Plotting Random Effects

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Blood Data

```
# Systolic blood pressure measurements made
# simultaneously by two observers (J and R)
# and an automatic blood pressure measuring
# machine (S), each making three observations
# in quick succession (supplied by Dr E O'Brien)
library(nlme)

Blood <- matrix(data=c(100, 106, 107, 98, 98, 111,
122, 128, 124, 108, 110, 108, 108, 112, 110, 121,
127, 128, 76, 84, 82, 76, 88, 82, 95, 94, 98,
108, 104, 104, 110, 100, 106, 127, 127, 135,
124, 112, 112, 128, 112, 114, 140, 131, 124,
122, 140, 124, 124, 140, 126, 139, 142, 136,
116, 108, 102, 118, 110, 102, 122, 112, 112,
114, 110, 112, 112, 108, 112, 130, 129, 135,
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108, 92, 100, 108, 98, 100, 126, 113, 111,
100, 106, 104, 102, 108, 106, 107, 113, 111,
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112, 112, 110, 114, 112, 110, 131, 129, 122,
104, 108, 104, 104, 108, 104, 123, 126, 114,
106, 108, 102, 104, 106, 102, 127, 119, 126,
122, 122, 114, 118, 122, 114, 142, 133, 137,
100, 102, 102, 102, 102, 100, 104, 116, 115,
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140, 134, 138, 138, 136, 134, 139, 127, 113,
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166, 154, 154, 164, 154, 148, 181, 170, 166,
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140, 144, 144, 140, 144, 144, 158, 152, 154,
128, 134, 130, 128, 134, 130, 139, 144, 141,
146, 138, 140, 146, 138, 138, 153, 150, 154,
146, 152, 148, 146, 152, 148, 138, 144, 131,
220, 218, 220, 220, 218, 220, 228, 228, 226,
208, 200, 192, 204, 200, 190, 190, 183, 184,
94, 84, 86, 94, 84, 88, 103, 99, 106,
114, 124, 116, 112, 126, 118, 131, 131, 124,
126, 120, 122, 124, 120, 120, 131, 123, 124,
124, 124, 132, 126, 126, 120, 126, 129, 125,
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110, 120, 128, 110, 122, 126, 121, 114, 125,
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106, 106, 110, 106, 108, 110, 116, 121, 127,
218, 202, 208, 218, 200, 206, 215, 201, 207,
130, 128, 130, 128, 126, 128, 141, 133, 146,
136, 136, 130, 136, 138, 128, 153, 143, 138,
100, 96, 88, 100, 96, 86, 113, 107, 102,
100, 98, 88, 100, 98, 88, 109, 105, 97,
124, 116, 122, 126, 116, 122, 145, 102, 137,
164, 168, 154, 164, 168, 154, 192, 178, 171,
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136, 126, 122, 136, 124, 122, 152, 144, 147,
114, 108, 122, 114, 108, 122, 141, 141, 137,
148, 120, 132, 146, 130, 132, 206, 188, 166,
160, 150, 148, 160, 152, 146, 151, 147, 136,
84, 92, 98, 86, 92, 98, 112, 125, 124,
156, 162, 152, 156, 158, 152, 162, 165, 189,
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86, 74, 76, 88, 76, 76, 112, 115, 104,
106, 100, 110, 106, 100, 108, 120, 118, 132,
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168, 188, 178, 170, 188, 182, 194, 191, 196,
166, 150, 154, 164, 150, 154, 167, 160, 161,
146, 142, 132, 144, 142, 130, 173, 161, 154,
204, 198, 188, 206, 198, 188, 228, 218, 189,
96, 94, 86, 96, 94, 84, 77, 89, 101,
134, 126, 124, 132, 126, 124, 154, 156, 141,
138, 144, 140, 140, 142, 138, 154, 155, 148,
134, 136, 142, 136, 134, 140, 145, 154, 166,
156, 160, 154, 156, 162, 156, 200, 180, 179,
124, 138, 138, 122, 140, 136, 188, 147, 139,
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112, 116, 134, 114, 114, 136, 128, 125, 142,
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132, 136, 134, 134, 136, 132, 184, 187, 192,
158, 162, 152, 158, 164, 150, 163, 160, 152,
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170, 174, 176, 172, 174, 178, 178, 181, 181,
182, 176, 180, 184, 174, 178, 202, 199, 195,
112, 114, 124, 112, 112, 126, 162, 166, 148,
120, 118, 120, 118, 116, 120, 227, 227, 219,
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112, 112, 106, 112, 110, 106, 202, 190, 213,
154, 134, 130, 156, 136, 132, 158, 121, 134,
116, 112, 94, 118, 114, 96, 124, 149, 137,
108, 110, 114, 106, 110, 114, 114, 118, 126,
106, 98, 100, 104, 100, 100, 137, 135, 134,

```
122, 112, 112, 122, 114, 114, 121, 123, 128),
nrow = 85, ncol = 9, byrow = TRUE,
dimnames = list(NULL, c("J1","J2","J3","R1","R2","R3","S1","S2","S3")) )
```

Working on the JS comparison

```
blood = groupedData( BP ~ method | subject ,
  data = data.frame( BP = c(Blood),
    subject = rep(seq(nrow(Blood)), ncol(Blood)),
    method = rep(c("J","R","S"), rep(nrow(Blood)*3, 3)),
        repl = rep(rep(c(1:3), rep(nrow(Blood), 3)), 3) ),
    labels = list(BP = "Systolic Blood Pressure", method = "Measurement Device"),
    )
```

```
# consider on methods "J" and "S"
dat = subset(blood, subset = method != "R") # fixed-effects X_i with(subset(dat, subset = subject
== "1"), model.matrix(BP ~ method)) # random-effects Z_i with(subset(dat, subset = subject ==
"1"), model.matrix( ~ method -1))


# consider J and S groups only:
# J.sd = c(with(subset(blood, subset = method == "J"), by(BP, subject, sd)))
# S.sd = c(with(subset(blood, subset = method == "S"), by(BP, subject, sd)))
# min(J.sd) ; max(J.sd)
# min(S.sd) ; max(S.sd)
# plot(J.sd, S.sd)
```
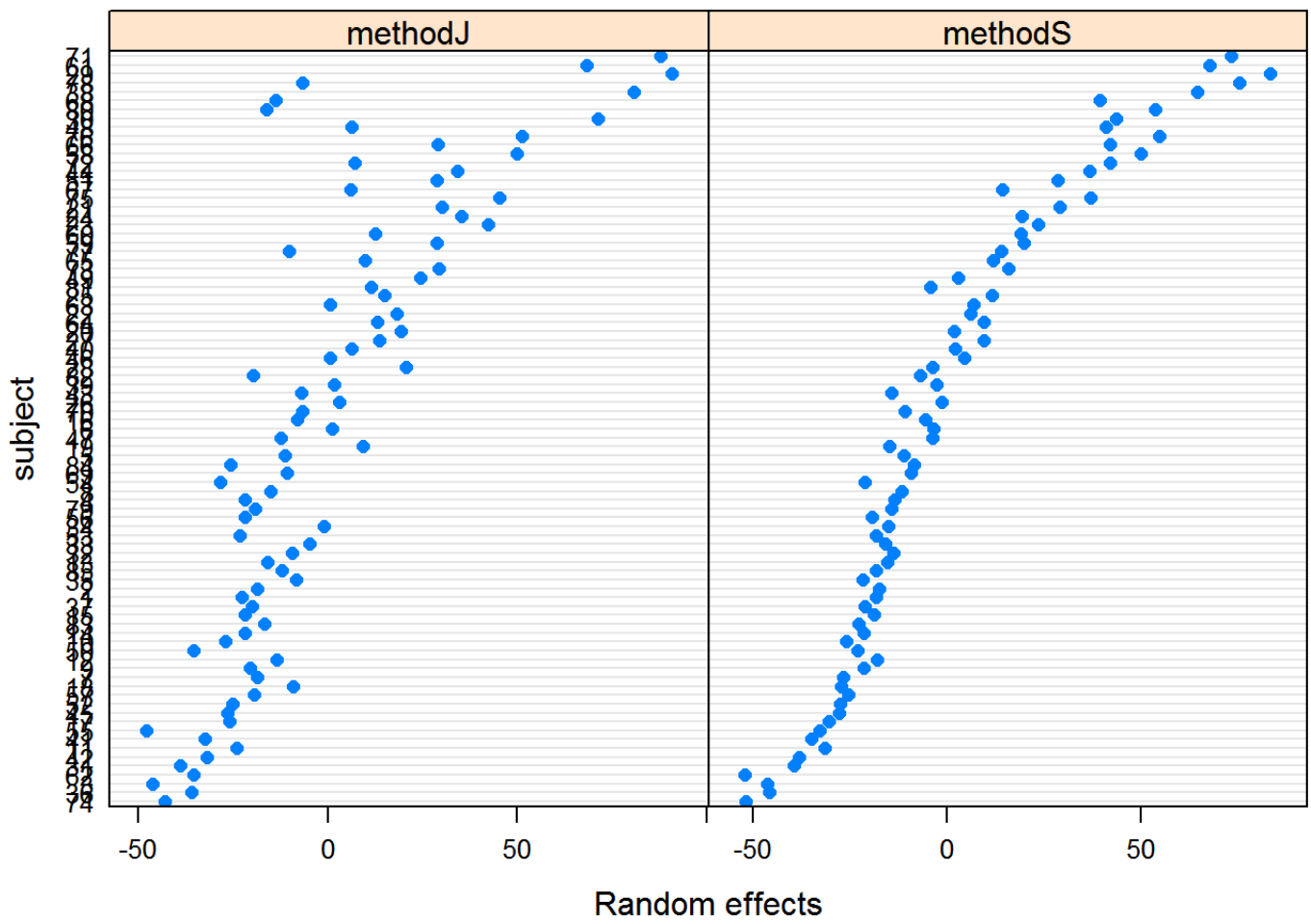
```
# make a data frame containing J and S groups only:
dat = subset(blood, subset = method != "R")
```
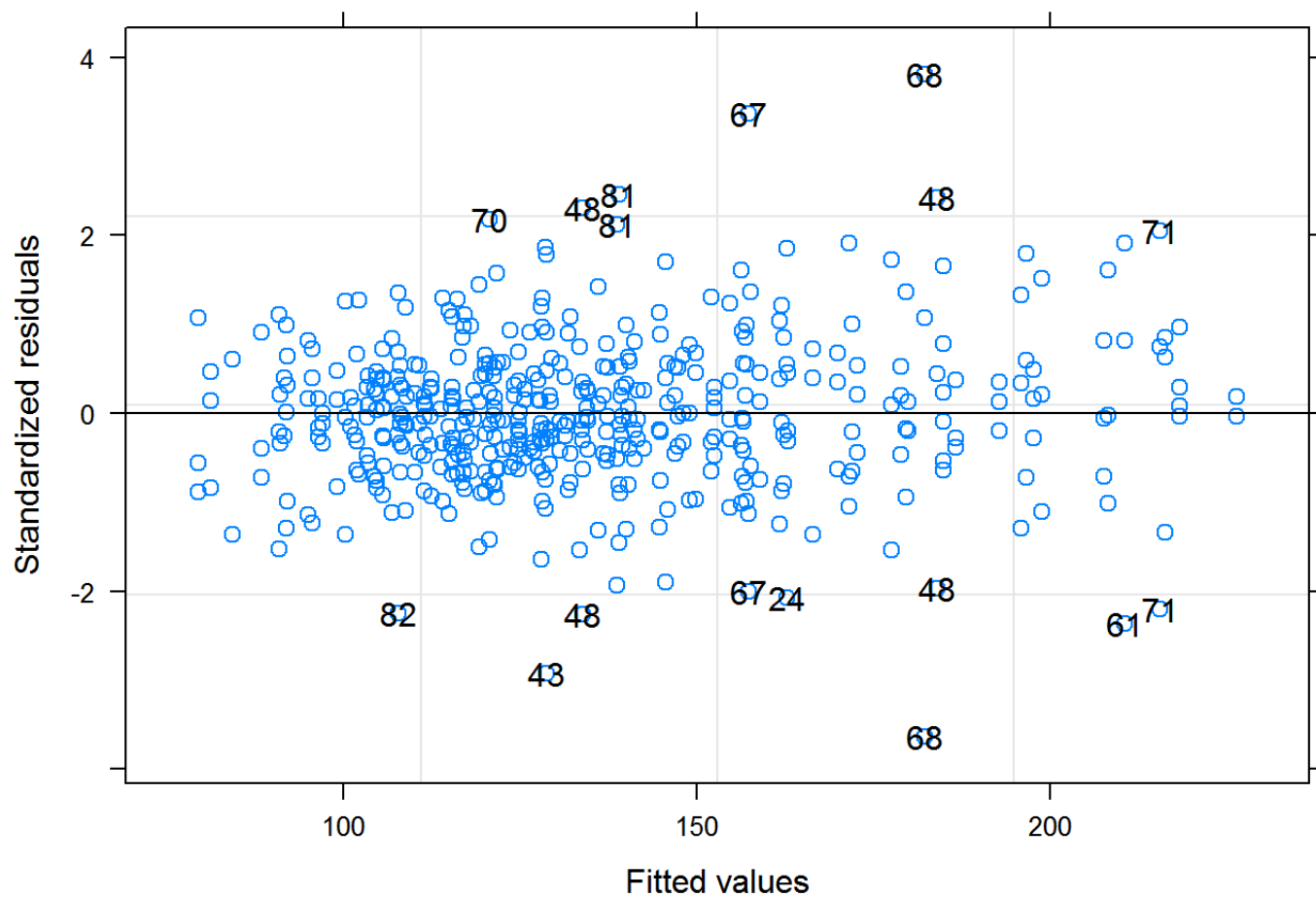
```
JS.roy1 = lme(BP ~ method-1, data = dat,random = list(subject=pdSymm(~ method-1)), weights=varIden
t(form=~1|method),correlation = corSymm(form=~1 | subject/repl), method="ML")
```
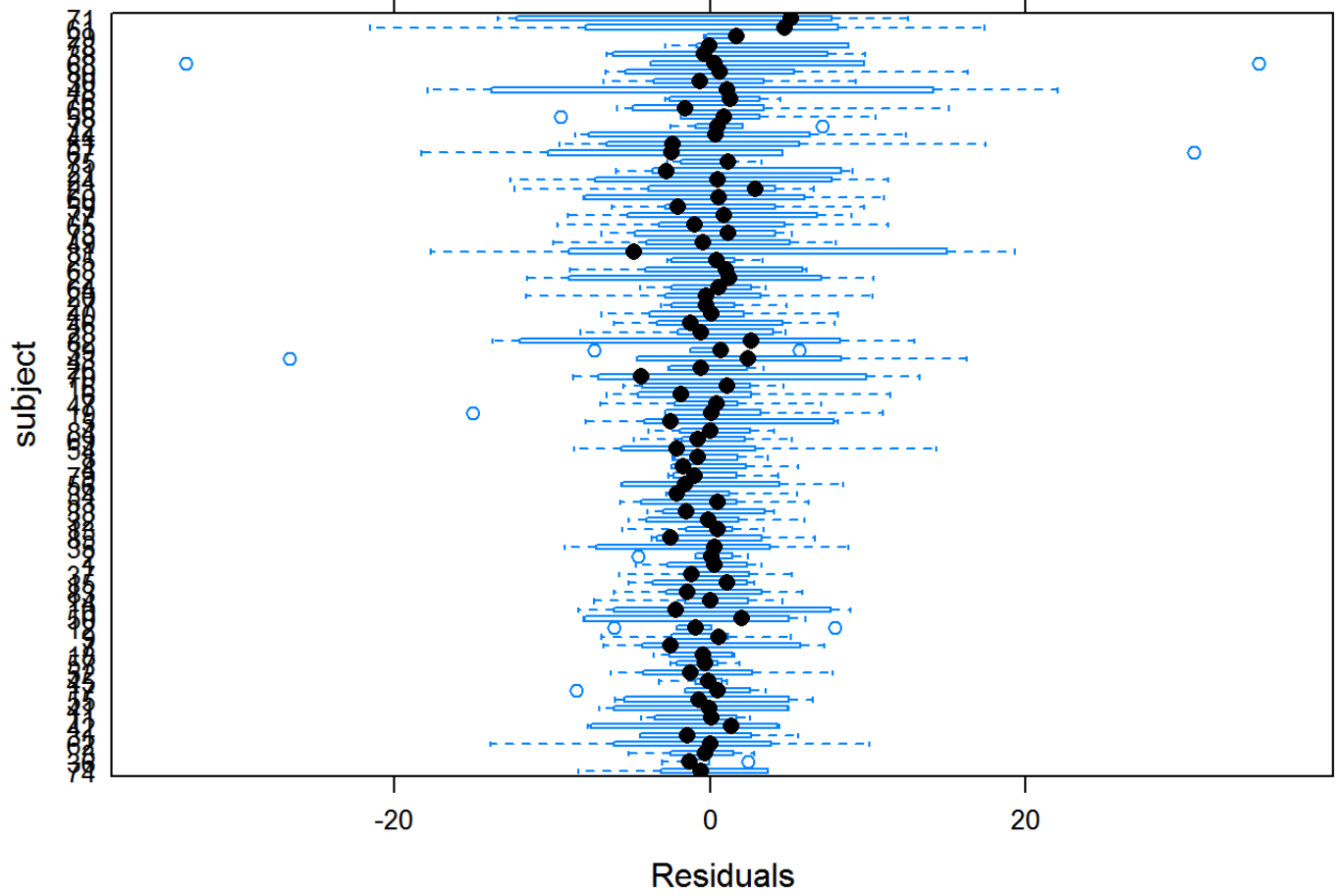
Diagnostic Plots

```
plot(ranef(JS.roy1,aug=TRUE))
```

```
# standardized residuals versus fitted values by gender
plot(JS.roy1, resid(., type = "pearson") ~ fitted(.) , abline = 0, id = 0.05)
```

```
# box-plots of residuals by Subject
plot(JS.roy1, subject ~ resid(.))
```

```
# observed versus fitted values by Subject
plot(JS.roy1, BP ~ fitted(.) | subject, abline = c(0,1))
```