Dirichlet Regression for Compositional Data in R

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Abstract

Full R Code for

Maier, M. J. (2014). DirichletReg: Dirichlet Regression for Compositional Data in R. Research Report Series/Department of Statistics and Mathematics, 125. WU Vienna University of Economics and Business, Vienna. http://epub.wu.ac.at/4077/

Keywords:~ Dirichlet regression, Dirichlet distribution, multivariate generalized linear model, rates, proportions, rates, compositional data, simplex, R.

4. Application examples

4.1. The Arctic lake (common parametrization)

```
> library("DirichletReg")
> head(ArcticLake)
  sand silt clay depth
1 0.775 0.195 0.030 10.4
2 0.719 0.249 0.032 11.7
3 0.507 0.361 0.132 12.8
4 0.522 0.409 0.066 13.0
5 0.700 0.265 0.035 15.7
6 0.665 0.322 0.013 16.3
> AL <- DR_data(ArcticLake[, 1:3])</pre>
> AL[1:6, ]
      sand
                silt
1 0.7750000 0.1950000 0.0300000
2 0.7190000 0.2490000 0.0320000
3 0.5070000 0.3610000 0.1320000
4 0.5235707 0.4102307 0.0661986
5 0.7000000 0.2650000 0.0350000
6 0.6650000 0.3220000 0.0130000
Code for Fig.\sim 1 (left):
> plot(AL, cex = 0.5, a2d = list(colored = FALSE, c.grid = FALSE))
```

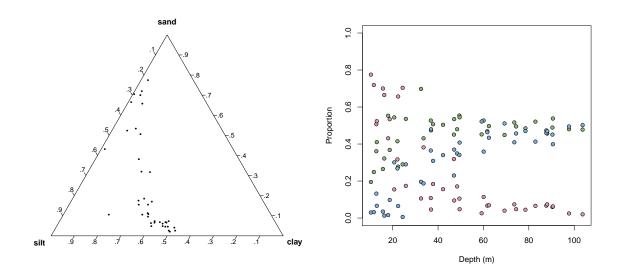


Figure 1: Arctic lake: Ternary plot and depth vs. composition.

```
Code for Fig.\sim 1 (right):
> plot(rep(ArcticLake$depth, 3), as.numeric(AL), pch = 21, bg = rep(c("#E495A5",
       "#86B875", "#7DB0DD"), each = 39), xlab = "Depth (m)", ylab = "Proportion",
      ylim = 0:1)
> lake1 <- DirichReg(AL ~ depth, ArcticLake)</pre>
> lake1
Call:
DirichReg(formula = AL ~ depth, data = ArcticLake)
using the common parametrization
Log-likelihood: 101.4 on 6 df (100 BFGS + 1 NR Iterations)
Coefficients for variable no. 1: sand
(Intercept)
                 depth
   0.11662
               0.02335
Coefficients for variable no. 2: silt
(Intercept)
                 depth
   -0.31060
                0.05557
Coefficients for variable no. 3: clay
(Intercept)
                 depth
   -1.1520
                 0.0643
> coef(lake1)
$sand
(Intercept)
                 depth
0.11662480 0.02335114
$silt
```

```
(Intercept)
                  depth
-0.31059591 0.05556745
$clay
(Intercept)
                  depth
-1.15195642 0.06430175
> lake2 <- update(lake1, . ~ . + I(depth^2) | . + I(depth^2) | . + I(depth^2))
> anova(lake1, lake2)
Analysis of Deviance Table
Model 1: DirichReg(formula = AL ~ depth, data = ArcticLake)
Model 2: DirichReg(formula = AL ~ depth + I(depth^2) | depth + I(depth^2) | depth + I(depth^2),
 data = ArcticLake)
       Deviance N. par Difference df Pr(>Chi)
Model 1 -202.74 6
                            15.254 3 0.001612 **
Model 2 -217.99
                    9
Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' ' 1
> summary(lake2)
DirichReg(formula = AL ~ depth + I(depth^2) | depth + I(depth^2) | depth + I(depth^2), data =
ArcticLake)
Standardized Residuals:
        Min 1Q Median
                                   3Q
sand -1.7647 -0.7080 -0.1786 0.9598 3.0460
silt -1.1379 -0.5330 -0.1546 0.2788 1.5604
clay -1.7661 -0.6583 -0.0454 0.6584 2.0152
Beta-Coefficients for variable no. 1: sand
             Estimate Std. Error z value Pr(>|z|)
(Intercept) 1.4361967 0.8026814 1.789 0.0736.
         -0.0072382 0.0329433 -0.220 0.8261
I(depth^2) 0.0001324 0.0002761 0.480 0.6315
Beta-Coefficients for variable no. 2: silt
             Estimate Std. Error z value Pr(>|z|)
I(depth^2) -0.0002679 0.0003088 -0.867 0.3857
Beta-Coefficients for variable no. 3: clay
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -1.7931487 0.7362293 -2.436 0.01487 * depth 0.1107906 0.0357705 3.097 0.00195 **
I(depth^2) -0.0004872 0.0003308 -1.473 0.14079
Significance codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Log-likelihood: 109 on 9 df (162 BFGS + 2 NR Iterations)
AIC: -200, BIC: -185
Number of Observations: 39
Link: Log
Parametrization: common
```

Code for Fig.~2:

Sediment Composition in an Arctic Lake

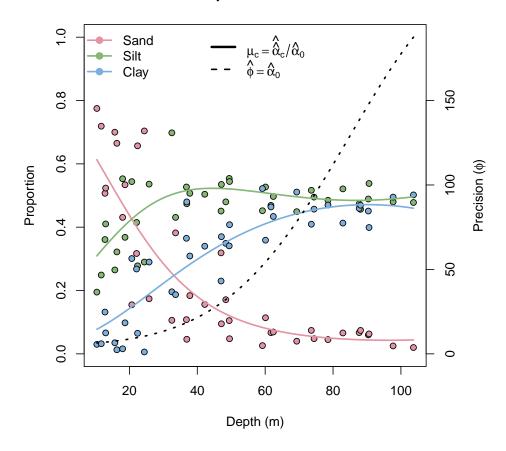


Figure 2: Arctic lake: Fitted values of the quadratic model.

```
> par(mar = c(4, 4, 4, 4) + 0.1)
> plot(rep(ArcticLake$depth, 3), as.numeric(AL), pch = 21, bg = rep(c("#E495A5",
                 "#86B875", "#7DB0DD"), each = 39), xlab = "Depth (m)", ylab = "Proportion",
                ylim = 0:1, main = "Sediment Composition in an Arctic Lake")
    Xnew <- data.frame(depth = seq(min(ArcticLake$depth), max(ArcticLake$depth),</pre>
                length.out = 100))
    for (i in 1:3) lines(cbind(Xnew, predict(lake2, Xnew)[, i]), col = c("\#E495A5",
                 "#86B875", "#7DB0DD")[i], 1wd = 2)
    legend("topleft", legend = c("Sand", "Silt", "Clay"), \ lwd = 2, \ col = c("\#E495A5", \ legend("topleft", legend = c("Sand", "Silt", "Clay"), \ lwd = 2, \ logend("topleft", legend = c("Sand", "Silt", "Clay"), \ lwd = 2, \ logend("topleft", legend = c("Sand", "Silt", "Clay"), \ lwd = 2, \ logend("topleft", legend = c("Sand", "Silt", "Clay"), \ lwd = 2, \ logend("topleft", legend = c("Sand", "Silt", "Clay"), \ lwd = 2, \ logend("silt", "logend = c("Sand", "Silt", "Clay"), \ lwd = 2, \ logend("silt", "logend = c("Sand", "Silt", "Clay"), \ lwd = 2, \ logend("silt", "logend = c("Sand", "Silt", "Clay"), \ lwd = 2, \ logend("silt", "logend = c("Sand", "Silt", "Clay"), \ lwd = 2, \ logend("silt", "logend = c("Sand", "Silt", "Silt", "logend = c("Sand", "Silt", "Silt", "logend = c("Sand", "Silt", "S
                 "#86B875", "#7DB0DD"), pt.bg = c("#E495A5", "#86B875", "#7DB0DD"), pch = 21,
                bty = "n")
> par(new = TRUE)
> plot(cbind(Xnew, predict(lake2, Xnew, F, F, T)), lty = "24", type = "1", ylim = c(0,
                \max(\text{predict}(\text{lake2, Xnew, F, F, T}))), axes = F, ann = F, \text{lwd} = 2)
> axis(4)
> mtext(expression(paste("Precision (", phi, ")", sep = "")), 4, line = 3)
> legend("top", legend = c(expression(hat(mu[c] == hat(alpha)[c]/hat(alpha)[0])),
                \texttt{expression(hat(phi) == hat(alpha)[0])), lty = c(1, 2), lwd = c(3, 2), bty = "n")}
> AL <- ArcticLake
> AL$AL <- DR_data(ArcticLake[, 1:3])</pre>
```

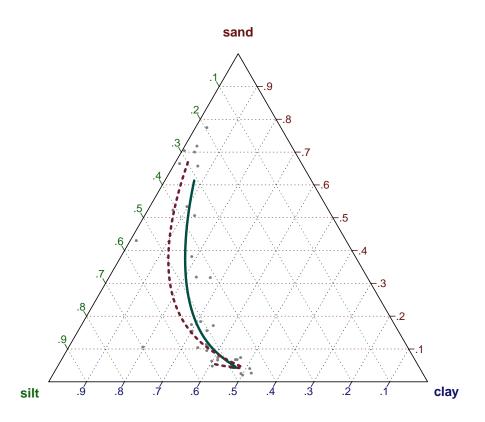


Figure 3: Arctic lake: OLS (dashed) vs. Dirichlet regression (solid) predictions.

```
> dd <- range(ArcticLake$depth)
> X <- data.frame(depth = seq(dd[1], dd[2], length.out = 200))
> pp <- predict(DirichReg(AL ~ depth + I(depth^2), AL), X)

Code for Fig.~3:
> plot(AL$AL, cex = 0.1, reset_par = FALSE)
> points(toSimplex(AL$AL), pch = 16, cex = 0.5, col = gray(0.5))
> lines(toSimplex(pp), lwd = 3, col = c("#6E1D34", "#004E42")[2])
> Dols <- log(cbind(ArcticLake[, 2]/ArcticLake[, 1], ArcticLake[, 3]/ArcticLake[, + 1]))
> ols <- lm(Dols ~ depth + I(depth^2), ArcticLake)
> p2 <- predict(ols, X)
> p2m <- exp(cbind(0, p2[, 1], p2[, 2]))/rowSums(exp(cbind(0, p2[, 1], p2[, 2])))
> lines(toSimplex(p2m), lwd = 3, col = c("#6E1D34", "#004E42")[1], lty = "21")
```

4.2. Blood samples (alternative parametrization)

```
> Bld <- BloodSamples
> Bld$Smp <- DR_data(Bld[, 1:4])</pre>
```

```
> blood1 <- DirichReg(Smp ~ Disease | 1, Bld, model = "alternative", base = 3)
> blood2 <- DirichReg(Smp ~ Disease | Disease, Bld, model = "alternative", base = 3)
> anova(blood1, blood2)
Analysis of Deviance Table
Model 1: DirichReg(formula = Smp ~ Disease | 1, data = Bld, model = "alternative", base = 3)
Model 2: DirichReg(formula = Smp ~ Disease | Disease, data = Bld, model = "alternative", base = 3)
       Deviance N. par Difference df Pr(>Chi)
Model 1 -303.86 7
Model 2 -304.61
                          0.7587 1 0.3837
> summary(blood1)
Call:
DirichReg(formula = Smp ~ Disease | 1, data = Bld, model = "alternative", base = 3)
Standardized Residuals:
          Min 1Q Median 3Q Max
-2.1310 -0.9307 -0.1234 0.8149 2.8429
Pre.Albumin -1.0687 -0.4054 -0.0789 0.1947 1.5691
Globulin.A -2.0503 -1.0392 0.1938 0.7927 2.2393
Globulin.B -1.8176 -0.5347 0.1488 0.5115 1.3284
MEAN MODELS:
Coefficients for variable no. 1: Albumin
          Estimate Std. Error z value Pr(>|z|)
(Intercept) 1.11639 0.09935 11.237 <2e-16 ***
DiseaseB -0.07002 0.13604 -0.515 0.607
______
Coefficients for variable no. 2: Pre.Albumin
          Estimate Std. Error z value Pr(>|z|)
(Intercept) 0.5490 0.1082 5.076 3.86e-07 ***
DiseaseB -0.1276 0.1493 -0.855 0.393
Coefficients for variable no. 3: Globulin.A
- variable omitted (reference category) -
Coefficients for variable no. 4: Globulin.B
          Estimate Std. Error z value Pr(>|z|)
(Intercept) 0.4863 0.1094 4.445 8.8e-06 ***
DiseaseB 0.1819 0.1472 1.236 0.216
DiseaseB 0.1819
PRECISION MODEL:
          Estimate Std. Error z value Pr(>|z|)
(Intercept) 4.2227 0.1475 28.64 <2e-16 ***
Significance codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' 1
Log-likelihood: 151.9 on 7 df (44 BFGS + 1 NR Iterations)
AIC: -289.9, BIC: -280
Number of Observations: 30
Links: Logit (Means) and Log (Precision)
{\tt Parametrization:\ alternative}
Code for Fig.~4:
> par(mfrow = c(1, 4), mar = c(4, 4, 4, 2) + 0.25)
> for (i in 1:4) {
+ boxplot(Bld$Smp[, i] ~ Bld$Disease, ylim = range(Bld$Smp[, 1:4]), main = paste(names(Bld)[i]),
```

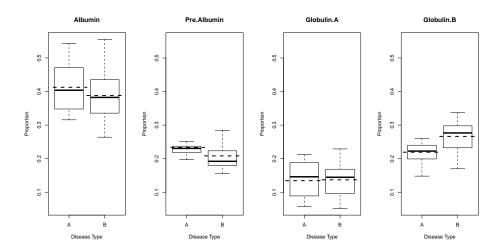


Figure 4: Blood samples: Box plots and fitted values (dashed lines indicate the fitted values for each group).

```
xlab = "Disease Type", ylab = "Proportion")
               segments(c(-5,\ 1.5),\ unique(fitted(blood2)[,\ i]),\ c(1.5,\ 5),\ unique(fitted(blood2)[,\ i]),\ unique(f
                         i]), 1wd = 2, 1ty = 2)
+ }
> alpha <- predict(blood2, data.frame(Disease = factor(c("A", "B"))), F, T, F)</pre>
> L <- sapply(1:2, function(i) ddirichlet(DR_data(Bld[31:36, 1:4]), unlist(alpha[i,
               ])))
> LP <- L/rowSums(L)
> dimnames(LP) <- list(paste("C", 1:6), c("A", "B"))</pre>
> print(data.frame(round(LP * 100, 1), pred. = as.factor(ifelse(LP[, 1] > LP[,
               2], "==> A", "==> B"))), print.gap = 2)
                               B pred.
           59.4
C 1
                        40.6
                                      ==> A
C 2
           43.2
                        56.8
                                     ==> B
С 3
          38.4
                        61.6
                                     ==> B
C 4
           43.8
                        56.2
                                     ==> B
           36.6
                        63.4
C 6 70.2
                        29.8
                                     ==> A
Code for Fig.~5:
> B2 \leftarrow DR data(BloodSamples[, c(1, 2, 4)])
> plot(B2, cex = 0.001, reset par = FALSE)
> div.col <- colorRampPalette(c("#023FA5", "#c0c0c0", "#8E063B"))(100)</pre>
> temp <- (alpha/rowSums(alpha))[, c(1, 2, 4)]
> points(toSimplex(temp/rowSums(temp)), pch = 22, bg = div.col[c(1, 100)], cex = 2,
               1wd = 0.25)
> temp <- B2[1:30, ]
> points(toSimplex(temp/rowSums(temp)), pch = 21, bg = (div.col[c(1, 100)])[BloodSamples$Disease[1:30]],
               cex = 0.5, 1wd = 0.25)
> temp <- B2[31:36, ]</pre>
> points(toSimplex(temp/rowSums(temp)), pch = 21, bg = div.col[round(100 * LP[,
               2], 0)], cex = 1, lwd = 0.5)
> legend("topright", bty = "n", legend = c("Disease A", "Disease B", NA, "Expected Values"),
               pch = c(21, 21, NA, 22), pt.bg = c(div.col[c(1, 100)], NA, "white"))
```

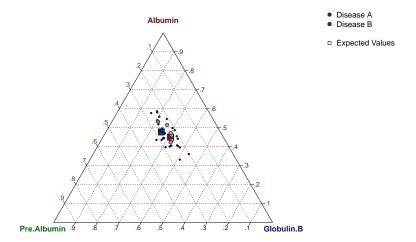


Figure 5: Blood samples: Observed values and predictions

4.3. Reading skills data (alternative parametrization)

```
> RS <- ReadingSkills
> RS$acc <- DR_data(RS$accuracy)</pre>
> RS$dyslexia <- C(RS$dyslexia, treatment)
> rs1 <- DirichReg(acc ~ dyslexia * iq | dyslexia * iq, RS, model = "alternative")
> rs2 <- DirichReg(acc ~ dyslexia * iq | dyslexia + iq, RS, model = "alternative")
> anova(rs1, rs2)
Analysis of Deviance Table
Model 1: DirichReg(formula = acc ~ dyslexia * iq | dyslexia * iq, data = RS, model = "alternative")
Model 2: DirichReg(formula = acc ~ dyslexia * iq | dyslexia + iq, data = RS, model = "alternative")
       Deviance N. par Difference df Pr(>Chi)
Model 1 -133.47
Model 2 -131.80
                          1.6645 1
Code for Fig.~6:
> g.ind <- as.numeric(RS$dyslexia)
> g1 <- g.ind == 1
> g2 <- g.ind != 1
> par(mar = c(4, 4, 4, 4) + 0.25)
> plot(accuracy ~ iq, RS, pch = 21, bg = c("#E495A5", "#39BEB1")[3 - g.ind], cex = 1.5,
      main = "Dyslexic (Red) vs. Control (Green) Group", xlab = "IQ Score", ylab = "Reading Accuracy",
      xlim = range(ReadingSkills$iq))
> x1 \leftarrow seq(min(RS$iq[g1]), max(RS$iq[g1]), length.out = 200)
> x2 \leftarrow seq(min(RS$iq[g2]), max(RS$iq[g2]), length.out = 200)
> n <- length(x1)
> X <- data.frame(dyslexia = factor(rep(0:1, each = n), levels = 0:1, labels = c("no",
      "yes")), iq = c(x1, x2))
> pv <- predict(rs2, X, TRUE, TRUE, TRUE)
> lines(x1, pv$mu[1:n, 2], col = c("#E495A5", "#39BEB1")[2], lwd = 3)
> lines(x2, pv mu[(n + 1):(2 * n), 2], col = c("#E495A5", "#39BEB1")[1], lwd = 3)
> a <- RS$accuracy
> logRa_a <- log(a/(1 - a))</pre>
> rlr <- lm(logRa_a ~ dyslexia * iq, RS)
```

Dyslexic (Red) vs. Control (Green) Group

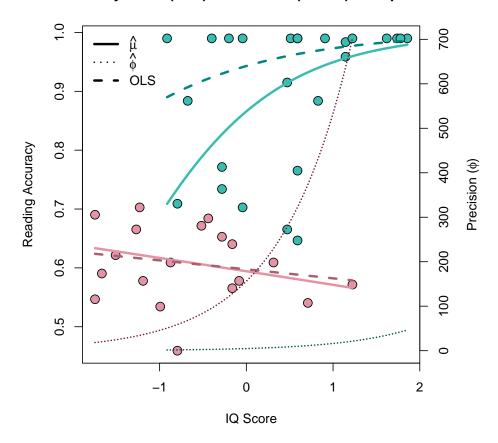


Figure 6: Reading skills: Predicted values of Dirichlet regression and OLS regression.

```
> ols <- 1/(1 + exp(-predict(rlr, X)))</pre>
> lines(x1, ols[1:n], col = c("#AD6071", "#00897D")[2], lwd = 3, lty = 2)
> lines(x2, ols[(n + 1):(2 * n)], col = c("#AD6071", "#00897D")[1], lwd = 3, lty = 2)
> par(new = TRUE)
> plot(x1, pv\$phi[1:n], col = c("#6E1D34", "#004E42")[2], lty = "11", type = "1",
      ylim = c(0, max(pv\$phi)), axes = F, ann = F, lwd = 2, xlim = range(RS\$iq))
> lines(x2, pv\$phi[(n + 1):(2 * n)], col = c("#6E1D34", "#004E42")[1], lty = "11",
      type = "1", 1wd = 2)
> axis(4)
> mtext(expression(paste("Precision (", phi, ")", sep = "")), 4, line = 3)
> legend("topleft", legend = c(expression(hat(mu)), expression(hat(phi)), "OLS"),
      1ty = c(1, 3, 2), 1wd = c(3, 2, 3), bty = "n")
> a <- RS$accuracy
> logRa_a <- log(a/(1 - a))
> rlr <- lm(logRa_a ~ dyslexia * iq, RS)
> summary(rlr)
lm(formula = logRa_a ~ dyslexia * iq, data = RS)
```

variable omitted

```
Residuals:
   Min
              1Q Median
                               3Q
                                        Max
-2.66405 -0.37966 0.03687 0.40887 2.50345
Coefficients:
              Estimate Std. Error t value Pr(>|t|)
              (Intercept)
dyslexiayes
               dyslexiayes:iq -0.8457 0.4510 -1.875 0.0681.
Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' ' 1
Residual standard error: 1.2 on 40 degrees of freedom
Multiple R-squared: 0.6151, Adjusted R-squared: 0.5862 F-statistic: 21.31 on 3 and 40 DF, p-value: 2.083e-08
> summary(rs2)
Call:
DirichReg(formula = acc ~ dyslexia * iq | dyslexia + iq, data = RS, model = "alternative")
Standardized Residuals:
                           1Q Median
                                           3Q
1 - accuracy -1.5661 -0.8204 -0.5112 0.5211 3.4334
            -3.4334 -0.5211 0.5112 0.8204 1.5661
accuracy
MEAN MODELS:
Coefficients for variable no. 1: 1 - accuracy
- variable omitted (reference category) -
Coefficients for variable no. 2: accuracy
             Estimate Std. Error z value Pr(>|z|)
(Intercept) 1.8649 0.2991 6.235 4.52e-10 ***
dyslexiayes -1.4833 0.3029 -4.897 9.74e-07 ***
iq 1.0676 0.3359 3.178 0.001482 **
dyslexiayes:iq -1.1625 0.3452 -3.368 0.000757 ***
PRECISION MODEL:
          Estimate Std. Error z value Pr(>|z|)
(Intercept) 1.5579 0.3336 4.670 3.01e-06 ***
dyslexiayes 3.4931 0.5880 5.941 2.83e-09 ***
iq 1.2291 0.4596 2.674 0.00749 **
Significance codes: 0 '***, 0.001 '**, 0.01 '*, 0.05 '., 0.1 ', 1
Log-likelihood: 65.9 on 7 df (56 BFGS + 2 NR Iterations)
AIC: -117.8, BIC: -105.3
Number of Observations: 44
Links: Logit (Means) and Log (Precision)
Parametrization: alternative
> confint(rs2)
95% Confidence Intervals (original form)
- Beta-Parameters:
Variable: 1 - accuracy
```

```
Variable: accuracy
                2.5% Est. 97.5%
               1.279 1.86 2.451
(Intercept)
dyslexiayes
               -2.077 -1.48 -0.890
               0.409 1.07 1.726
dyslexiayes:iq -1.839 -1.16 -0.486
- Gamma-Parameters
            2.5% Est. 97.5%
(Intercept) 0.904 1.56
                        2.21
dyslexiayes 2.341 3.49
                        4.65
           0.328 1.23 2.13
> confint(rs2, exp = TRUE)
95% Confidence Intervals (exponentiated)
- Beta-Parameters:
Variable: 1 - accuracy
 variable omitted
Variable: accuracy
               2.5% exp(Est.) 97.5%
                        6.455 11.601
(Intercept)
              3.592
dyslexiayes
              0.125
                        0.227 0.411
                        2.908 5.618
0.313 0.615
iq
              1.506
dyslexiayes:iq 0.159
- Gamma-Parameters
            2.5% exp(Est.)
                             97.5%
(Intercept)
           2.47
                      4.75
                             9.13
dyslexiayes 10.39
                      32.89 104.12
                      3.42
                              8.41
Code for Fig.~7:
> gcol <- c("#E495A5", "#39BEB1")[3 - as.numeric(RS$dyslexia)]
> tmt <- c(-3, 3)
> par(mfrow = c(3, 2), cex = 0.8)
> qqnorm(residuals(rlr, "pearson"), ylim = tmt, xlim = tmt, pch = 21, bg = gcol,
      main = "Normal Q-Q-Plot: OLS Residuals", cex = 0.75, lwd = 0.5)
> abline(0, 1, lwd = 2)
> qqline(residuals(rlr, "pearson"), lty = 2)
> qqnorm(residuals(rs2, "standardized")[, 2], ylim = tmt, xlim = tmt, pch = 21,
      bg = gcol, main = "Normal Q-Q-Plot: DirichReg Residuals", cex = 0.75, lwd = 0.5)
> abline(0, 1, lwd = 2)
> qqline(residuals(rs2, "standardized")[, 2], 1ty = 2)
> plot(ReadingSkillsiq, residuals(rlr, "pearson"), pch = 21, bg = gcol, ylim = c(-3,
      3), main = "OLS Residuals", xlab = "IQ", ylab = "Pearson Residuals", cex = 0.75,
      1wd = 0.5)
> abline(h = 0, lty = 2)
> plot(ReadingSkills$iq, residuals(rs2, "standardized")[, 2], pch = 21, bg = gcol,
      ylim = c(-3, 3), main = "DirichReg Residuals", xlab = "IQ", ylab = "Standardized Residuals",
      cex = 0.75, 1wd = 0.5)
> abline(h = 0, lty = 2)
> plot(fitted(rlr), residuals(rlr, "pearson"), pch = 21, bg = gcol, ylim = c(-3, -3)
      3), main = "OLS Residuals", xlab = "Fitted", ylab = "Pearson Residuals",
      cex = 0.75, 1wd = 0.5)
> abline(h = 0, lty = 2)
> plot(fitted(rs2)[, 2], residuals(rs2, "standardized")[, 2], pch = 21, bg = gcol,
     ylim = c(-3, 3), main = "DirichReg Residuals", xlab = "Fitted", ylab = "Standardized Residuals",
```

```
+ cex = 0.75, lwd = 0.5)
> abline(h = 0, lty = 2)
```

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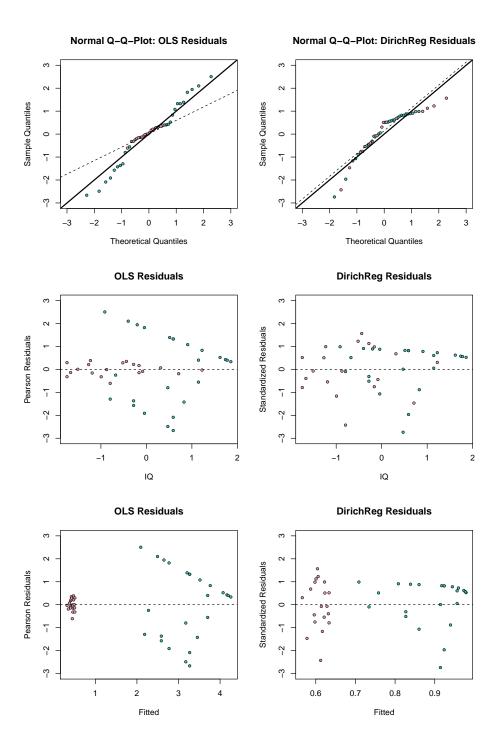


Figure 7: Reading skills: residual plots of OLS and Dirichlet regression models.