## Age               1 0.12673 0.126734 0.052661 29.0071           0.023 *
## Block:Fungus      6 0.06827 0.011378 0.028368  6.5250  1.77838  0.036 *
## Block:Age         1 0.02862 0.028619 0.011892  6.5505           0.025 *
```

```
## Fungus:Age        8 0.03616 0.004520 0.015025  1.0345 -0.42391  0.658
## Block:Fungus:Age  6 0.02621 0.004369 0.010893  2.5055  1.16914  0.104
## Residuals         8 0.01395 0.001744 0.005797
## Total            39 2.40657
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Call: lm.rrpp(f1 = Chl.b.a.ratio ~ Block * Fungus * Age, SS.type = "III",
##     data = high, print.progress = F)
```

```
lowANOVA <- anova(lowLM, effect.type = "F", error = c("Residuals",
    "Block:Fungus", "Block:Fungus:Age", "Residuals", "Block:Fungus:Age",
    "Block:Fungus:Age", "Residuals"))
summary(lowANOVA)
```

```
##
## Analysis of Variance, using Residual Randomization
## Permutation procedure: Randomization of null model residuals
## Number of permutations: 1000
## Estimation method: Ordinary Least Squares
## Sums of Squares and Cross-products: Type III
## Effect sizes (Z) based on F distributions
##
##                  Df     SS     MS      Rsq      F        Z Pr(>F)
## Block             1  0.651 0.6509 0.015217 1.8200           0.215
## Fungus            8 10.522 1.3153 0.245979 3.9387  0.88560  0.196
## Age               1  2.607 2.6069 0.060944 2.1006  1.16837  0.088 .
## Block:Fungus      7  2.338 0.3339 0.054645 0.9336  0.00261  0.480
## Block:Age         1  5.149 5.1489 0.120369 4.1489           0.036 *
## Fungus:Age        8  9.881 1.2351 0.230997 0.9953 -0.21371  0.566
## Block:Fungus:Age  7  8.687 1.2410 0.203084 3.4698  1.83670  0.034 *
## Residuals        12  4.292 0.3577 0.100336
## Total            45 42.776
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Call: lm.rrpp(f1 = Chl.b.a.ratio ~ Block * Fungus * Age, SS.type = "III",
##     data = low, print.progress = F)
```

6. Test pairwise differences between least squares means. Similar to tukeyHSD function in the r stats package. The pairwise function will generate tables with confidence intervals and p-values for the pairwise statistic, Euclidean distance between least-squares means.

```
# chl b/a ratio pairwise
highpw <- pairwise(highLM, groups = high$Fungus)
summary(highpw, confidence = 0.95, stat.table = T)
```

```
##
## Pairwise comparisons
##
## Groups: Asp Cer Cok Ctrl Nig Pen Pod Pre Xyl
##
## RRPP: 1000 permutations
##
## LS means:
## Vectors hidden (use show.vectors = TRUE to view)
```

```
##
## Pairwise distances between means, plus statistics
##                     d  UCL (95%)            Z Pr > d
## Asp:Cer  0.058187450 0.10320322 -0.044024032  0.502
## Asp:Cok  0.105451323 0.14814480  0.041087763  0.459
## Asp:Ctrl 0.000905116 0.03538716 -1.237179248  0.954
## Asp:Nig  0.062926762 0.09129584  0.021800062  0.496
## Asp:Pen  0.079731152 0.10842561  0.010537412  0.484
## Asp:Pod  0.118743037 0.15235664  0.016767643  0.505
## Asp:Pre  0.060104737 0.09291459  0.004794364  0.505
## Asp:Xyl  0.074021132 0.10700516  0.015703933  0.489
## Cer:Cok  0.047263873 0.10101312  0.002161435  0.472
## Cer:Ctrl 0.057282333 0.10012902 -0.042094826  0.514
## Cer:Nig  0.004739313 0.04883312 -1.076294211  0.872
## Cer:Pen  0.021543703 0.06225822 -0.286323700  0.553
## Cer:Pod  0.060555587 0.10416286  0.035535283  0.479
## Cer:Pre  0.001917287 0.05311203 -1.220478644  0.946
## Cer:Xyl  0.015833683 0.06087528 -0.489894704  0.619
## Cok:Ctrl 0.104546207 0.14777001  0.040224596  0.475
## Cok:Nig  0.042524561 0.08314593 -0.012700058  0.487
## Cok:Pen  0.025720171 0.06850836 -0.157550447  0.499
## Cok:Pod  0.013291714 0.06150881 -0.636031187  0.681
## Cok:Pre  0.045346586 0.08738173  0.009293654  0.484
## Cok:Xyl  0.031430191 0.07517390 -0.125850341  0.503
## Ctrl:Nig 0.062021646 0.08977578  0.020903726  0.481
## Ctrl:Pen 0.078826036 0.10927781  0.009019397  0.490
## Ctrl:Pod 0.117837921 0.15023118  0.015882660  0.492
## Ctrl:Pre 0.059199621 0.09347071  0.003756734  0.493
## Ctrl:Xyl 0.073116016 0.10799845  0.014913400  0.504
## Nig:Pen  0.016804390 0.04686381 -0.245379009  0.530
## Nig:Pod  0.055816275 0.09024489 -0.003497201  0.494
## Nig:Pre  0.002822025 0.03919538 -1.143384126  0.894
## Nig:Xyl  0.011094370 0.04488742 -0.556207991  0.651
## Pen:Pod  0.039011885 0.07297390 -0.013586489  0.490
## Pen:Pre  0.019626415 0.05038415 -0.231720558  0.549
## Pen:Xyl  0.005710020 0.04160410 -0.957946450  0.823
## Pod:Pre  0.058638300 0.09500790  0.009237436  0.496
## Pod:Xyl  0.044721905 0.08167184 -0.011530614  0.502
## Pre:Xyl  0.013916396 0.05103364 -0.428795664  0.587
```

```
highpw2 <- pairwise(highLM, groups = high$Age)
summary(highpw2, confidence = 0.95, stat.table = T)
```

```
##
## Pairwise comparisons
##
## Groups: Old Young
##
## RRPP: 1000 permutations
##
## LS means:
## Vectors hidden (use show.vectors = TRUE to view)
##
## Pairwise distances between means, plus statistics
##                   d UCL (95%)           Z Pr > d
```

```
## Old:Young 0.4570754 0.4736502 0.006216987  0.498
```

```
lowpw <- pairwise(lowLM, groups = low$Fungus)
summary(lowpw, confidence = 0.95, stat.table = T)
```

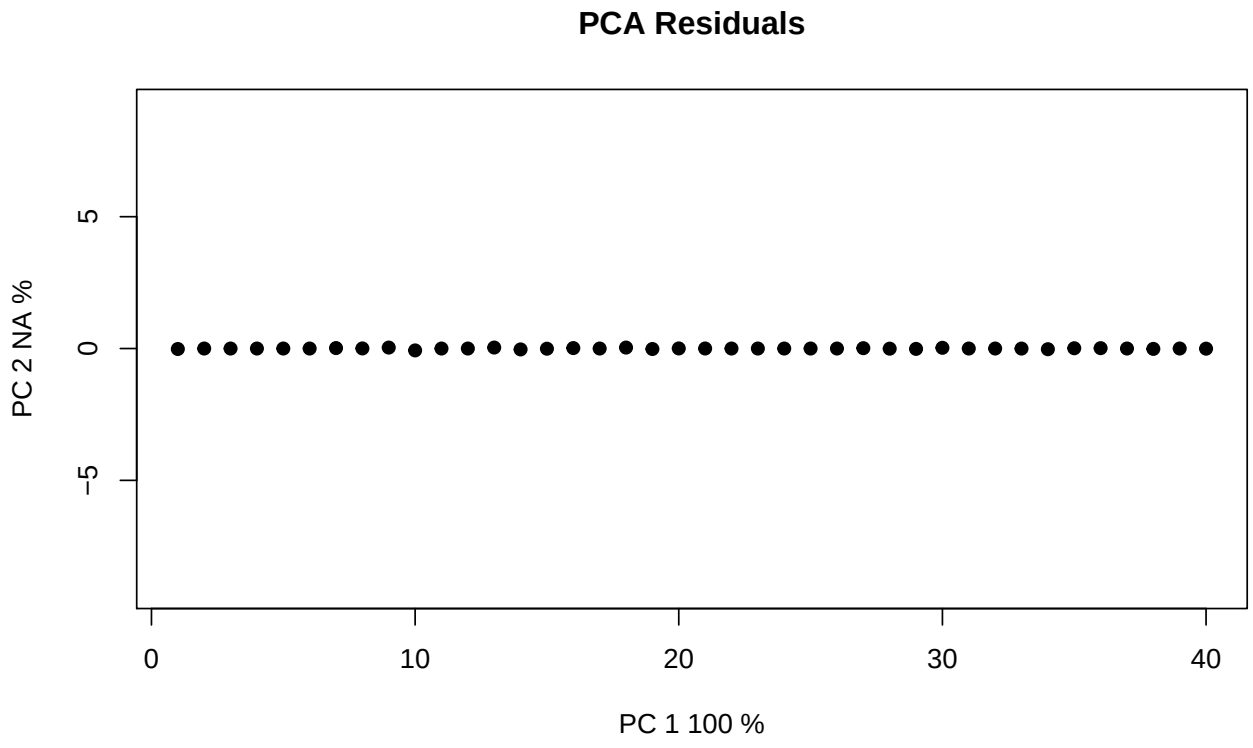
```
##
## Pairwise comparisons
##
## Groups: Asp Cer Cok Ctrl Nig Pen Pod Pre Xyl
##
## RRPP: 1000 permutations
##
## LS means:
## Vectors hidden (use show.vectors = TRUE to view)
##
## Pairwise distances between means, plus statistics
##                     d UCL (95%)             Z Pr > d
## Asp:Cer  0.370507246 0.8853904 -0.1478610225  0.510
## Asp:Cok  0.779278707 1.3278286 -0.0301422487  0.513
## Asp:Ctrl 0.900704655 1.4166997  0.0486720988  0.485
## Asp:Nig  0.364673628 0.9258853 -0.1976350688  0.536
## Asp:Pen  0.784038739 1.2985573  0.0088839580  0.495
## Asp:Pod  1.039088154 1.5506775  0.0209061636  0.481
## Asp:Pre  0.739014926 1.2434961 -0.0191867912  0.505
## Asp:Xyl  0.897521008 1.6177589 -0.0001802989  0.475
## Cer:Cok  0.408771460 0.9782648 -0.1582706790  0.527
## Cer:Ctrl 0.530197409 1.0277899  0.0238848355  0.478
## Cer:Nig  0.735180874 1.3045299 -0.0315741826  0.511
## Cer:Pen  0.413531493 0.9050760 -0.0688173046  0.483
## Cer:Pod  0.668580908 1.1598071  0.0258294564  0.487
## Cer:Pre  0.368507680 0.8352309 -0.1049670821  0.503
## Cer:Xyl  1.268028254 2.0212365  0.0033059568  0.467
## Cok:Ctrl 0.121425948 0.7199995 -0.7945657985  0.753
## Cok:Nig  1.143952335 1.7831922 -0.0328399848  0.541
## Cok:Pen  0.004760032 0.6678481 -1.3446792124  0.992
## Cok:Pod  0.259809448 0.7947886 -0.3253185841  0.556
## Cok:Pre  0.040263781 0.6994316 -1.1684395589  0.926
## Cok:Xyl  1.676799715 2.4291577 -0.0067111061  0.504
## Ctrl:Nig 1.265378283 1.8612714  0.0336356330  0.491
## Ctrl:Pen 0.116665916 0.6621089 -0.7131360410  0.722
## Ctrl:Pod 0.138383499 0.6261081 -0.6820100797  0.697
## Ctrl:Pre 0.161689729 0.6341678 -0.5632679557  0.635
## Ctrl:Xyl 1.798225663 2.4793894  0.0473879461  0.481
## Nig:Pen  1.148712367 1.7261930 -0.0020162903  0.496
## Nig:Pod  1.403761782 1.9775184  0.0071805840  0.497
## Nig:Pre  1.103688554 1.6846964 -0.0219302947  0.507
## Nig:Xyl  0.532847380 1.3106403 -0.0995566621  0.491
## Pen:Pod  0.255049415 0.7280045 -0.2874635575  0.553
## Pen:Pre  0.045023813 0.6042290 -1.0595525678  0.870
## Pen:Xyl  1.681559747 2.4276324  0.0190719930  0.472
## Pod:Pre  0.300073228 0.7769037 -0.2061556458  0.526
## Pod:Xyl  1.936609162 2.6851716  0.0257284921  0.473
## Pre:Xyl  1.636535934 2.3562280  0.0036599286  0.477
```

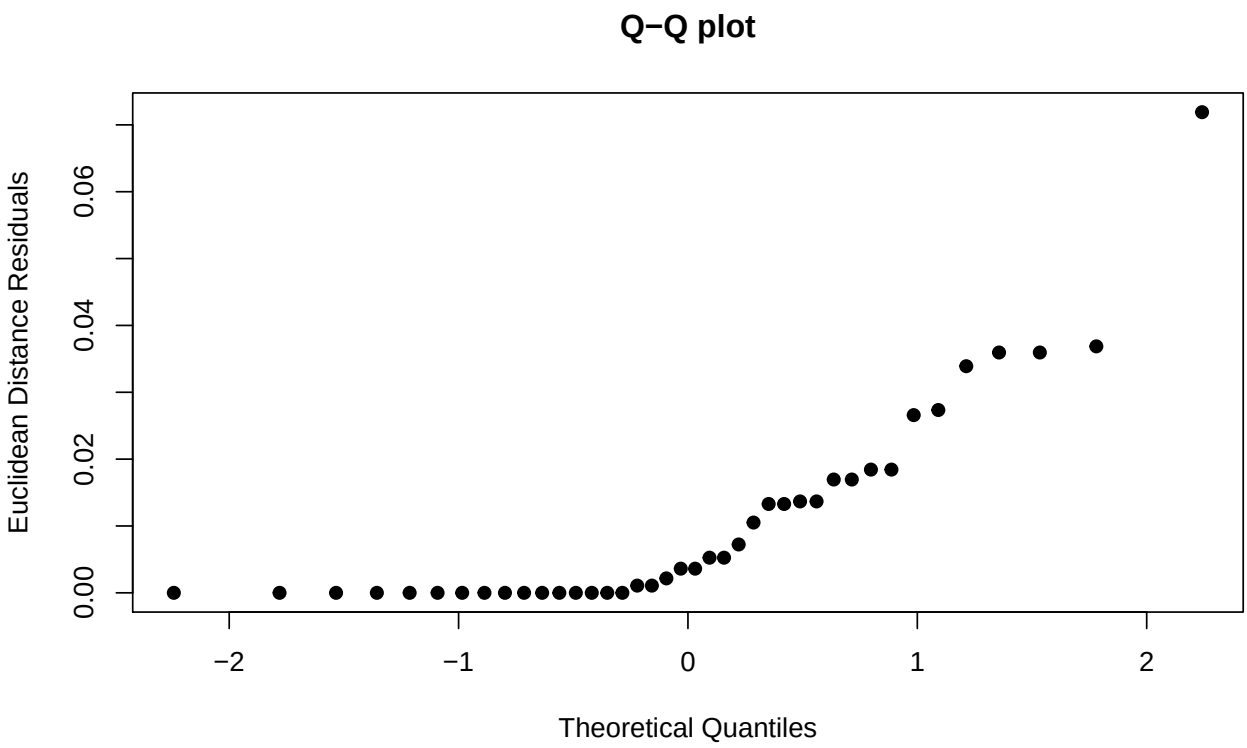
```r
lowpw2 <- pairwise(lowLM, groups = low$Age)
summary(lowpw2, confidence = 0.95, stat.table = T)
```

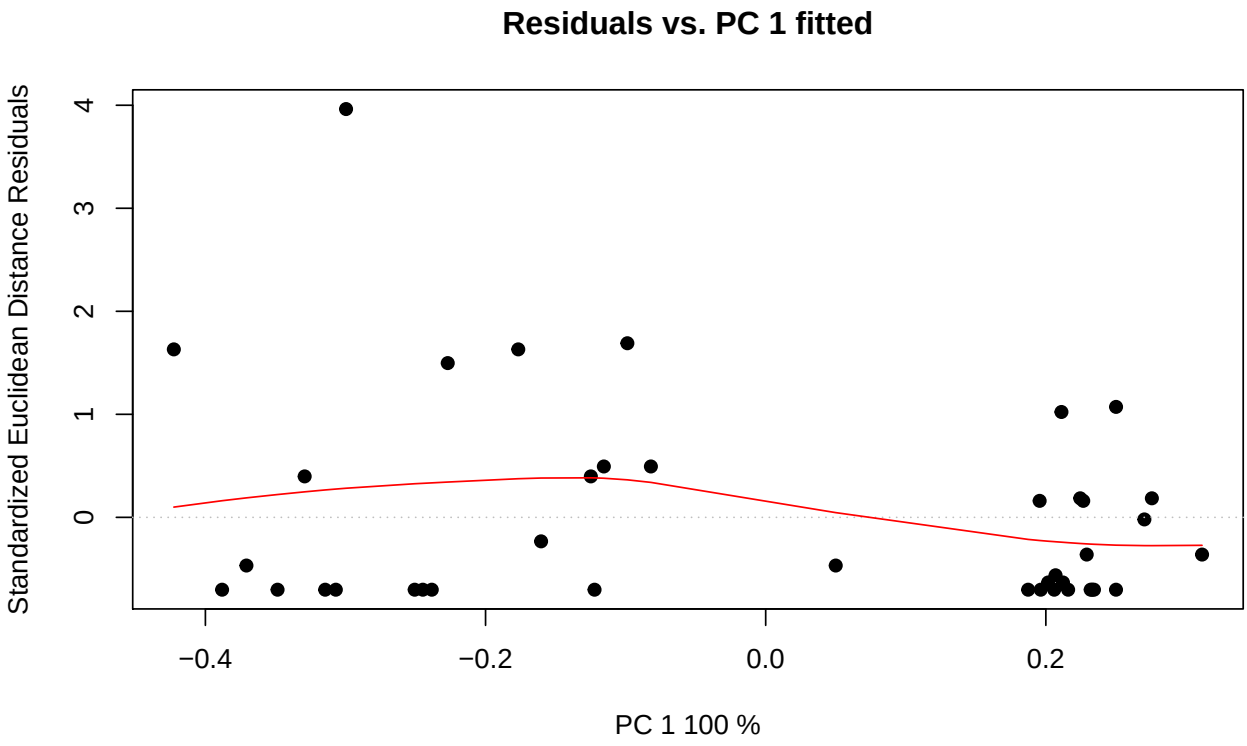
```
##
## Pairwise comparisons
##
## Groups: Old Young
##
## RRPP: 1000 permutations
##
## LS means:
## Vectors hidden (use show.vectors = TRUE to view)
##
## Pairwise distances between means, plus statistics
##                    d UCL (95%)          Z Pr > d
## Old:Young 0.1482125 0.4063939 -0.2117849  0.515
```

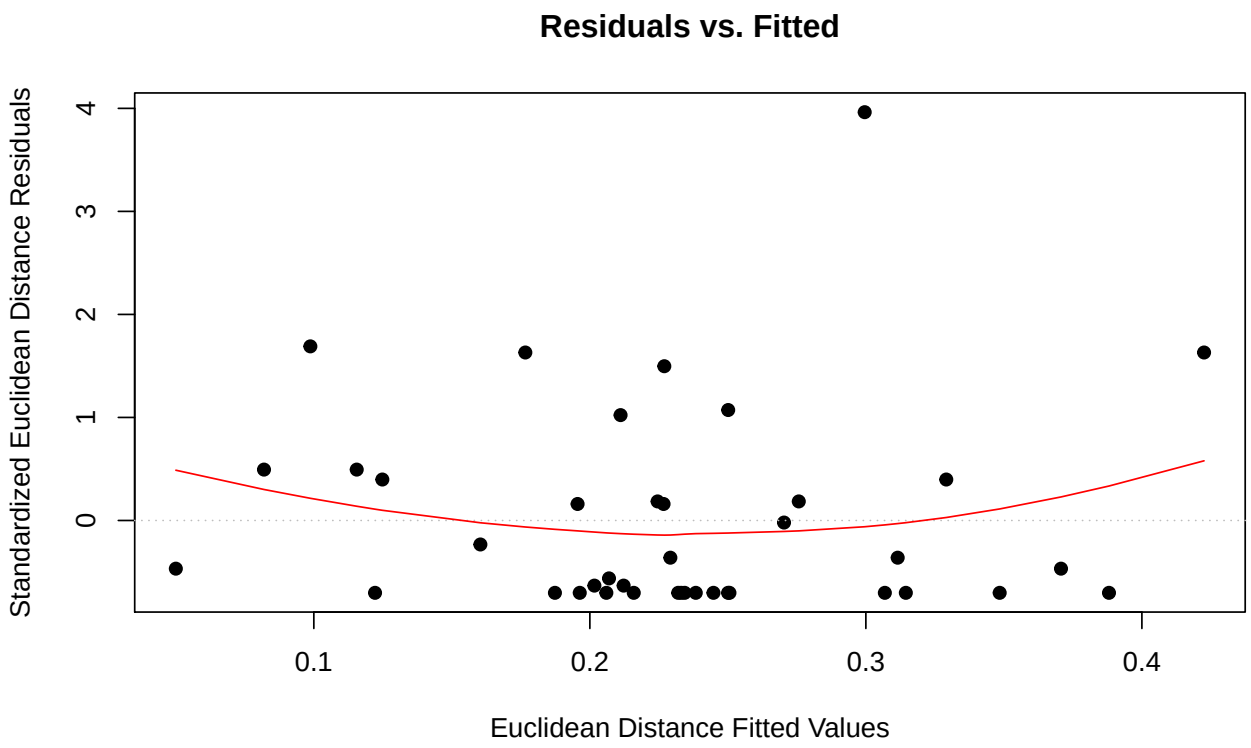
7. Examine RRPP plots to check for assumptions.

```r
## chl b/a ratio residuals vs fitted values (homoscedasticity
## check)
hdiagnostics <- plot(highLM, type = "diagnostics")
```

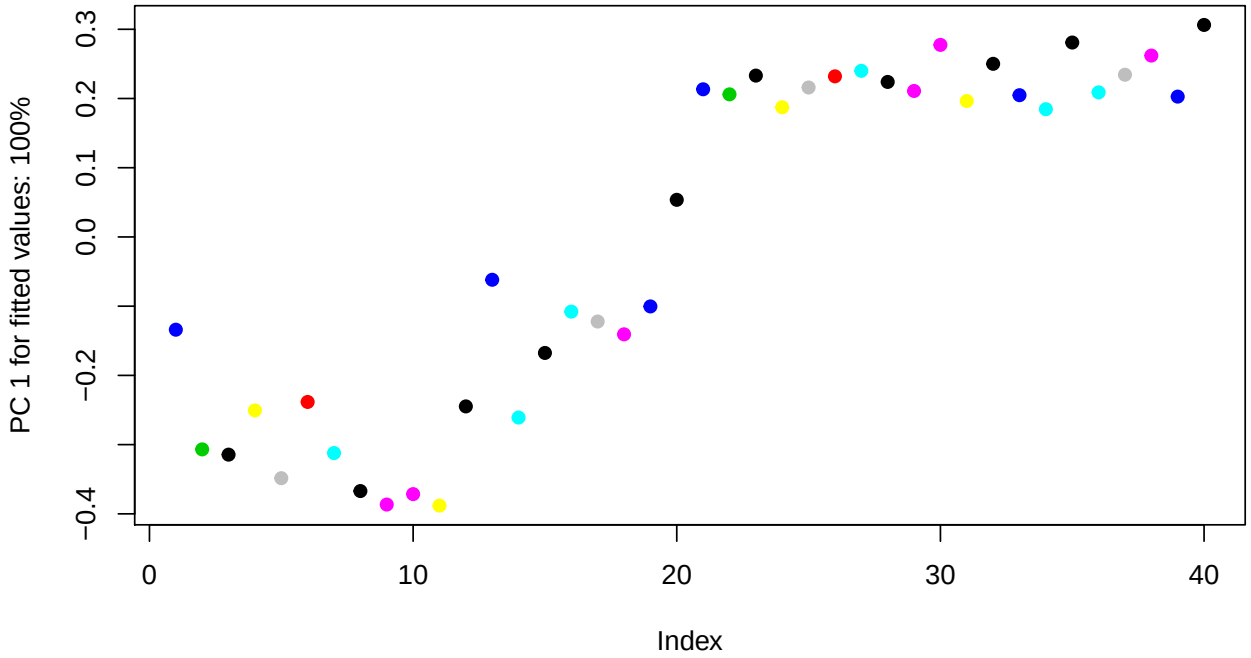



Q−Q plot
Euclidean Distance Residuals
0.00
0.02
0.04
0.06
−2
−1
0
1
2
Theoretical Quantiles

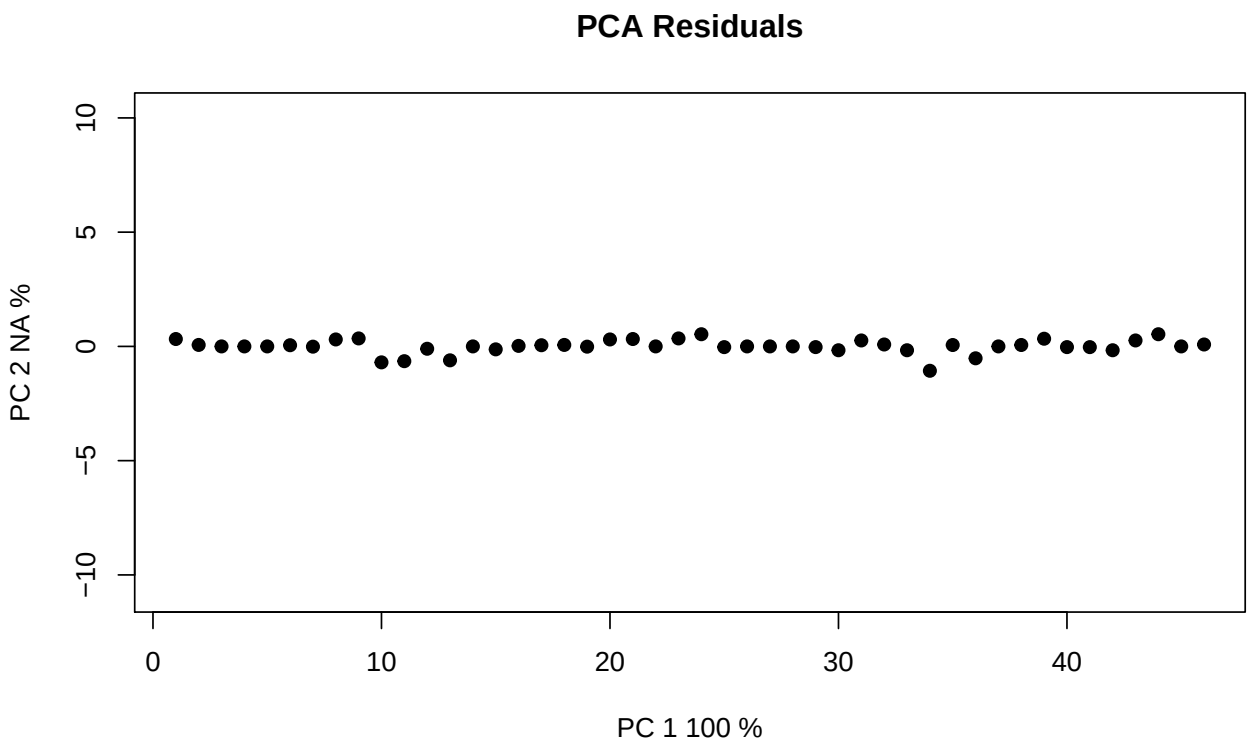

Residuals vs. PC 1 fitted
Standardized Euclidean Distance Residuals
0
1
2
3
4
−0.4
−0.2
0.0
0.2
PC 1 100 %

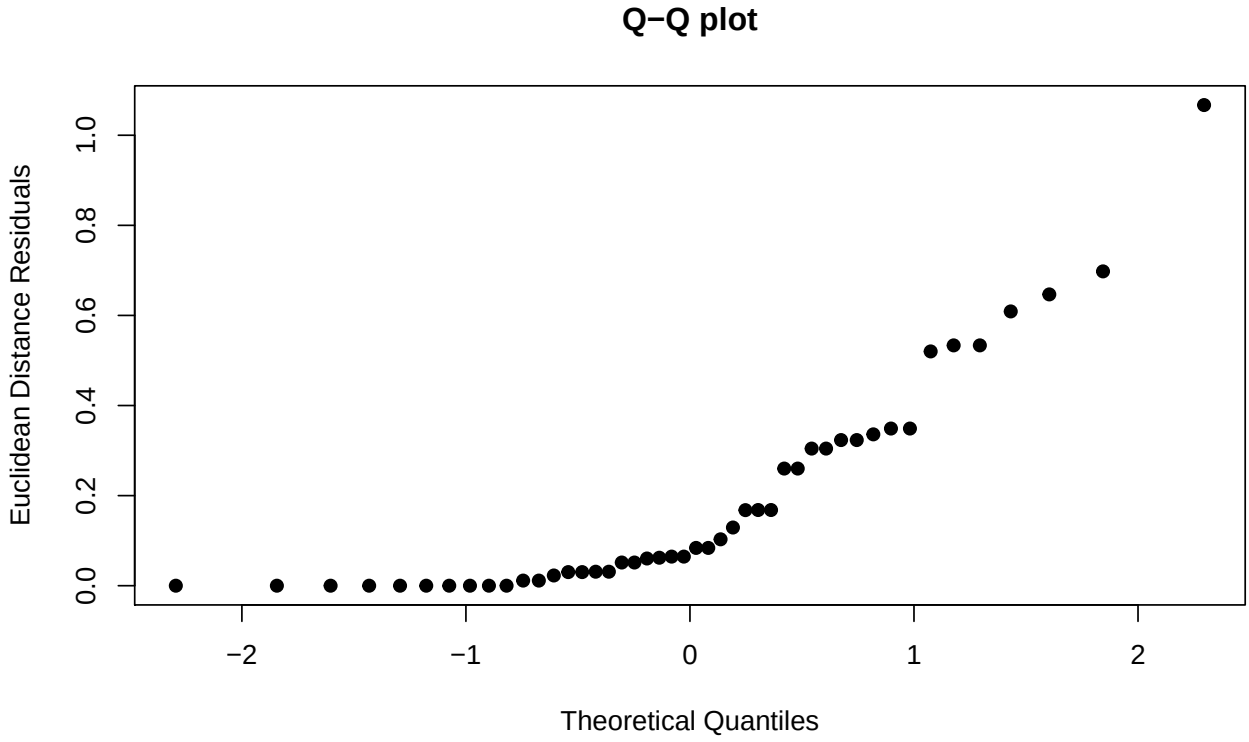


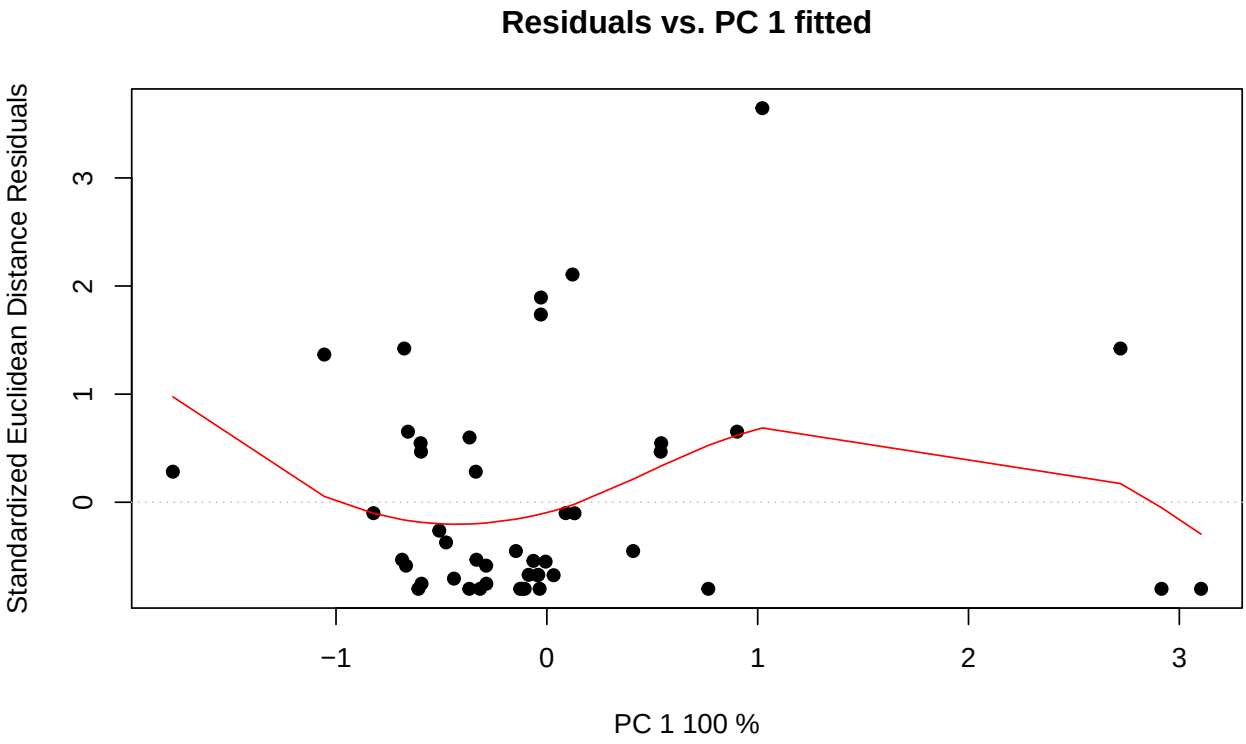

```
# pca plot
hpcplot <- plot(highLM, type = "PC", pch = 19, col = interaction(high$Water,
    high$Fungus))
```

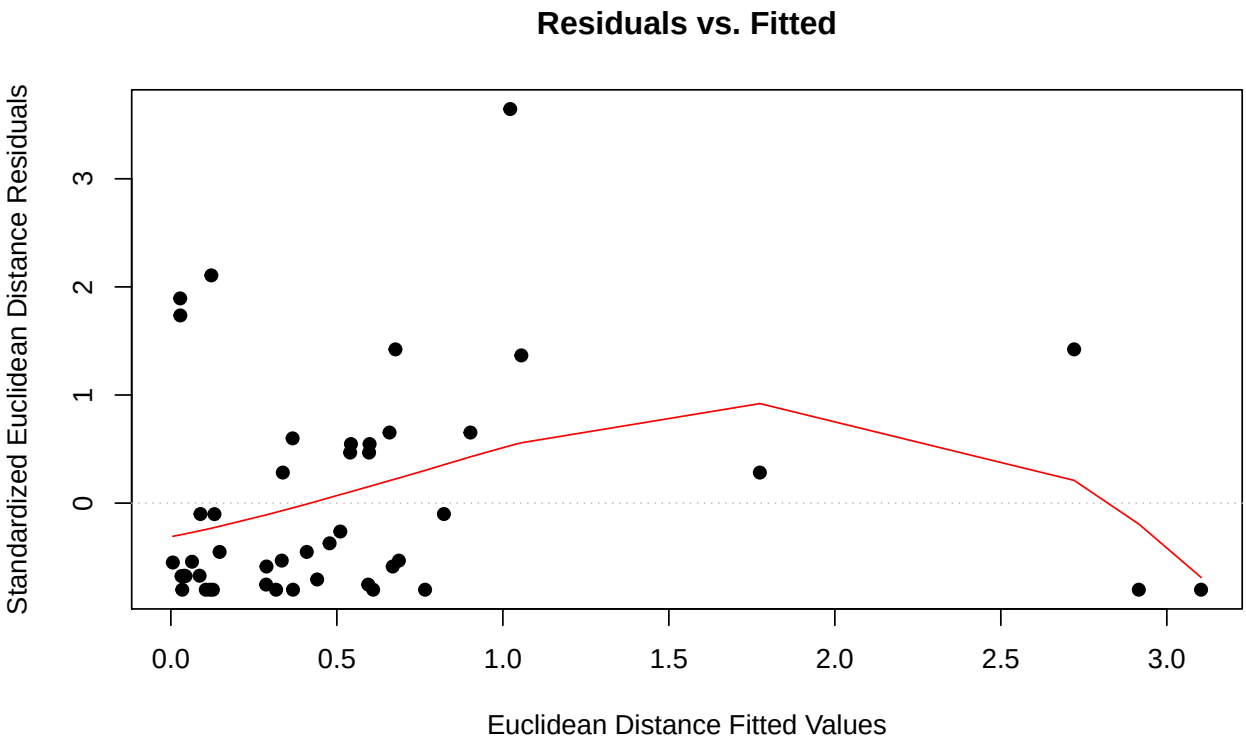



```
# residuals vs fitted values (homoscedasticity check)
ldiagnostics <- plot(lowLM, type = "diagnostics")
```

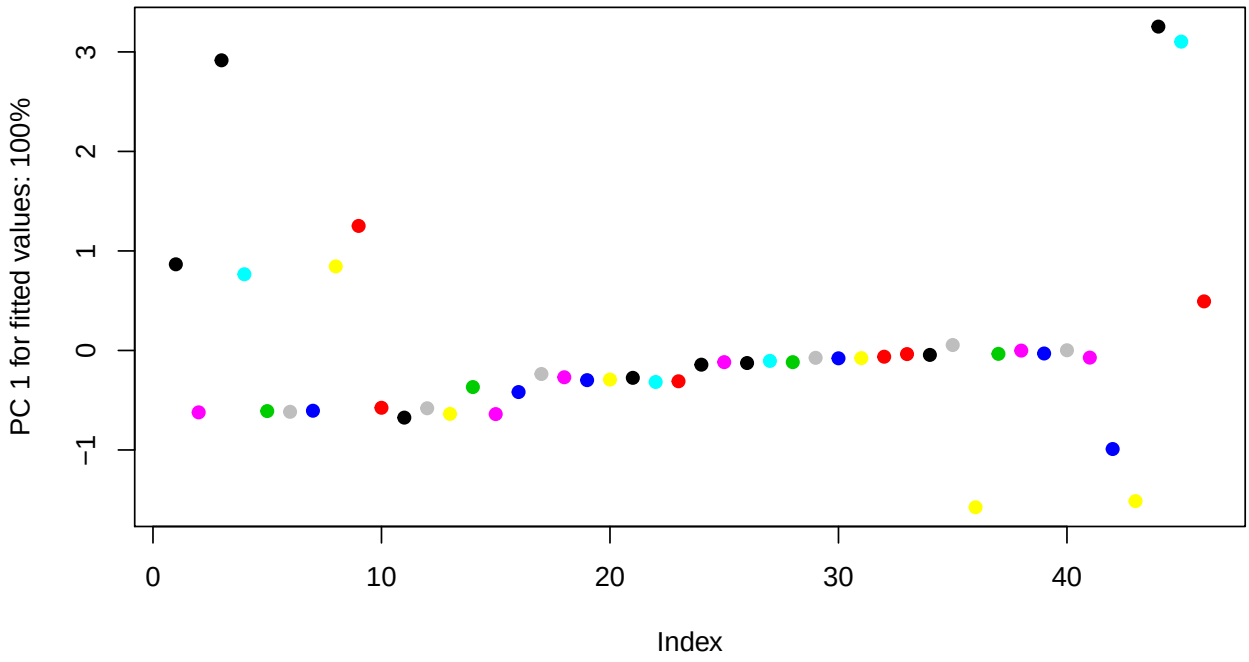

PCA Residuals
PC 2 NA %
10
5
0
−5
−10
0
10
20
30
40
PC 1 100 %


Q−Q plot
Euclidean Distance Residuals
0.0
0.2
0.4
0.6
0.8
1.0
−2
−1
0
1
2
Theoretical Quantiles






```
# pca plot
lpcplot <- plot(lowLM, type = "PC", pch = 19, col = interaction(low$Water,
    low$Fungus))
```



8. Repeat steps 4 - 7 for chlorophyll a and b

```
## chl a linear models and coefficient tests
highLM <- lm.rrpp(Chl.a ~ Block * Fungus * Age, data = high,
    SS.type = "III", print.progress = F)
```

```
##
## Warning: Because variables in the linear model are redundant,
## the linear model design has been truncated (via QR decomposition).
## Original X columns: 36
## Final X columns (rank): 32
## Check coefficients or degrees of freedom in ANOVA to see changes.
```

```
summary(highLM)
```

```
##
## Warning: Because variables in the linear model are redundant,
## the linear model design has been truncated (via QR decomposition).
## Original X columns: 36
## Final X columns (rank): 32
## Check coefficients or degrees of freedom in ANOVA to see changes.
```

```
##
## Linear Model fit with lm.rrpp
##
## Number of observations: 40
## Number of dependent variables: 1
## Data space dimensions: 1
## Sums of Squares and Cross-products: Type III
## Number of permutations: 1000
##
## Full Model Analysis of Variance
##
##                       Df Residual Df       SS Residual SS       Rsq        F
## Block * Fungus * Age 31           8 34.62868    4.896895 0.8761082 1.824918
```

```
##                       Z (from F) Pr(>F)
## Block * Fungus * Age  0.8611391  0.191
##
##
## Redundancy Analysis (PCA on fitted values and residuals)
##
##               Trace Proportion Rank
## Fitted    0.8879149  0.8761082    1
## Residuals 0.1255614  0.1238918    1
## Total     1.0134763  1.0000000    1
##
## Eigenvalues
##
##                  PC1
## Fitted    0.8879149
## Residuals 0.1255614
## Total     1.0134763
```

```
coef(highLM, test = T)
```

```
##
## Linear Model fit with lm.rrpp
##
## Number of observations: 40
## Number of dependent variables: 1
## Data space dimensions: 1
## Sums of Squares and Cross-products: Type III
## Number of permutations: 1000
##
## Statistics (distances) of coefficients with 95 percent confidence intervals,
## effect sizes, and probabilities of exceeding observed values based on
## 1000 random permutations using RRPP
##
##                               d.obs UCL (95%)          Zd Pr(>d)
## (Intercept)               1.4887000 3.1132605 -0.88671633  0.844
## Block                     0.0189000 0.5625146 -0.98230634  0.800
## FungusCer                 0.8958000 1.7774671  0.66888479  0.181
## FungusCok                 3.1225000 1.6911105  4.86491341  0.003
## FungusCtrl                0.4613333 2.7235718 -0.58767526  0.646
## FungusNig                 2.5825333 2.4298071  2.25902054  0.045
## FungusPen                 1.2428667 2.3409168  0.54841450  0.238
## FungusPod                 1.1789000 3.1386469  0.10645855  0.327
## FungusPre                 1.2563500 2.7923820  0.39384042  0.248
## FungusXyl                 1.0466000 3.3762310 -0.08388678  0.398
## AgeYoung                  1.3735000 1.6506508  1.43495466  0.099
## Block:FungusCtrl          0.0708500 0.7875661 -1.01948406  0.868
## Block:FungusNig           1.0067000 0.7849443  2.89710866  0.009
## Block:FungusPen           0.3558500 0.7568903  0.17981382  0.374
## Block:FungusPod           0.2273000 1.2103392 -0.67305703  0.706
## Block:FungusPre           0.0790500 0.7999934 -0.95453805  0.853
## Block:FungusXyl           0.2903000 1.3270783 -0.47649035  0.604
## Block:AgeYoung            0.4828500 0.7235837  0.84909850  0.191
## FungusCer:AgeYoung        0.1345500 1.6145549 -1.03855928  0.867
## FungusCok:AgeYoung        1.2665500 1.6356655  1.18829425  0.134
## FungusCtrl:AgeYoung       1.1549333 2.7405931  0.06908845  0.393
```

```
## FungusNig:AgeYoung        2.1915667 2.7141535  1.33164332  0.115
## FungusPen:AgeYoung        0.8735667 2.5730234 -0.26025976  0.518
## FungusPod:AgeYoung        0.7334000 3.2372444 -0.60698556  0.671
## FungusPre:AgeYoung        1.7795000 2.6980775  0.85127825  0.193
## FungusXyl:AgeYoung        1.8918000 3.3456213  0.56228249  0.240
## Block:FungusCtrl:AgeYoung 0.0221500 1.1421181 -1.29161849  0.977
## Block:FungusNig:AgeYoung  1.5067000 1.1835913  2.78562240  0.011
## Block:FungusPen:AgeYoung  0.2853000 1.1521380 -0.56824518  0.656
## Block:FungusPod:AgeYoung  0.7454500 1.7567748  0.05991203  0.410
## Block:FungusPre:AgeYoung  0.8015500 1.1512449  0.95806001  0.174
## Block:FungusXyl:AgeYoung  1.0046500 1.8482219  0.47163597  0.267
```

```
lowLM <- lm.rrpp(Chl.a ~ Block * Fungus * Age, data = low, SS.type = "III",
    print.progress = F)
```

```
##
## Warning: Because variables in the linear model are redundant,
## the linear model design has been truncated (via QR decomposition).
## Original X columns: 36
## Final X columns (rank): 34
## Check coefficients or degrees of freedom in ANOVA to see changes.
```

```
summary(lowLM)
```

```
##
## Warning: Because variables in the linear model are redundant,
## the linear model design has been truncated (via QR decomposition).
## Original X columns: 36
## Final X columns (rank): 34
## Check coefficients or degrees of freedom in ANOVA to see changes.
```

```
##
## Linear Model fit with lm.rrpp
##
## Number of observations: 46
## Number of dependent variables: 1
## Data space dimensions: 1
## Sums of Squares and Cross-products: Type III
## Number of permutations: 1000
##
## Full Model Analysis of Variance
##
##                       Df Residual Df       SS Residual SS       Rsq        F
## Block * Fungus * Age 33          12 67.19567    13.12627 0.8365793 1.861519
##                       Z (from F) Pr(>F)
## Block * Fungus * Age   1.033254  0.139
##
##
## Redundancy Analysis (PCA on fitted values and residuals)
##
##               Trace Proportion Rank
## Fitted    1.4932372  0.8365793    1
## Residuals 0.2916948  0.1634207    1
## Total     1.7849320  1.0000000    1
##
## Eigenvalues
```

```
##
##                 PC1
## Fitted    1.4932372
## Residuals 0.2916948
## Total     1.7849320
```

```
coef(lowLM, test = T)
```

```
##
## Linear Model fit with lm.rrpp
##
## Number of observations: 46
## Number of dependent variables: 1
## Data space dimensions: 1
## Sums of Squares and Cross-products: Type III
## Number of permutations: 1000
##
## Statistics (distances) of coefficients with 95 percent confidence intervals,
## effect sizes, and probabilities of exceeding observed values based on
## 1000 random permutations using RRPP
##
##                                d.obs UCL (95%)         Zd Pr(>d)
## (Intercept)                4.3430667 6.5795080 -0.5677956  0.736
## Block                      0.7142000 0.9534942  1.5016766  0.083
## FungusCer                  2.7943333 3.2320490  1.5055108  0.085
## FungusCok                  2.6333333 4.2156378  0.7341268  0.213
## FungusCtrl                 2.5017333 3.3287671  1.1785583  0.134
## FungusNig                  1.1112667 3.5222104 -0.2301015  0.501
## FungusPen                  1.6043667 3.3251946  0.2064703  0.361
## FungusPod                  1.5069667 3.4805683  0.1252120  0.374
## FungusPre                  0.2210000 3.3565091 -1.0215211  0.881
## FungusXyl                  2.1914667 2.0939637  2.1208716  0.042
## AgeYoung                   1.0963333 2.5607897  0.1976930  0.323
## Block:FungusCer            0.8895000 1.3143093  0.8830000  0.197
## Block:FungusCok            1.5832000 2.0953984  1.1345885  0.144
## Block:FungusCtrl           1.2090500 1.2828312  1.6897109  0.067
## Block:FungusNig            0.2778000 1.3244636 -0.6598018  0.695
## Block:FungusPen            1.0023500 1.3873875  0.9907349  0.164
## Block:FungusPod            0.1797000 1.3821395 -0.9159896  0.796
## Block:FungusPre            0.6740500 1.2605982  0.3783323  0.298
## Block:AgeYoung             0.3849000 1.1710396 -0.1370970  0.446
## FungusCer:AgeYoung         0.9018000 4.1265671 -0.6110257  0.664
## FungusCok:AgeYoung         3.0812333 5.0500914  0.5812771  0.263
## FungusCtrl:AgeYoung        4.2113000 4.2977626  1.8382194  0.058
## FungusNig:AgeYoung         1.1608667 4.0980392 -0.3985153  0.571
## FungusPen:AgeYoung         1.2637000 4.2613209 -0.2857590  0.518
## FungusPod:AgeYoung         2.8811000 4.2696158  0.9053959  0.175
## FungusPre:AgeYoung         0.1191667 4.1067099 -1.2141235  0.962
## FungusXyl:AgeYoung         2.0379667 2.5317165  1.2242357  0.113
## Block:FungusCer:AgeYoung   0.3556500 1.9430340 -0.7476500  0.728
## Block:FungusCok:AgeYoung   1.7435000 3.0711511  0.5126096  0.268
## Block:FungusCtrl:AgeYoung 2.0082000 2.0210904  1.9235037  0.055
## Block:FungusNig:AgeYoung   0.5530000 1.9265238 -0.3930890  0.560
## Block:FungusPen:AgeYoung   0.6282000 1.9548830 -0.2591984  0.505
## Block:FungusPod:AgeYoung   2.4821000 2.0151741  2.7198075  0.011
```

```
## Block:FungusPre:AgeYoung  0.1321000 1.9961832 -1.0811244  0.885
```

```
# ratio anovas
highANOVA <- anova(highLM, effect.type = "F", error = c("Residuals",
    "Block:Fungus", "Block:Fungus:Age", "Residuals", "Block:Fungus:Age",
    "Block:Fungus:Age", "Residuals"))
summary(highANOVA)
```

```
##
## Analysis of Variance, using Residual Randomization
## Permutation procedure: Randomization of null model residuals
## Number of permutations: 1000
## Estimation method: Ordinary Least Squares
## Sums of Squares and Cross-products: Type III
## Effect sizes (Z) based on F distributions
##
##                  Df     SS      MS      Rsq      F        Z Pr(>F)
## Block             1  0.001 0.00071 0.000018 0.0012           0.843
## Fungus            8  6.835 0.85442 0.172936 3.6871  0.81970  0.207
## Age               1  0.404 0.40425 0.010228 1.3942           0.223
## Block:Fungus      6  1.390 0.23174 0.035178 0.3786 -0.91017  0.813
## Block:Age         1  0.233 0.23314 0.005899 0.8041           0.339
## Fungus:Age        8  2.416 0.30205 0.061134 1.0417 -0.17869  0.556
## Block:Fungus:Age  6  1.740 0.28994 0.044013 0.4737 -0.82082  0.817
## Residuals         8  4.897 0.61211 0.123892
## Total            39 39.526
##
## Call: lm.rrpp(f1 = Chl.a ~ Block * Fungus * Age, SS.type = "III", data = high,
##     print.progress = F)
```

```
lowANOVA <- anova(lowLM, effect.type = "F", error = c("Residuals",
    "Block:Fungus", "Block:Fungus:Age", "Residuals", "Block:Fungus:Age",
    "Block:Fungus:Age", "Residuals"))
summary(lowANOVA)
```

```
##
## Analysis of Variance, using Residual Randomization
## Permutation procedure: Randomization of null model residuals
## Number of permutations: 1000
## Estimation method: Ordinary Least Squares
## Sums of Squares and Cross-products: Type III
## Effect sizes (Z) based on F distributions
##
##                  Df     SS      MS      Rsq      F        Z Pr(>F)
## Block             1  1.020 1.02016 0.012701 0.9326           0.287
## Fungus            8 14.156 1.76956 0.176246 1.5751  0.34461  0.330
## Age               1  0.258 0.25756 0.003207 0.2084  0.08224  0.542
## Block:Fungus      7  7.864 1.12346 0.097909 1.0271  0.06854  0.469
## Block:Age         1  0.148 0.14815 0.001844 0.1199           0.648
## Fungus:Age        8  8.488 1.06096 0.105671 0.8586 -0.27319  0.623
## Block:Fungus:Age  7  8.649 1.23563 0.107684 1.1296  0.15859  0.444
## Residuals        12 13.126 1.09386 0.163421
## Total            45 80.322
##
## Call: lm.rrpp(f1 = Chl.a ~ Block * Fungus * Age, SS.type = "III", data = low,
```

```
##     print.progress = F)
# pairwise
highpw <- pairwise(highLM, groups = high$Fungus)
summary(highpw, confidence = 0.95, stat.table = T)
```

```
##
## Pairwise comparisons
##
## Groups: Asp Cer Cok Ctrl Nig Pen Pod Pre Xyl
##
## RRPP: 1000 permutations
##
## LS means:
## Vectors hidden (use show.vectors = TRUE to view)
##
## Pairwise distances between means, plus statistics
##                   d UCL (95%)             Z Pr > d
## Asp:Cer  1.1856000 1.7444579 -0.0397153304  0.529
## Asp:Cok  2.7117500 3.2527296 -0.0138542613  0.524
## Asp:Ctrl 0.8749500 1.2538255  0.0044563947  0.513
## Asp:Nig  0.9800500 1.3816918 -0.0173411982  0.519
## Asp:Pen  0.3796833 0.7757114 -0.1107287911  0.510
## Asp:Pod  1.8750000 2.2842005  0.0036071225  0.509
## Asp:Pre  1.0100500 1.4193045 -0.0263544834  0.522
## Asp:Xyl  0.5300000 0.9526171 -0.0065051864  0.499
## Cer:Cok  1.5261500 2.1563458  0.0217534315  0.521
## Cer:Ctrl 0.3106500 0.8739857 -0.3158461812  0.587
## Cer:Nig  0.2055500 0.7563966 -0.5139173573  0.636
## Cer:Pen  0.8059167 1.3612361 -0.0010300757  0.506
## Cer:Pod  0.6894000 1.2618955  0.0155048542  0.488
## Cer:Pre  0.1755500 0.7747262 -0.6314269116  0.670
## Cer:Xyl  0.6556000 1.2782708 -0.0756869893  0.505
## Cok:Ctrl 1.8368000 2.3667611 -0.0172371496  0.516
## Cok:Nig  1.7317000 2.2762065 -0.0015446047  0.519
## Cok:Pen  2.3320667 2.8416513  0.0340602484  0.511
## Cok:Pod  0.8367500 1.4346393 -0.0192224934  0.511
## Cok:Pre  1.7017000 2.2525063  0.0063877794  0.505
## Cok:Xyl  2.1817500 2.7618799 -0.0257520695  0.517
## Ctrl:Nig 0.1051000 0.5202463 -0.6938997811  0.706
## Ctrl:Pen 0.4952667 0.8692005  0.0585394076  0.469
## Ctrl:Pod 1.0000500 1.4013555 -0.0003978616  0.525
## Ctrl:Pre 0.1351000 0.5844879 -0.6359027729  0.677
## Ctrl:Xyl 0.3449500 0.8074781 -0.1043138089  0.490
## Nig:Pen  0.6003667 0.9585536  0.0489269640  0.483
## Nig:Pod  0.8949500 1.3359137  0.0185405734  0.494
## Nig:Pre  0.0300000 0.5394487 -1.1504355699  0.929
## Nig:Xyl  0.4500500 0.9370759 -0.0728146707  0.512
## Pen:Pod  1.4953167 1.9238148  0.0628278002  0.471
## Pen:Pre  0.6303667 1.0312906  0.0285803512  0.505
## Pen:Xyl  0.1503167 0.5646290 -0.5158031070  0.630
## Pod:Pre  0.8649500 1.3322021  0.0255257998  0.483
## Pod:Xyl  1.3450000 1.8434605 -0.0118110166  0.489
## Pre:Xyl  0.4800500 0.9827610 -0.0830715955  0.502
```

```
highpw2 <- pairwise(highLM, groups = high$Age)
summary(highpw2, confidence = 0.95, stat.table = T)
```

```
##
## Pairwise comparisons
##
## Groups: Old Young
##
## RRPP: 1000 permutations
##
## LS means:
## Vectors hidden (use show.vectors = TRUE to view)
##
## Pairwise distances between means, plus statistics
##                 d UCL (95%)           Z Pr > d
## Old:Young 0.82123  1.037333 -0.02091859  0.511
```

```
lowpw <- pairwise(lowLM, groups = low$Fungus)
summary(lowpw, confidence = 0.95, stat.table = T)
```

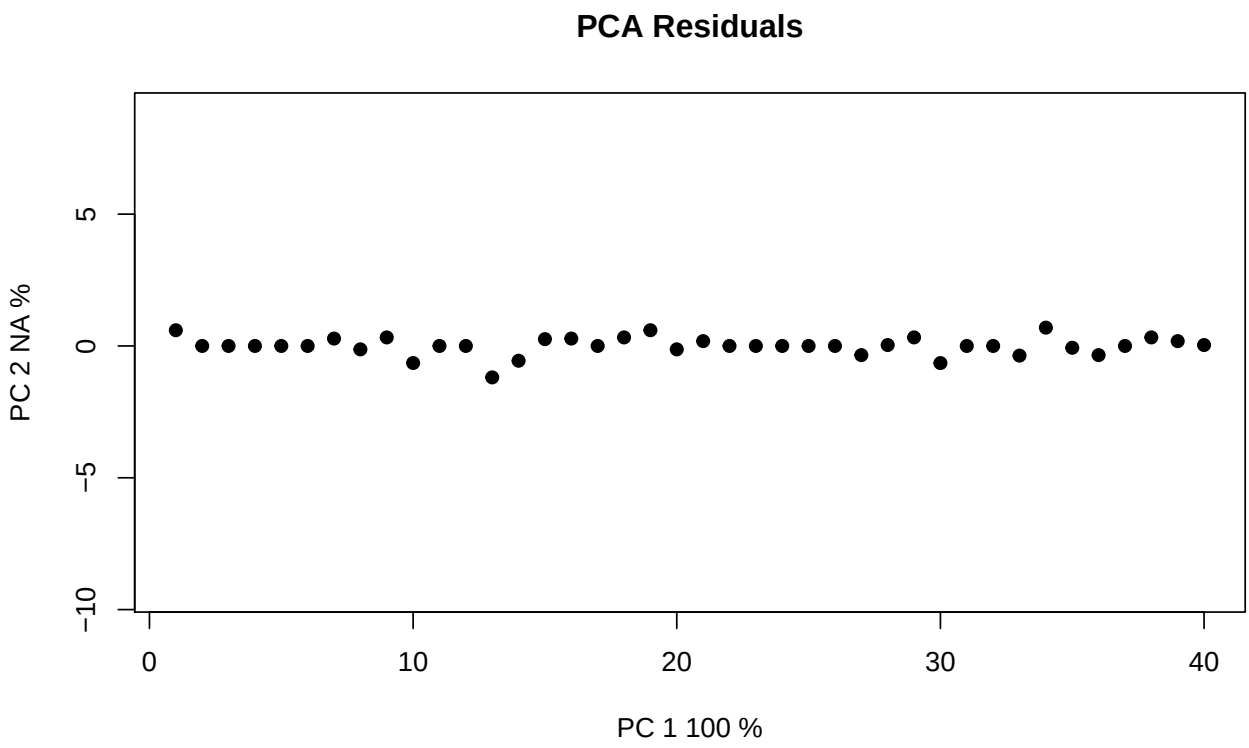
```
##
## Pairwise comparisons
##
## Groups: Asp Cer Cok Ctrl Nig Pen Pod Pre Xyl
##
## RRPP: 1000 permutations
##
## LS means:
## Vectors hidden (use show.vectors = TRUE to view)
##
## Pairwise distances between means, plus statistics
##                   d UCL (95%)            Z Pr > d
## Asp:Cer  0.92008333 1.5637361  0.034915227  0.486
## Asp:Cok  0.47886667 1.2148622 -0.237263641  0.544
## Asp:Ctrl 0.01381667 0.8055051 -1.284002224  0.974
## Asp:Nig  0.52823333 1.2857103 -0.142772260  0.516
## Asp:Pen  0.40398333 1.0660547 -0.185969668  0.499
## Asp:Pod  0.10601667 0.8330731 -0.912835344  0.809
## Asp:Pre  1.05458333 1.6798158  0.055895891  0.479
## Asp:Xyl  0.26583333 1.2734648 -0.611330189  0.661
## Cer:Cok  1.39895000 2.1223384 -0.001324945  0.510
## Cer:Ctrl 0.90626667 1.5679645  0.019518183  0.488
## Cer:Nig  0.39185000 1.1775226 -0.267746528  0.528
## Cer:Pen  0.51610000 1.1430992 -0.094326711  0.508
## Cer:Pod  0.81406667 1.4922583 -0.014336746  0.510
## Cer:Pre  0.13450000 0.7951180 -0.779960179  0.740
## Cer:Xyl  0.65425000 1.5515824 -0.117681477  0.490
## Cok:Ctrl 0.49268333 1.2511124 -0.196753111  0.534
## Cok:Nig  1.00710000 1.8471925 -0.045723063  0.489
## Cok:Pen  0.88285000 1.6387334 -0.019665302  0.490
## Cok:Pod  0.58488333 1.3201755 -0.098747059  0.498
## Cok:Pre  1.53345000 2.2844860  0.013598997  0.504
## Cok:Xyl  0.74470000 1.7943119 -0.192932164  0.547
## Ctrl:Nig 0.51441667 1.2486167 -0.159330575  0.511
```

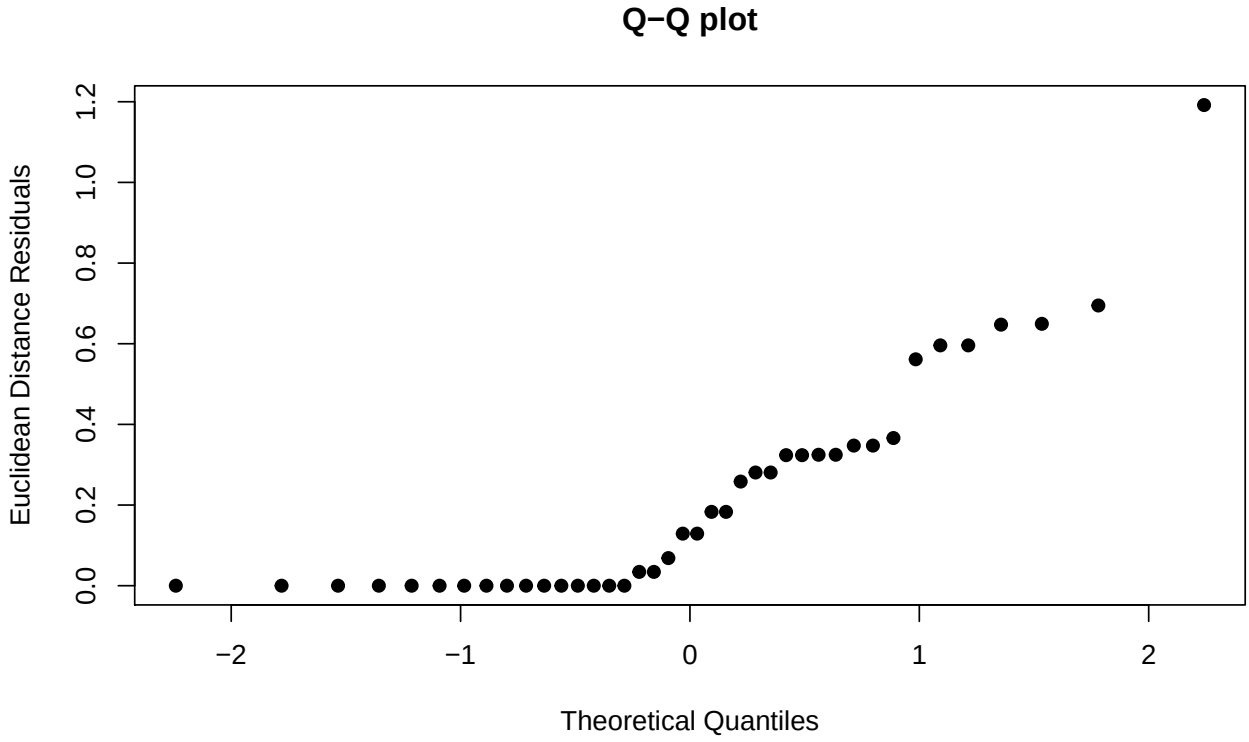
```
## Ctrl:Pen 0.39016667 1.0559846 -0.201126915  0.533
## Ctrl:Pod 0.09220000 0.7990792 -0.938361296  0.811
## Ctrl:Pre 1.04076667 1.6776556  0.044181027  0.503
## Ctrl:Xyl 0.25201667 1.2459252 -0.646607176  0.688
## Nig:Pen  0.12425000 0.9377064 -0.884333831  0.799
## Nig:Pod  0.42221667 1.2071220 -0.265216655  0.530
## Nig:Pre  0.52635000 1.2571673 -0.095886477  0.481
## Nig:Xyl  0.26240000 1.3506374 -0.641769147  0.698
## Pen:Pod  0.29796667 0.9418610 -0.378561888  0.576
## Pen:Pre  0.65060000 1.2658125 -0.027096504  0.502
## Pen:Xyl  0.13815000 1.1938933 -0.859080303  0.788
## Pod:Pre  0.94856667 1.5939658  0.010123718  0.485
## Pod:Xyl  0.15981667 1.2629318 -0.856348834  0.782
## Pre:Xyl  0.78875000 1.6942014 -0.034614641  0.475
```

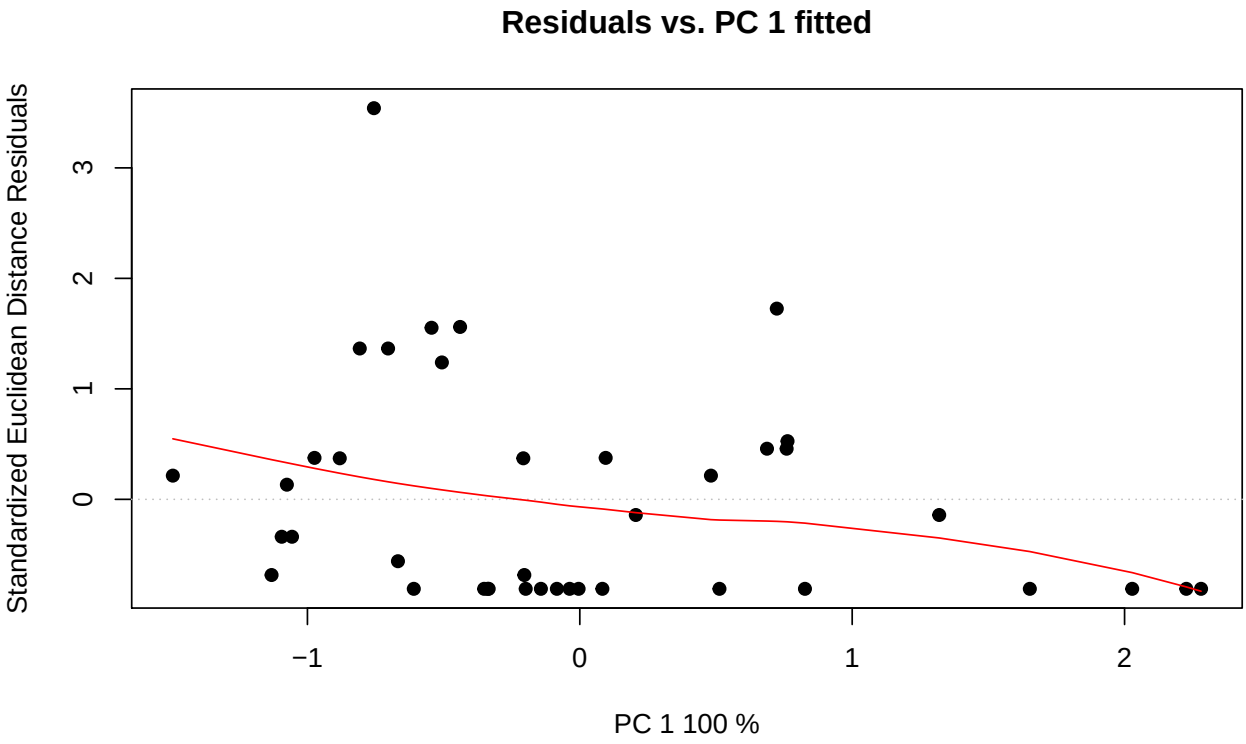
```
lowpw2 <- pairwise(lowLM, groups = low$Age)
summary(lowpw2, confidence = 0.95, stat.table = T)
```

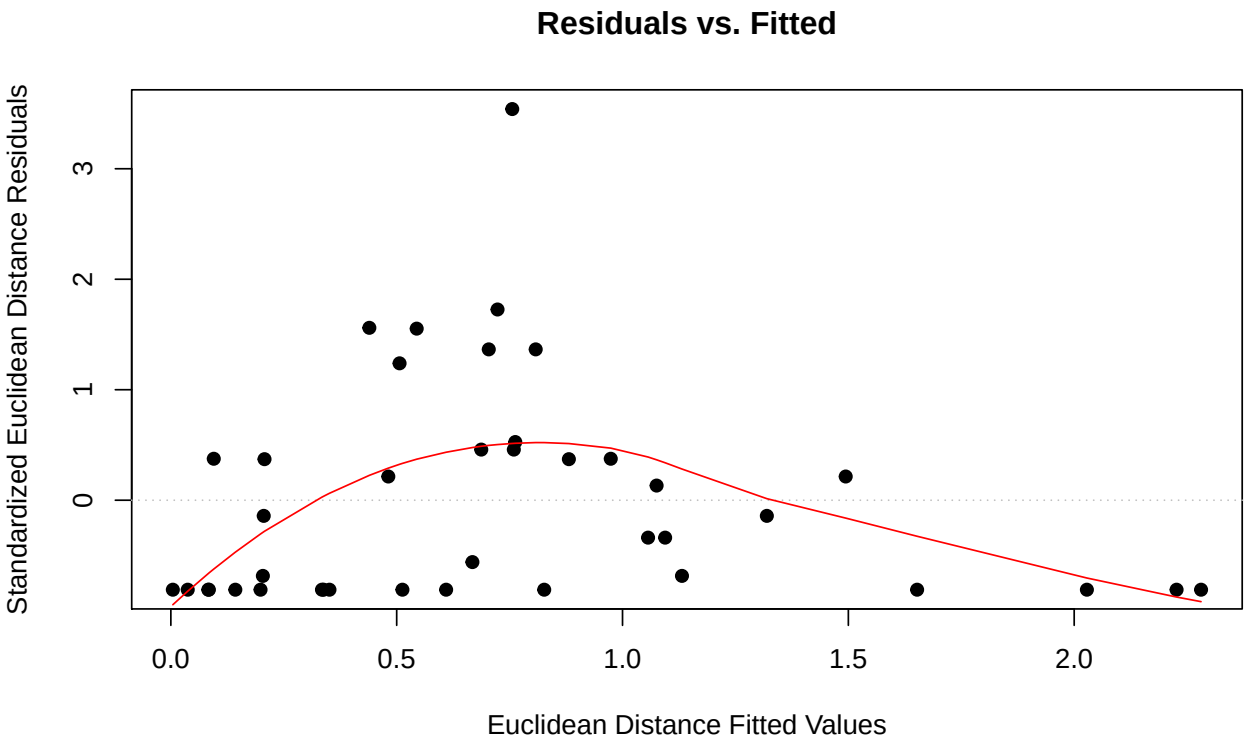
```
##
## Pairwise comparisons
##
## Groups: Old Young
##
## RRPP: 1000 permutations
##
## LS means:
## Vectors hidden (use show.vectors = TRUE to view)
##
## Pairwise distances between means, plus statistics
##                   d UCL (95%)          Z Pr > d
## Old:Young 0.7019609  1.050308 0.01081928  0.496
```

```
# residuals vs fitted values (homoscedasticity check)
hdiagnostics <- plot(highLM, type = "diagnostics")
```

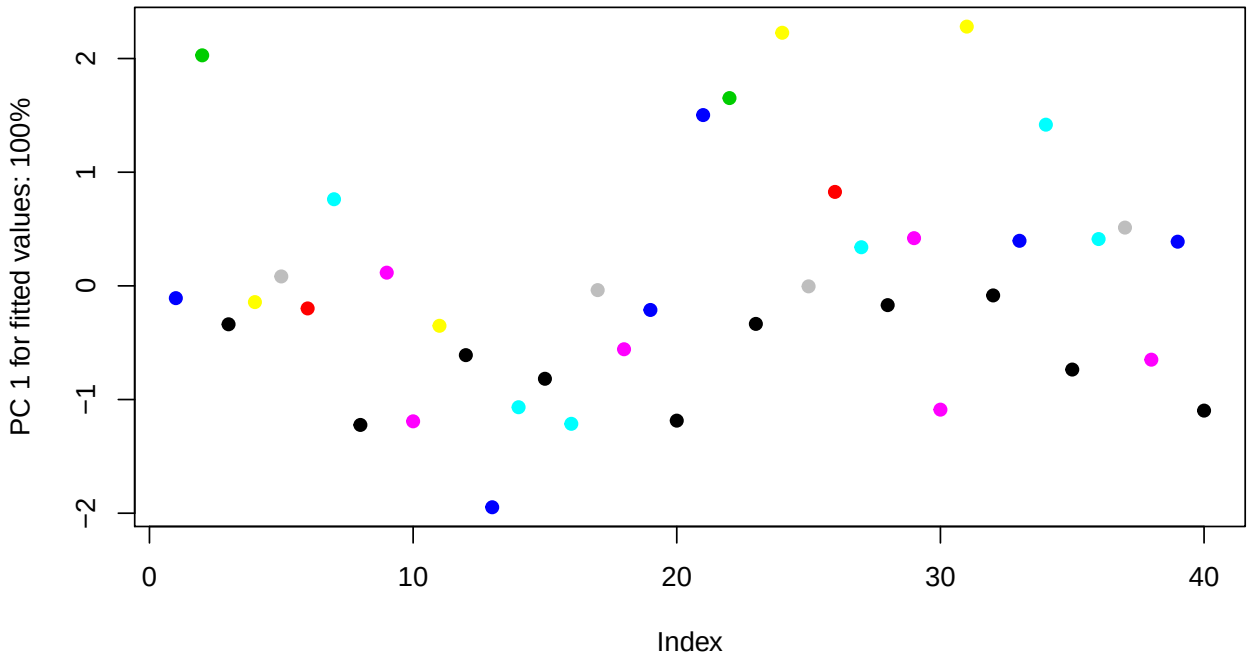

PCA Residuals
PC 2 NA %
5
0
−5
−10
0
10
20
30
40
PC 1 100 %


Q−Q plot
Euclidean Distance Residuals
0.0
0.2
0.4
0.6
0.8
1.0
1.2
−2
−1
0
1
2
Theoretical Quantiles

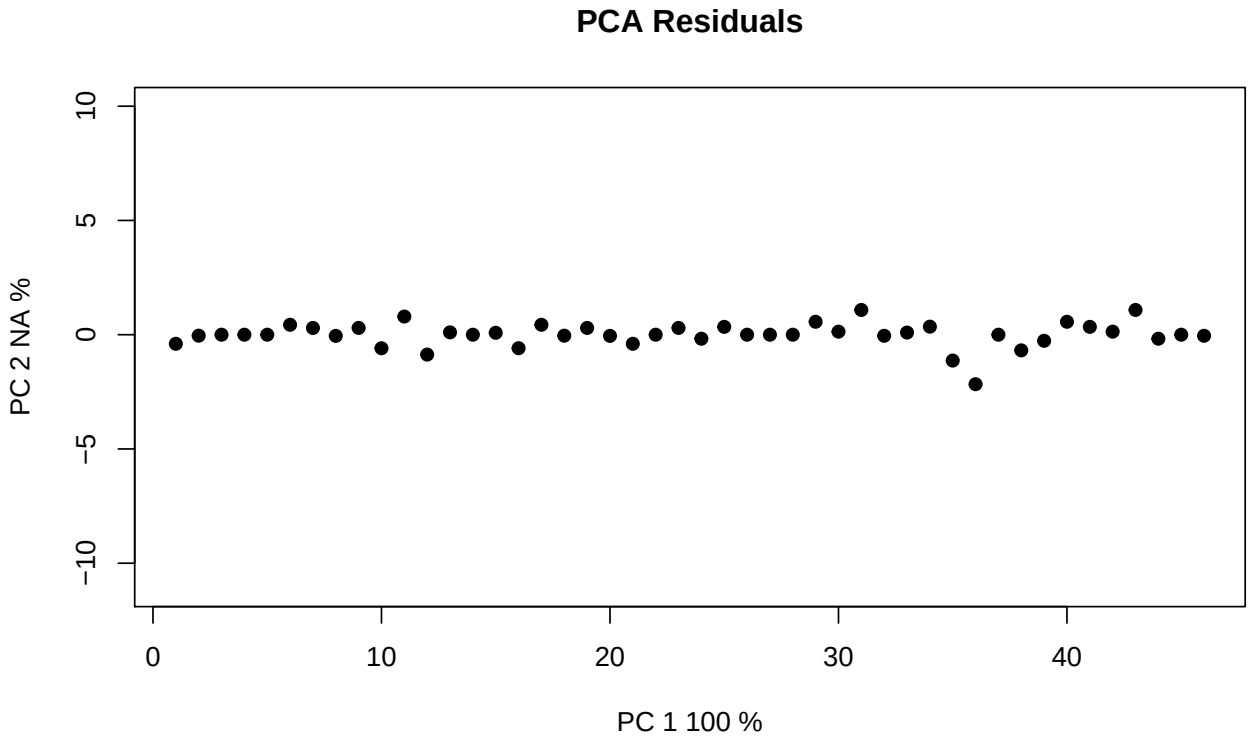


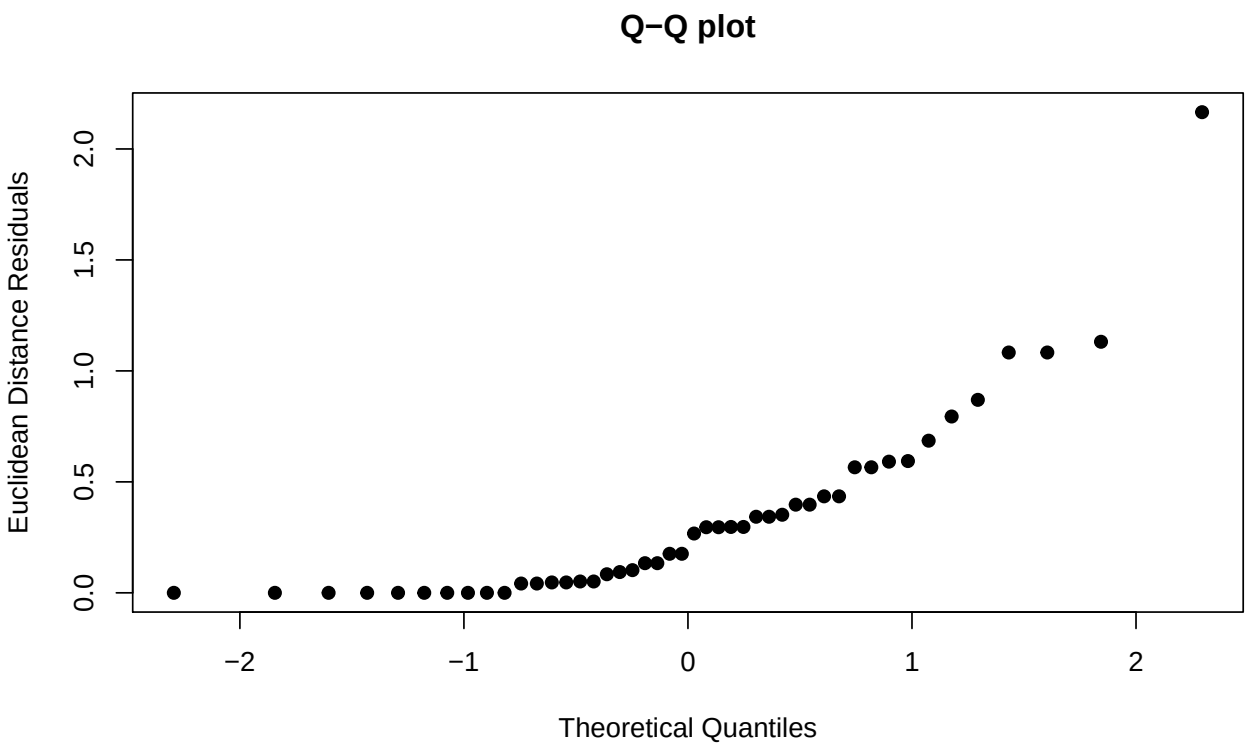


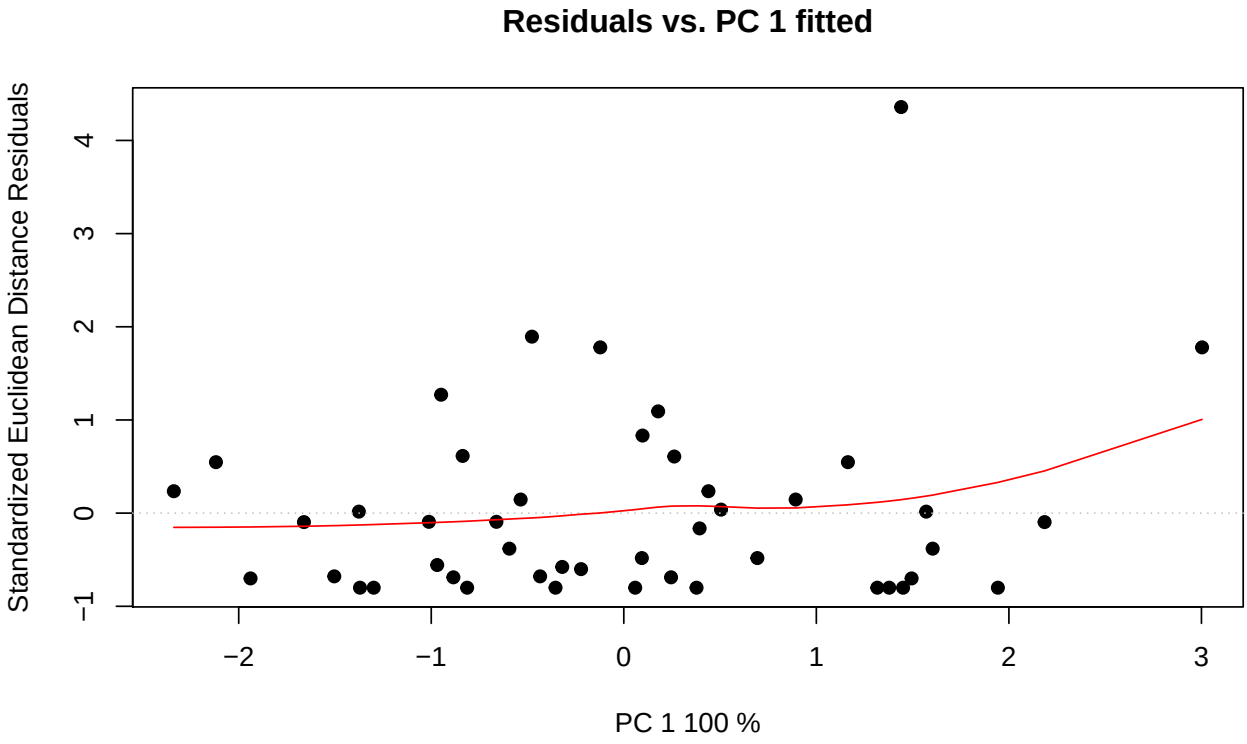

```
# pca plot
hpcplot <- plot(highLM, type = "PC", pch = 19, col = interaction(high$Water,
    high$Fungus))
```

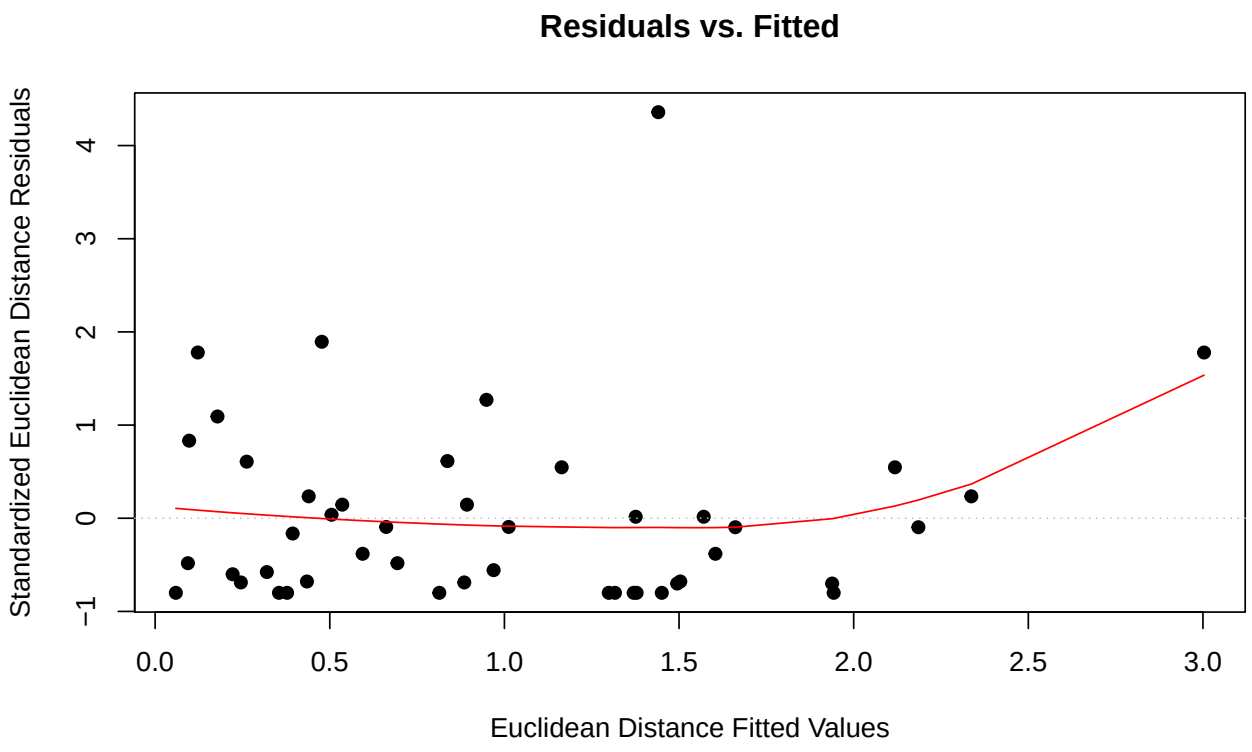



```
# residuals vs fitted values (homoscedasticity check)
ldiagnostics <- plot(lowLM, type = "diagnostics")
```

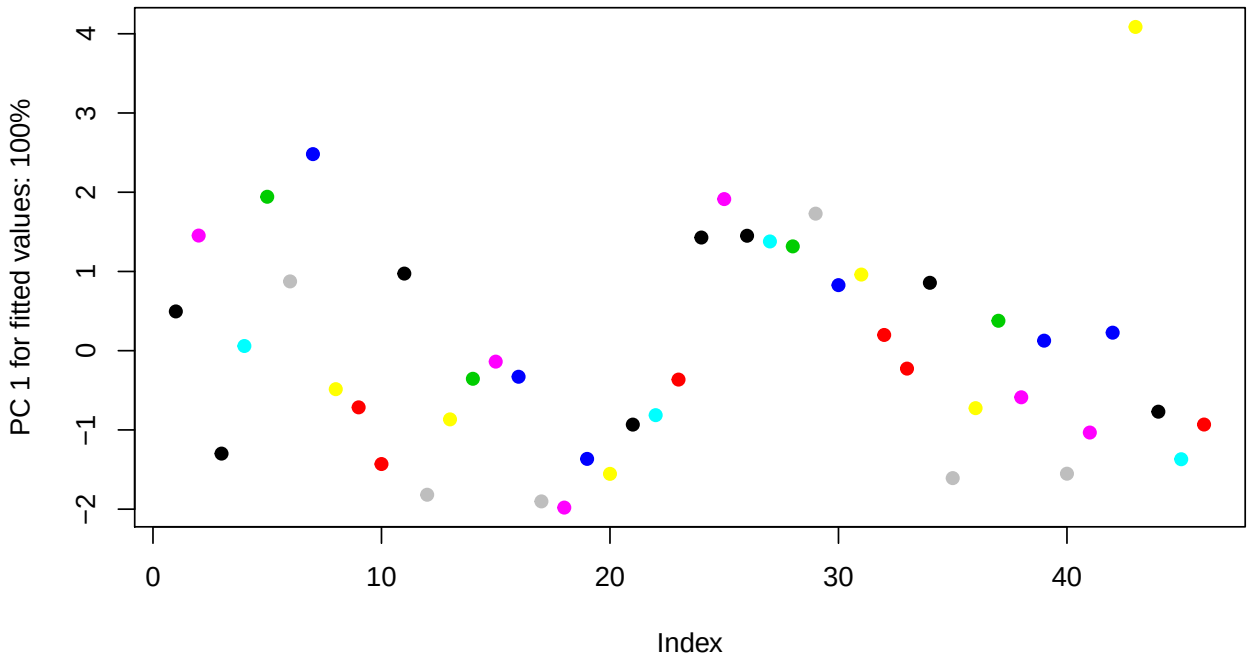



Q−Q plot
Euclidean Distance Residuals
0.0
0.5
1.0
1.5
2.0
−2
−1
0
1
2
Theoretical Quantiles


Residuals vs. PC 1 fitted
Standardized Euclidean Distance Residuals
−1
0
1
2
3
4
−2
−1
0
1
2
3
PC 1 100 %




```
# pca plot
lpcplot <- plot(lowLM, type = "PC", pch = 19, col = interaction(low$Water,
    low$Fungus))
```




```
## chl b linear models and coefficient tests
highLM <- lm.rrpp(Chl.b ~ Block * Fungus * Age, data = high,
    SS.type = "III", print.progress = F)
```

```
##
```

```
## Warning: Because variables in the linear model are redundant,
## the linear model design has been truncated (via QR decomposition).
## Original X columns: 36
## Final X columns (rank): 32
## Check coefficients or degrees of freedom in ANOVA to see changes.
```

```
summary(highLM)
```

```
##
## Warning: Because variables in the linear model are redundant,
## the linear model design has been truncated (via QR decomposition).
## Original X columns: 36
## Final X columns (rank): 32
## Check coefficients or degrees of freedom in ANOVA to see changes.
```

```
##
## Linear Model fit with lm.rrpp
##
## Number of observations: 40
## Number of dependent variables: 1
## Data space dimensions: 1
## Sums of Squares and Cross-products: Type III
## Number of permutations: 1000
##
## Full Model Analysis of Variance
##
##                       Df Residual Df       SS Residual SS       Rsq        F
## Block * Fungus * Age 31           8 87.50118    6.465898 0.9311898 3.492315
##                       Z (from F) Pr(>F)
## Block * Fungus * Age   2.036384  0.034
##
##
## Redundancy Analysis (PCA on fitted values and residuals)
##
##               Trace Proportion Rank
## Fitted    2.2436201  0.9311898    1
## Residuals 0.1657923  0.0688103    1
## Total     2.4094123  1.0000000    1
##
## Eigenvalues
##
##                 PC1
## Fitted    2.2436201
## Residuals 0.1657923
## Total     2.4094123
```

```
coef(highLM, test = T)
```

```
##
## Linear Model fit with lm.rrpp
##
## Number of observations: 40
## Number of dependent variables: 1
## Data space dimensions: 1
## Sums of Squares and Cross-products: Type III
## Number of permutations: 1000
```

```
##
## Statistics (distances) of coefficients with 95 percent confidence intervals,
## effect sizes, and probabilities of exceeding observed values based on
## 1000 random permutations using RRPP
##
##                                d.obs UCL (95%)          Zd Pr(>d)
## (Intercept)                0.9718000 2.8586074 -1.03555526  0.846
## Block                      0.3138000 0.6370833  0.48006561  0.291
## FungusCer                  1.0423000 1.5886509  0.95618364  0.156
## FungusCok                  2.8819000 1.5980151  4.60564538  0.003
## FungusCtrl                 1.0827667 2.5596319  0.13473711  0.357
## FungusNig                  2.5081667 2.3652114  2.19739768  0.038
## FungusPen                  0.9413333 2.3066913  0.09063560  0.366
## FungusPod                  1.8891000 3.0356122  0.79880817  0.186
## FungusPre                  1.0948000 2.6725431  0.17522571  0.336
## FungusXyl                  1.1520000 3.4087934 -0.02631461  0.390
## AgeYoung                   3.0766333 2.0489802  3.55937998  0.002
## Block:FungusCtrl           0.3293500 0.8954640 -0.14763723  0.484
## Block:FungusNig            1.0558000 0.8658242  2.64201607  0.011
## Block:FungusPen            0.3389500 0.8589332 -0.06408513  0.464
## Block:FungusPod            0.8227000 1.3600749  0.65215662  0.234
## Block:FungusPre            0.0753000 0.9176346 -1.01598028  0.871
## Block:FungusXyl            0.4171000 1.4458540 -0.30661780  0.531
## Block:AgeYoung             0.9157500 0.8609529  2.11985292  0.040
## FungusCer:AgeYoung         0.4449167 1.8168762 -0.47636122  0.610
## FungusCok:AgeYoung         0.3173833 1.7661016 -0.74526101  0.725
## FungusCtrl:AgeYoung        1.2420667 2.9113518  0.04990791  0.404
## FungusNig:AgeYoung         1.8611000 3.0423215  0.72779843  0.234
## FungusPen:AgeYoung         0.4409667 2.8346250 -0.85528411  0.770
## FungusPod:AgeYoung         0.6755667 3.5070109 -0.72511390  0.719
## FungusPre:AgeYoung         1.8436833 2.8716802  0.75353808  0.220
## FungusXyl:AgeYoung         2.3386333 3.6527518  0.82694472  0.185
## Block:FungusCtrl:AgeYoung  0.1244500 1.3340999 -1.06173665  0.865
## Block:FungusNig:AgeYoung   1.6630000 1.3789928  2.57631759  0.017
## Block:FungusPen:AgeYoung   0.2330000 1.3324569 -0.79560761  0.742
## Block:FungusPod:AgeYoung   1.5442500 2.0773416  1.14486290  0.139
## Block:FungusPre:AgeYoung   1.0738000 1.3315547  1.31612559  0.109
## Block:FungusXyl:AgeYoung   1.4224500 2.1255591  0.87637559  0.181
```

```
lowLM <- lm.rrpp(Chl.b ~ Block * Fungus * Age, data = low, SS.type = "III",
    print.progress = F)
```

```
##
## Warning: Because variables in the linear model are redundant,
## the linear model design has been truncated (via QR decomposition).
## Original X columns: 36
## Final X columns (rank): 34
## Check coefficients or degrees of freedom in ANOVA to see changes.
```

```
summary(lowLM)
```

```
##
## Warning: Because variables in the linear model are redundant,
## the linear model design has been truncated (via QR decomposition).
## Original X columns: 36
```

```
## Final X columns (rank): 34
## Check coefficients or degrees of freedom in ANOVA to see changes.
```

```
##
## Linear Model fit with lm.rrpp
##
## Number of observations: 46
## Number of dependent variables: 1
## Data space dimensions: 1
## Sums of Squares and Cross-products: Type III
## Number of permutations: 1000
##
## Full Model Analysis of Variance
##
##                       Df Residual Df       SS Residual SS       Rsq        F
## Block * Fungus * Age 33          12 183.9456    24.99044 0.8803919 2.676596
##                       Z (from F) Pr(>F)
## Block * Fungus * Age   1.937795  0.028
##
##
## Redundancy Analysis (PCA on fitted values and residuals)
##
##              Trace Proportion Rank
## Fitted    4.087680  0.8803919    1
## Residuals 0.555343  0.1196081    1
## Total     4.643023  0.9999999    1
##
## Eigenvalues
##
##                PC1
## Fitted    4.087680
## Residuals 0.555343
## Total     4.643023
```

```
coef(lowLM, test = T)
```

```
##
## Linear Model fit with lm.rrpp
##
## Number of observations: 46
## Number of dependent variables: 1
## Data space dimensions: 1
## Sums of Squares and Cross-products: Type III
## Number of permutations: 1000
##
## Statistics (distances) of coefficients with 95 percent confidence intervals,
## effect sizes, and probabilities of exceeding observed values based on
## 1000 random permutations using RRPP
##
##                               d.obs UCL (95%)          Zd Pr(>d)
## (Intercept)               9.7034333  8.816860  2.33761312  0.016
## Block                     2.7120500  1.422906  4.74788676  0.001
## FungusCer                 3.7832333  3.768123  1.96151405  0.050
## FungusCok                 4.1255333  4.457614  1.60711471  0.077
## FungusCtrl                3.7724667  3.819256  1.85177735  0.058
```

```
## FungusNig                  1.3687333  3.911751 -0.24312995  0.528
## FungusPen                  4.7273333  3.880863  2.59762256  0.017
## FungusPod                  3.1066000  3.901550  1.28390922  0.116
## FungusPre                  5.9124000  3.676641  3.75924811  0.003
## FungusXyl                  0.6566833  2.421600 -0.46066377  0.604
## AgeYoung                   6.7049333  3.942629  4.20728026  0.002
## Block:FungusCer            1.3418000  1.550478  1.51614632  0.095
## Block:FungusCok            1.2609500  2.364624  0.39779491  0.306
## Block:FungusCtrl           1.2197000  1.597281  1.14330704  0.137
## Block:FungusNig            0.6864500  1.642021  0.08730734  0.390
## Block:FungusPen            1.3535000  1.638861  1.36514635  0.105
## Block:FungusPod            0.7918000  1.517556  0.31453734  0.332
## Block:FungusPre            1.6565000  1.583976  2.10592274  0.036
## Block:AgeYoung             4.5699500  2.113529  5.55921594  0.001
## FungusCer:AgeYoung         5.2040333  6.041119  1.50370100  0.097
## FungusCok:AgeYoung         7.7240333  7.405409  2.05086828  0.038
## FungusCtrl:AgeYoung        7.8890333  6.050129  2.93704559  0.011
## FungusNig:AgeYoung         3.7873833  6.208656  0.69611436  0.220
## FungusPen:AgeYoung         9.7007000  6.213026  3.80655669  0.002
## FungusPod:AgeYoung         7.1257000  6.062376  2.59846744  0.020
## FungusPre:AgeYoung        10.7553667  6.072150  4.37963889  0.002
## FungusXyl:AgeYoung         1.5143833  3.614567  0.01095824  0.419
## Block:FungusCer:AgeYoung   3.5053500  3.096614  2.51432025  0.026
## Block:FungusCok:AgeYoung   4.1488500  4.741278  1.61552360  0.084
## Block:FungusCtrl:AgeYoung  4.8520000  2.971325  3.92849142  0.003
## Block:FungusNig:AgeYoung   2.2579000  2.970890  1.12751412  0.155
## Block:FungusPen:AgeYoung   5.1965000  3.174421  4.17789026  0.001
## Block:FungusPod:AgeYoung   5.3413500  2.962565  4.47570144  0.002
## Block:FungusPre:AgeYoung   5.7951500  3.018835  4.86979362  0.001
```

```
# ratio anovas
highANOVA <- anova(highLM, effect.type = "F", error = c("Residuals",
    "Block:Fungus", "Block:Fungus:Age", "Residuals", "Block:Fungus:Age",
    "Block:Fungus:Age", "Residuals"))
summary(highANOVA)
```

```
##
## Analysis of Variance, using Residual Randomization
## Permutation procedure: Randomization of null model residuals
## Number of permutations: 1000
## Estimation method: Ordinary Least Squares
## Sums of Squares and Cross-products: Type III
## Effect sizes (Z) based on F distributions
##
##                  Df     SS      MS      Rsq      F        Z Pr(>F)
## Block             1  0.197 0.19694 0.002096 0.2437           0.611
## Fungus            8  5.524 0.69044 0.058781 2.7711  0.83328  0.197
## Age               1  2.028 2.02836 0.021586 5.0392  1.30952  0.044 *
## Block:Fungus      6  1.495 0.24916 0.015909 0.3083 -1.26420  0.894
## Block:Age         1  0.839 0.83860 0.008924 2.0834           0.140
## Fungus:Age        8  2.190 0.27375 0.023306 0.6801 -0.74888  0.796
## Block:Fungus:Age  6  2.415 0.40251 0.025701 0.4980 -0.78923  0.793
## Residuals         8  6.466 0.80824 0.068810
## Total            39 93.967
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Call: lm.rrpp(f1 = Chl.b ~ Block * Fungus * Age, SS.type = "III", data = high,
##     print.progress = F)
```

```
lowANOVA <- anova(lowLM, effect.type = "F", error = c("Residuals",
    "Block:Fungus", "Block:Fungus:Age", "Residuals", "Block:Fungus:Age",
    "Block:Fungus:Age", "Residuals"))
summary(lowANOVA)
```

```
##
## Analysis of Variance, using Residual Randomization
## Permutation procedure: Randomization of null model residuals
## Number of permutations: 1000
## Estimation method: Ordinary Least Squares
## Sums of Squares and Cross-products: Type III
## Effect sizes (Z) based on F distributions
##
##                  Df      SS      MS      Rsq      F        Z Pr(>F)
## Block             1  14.710 14.7104 0.070406 7.0637           0.034 *
## Fungus            8  11.605  1.4506 0.055542 2.7036  1.62775  0.070 .
## Age               1   9.633  9.6335 0.046107 2.5619  1.04319  0.089 .
## Block:Fungus      7   3.756  0.5365 0.017976 0.2576 -1.68648  0.945
## Block:Age         1  20.884 20.8844 0.099956 5.5539           0.019 *
## Fungus:Age        8  19.625  2.4531 0.093927 0.6524 -0.70537  0.776
## Block:Fungus:Age  7  26.322  3.7604 0.125983 1.8057  0.97428  0.160
## Residuals        12  24.990  2.0825 0.119608
## Total            45 208.936
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Call: lm.rrpp(f1 = Chl.b ~ Block * Fungus * Age, SS.type = "III", data = low,
##     print.progress = F)
```

```
# pairwise
highpw <- pairwise(highLM, groups = high$Fungus)
summary(highpw, confidence = 0.95, stat.table = T)
```

```
##
## Pairwise comparisons
##
## Groups: Asp Cer Cok Ctrl Nig Pen Pod Pre Xyl
##
## RRPP: 1000 permutations
##
## LS means:
## Vectors hidden (use show.vectors = TRUE to view)
##
## Pairwise distances between means, plus statistics
##                    d UCL (95%)             Z Pr > d
## Asp:Cer  1.40883333 2.0532160 -0.0391402115  0.530
## Asp:Cok  2.86728333 3.5092806 -0.0134255369  0.527
## Asp:Ctrl 1.16955000 1.6009888  0.0033440133  0.489
## Asp:Nig  1.12901667 1.5862536 -0.0210603207  0.524
## Asp:Pen  0.27595000 0.7440610 -0.2560781352  0.546
```

```
## Asp:Pod  2.22305833 2.7093197  0.0020466769  0.512
## Asp:Pre  1.09615833 1.6013929 -0.0224875134  0.529
## Asp:Xyl  0.49590833 0.9711726 -0.0503802905  0.508
## Cer:Cok  1.45845000 2.1850596  0.0209170861  0.516
## Cer:Ctrl 0.23928333 0.8741738 -0.5177538498  0.643
## Cer:Nig  0.27981667 0.8940755 -0.4278919033  0.591
## Cer:Pen  1.13288333 1.7934800  0.0098670038  0.497
## Cer:Pod  0.81422500 1.4804144  0.0191380830  0.484
## Cer:Pre  0.31267500 0.9778259 -0.3690143297  0.580
## Cer:Xyl  0.91292500 1.6322366 -0.0459847725  0.500
## Cok:Ctrl 1.69773333 2.3133186 -0.0159375395  0.506
## Cok:Nig  1.73826667 2.3711863  0.0013238243  0.514
## Cok:Pen  2.59133333 3.1784924  0.0368552549  0.516
## Cok:Pod  0.64422500 1.3186784 -0.0638176448  0.517
## Cok:Pre  1.77112500 2.4275900  0.0038223452  0.509
## Cok:Xyl  2.37137500 3.0480770 -0.0160075182  0.512
## Ctrl:Nig 0.04053333 0.5490805 -1.1279636621  0.890
## Ctrl:Pen 0.89360000 1.3344906  0.0741060292  0.463
## Ctrl:Pod 1.05350833 1.5178074 -0.0009301432  0.519
## Ctrl:Pre 0.07339167 0.5959994 -0.9744038737  0.837
## Ctrl:Xyl 0.67364167 1.1927018 -0.0092211324  0.488
## Nig:Pen  0.85306667 1.2725337  0.0512371617  0.481
## Nig:Pod  1.09404167 1.6021957  0.0206345254  0.501
## Nig:Pre  0.03285833 0.6268016 -1.1470251872  0.915
## Nig:Xyl  0.63310833 1.1760572 -0.0365071319  0.512
## Pen:Pod  1.94710833 2.4327228  0.0649084515  0.477
## Pen:Pre  0.82020833 1.2881646  0.0397701337  0.491
## Pen:Xyl  0.21995833 0.7078684 -0.3647109876  0.579
## Pod:Pre  1.12690000 1.6651442  0.0217463297  0.487
## Pod:Xyl  1.72715000 2.3004922 -0.0017083427  0.484
## Pre:Xyl  0.60025000 1.1600314 -0.0558601571  0.495
```

```
highpw2 <- pairwise(highLM, groups = high$Age)
summary(highpw2, confidence = 0.95, stat.table = T)
```

```
##
## Pairwise comparisons
##
## Groups: Old Young
##
## RRPP: 1000 permutations
##
## LS means:
## Vectors hidden (use show.vectors = TRUE to view)
##
## Pairwise distances between means, plus statistics
##                   d UCL (95%)          Z Pr > d
## Old:Young 2.190885  2.437061 -0.0217629  0.516
```

```
lowpw <- pairwise(lowLM, groups = low$Fungus)
summary(lowpw, confidence = 0.95, stat.table = T)
```

```
##
## Pairwise comparisons
##
```

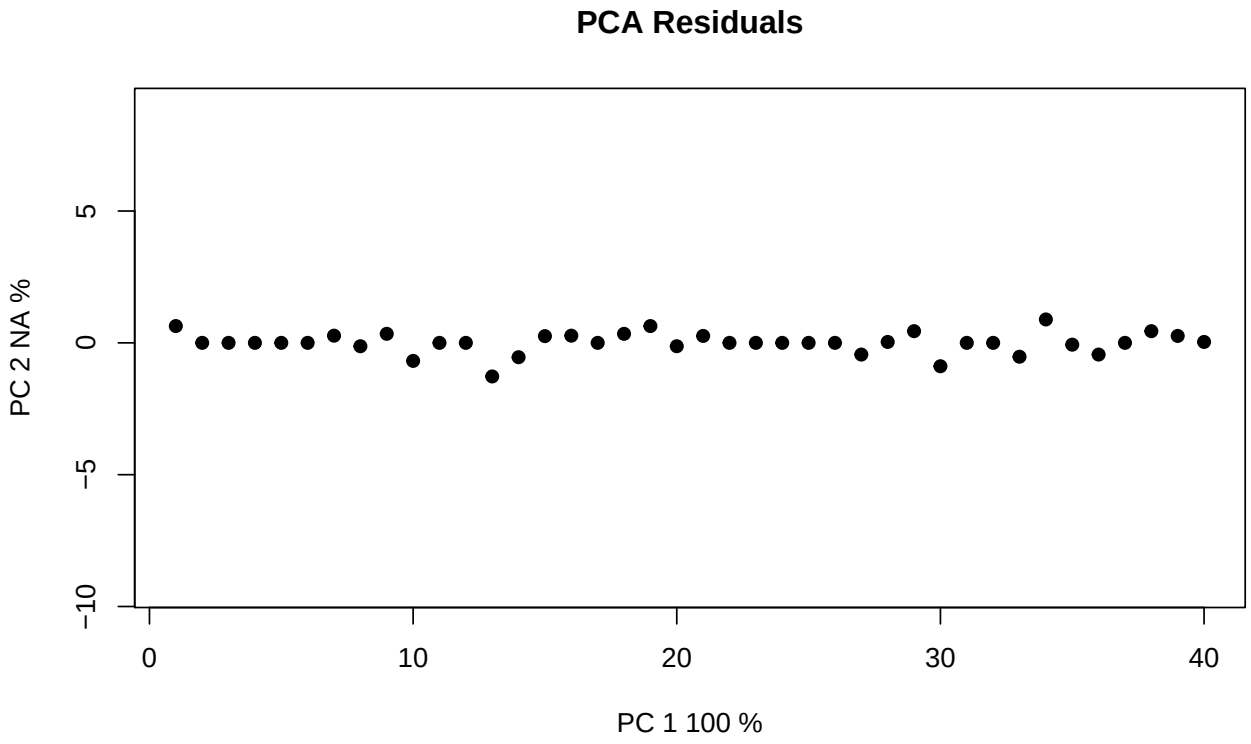
```
## Groups: Asp Cer Cok Ctrl Nig Pen Pod Pre Xyl
##
## RRPP: 1000 permutations
##
## LS means:
## Vectors hidden (use show.vectors = TRUE to view)
##
## Pairwise distances between means, plus statistics
##                   d UCL (95%)             Z Pr > d
## Asp:Cer  2.0029667  3.036590  0.0006948353  0.508
## Asp:Cok  1.2701917  2.449669 -0.0369686944  0.499
## Asp:Ctrl 2.2405500  3.208026  0.0591384880  0.485
## Asp:Nig  0.3600417  1.541545 -0.5661175530  0.642
## Asp:Pen  2.3664833  3.420721  0.0346965415  0.477
## Asp:Pod  3.3015000  4.329931  0.0381348759  0.496
## Asp:Pre  3.0168667  4.022630  0.0078963105  0.485
## Asp:Xyl  0.5275833  2.039301 -0.4596796837  0.588
## Cer:Cok  0.7327750  1.817063 -0.1786804299  0.519
## Cer:Ctrl 0.2375833  1.290320 -0.7064443750  0.706
## Cer:Nig  1.6429250  2.704958 -0.0025738725  0.520
## Cer:Pen  0.3635167  1.390792 -0.4524038522  0.593
## Cer:Pod  1.2985333  2.256281  0.0333987898  0.484
## Cer:Pre  1.0139000  1.982522 -0.0204402406  0.479
## Cer:Xyl  2.5305500  4.004337  0.0081304370  0.478
## Cok:Ctrl 0.9703583  2.116997 -0.0140104255  0.467
## Cok:Nig  0.9101500  2.106143 -0.1512865037  0.529
## Cok:Pen  1.0962917  2.151256 -0.0135297032  0.479
## Cok:Pod  2.0313083  3.148278  0.0424149024  0.475
## Cok:Pre  1.7466750  2.915110  0.0131353986  0.474
## Cok:Xyl  1.7977750  3.312103 -0.0238677671  0.497
## Ctrl:Nig 1.8805083  2.978263  0.0550075896  0.473
## Ctrl:Pen 0.1259333  1.216929 -1.0020940115  0.842
## Ctrl:Pod 1.0609500  2.034873 -0.0520971158  0.514
## Ctrl:Pre 0.7763167  1.818599 -0.1372043863  0.516
## Ctrl:Xyl 2.7681333  4.270618  0.0498277153  0.462
## Nig:Pen  2.0064417  3.137083  0.0329286981  0.477
## Nig:Pod  2.9414583  4.073581  0.0357682822  0.496
## Nig:Pre  2.6568250  3.772914  0.0086836026  0.484
## Nig:Xyl  0.8876250  2.423975 -0.1882226477  0.503
## Pen:Pod  0.9350167  1.975069 -0.0565680218  0.501
## Pen:Pre  0.6503833  1.666200 -0.2064797620  0.538
## Pen:Xyl  2.8940667  4.355614  0.0319462746  0.475
## Pod:Pre  0.2846333  1.295458 -0.6190877269  0.672
## Pod:Xyl  3.8290833  5.340200  0.0338894566  0.472
## Pre:Xyl  3.5444500  4.991688  0.0131360352  0.484
```

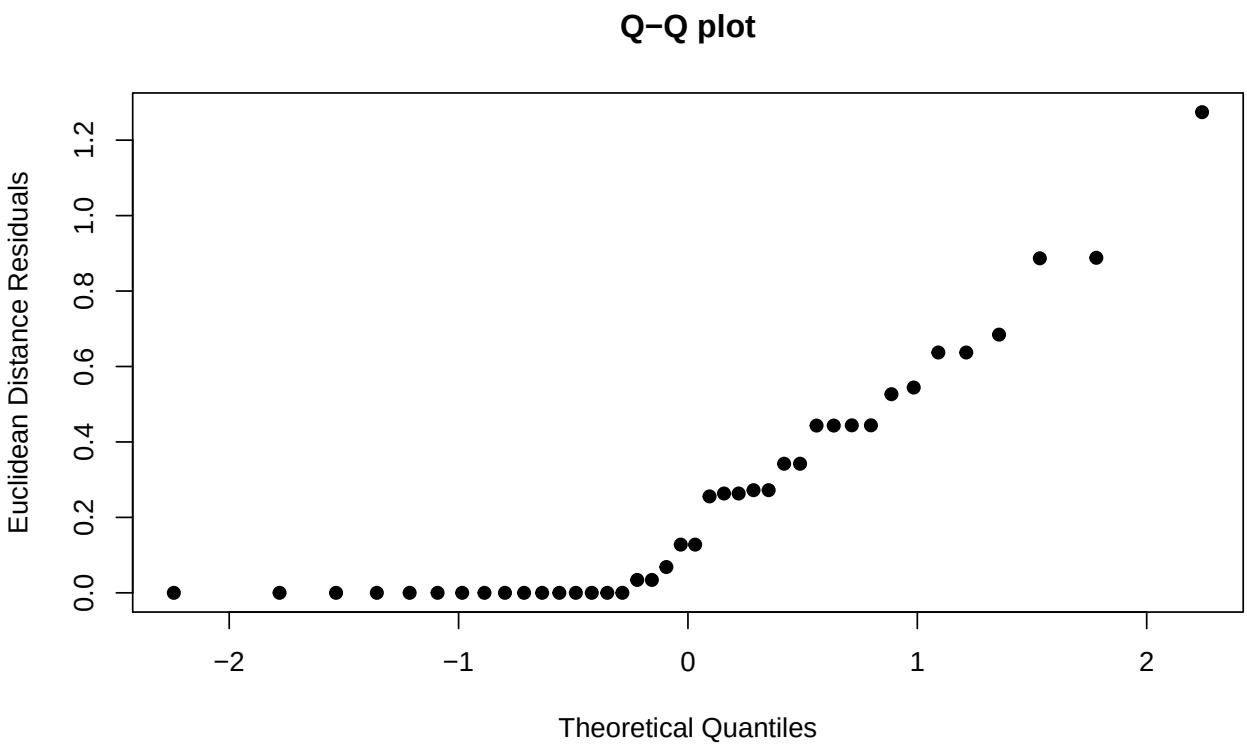
```
lowpw2 <- pairwise(lowLM, groups = low$Age)
summary(lowpw2, confidence = 0.95, stat.table = T)
```

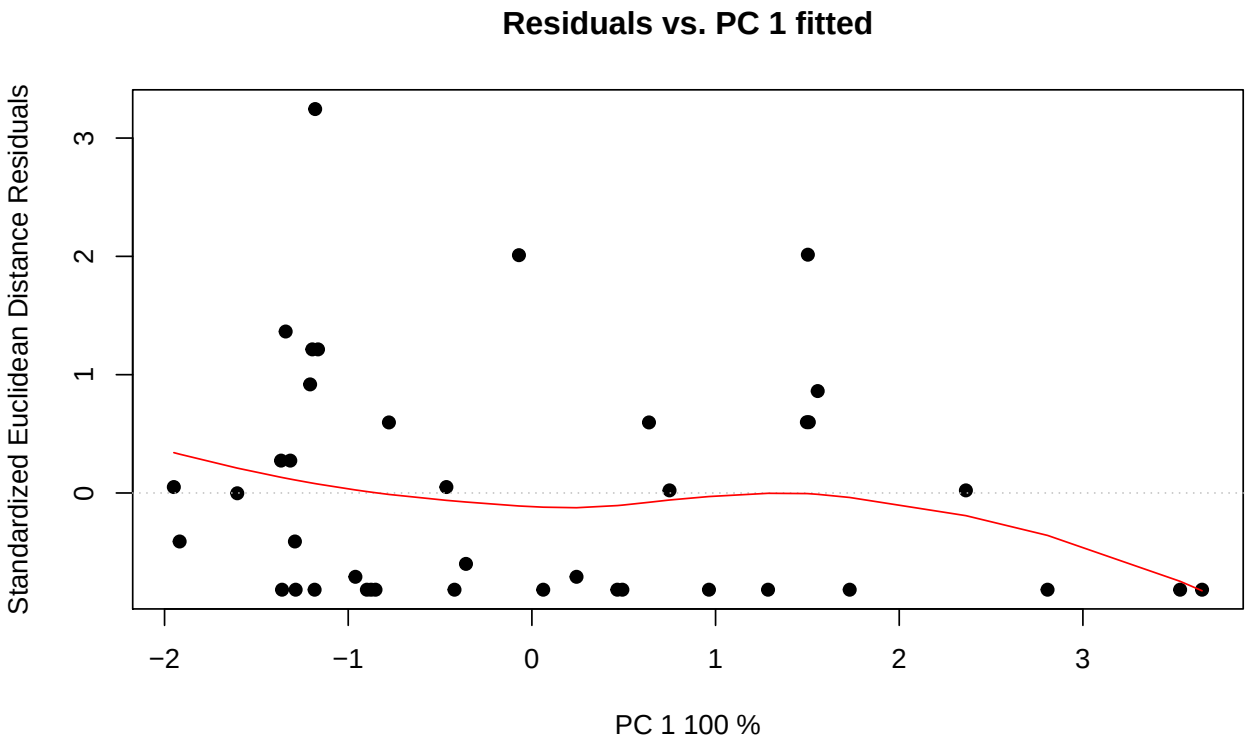
```
##
## Pairwise comparisons
##
## Groups: Old Young
##
## RRPP: 1000 permutations
```

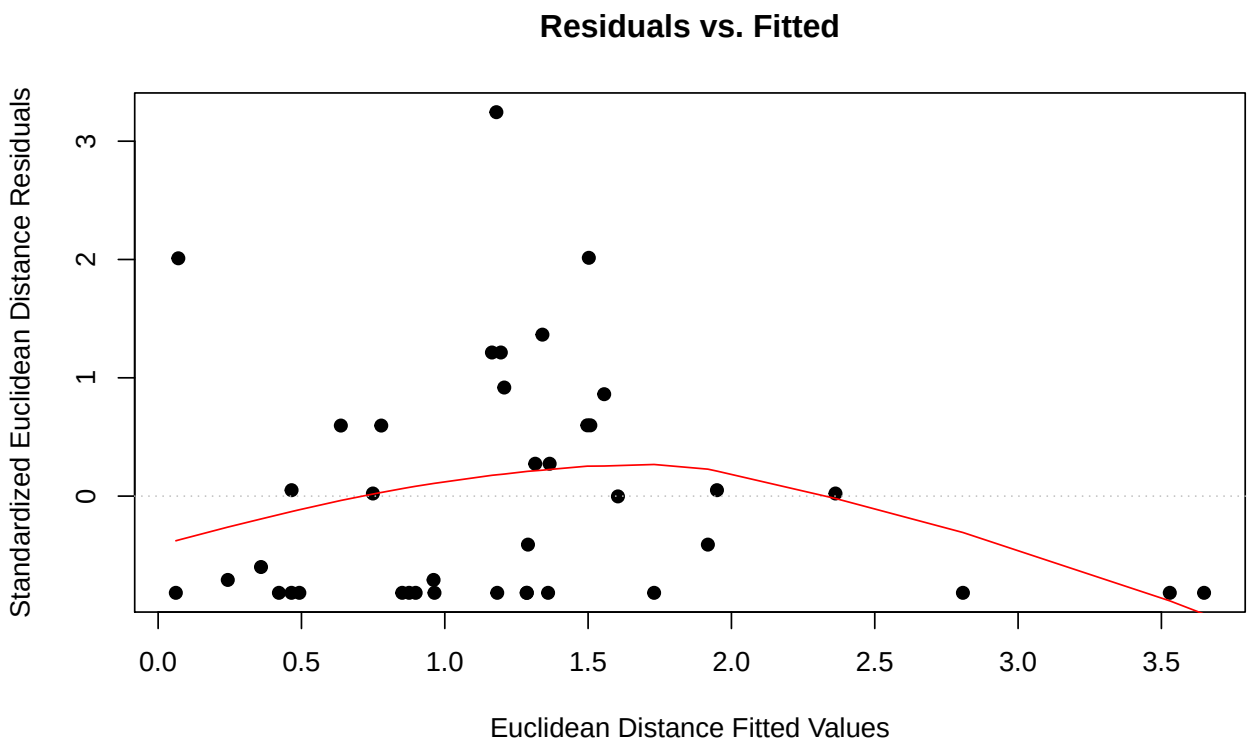
```
##
## LS means:
## Vectors hidden (use show.vectors = TRUE to view)
##
## Pairwise distances between means, plus statistics
##                   d UCL (95%)          Z Pr > d
## Old:Young 1.035035  1.546003 0.01878663  0.489
```

```r
# residuals vs fitted values (homoscedasticity check)
hdiagnostics <- plot(highLM, type = "diagnostics")
```

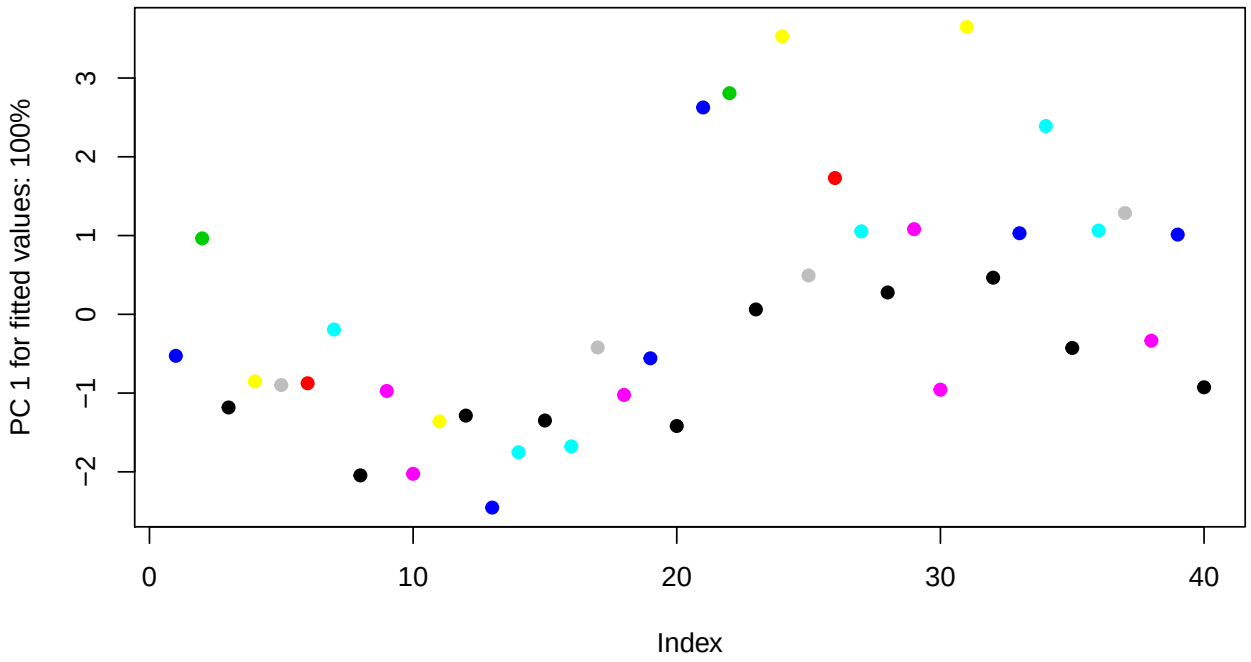



Q−Q plot
Euclidean Distance Residuals
0.0
0.2
0.4
0.6
0.8
1.0
1.2
−2
−1
0
1
2
Theoretical Quantiles

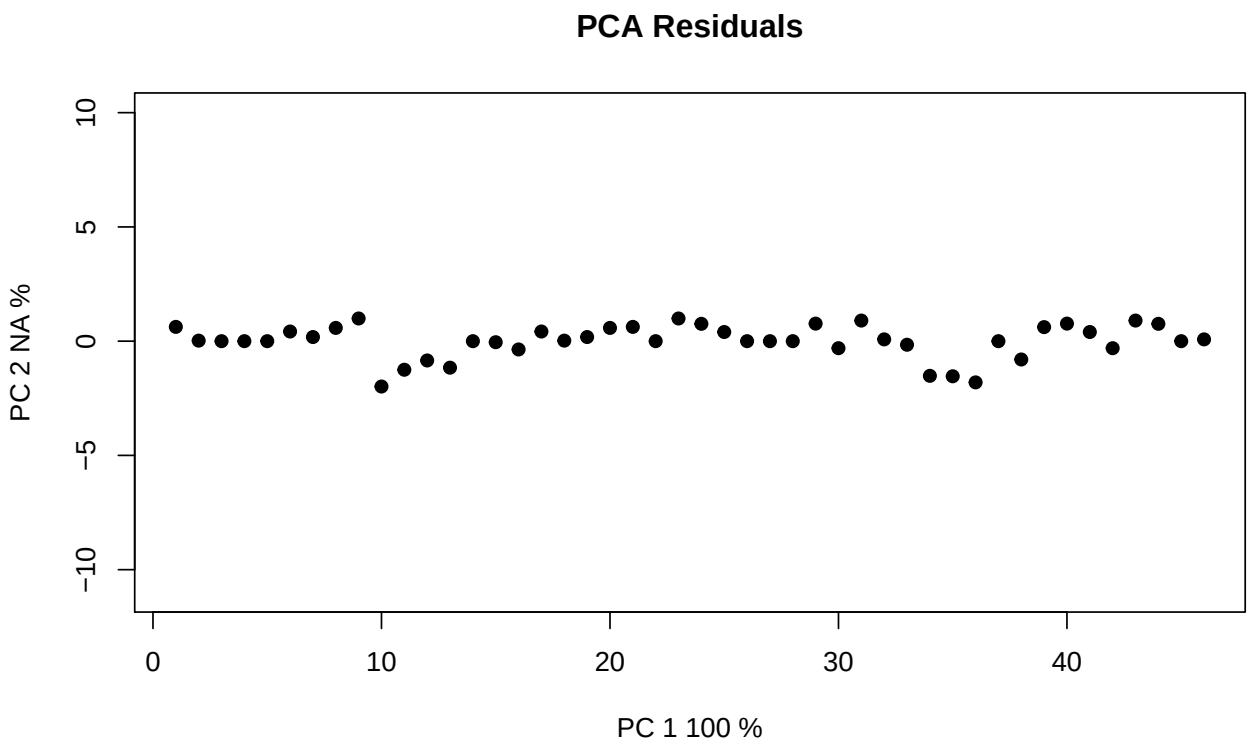

Residuals vs. PC 1 fitted
Standardized Euclidean Distance Residuals
0
1
2
3
−2
−1
0
1
2
3
PC 1 100 %

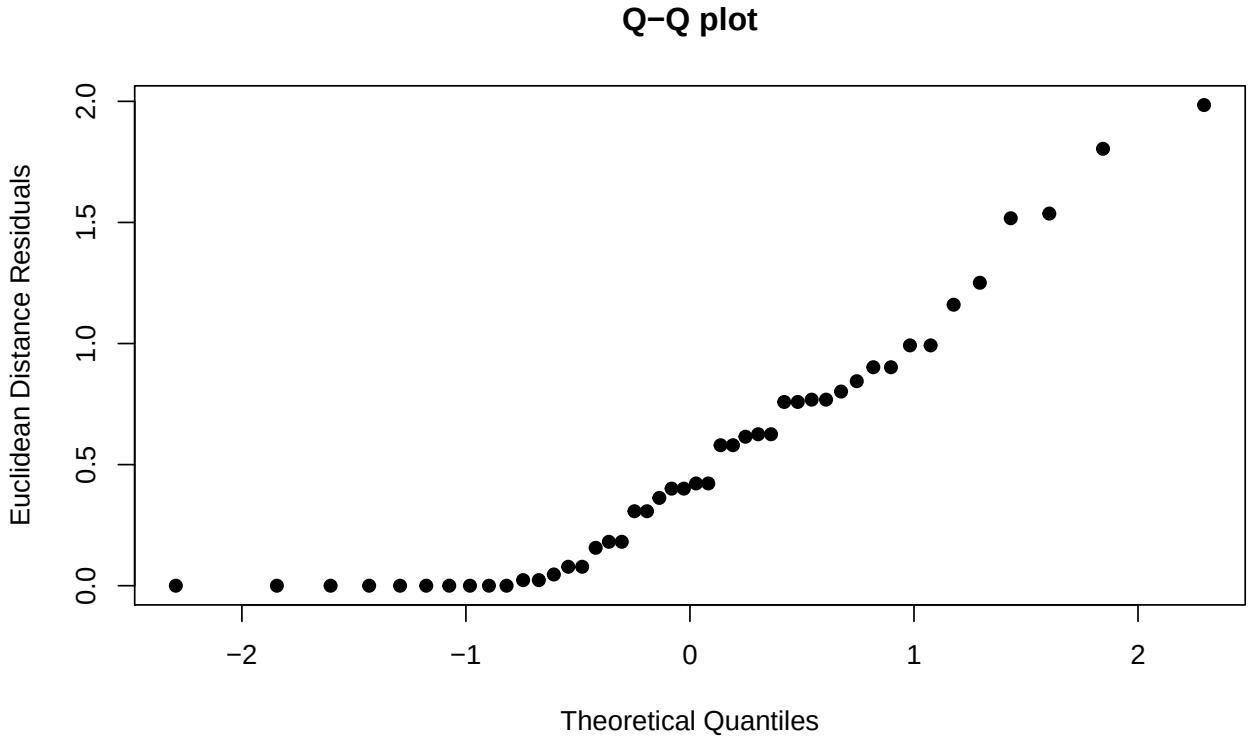


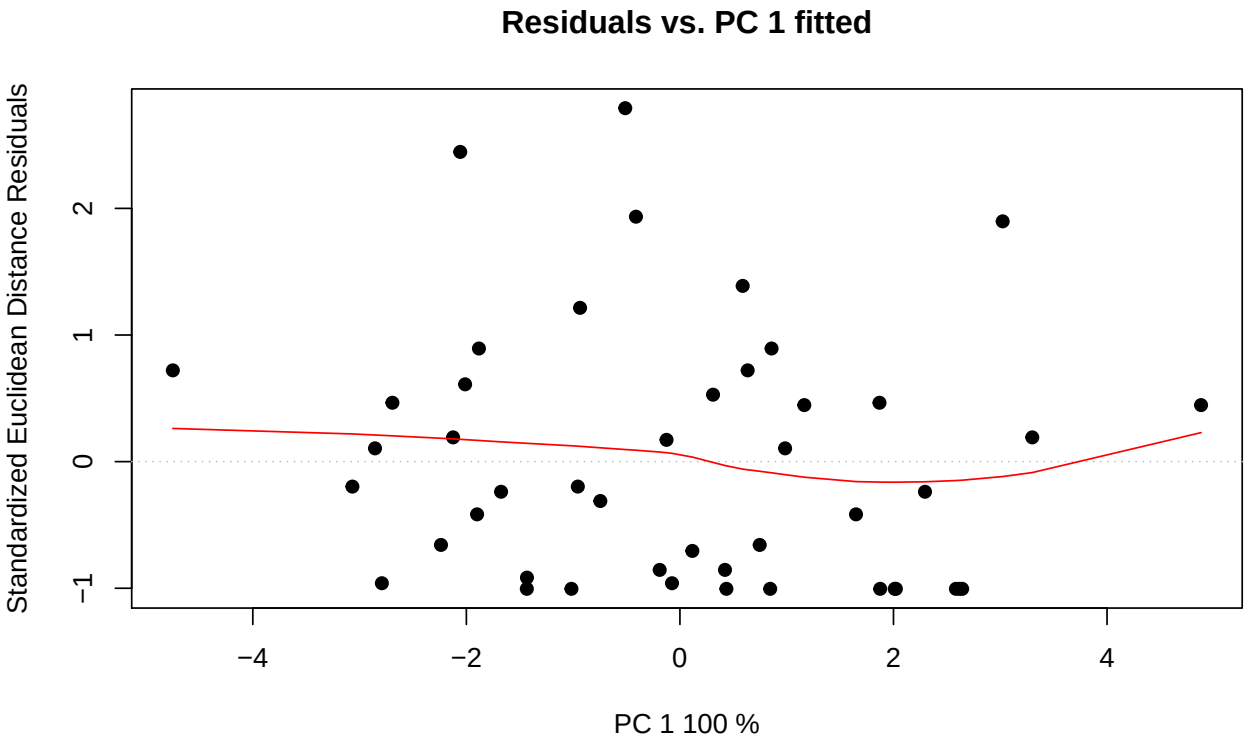

```
# pca plot
hpcplot <- plot(highLM, type = "PC", pch = 19, col = interaction(high$Water,
    high$Fungus))
```

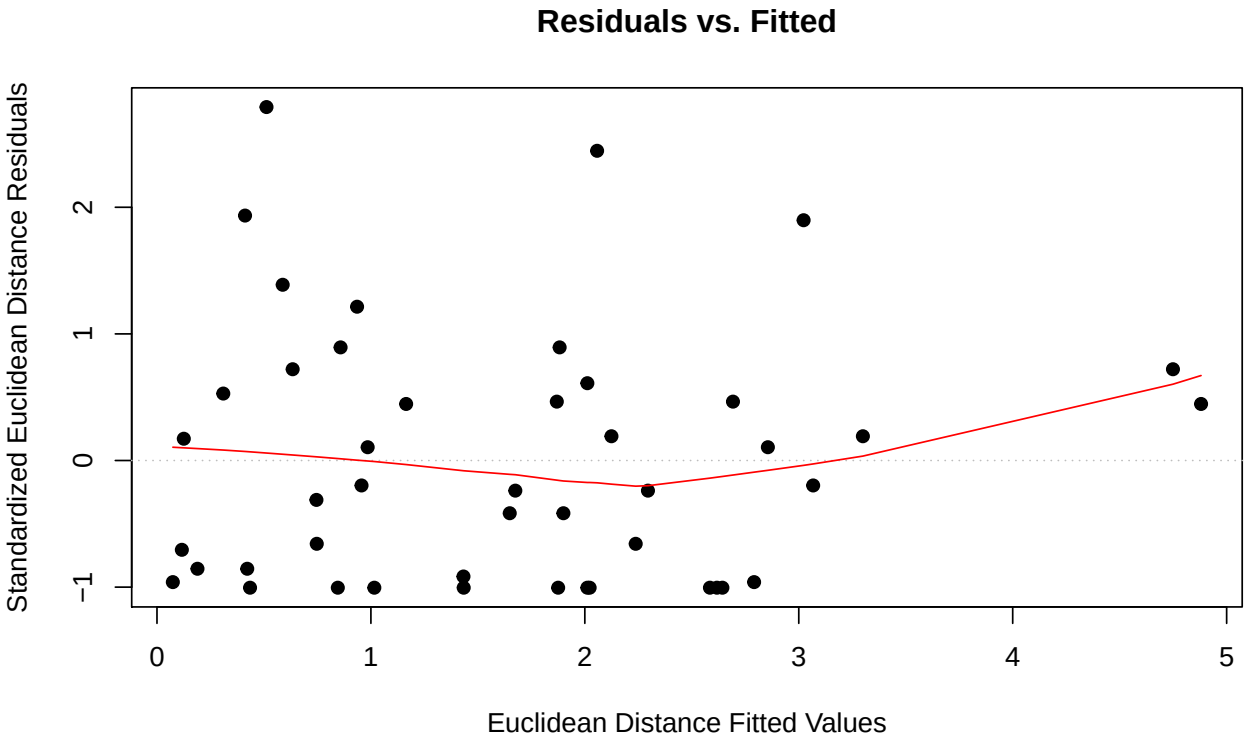



```
# residuals vs fitted values (homoscedasticity check)
ldiagnostics <- plot(lowLM, type = "diagnostics")
```

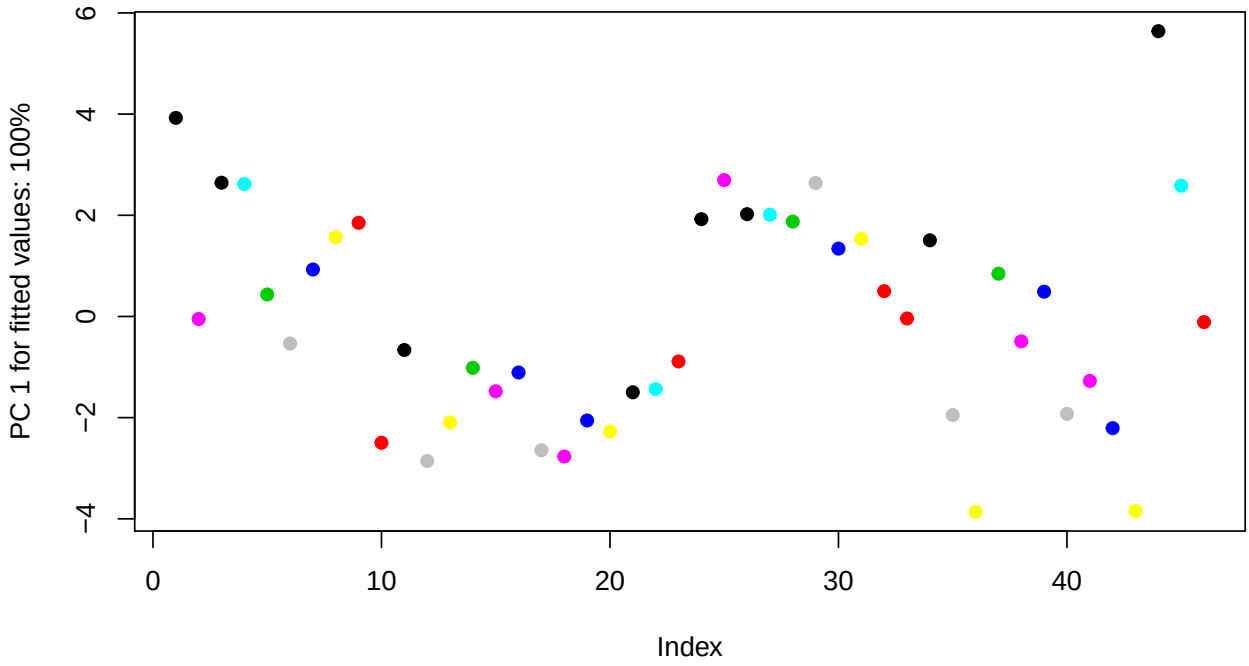

PCA Residuals
PC 2 NA %
10
5
0
−5
−10
0
10
20
30
40
PC 1 100 %


Q−Q plot
Euclidean Distance Residuals
2.0
1.5
1.0
0.5
0.0
−2
−1
0
1
2
Theoretical Quantiles






```
# pca plot
lpcplot <- plot(lowLM, type = "PC", pch = 19, col = interaction(low$Water,
    low$Fungus))
```




```
## Total linear models and coefficient tests
highLM <- lm.rrpp(Total ~ Block * Fungus * Age, data = high,
    SS.type = "III", print.progress = F)
```

```
##
## Warning: Because variables in the linear model are redundant,
## the linear model design has been truncated (via QR decomposition).
## Original X columns: 36
## Final X columns (rank): 32
## Check coefficients or degrees of freedom in ANOVA to see changes.
```

```
summary(highLM)
```

```
##
## Warning: Because variables in the linear model are redundant,
## the linear model design has been truncated (via QR decomposition).
## Original X columns: 36
## Final X columns (rank): 32
## Check coefficients or degrees of freedom in ANOVA to see changes.
```

```
##
## Linear Model fit with lm.rrpp
##
## Number of observations: 40
## Number of dependent variables: 1
## Data space dimensions: 1
## Sums of Squares and Cross-products: Type III
## Number of permutations: 1000
##
## Full Model Analysis of Variance
##
##                       Df Residual Df       SS Residual SS       Rsq        F
## Block * Fungus * Age 31           8 221.9666    22.53375 0.9078376 2.542041
##                       Z (from F) Pr(>F)
```

```
## Block * Fungus * Age    1.45138  0.083
##
##
## Redundancy Analysis (PCA on fitted values and residuals)
##
##              Trace Proportion Rank
## Fitted    5.691452  0.9078375    1
## Residuals 0.577788  0.0921624    1
## Total     6.269241  1.0000000    1
##
## Eigenvalues
##
##                PC1
## Fitted    5.691452
## Residuals 0.577788
## Total     6.269241
```

```
coef(highLM, test = T)
```

```
##
## Linear Model fit with lm.rrpp
##
## Number of observations: 40
## Number of dependent variables: 1
## Data space dimensions: 1
## Sums of Squares and Cross-products: Type III
## Number of permutations: 1000
##
## Statistics (distances) of coefficients with 95 percent confidence intervals,
## effect sizes, and probabilities of exceeding observed values based on
## 1000 random permutations using RRPP
##
##                               d.obs UCL (95%)          Zd Pr(>d)
## (Intercept)               2.4605000  5.965483 -0.95729564  0.842
## Block                     0.3327000  1.170195 -0.19550994  0.524
## FungusCer                 1.9381000  3.371012  0.81834791  0.168
## FungusCok                 6.0044000  3.262008  4.75793997  0.003
## FungusCtrl                1.5441000  5.092658 -0.23232550  0.491
## FungusNig                 5.0907000  4.756851  2.24948871  0.040
## FungusPen                 2.1842000  4.664580  0.33220964  0.292
## FungusPod                 3.0680000  6.215268  0.45468859  0.242
## FungusPre                 2.3511500  5.412914  0.29631293  0.283
## FungusXyl                 2.1986000  6.671164 -0.04890224  0.403
## AgeYoung                  4.4501333  3.592018  2.65381638  0.017
## Block:FungusCtrl          0.4002000  1.665440 -0.55555368  0.636
## Block:FungusNig           2.0625000  1.641081  2.79178268  0.009
## Block:FungusPen           0.6948000  1.594835  0.05782493  0.415
## Block:FungusPod           1.0500000  2.609495  0.03176724  0.401
## Block:FungusPre           0.1543500  1.713732 -0.98513696  0.855
## Block:FungusXyl           0.7074000  2.734658 -0.38407267  0.556
## Block:AgeYoung            1.3986000  1.565950  1.55086533  0.081
## FungusCer:AgeYoung        0.5794667  3.367753 -0.74130802  0.746
## FungusCok:AgeYoung        1.5839333  3.410924  0.20011719  0.354
## FungusCtrl:AgeYoung       2.3970000  5.642273  0.07070170  0.394
## FungusNig:AgeYoung        4.0526667  5.726562  1.03328104  0.166
```

```
## FungusPen:AgeYoung        1.3145333  5.410354 -0.56281946  0.647
## FungusPod:AgeYoung        1.4089667  6.736242 -0.65953491  0.704
## FungusPre:AgeYoung        3.6231833  5.582544  0.81975980  0.205
## FungusXyl:AgeYoung        4.2304333  6.870825  0.71704352  0.197
## Block:FungusCtrl:AgeYoung 0.1023000  2.455576 -1.22318440  0.939
## Block:FungusNig:AgeYoung  3.1697000  2.543829  2.68840384  0.014
## Block:FungusPen:AgeYoung  0.5183000  2.468054 -0.69008022  0.701
## Block:FungusPod:AgeYoung  2.2897000  3.856709  0.65193013  0.221
## Block:FungusPre:AgeYoung  1.8753500  2.470363  1.15902044  0.131
## Block:FungusXyl:AgeYoung  2.4271000  3.971562  0.69529753  0.221
```

```
lowLM <- lm.rrpp(Total ~ Block * Fungus * Age, data = low, SS.type = "III",
    print.progress = F)
```

```
##
## Warning: Because variables in the linear model are redundant,
## the linear model design has been truncated (via QR decomposition).
## Original X columns: 36
## Final X columns (rank): 34
## Check coefficients or degrees of freedom in ANOVA to see changes.
```

```
summary(lowLM)
```

```
##
## Warning: Because variables in the linear model are redundant,
## the linear model design has been truncated (via QR decomposition).
## Original X columns: 36
## Final X columns (rank): 34
## Check coefficients or degrees of freedom in ANOVA to see changes.
```

```
##
## Linear Model fit with lm.rrpp
##
## Number of observations: 46
## Number of dependent variables: 1
## Data space dimensions: 1
## Sums of Squares and Cross-products: Type III
## Number of permutations: 1000
##
## Full Model Analysis of Variance
##
##                       Df Residual Df       SS Residual SS       Rsq        F
## Block * Fungus * Age 33          12 314.3371    57.59527 0.8451458 1.984614
##                       Z (from F) Pr(>F)
## Block * Fungus * Age   1.404311   0.09
##
##
## Redundancy Analysis (PCA on fitted values and residuals)
##
##              Trace Proportion Rank
## Fitted    6.985269  0.8451459    1
## Residuals 1.279895  0.1548542    1
## Total     8.265164  1.0000000    1
##
## Eigenvalues
##
```

```
##                PC1
## Fitted    6.985269
## Residuals 1.279895
## Total     8.265164
```

```
coef(lowLM, test = T)
```

```
##
## Linear Model fit with lm.rrpp
##
## Number of observations: 46
## Number of dependent variables: 1
## Data space dimensions: 1
## Sums of Squares and Cross-products: Type III
## Number of permutations: 1000
##
## Statistics (distances) of coefficients with 95 percent confidence intervals,
## effect sizes, and probabilities of exceeding observed values based on
## 1000 random permutations using RRPP
##
##                               d.obs UCL (95%)           Zd Pr(>d)
## (Intercept)               14.046500 13.965178  1.598502712  0.045
## Block                      3.426250  1.984917  4.119848819  0.001
## FungusCer                  6.577567  5.511842  2.719404246  0.017
## FungusCok                  1.492200  6.902350 -0.552599128  0.640
## FungusCtrl                 1.270733  5.781253 -0.499083591  0.601
## FungusNig                  2.480000  5.710512  0.127061132  0.377
## FungusPen                  3.122967  5.753718  0.477962269  0.270
## FungusPod                  4.613567  5.726922  1.352948507  0.115
## FungusPre                  5.691400  5.417928  2.107465113  0.036
## FungusXyl                  2.848150  3.540888  1.375778288  0.110
## AgeYoung                   5.608600  5.420489  2.086786232  0.044
## Block:FungusCer            2.231300  2.310645  1.812591958  0.066
## Block:FungusCok            0.322250  3.716870 -0.947388077  0.844
## Block:FungusCtrl           0.010650  2.423836 -1.238000970  0.991
## Block:FungusNig            0.964250  2.379073 -0.004997778  0.417
## Block:FungusPen            0.351150  2.509073 -0.833822189  0.765
## Block:FungusPod            0.971500  2.415302 -0.001782977  0.428
## Block:FungusPre            0.982450  2.343578  0.088170677  0.394
## Block:AgeYoung             4.185050  2.642521  3.748898429  0.003
## FungusCer:AgeYoung         6.105833  7.714816  1.267998376  0.123
## FungusCok:AgeYoung         4.642800  9.503512  0.253820819  0.353
## FungusCtrl:AgeYoung        3.677733  7.795574  0.247276859  0.319
## FungusNig:AgeYoung         4.948250  7.609501  0.764640533  0.204
## FungusPen:AgeYoung         8.437000  7.892359  2.201506176  0.040
## FungusPod:AgeYoung         4.244600  7.824488  0.512062670  0.267
## FungusPre:AgeYoung        10.636200  7.769286  3.127722259  0.011
## FungusXyl:AgeYoung         3.552350  4.693658  1.159082705  0.131
## Block:FungusCer:AgeYoung   3.861000  3.700948  2.117453293  0.040
## Block:FungusCok:AgeYoung   2.405350  5.646958  0.053699113  0.412
## Block:FungusCtrl:AgeYoung  2.843800  3.702787  1.184145831  0.135
## Block:FungusNig:AgeYoung   2.810900  3.493581  1.226205299  0.124
## Block:FungusPen:AgeYoung   4.568300  3.804095  2.649358373  0.017
## Block:FungusPod:AgeYoung   2.859250  3.766930  1.227770762  0.131
## Block:FungusPre:AgeYoung   5.663050  3.580884  3.674304102  0.006
```

```r
# ratio anovas
highANOVA <- anova(highLM, effect.type = "F", error = c("Residuals",
    "Block:Fungus", "Block:Fungus:Age", "Residuals", "Block:Fungus:Age",
    "Block:Fungus:Age", "Residuals"))
summary(highANOVA)
```

```
##
## Analysis of Variance, using Residual Randomization
## Permutation procedure: Randomization of null model residuals
## Number of permutations: 1000
## Estimation method: Ordinary Least Squares
## Sums of Squares and Cross-products: Type III
## Effect sizes (Z) based on F distributions
##
##                  Df      SS     MS      Rsq      F        Z Pr(>F)
## Block             1   0.221 0.2214 0.000905 0.0786          0.712
## Fungus            8  24.327 3.0408 0.099495 3.3018  0.87448  0.188
## Age               1   4.244 4.2436 0.017356 3.1404          0.094 .
## Block:Fungus      6   5.526 0.9210 0.022600 0.3270 -1.13474  0.869
## Block:Age         1   1.956 1.9561 0.008000 1.4475          0.206
## Fungus:Age        8   8.799 1.0999 0.035989 0.8140 -0.49572  0.703
## Block:Fungus:Age  6   8.108 1.3513 0.033161 0.4797 -0.81835  0.811
## Residuals         8  22.534 2.8167 0.092162
## Total            39 244.500
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Call: lm.rrpp(f1 = Total ~ Block * Fungus * Age, SS.type = "III", data = high,
##     print.progress = F)
```

```r
lowANOVA <- anova(lowLM, effect.type = "F", error = c("Residuals",
    "Block:Fungus", "Block:Fungus:Age", "Residuals", "Block:Fungus:Age",
    "Block:Fungus:Age", "Residuals"))
summary(lowANOVA)
```

```
##
## Analysis of Variance, using Residual Randomization
## Permutation procedure: Randomization of null model residuals
## Number of permutations: 1000
## Estimation method: Ordinary Least Squares
## Sums of Squares and Cross-products: Type III
## Effect sizes (Z) based on F distributions
##
##                  Df     SS      MS      Rsq      F        Z Pr(>F)
## Block             1  23.48 23.4784 0.063125 4.8917          0.068 .
## Fungus            8  15.97  1.9959 0.042930 1.7917  0.91703  0.153
## Age               1   6.74  6.7407 0.018123 2.4616  0.97890  0.122
## Block:Fungus      7   7.80  1.1140 0.020966 0.2321 -1.60813  0.939
## Block:Age         1  17.51 17.5146 0.047091 6.3962          0.014 *
## Fungus:Age        8  15.32  1.9152 0.041195 0.6994 -0.72922  0.784
## Block:Fungus:Age  7  19.17  2.7383 0.051536 0.5705 -0.62258  0.744
## Residuals        12  57.60  4.7996 0.154854
## Total            45 371.93
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Call: lm.rrpp(f1 = Total ~ Block * Fungus * Age, SS.type = "III", data = low,
##     print.progress = F)
```

```
# pairwise
highpw <- pairwise(highLM, groups = high$Fungus)
summary(highpw, confidence = 0.95, stat.table = T)
```

```
##
## Pairwise comparisons
##
## Groups: Asp Cer Cok Ctrl Nig Pen Pod Pre Xyl
##
## RRPP: 1000 permutations
##
## LS means:
## Vectors hidden (use show.vectors = TRUE to view)
##
## Pairwise distances between means, plus statistics
##                    d UCL (95%)             Z Pr > d
## Asp:Cer  2.594433333  3.812039 -3.954665e-02  0.533
## Asp:Cok  5.579033333  6.757072 -1.367275e-02  0.524
## Asp:Ctrl 2.044500000  2.865631  3.875306e-03  0.505
## Asp:Nig  2.109066667  2.953394 -1.940906e-02  0.525
## Asp:Pen  0.655633333  1.518069 -1.647441e-01  0.525
## Asp:Pod  4.098058333  5.001203  2.778474e-03  0.511
## Asp:Pre  2.106208333  3.012280 -2.436674e-02  0.529
## Asp:Xyl  1.025908333  1.915073 -2.668556e-02  0.503
## Cer:Cok  2.984600000  4.323065  2.153141e-02  0.515
## Cer:Ctrl 0.549933333  1.727749 -4.089082e-01  0.603
## Cer:Nig  0.485366667  1.636969 -4.659161e-01  0.612
## Cer:Pen  1.938800000  3.154183  5.623168e-03  0.499
## Cer:Pod  1.503625000  2.742521  1.824930e-02  0.480
## Cer:Pre  0.488225000  1.740016 -4.744391e-01  0.614
## Cer:Xyl  1.568525000  2.907379 -5.774385e-02  0.500
## Cok:Ctrl 3.534533333  4.676755 -1.659699e-02  0.508
## Cok:Nig  3.469966667  4.651340  2.638330e-06  0.518
## Cok:Pen  4.923400000  5.998903  3.570479e-02  0.513
## Cok:Pod  1.480975000  2.759216 -3.243378e-02  0.516
## Cok:Pre  3.472825000  4.669348  5.027707e-03  0.508
## Cok:Xyl  4.553125000  5.809938 -2.061802e-02  0.513
## Ctrl:Nig 0.064566667  1.040871 -1.170930e+00  0.913
## Ctrl:Pen 1.388866667  2.212370  7.117354e-02  0.461
## Ctrl:Pod 2.053558333  2.917332 -6.862494e-04  0.526
## Ctrl:Pre 0.061708333  1.103822 -1.193488e+00  0.920
## Ctrl:Xyl 1.018591667  1.991286 -2.842164e-02  0.492
## Nig:Pen  1.453433333  2.231779  5.055845e-02  0.482
## Nig:Pod  1.988991667  2.943447  1.983241e-02  0.496
## Nig:Pre  0.002858333  1.136061 -1.308734e+00  0.998
## Nig:Xyl  1.083158333  2.101251 -5.034647e-02  0.510
## Pen:Pod  3.442425000  4.356699  6.420656e-02  0.471
## Pen:Pre  1.450575000  2.304164  3.488796e-02  0.491
## Pen:Xyl  0.370275000  1.253998 -4.289162e-01  0.601
## Pod:Pre  1.991850000  3.006670  2.368274e-02  0.488
```

```
## Pod:Xyl  3.072150000  4.135326 -6.425890e-03  0.482
## Pre:Xyl  1.080300000  2.137962 -6.751978e-02  0.497
```

```
highpw2 <- pairwise(highLM, groups = high$Age)
summary(highpw2, confidence = 0.95, stat.table = T)
```

```
##
## Pairwise comparisons
##
## Groups: Old Young
##
## RRPP: 1000 permutations
##
## LS means:
## Vectors hidden (use show.vectors = TRUE to view)
##
## Pairwise distances between means, plus statistics
##                   d UCL (95%)           Z Pr > d
## Old:Young 3.012115  3.472667 -0.02145217  0.512
```

```
lowpw <- pairwise(lowLM, groups = low$Fungus)
summary(lowpw, confidence = 0.95, stat.table = T)
```

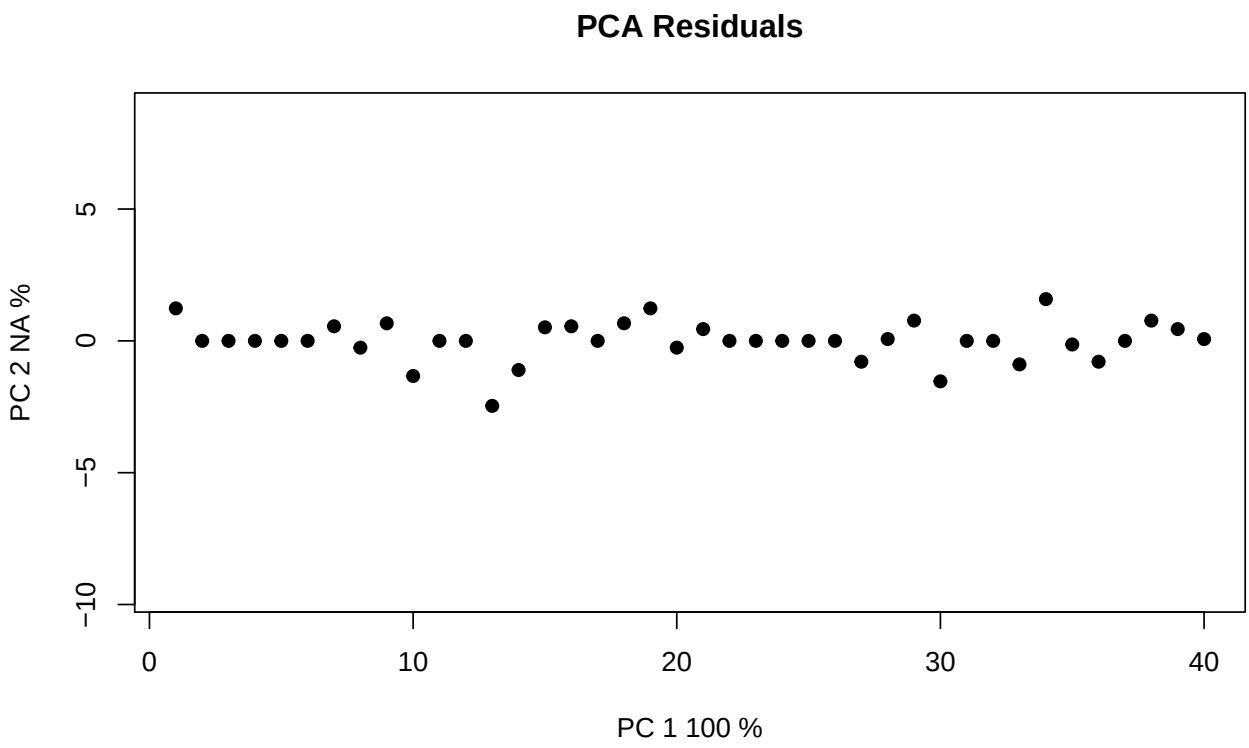
```
##
## Pairwise comparisons
##
## Groups: Asp Cer Cok Ctrl Nig Pen Pod Pre Xyl
##
## RRPP: 1000 permutations
##
## LS means:
## Vectors hidden (use show.vectors = TRUE to view)
##
## Pairwise distances between means, plus statistics
##                   d UCL (95%)            Z Pr > d
## Asp:Cer  2.9230500  4.191613  0.021014198  0.501
## Asp:Cok  0.7913250  2.275334 -0.218102220  0.501
## Asp:Ctrl 2.2543667  3.451344  0.053541805  0.473
## Asp:Nig  0.8882750  2.421483 -0.155071014  0.482
## Asp:Pen  2.7704667  3.989263  0.048371138  0.479
## Asp:Pod  3.4075167  4.581617  0.051997772  0.491
## Asp:Pre  4.0714500  5.330438  0.036290539  0.471
## Asp:Xyl  0.2617500  2.222896 -0.914283250  0.806
## Cer:Cok  2.1317250  3.437677  0.000642411  0.508
## Cer:Ctrl 0.6686833  1.864353 -0.310715671  0.571
## Cer:Nig  2.0347750  3.382907  0.011476309  0.496
## Cer:Pen  0.1525833  1.411810 -1.043842561  0.851
## Cer:Pod  0.4844667  1.657651 -0.402741842  0.586
## Cer:Pre  1.1484000  2.402595 -0.034185797  0.481
## Cer:Xyl  3.1848000  4.758612  0.034303087  0.507
## Cok:Ctrl 1.4630417  2.755800  0.001137154  0.490
## Cok:Nig  0.0969500  1.792232 -1.141932269  0.918
## Cok:Pen  1.9791417  3.298245  0.022819396  0.495
## Cok:Pod  2.6161917  4.017258  0.034244268  0.489
## Cok:Pre  3.2801250  4.669605  0.018793900  0.484
```

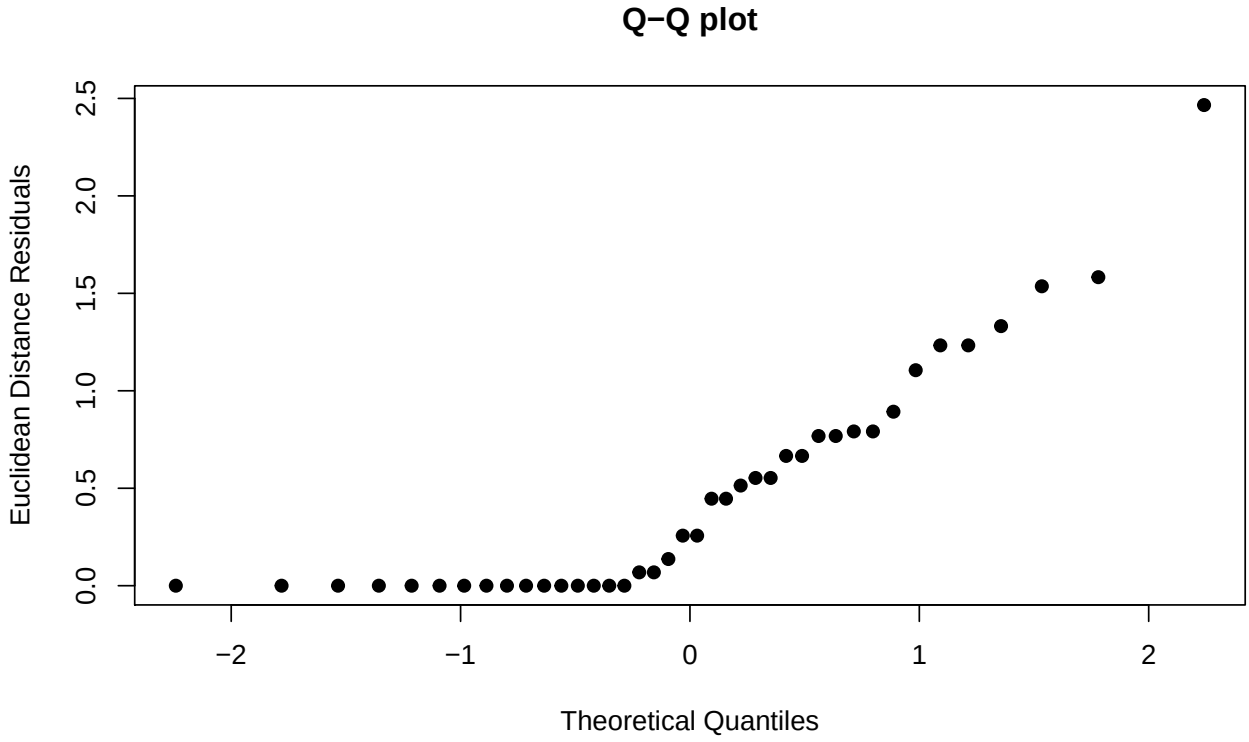
```
## Cok:Xyl  1.0530750  2.971412 -0.259364195  0.538
## Ctrl:Nig 1.3660917  2.664379 -0.021987340  0.479
## Ctrl:Pen 0.5161000  1.737725 -0.421214597  0.596
## Ctrl:Pod 1.1531500  2.305679 -0.053278230  0.510
## Ctrl:Pre 1.8170833  3.024396 -0.023286737  0.506
## Ctrl:Xyl 2.5161167  4.166173  0.045079752  0.484
## Nig:Pen  1.8821917  3.166039  0.030281828  0.483
## Nig:Pod  2.5192417  3.813857  0.040294181  0.501
## Nig:Pre  3.1831750  4.456738  0.031100619  0.481
## Nig:Xyl  1.1500250  3.066943 -0.200683755  0.520
## Pen:Pod  0.6370500  1.935758 -0.279985065  0.539
## Pen:Pre  1.3009833  2.552229 -0.047965977  0.512
## Pen:Xyl  3.0322167  4.664688  0.048599721  0.492
## Pod:Pre  0.6639333  1.994558 -0.259396330  0.526
## Pod:Xyl  3.6692667  5.352557  0.056020427  0.503
## Pre:Xyl  4.3332000  6.034100  0.045998381  0.490
```

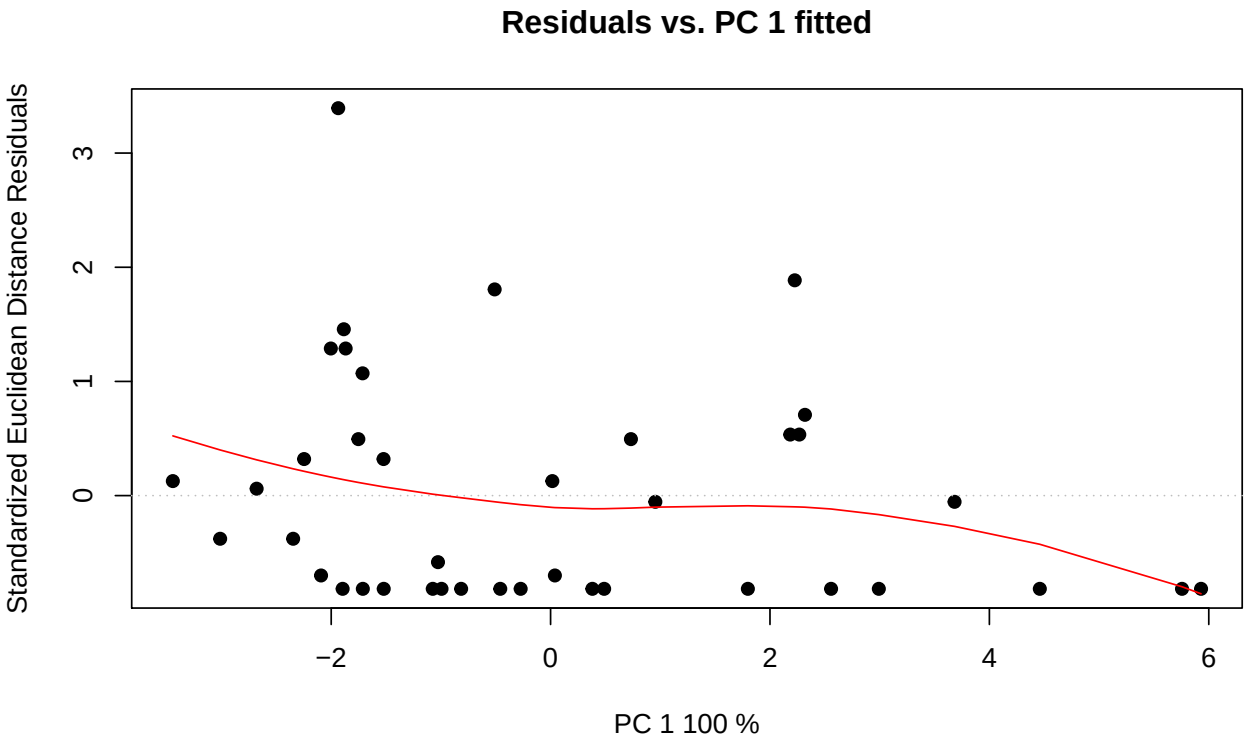
```
lowpw2 <- pairwise(lowLM, groups = low$Age)
summary(lowpw2, confidence = 0.95, stat.table = T)
```

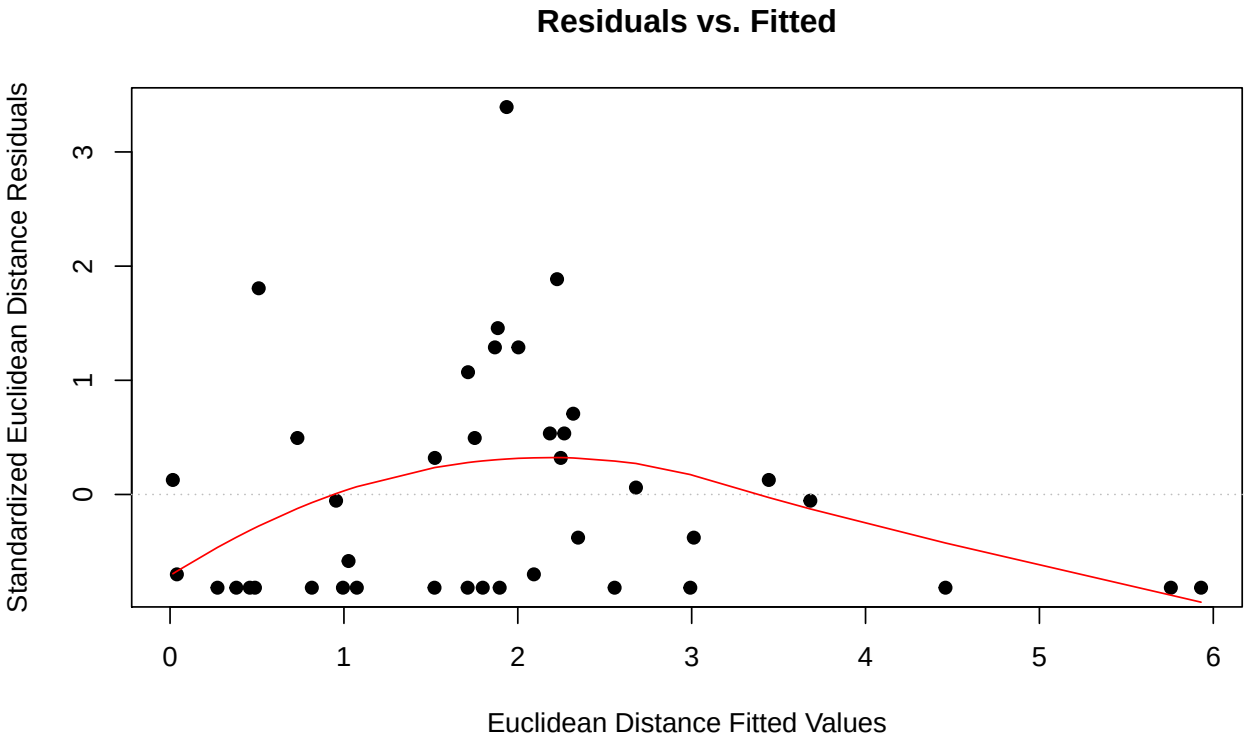
```
##
## Pairwise comparisons
##
## Groups: Old Young
##
## RRPP: 1000 permutations
##
## LS means:
## Vectors hidden (use show.vectors = TRUE to view)
##
## Pairwise distances between means, plus statistics
##                   d UCL (95%)          Z Pr > d
## Old:Young 1.736996  2.386233 0.02114367  0.496
```

```
# residuals vs fitted values (homoscedasticity check)
hdiagnostics <- plot(highLM, type = "diagnostics")
```

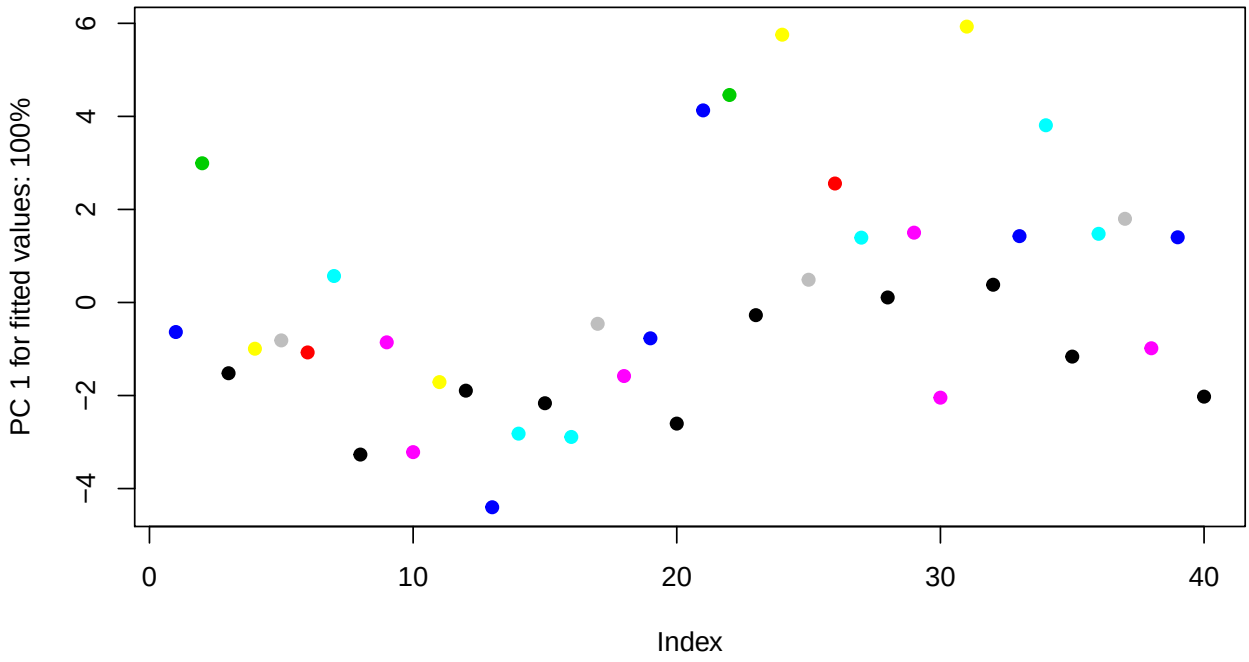

PCA Residuals
PC 2 NA %
5
0
−5
−10
0
10
20
30
40
PC 1 100 %


Q−Q plot
Euclidean Distance Residuals
0.0
0.5
1.0
1.5
2.0
2.5
−2
−1
0
1
2
Theoretical Quantiles

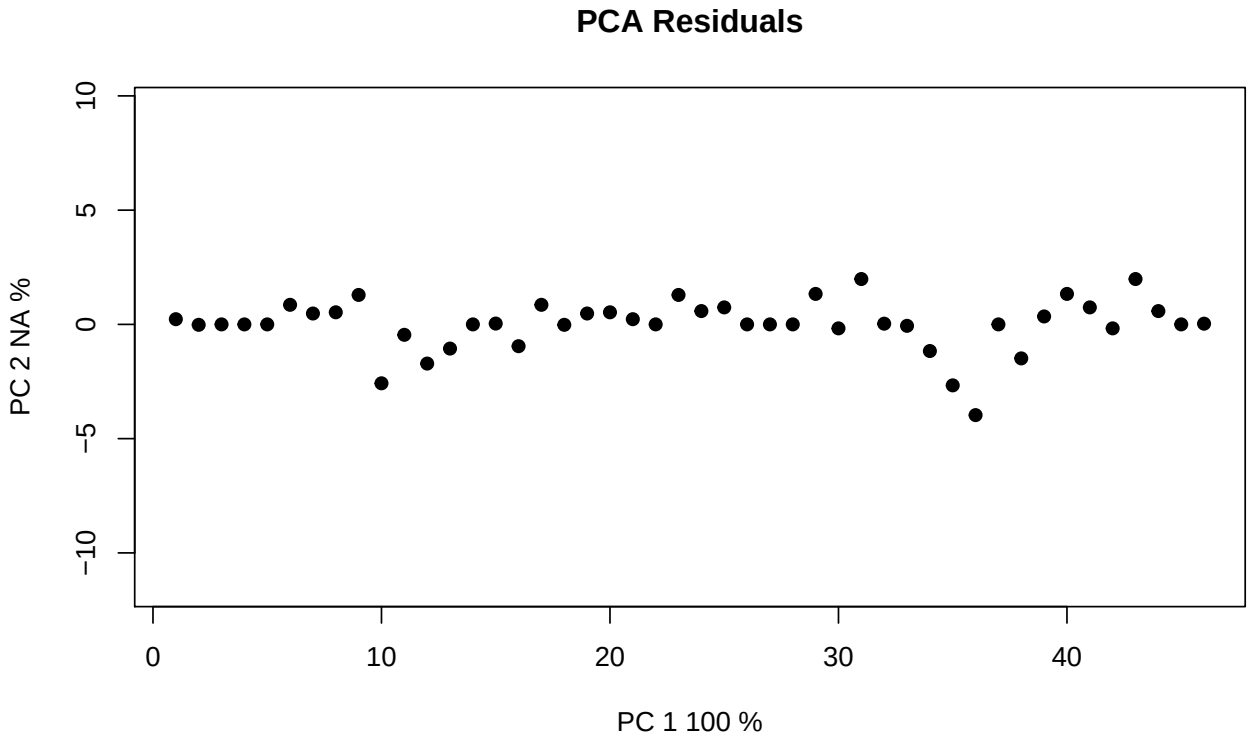


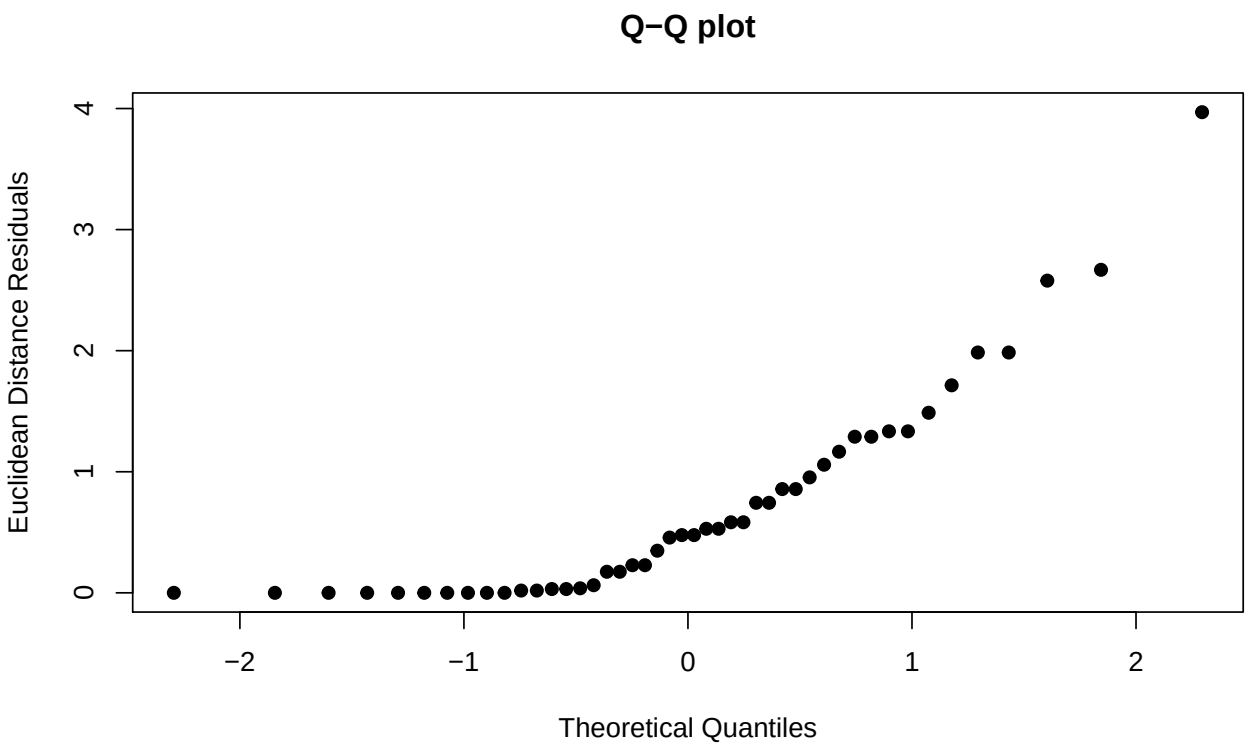


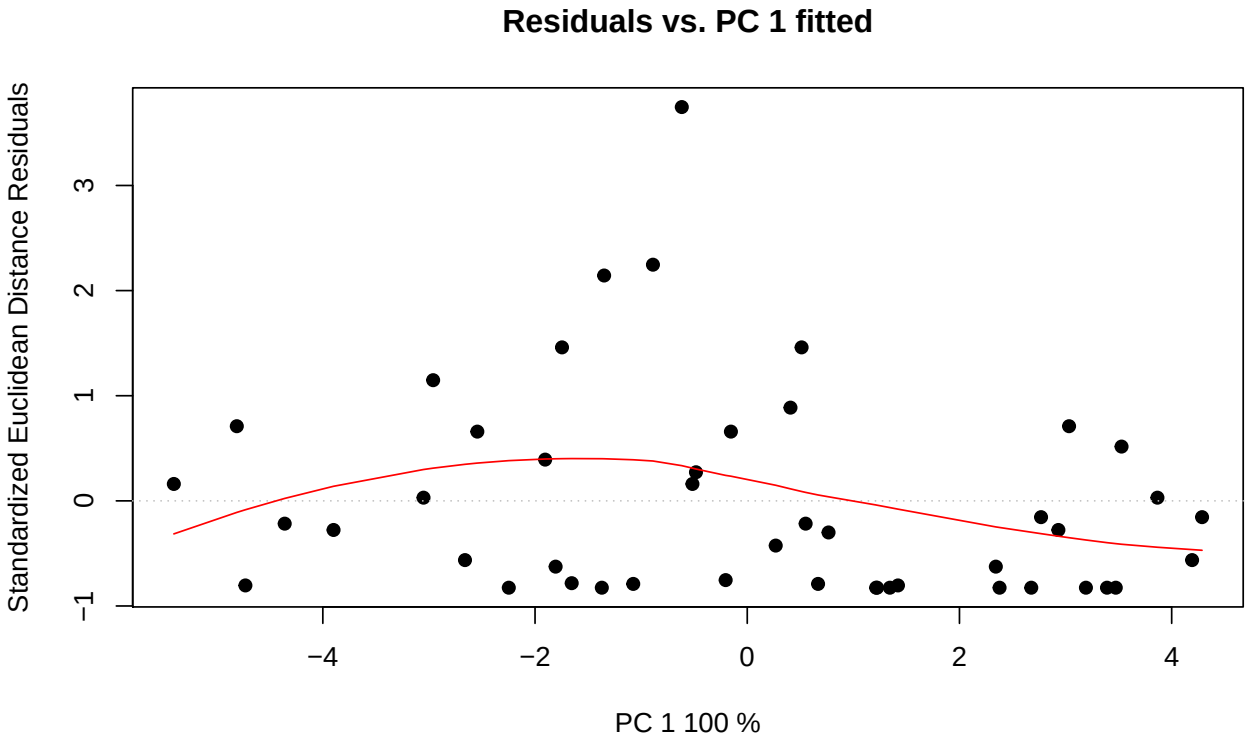

```
# pca plot
hpcplot <- plot(highLM, type = "PC", pch = 19, col = interaction(high$Water,
    high$Fungus))
```

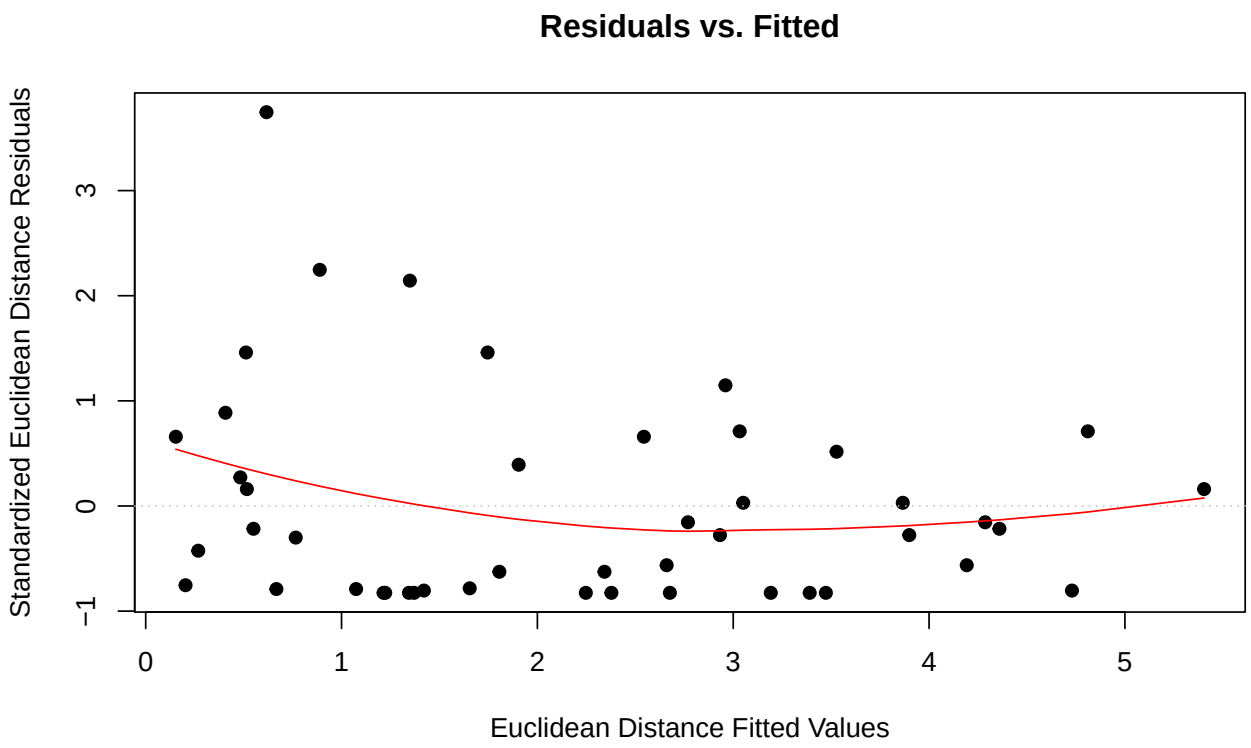



```
# residuals vs fitted values (homoscedasticity check)
ldiagnostics <- plot(lowLM, type = "diagnostics")
```




Q−Q plot
Euclidean Distance Residuals
0
1
2
3
4
−2
−1
0
1
2
Theoretical Quantiles


Residuals vs. PC 1 fitted
Standardized Euclidean Distance Residuals
−1
0
1
2
3
−4
−2
0
2
4
PC 1 100 %




```
# pca plot
lpcplot <- plot(lowLM, type = "PC", pch = 19, col = interaction(low$Water,
    low$Fungus))
```