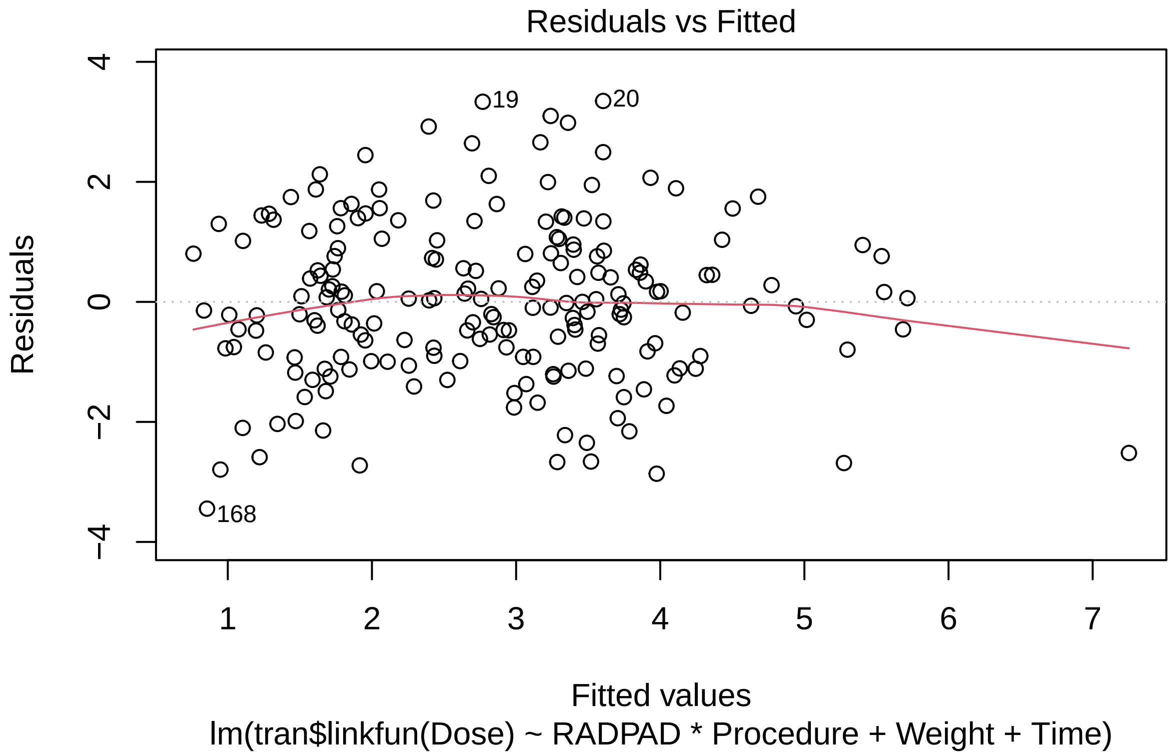
RADPAD Analysis by Occupation

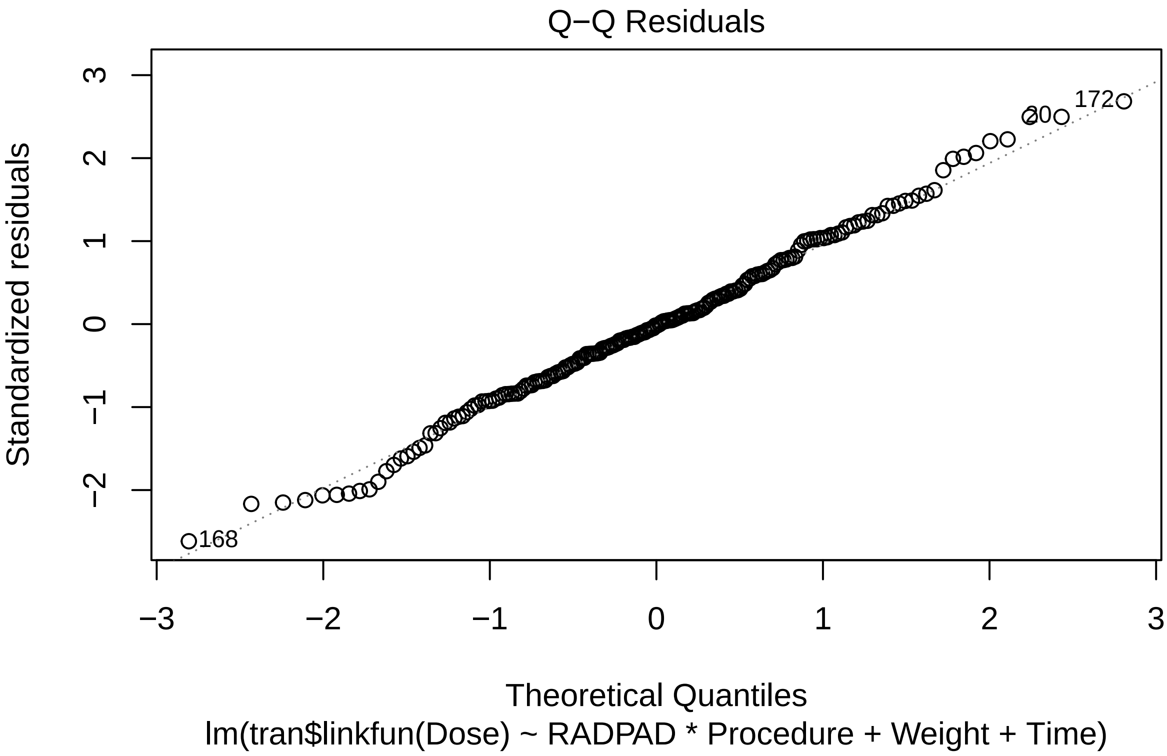
Resident 1 - OLS

```
## boxcox transformation on Dose
fit <- lm(Dose ~ RADPAD * Procedure + Weight + Time, data = r1)
b <- MASS::boxcox(fit, plotit = FALSE)
tran <- make.tran("boxcox", b$x[which.max(b$y)])

## OLS Fit
fit2 <- lm(tran$linkfun(Dose) ~ RADPAD*Procedure + Weight + Time,
           data = r1)

## emmeans on transformed scale
em0 <- emmeans(fit2, ~RADPAD|Procedure)
c0 <- contrast(em0, "revpairwise")
c0 <- update(c0, side =  "<")

## emmeans on response scale
grid <- ref_grid(fit2)
rg <- update(grid, tran = tran)
em <- emmeans(regrid(rg, transform = "response"), ~RADPAD|Procedure)
c <- contrast(em, method = "revpairwise", infer = FALSE)
c
```

```
## Procedure = BPV:
##  contrast estimate    SE  df
##  Y - N      -12.38  2.32 190
##
## Procedure = PDA:
##  contrast estimate    SE  df
##  Y - N       -4.13  2.27 190
##
## Procedure = PMI:
##  contrast estimate    SE  df
##  Y - N      -12.94  4.52 190
##
## Procedure = PV Stent:
##  contrast estimate    SE  df
##  Y - N      -32.22 15.10 190
```

```
## residual plots
plot(fit2, which = c(1,2))
```


Residuals vs Fitted
Residuals
Fitted values
lm(tran$linkfun(Dose) ~ RADPAD * Procedure + Weight + Time)
4
2
0
−2
−4
1
2
3
4
5
6
7
19
20
168


Q−Q Residuals
Standardized residuals
3
2
1
0
−1
−2
−3
−2
−1
0
1
2
3
Theoretical Quantiles
lm(tran$linkfun(Dose) ~ RADPAD * Procedure + Weight + Time)
168
20
172

Resident 2 - GLS

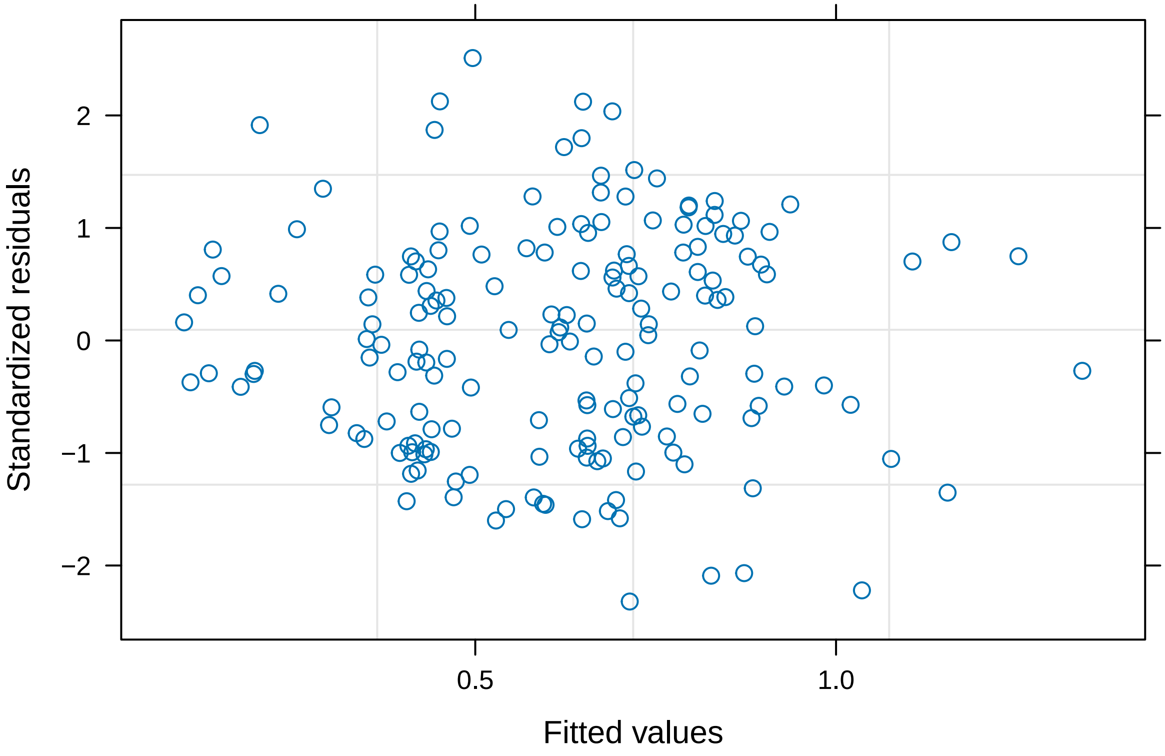
```
## boxcox transformation on Dose
fit <- lm(Dose+1 ~ RADPAD * Procedure  + Weight + Time, data = r2)
b <- MASS::boxcox(fit, plotit = FALSE)
tran <- make.tran("boxcox", b$x[which.max(b$y)])

## GLS models under different variance structures
gls.fit0 <- gls(tran$linkfun(Dose+1) ~ RADPAD*Procedure + Weight + Time,
                data = r2,
                weights = varIdent(form = ~ 1 | RADPAD))
gls.fit1 <- gls(tran$linkfun(Dose+1) ~ RADPAD*Procedure  + Weight + Time,
                data = r2,
                weights = varIdent(form = ~ 1 | Procedure))
gls.fit2 <- gls(tran$linkfun(Dose+1) ~ RADPAD*Procedure + Weight + Time,
                data = r2,
                weights = varIdent(form = ~ 1 | RADPAD*Procedure))

## identify best model
AIC(gls.fit0, gls.fit1, gls.fit2) ## lowest AIC for fit1
```

```
##          df      AIC
## gls.fit0 12 193.8632
## gls.fit1 14 191.1100
## gls.fit2 18 195.4573
```

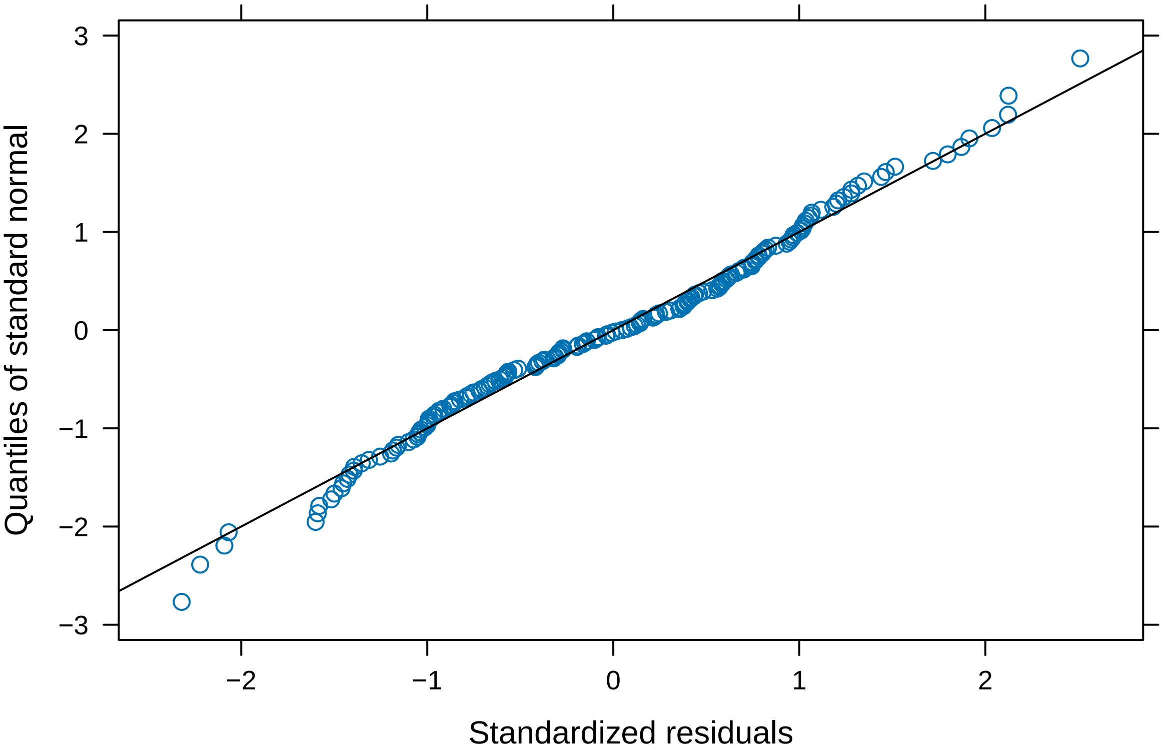
```
## emmeans on transformed scale
em0 <- emmeans(gls.fit1, ~RADPAD|Procedure)
c0 <- contrast(em0, "revpairwise")
c0 <- update(c0, side = "<")
## emmeans on response scale
grid <- ref_grid(gls.fit1)
rg <- update(grid, tran = tran)
em <- emmeans(regrid(rg, transform = "response"), ~RADPAD|Procedure)
contrast(em, method = "revpairwise", infer = FALSE)
```

```
## Procedure = BPV:
##  contrast estimate    SE   df
##  Y - N      -0.901 0.289 95.2
##
## Procedure = PDA:
##  contrast estimate    SE   df
##  Y - N      -0.683 0.193 54.3
##
## Procedure = PMI:
##  contrast estimate    SE   df
##  Y - N      -1.036 0.415 17.8
##
## Procedure = PV Stent:
##  contrast estimate    SE   df
##  Y - N       3.813 4.399 13.2
##
## Degrees-of-freedom method: inherited from satterthwaite when re-gridding
```

```r
## residual plots
plot(gls.fit1)
```



```r
qqnorm(gls.fit1, abline = c(0,1))
```



3
2
1
0
−1
−2
−3
Quantiles of standard normal
−2
−1
0
1
2
Standardized residuals

Faculty - GLS

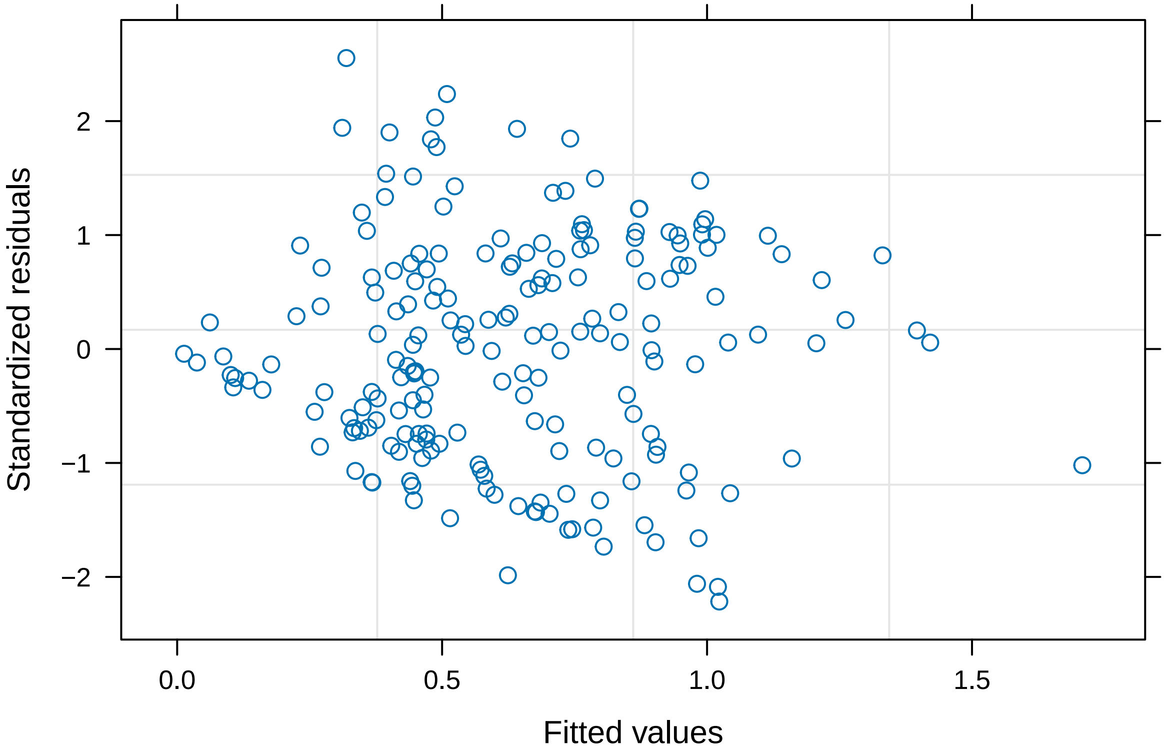
```
## boxcox transformation on Dose
fit <- lm(Dose+1 ~ RADPAD * Procedure  + Weight + Time, data = rF)
b <- MASS::boxcox(fit, plotit = FALSE)
tran <- make.tran("boxcox", b$x[which.max(b$y)])

## GLS models under different variance structures
gls.fit0 <- gls(tran$linkfun(Dose+1) ~ RADPAD*Procedure + Weight + Time,
                data = rF,
                weights = varIdent(form = ~ 1 | RADPAD))
gls.fit1 <- gls(tran$linkfun(Dose+1) ~ RADPAD*Procedure  + Weight + Time,
                data = rF,
                weights = varIdent(form = ~ 1 | Procedure))
gls.fit2 <- gls(tran$linkfun(Dose+1) ~ RADPAD*Procedure + Weight + Time,
                data = rF,
                weights = varIdent(form = ~ 1 | RADPAD*Procedure))

## identify best model
AIC(gls.fit0, gls.fit1, gls.fit2) ## lowest AIC for fit0
```

```
##          df      AIC
## gls.fit0 12 269.4288
## gls.fit1 14 279.6593
## gls.fit2 18 278.5581
```

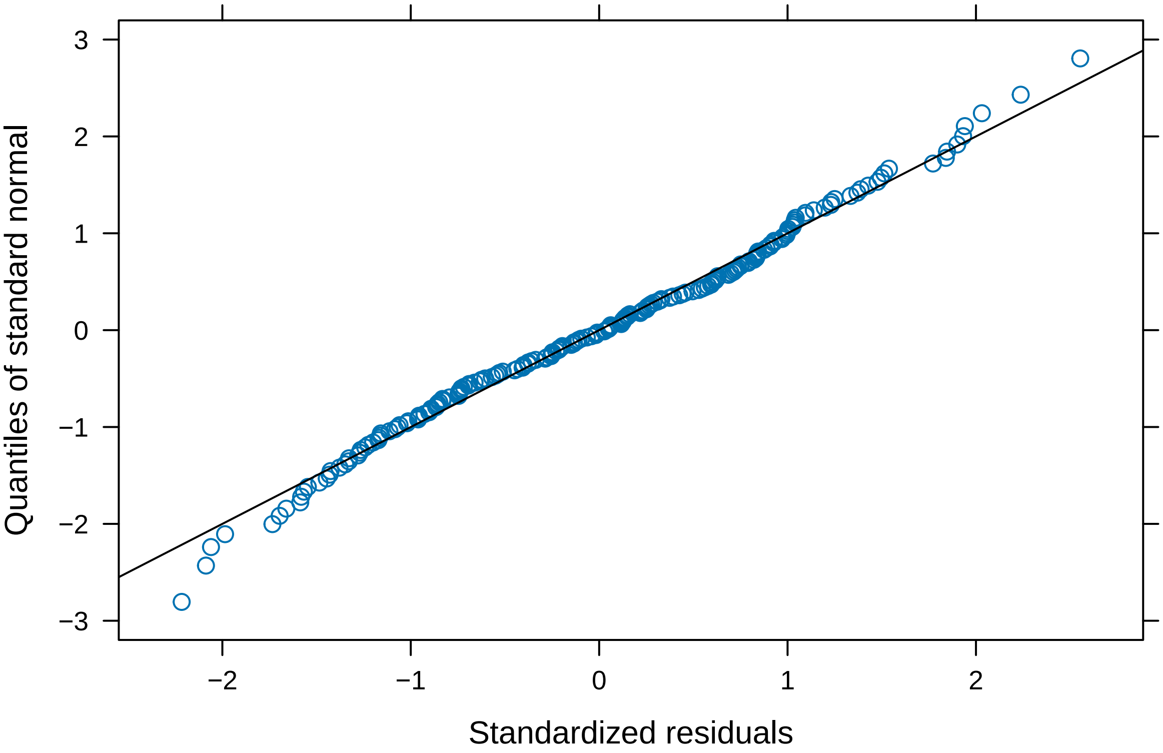
```
## emmeans on transformed scale
em0 <- emmeans(gls.fit0, ~RADPAD|Procedure)
c0 <- contrast(em0, "revpairwise")
c0 <- update(c0, side = "<")
## emmeans on response scale
grid <- ref_grid(gls.fit0)
rg <- update(grid, tran = tran)
em <- emmeans(regrid(rg, transform = "response"), ~RADPAD|Procedure)
contrast(em, method = "revpairwise", infer = FALSE)
```

```
## Procedure = BPV:
##  contrast estimate    SE   df
##  Y - N      -0.624 0.209 45.6
##
## Procedure = PDA:
##  contrast estimate    SE   df
##  Y - N      -0.768 0.281 47.1
##
## Procedure = PMI:
##  contrast estimate    SE   df
##  Y - N      -1.553 0.682 45.7
##
## Procedure = PV Stent:
##  contrast estimate    SE   df
##  Y - N      -0.694 0.813 55.6
##
## Degrees-of-freedom method: inherited from satterthwaite when re-gridding
```

```r
## residual plots
plot(gls.fit0)
```



```r
qqnorm(gls.fit0, abline = c(0,1))
```


Quantiles of standard normal
3
2
1
0
−1
−2
−3
−2
−1
0
1
2
Standardized residuals

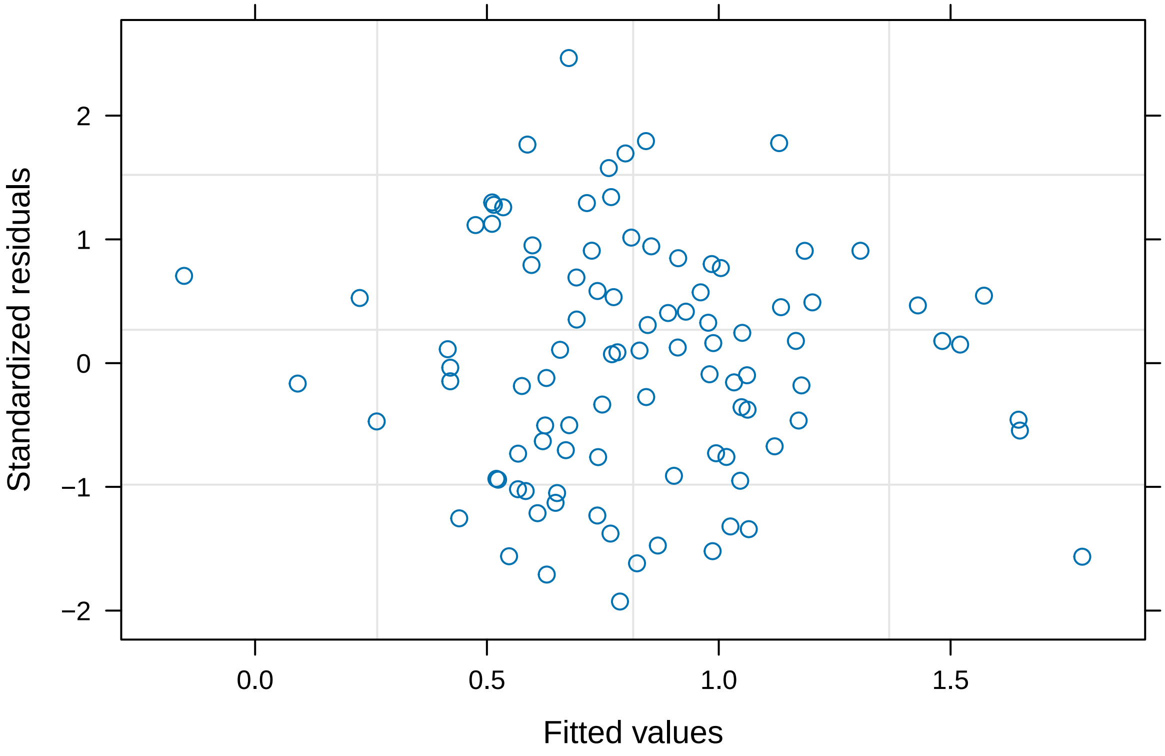
TEE - GLS

```r
## boxcox transformation on Dose
fit <- lm(Dose+1 ~ RADPAD * Procedure  + Weight + Time, data = rTee)
b <- MASS::boxcox(fit, plotit = FALSE)
tran <- make.tran("boxcox", b$x[which.max(b$y)])

## GLS models under different variance structures
gls.fit0 <- gls(tran$linkfun(Dose+1) ~ RADPAD*Procedure + Weight + Time,
                data = rTee,
                weights = varIdent(form = ~ 1 | RADPAD))
gls.fit1 <- gls(tran$linkfun(Dose+1) ~ RADPAD*Procedure  + Weight + Time,
                data = rTee,
                weights = varIdent(form = ~ 1 | Procedure))
gls.fit2 <- gls(tran$linkfun(Dose+1) ~ RADPAD*Procedure + Weight + Time,
                data = rTee,
                weights = varIdent(form = ~ 1 | RADPAD*Procedure))

## identify best model
AIC(gls.fit0, gls.fit1, gls.fit2) ## lowest AIC for fit1
```

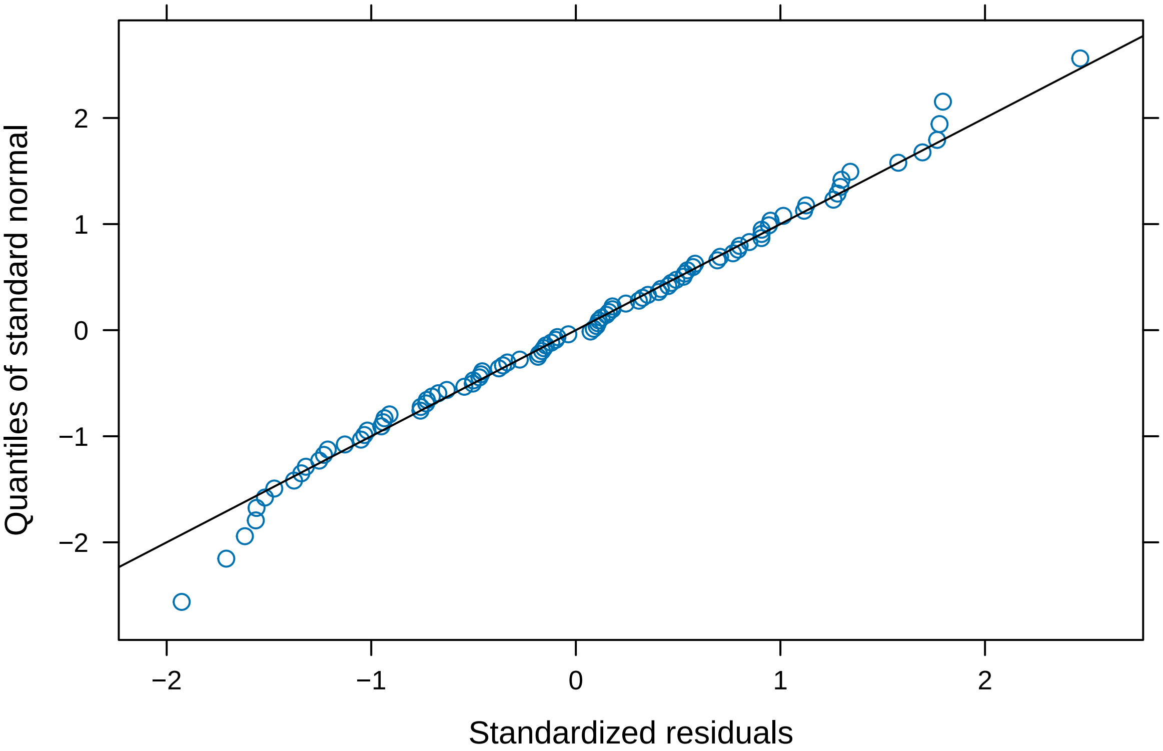
```
##          df      AIC
## gls.fit0 12 173.5750
## gls.fit1 14 167.8006
## gls.fit2 18 175.3866
```

```r
## emmeans on transformed scale
em0 <- emmeans(gls.fit1, ~RADPAD|Procedure)
c0 <- contrast(em0, "revpairwise")
c0 <- update(c0, side = "<")
## emmeans on response scale
grid <- ref_grid(gls.fit1)
rg <- update(grid, tran = tran)
em <- emmeans(regrid(rg, transform = "response"), ~RADPAD|Procedure)
contrast(em, method = "revpairwise", infer = FALSE)
```

```
## Procedure = BPV:
##  contrast estimate    SE    df
##  Y - N      -0.529 0.533 24.89
##
## Procedure = PDA:
##  contrast estimate    SE    df
##  Y - N      -1.159 0.663 51.13
##
## Procedure = PMI:
##  contrast estimate    SE    df
##  Y - N      -2.679 1.358  9.37
##
## Procedure = PV Stent:
##  contrast estimate    SE    df
##  Y - N       4.627 6.207  7.13
##
## Degrees-of-freedom method: inherited from satterthwaite when re-gridding
## residual plots
plot(gls.fit1)
```



```
qqnorm(gls.fit1, abline = c(0,1))
```


Quantiles of standard normal
2
1
0
−1
−2
−2
−1
0
1
2
Standardized residuals