

Data analysis pilots

Nathanael Larigaldie

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Dataset loading

```
datasets      <- list.files(file.path("final_data"), pattern="*.csv", full.names = TRUE)
datasets      <- lapply(datasets, read_csv, show_col_types = FALSE)

d <- datasets[[1]]
for (i in seq(from=2, to=length(datasets)))
{
  d <- rbind(d, datasets[[i]])
}
```

Dataset preparation

```
d <- d %>% mutate(Subject=rep(seq_len(length(datasets)), each=100))
```

Then we remove fixation times ≤ 1500 ms, scale the Agreement feature and take its square, and log-transform Fixation.Time

```
d_final <- d %>% filter(Fixation.Time > 1500) %>%
  mutate(Fixation.Time.Log = log(Fixation.Time),
         Agreement.Scaled = (Agreement-mean(Agreement))/sd(Agreement),
         Squared.Agreement.Scaled=Agreement.Scaled^2,
         Index=as.factor(Index), Subject=as.factor(Subject))
```

Variables plot (violin & boxplot + density)

```
violin_fixation <- ggplot(d_final, aes(x="Fixation time", y=Fixation.Time.Log)) +
  ylab("Fixation Time (log)") + theme_minimal() +
  theme(legend.position = "none") +
  geom_violin(width=1.2) + geom_boxplot(width=0.1, alpha=0.2)

violin_agreement <- ggplot(d_final, aes(x="Agreement", y=Agreement.Scaled)) +
  ylab("Agreement (scaled)") + theme_minimal() +
```

```

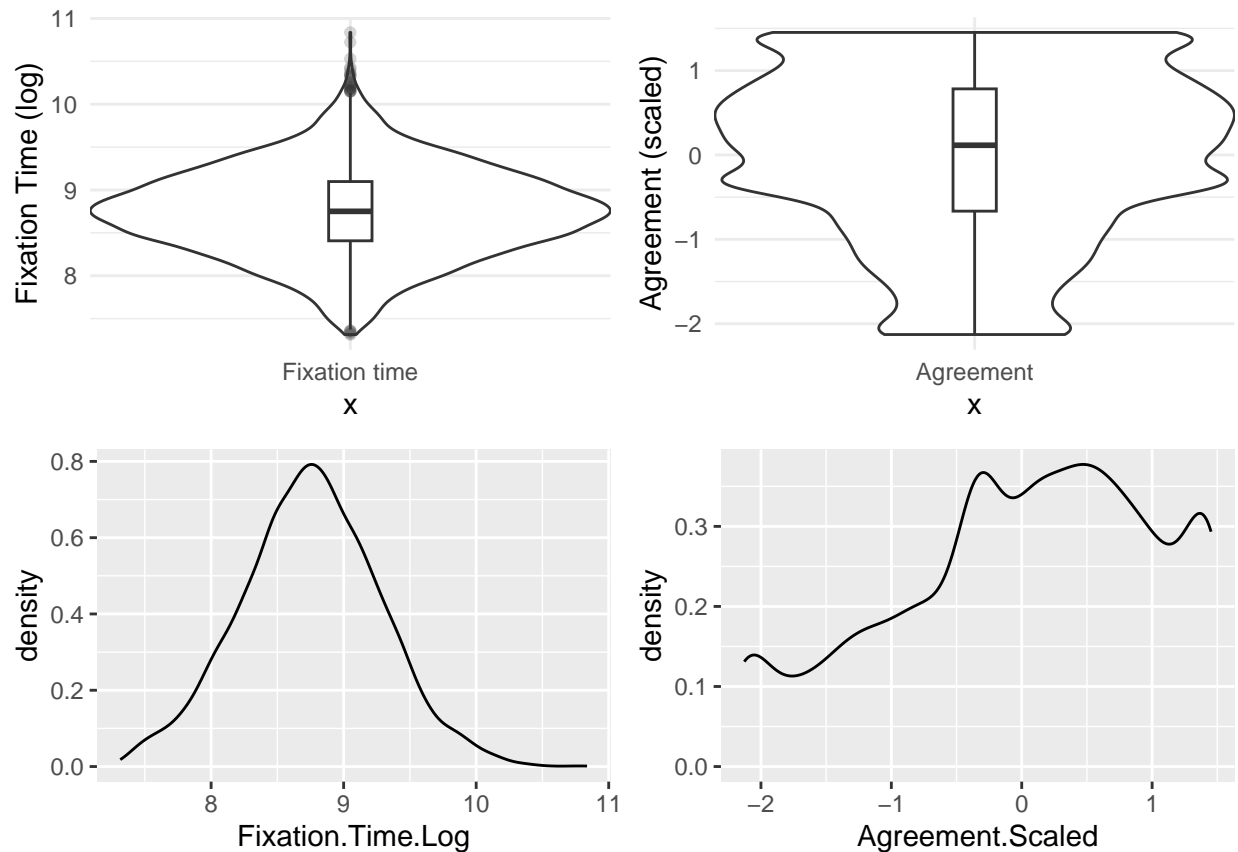
theme(legend.position = "none") +
geom_violin(width=1.2) + geom_boxplot(width=0.1, alpha=0.2)

density_fixation <- ggplot(d_final, aes(x=Fixation.Time.Log)) + geom_density()

density_agreement <- ggplot(d_final, aes(x=Agreement.Scaled)) + geom_density()

grid.arrange(violin_fixation, violin_agreement, density_fixation,
              density_agreement, nrow=2)

```



Statistical model

```

res_mixed <- lmer(Fixation.Time.Log ~ Agreement.Scaled +
                  Squared.Agreement.Scaled +
                  (1 | Index) +
                  (Agreement.Scaled + Squared.Agreement.Scaled | Subject),
                  data=d_final, control = lmerControl(optimizer = "bobyqa"))

summary(res_mixed)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: Fixation.Time.Log ~ Agreement.Scaled + Squared.Agreement.Scaled +
##      (1 | Index) + (Agreement.Scaled + Squared.Agreement.Scaled | Subject)
##      Data: d_final

```

```

## Control: lmerControl(optimizer = "bobyqa")
##
## REML criterion at convergence: 5400.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -4.3943 -0.6265 -0.0511  0.5946  4.7118
##
## Random effects:
##   Groups   Name                Variance Std.Dev. Corr
##   Index    (Intercept)          0.0306873 0.17518
##   Subject   (Intercept)          0.1167607 0.34170
##             Agreement.Scaled      0.0006924 0.02631 -0.32
##             Squared.Agreement.Scaled 0.0009278 0.03046 -0.84  0.28
##   Residual                        0.1488998 0.38588
## Number of obs: 5233, groups:  Index, 100; Subject, 54
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)      8.753405   0.050296  67.875373  174.039 < 2e-16 ***
## Agreement.Scaled  -0.022933   0.007933  83.551563   -2.891  0.00489 **
## Squared.Agreement.Scaled -0.013453   0.007030  43.252224   -1.914  0.06231 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Agrm.S
## Agrmnt.Scld -0.166
## Sqrd.Agrm.S -0.549  0.317

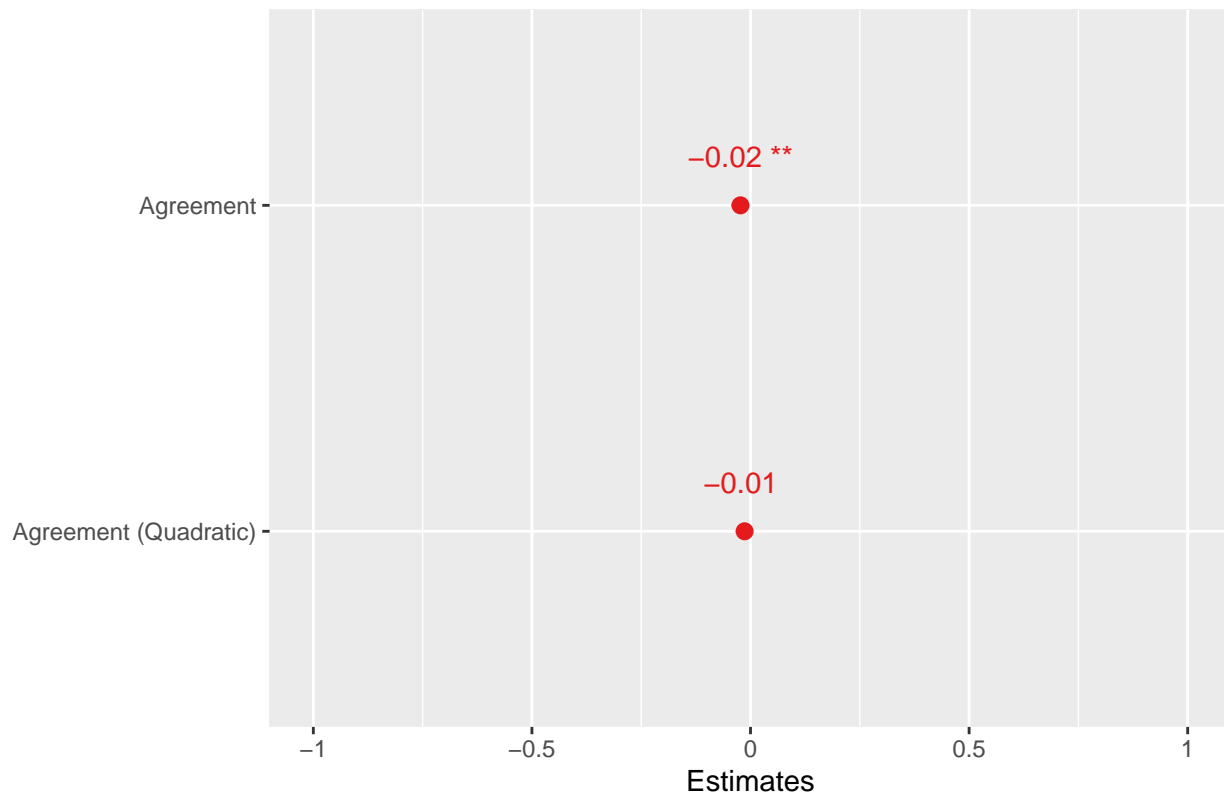
```

```

plot_model(res_mixed,
            axis.labels=c("Agreement (Quadratic)", "Agreement"),
            show.values=TRUE, show.p=TRUE,
            title="Quadratic effect of Agreement on Fixation Times")

```

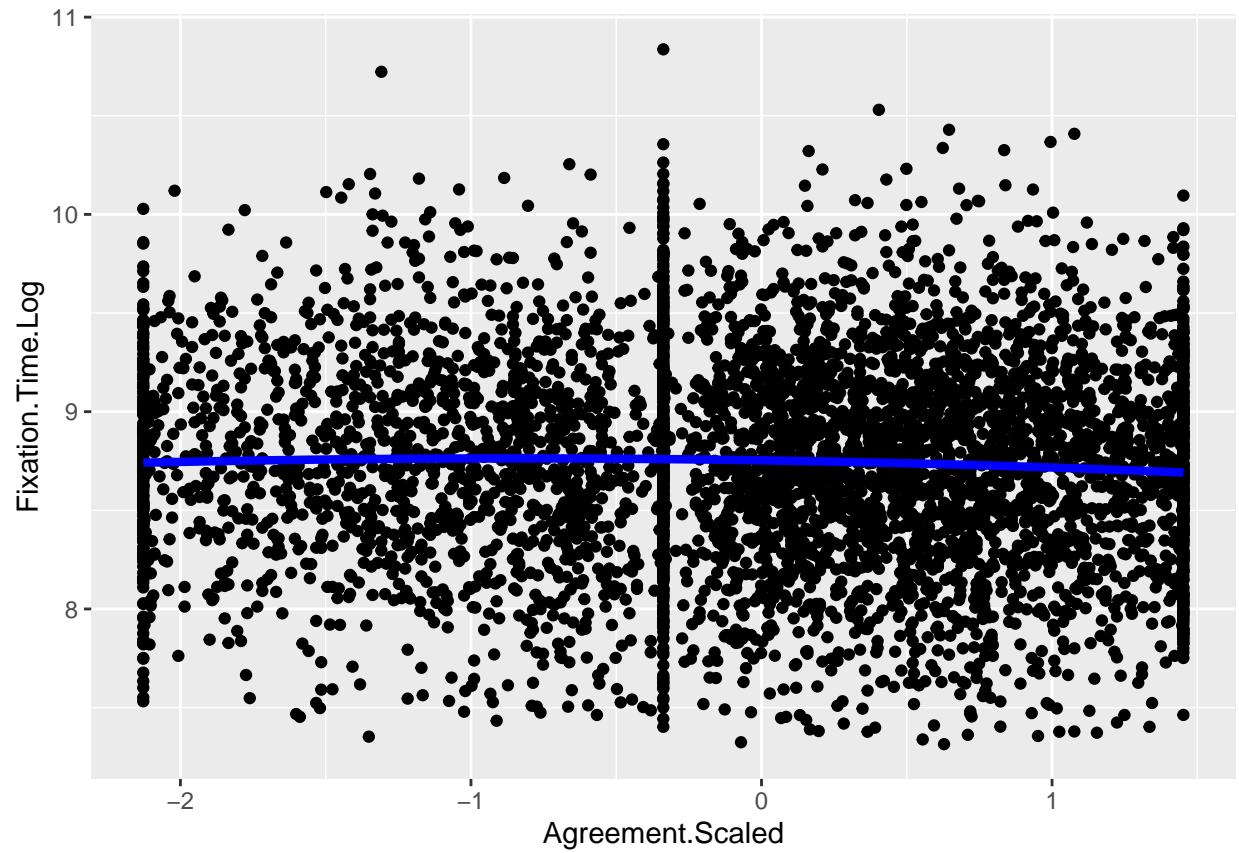
Quadratic effect of Agreement on Fixation Times



```
quad_function <- function(x, alpha, beta1, beta2)
{
  return(alpha + beta1*x + beta2*x^2)
}
```

Random effect plot

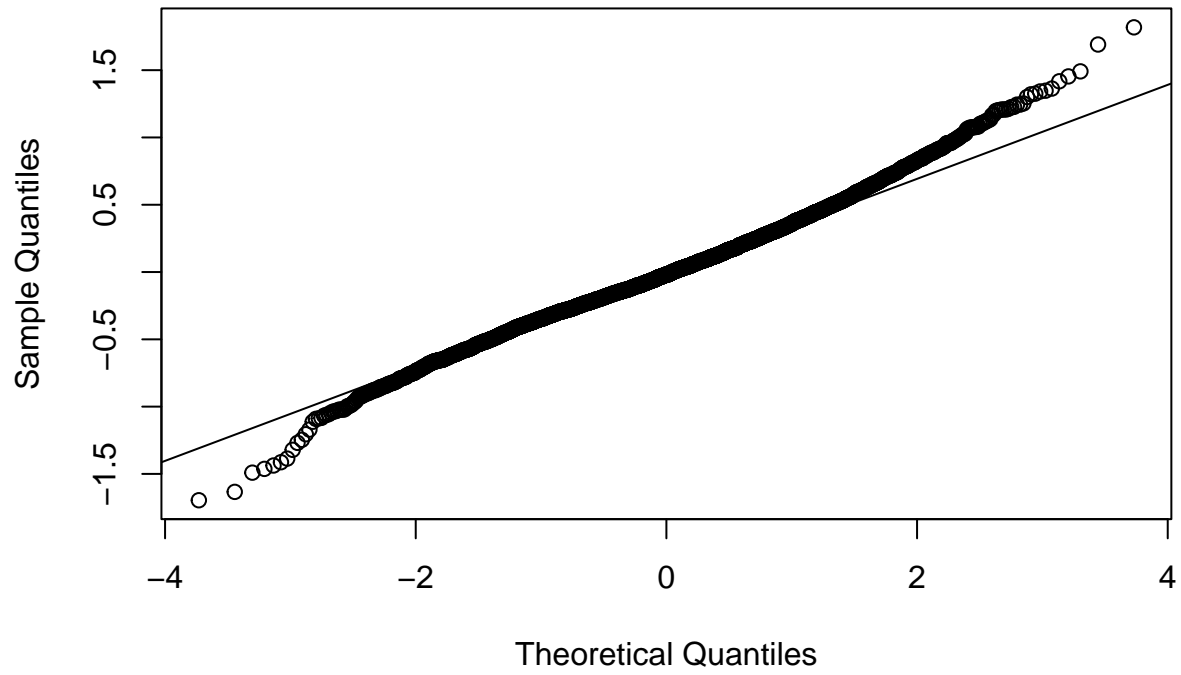
```
ggplot() +
  geom_point(data=d_final, aes(Agreement.Scaled, Fixation.Time.Log)) +
  geom_function(fun=quad_function,
    args=list(alpha=summary(res_mixed)[["coefficients"]][1],
              beta1=summary(res_mixed)[["coefficients"]][2],
              beta2=summary(res_mixed)[["coefficients"]][3]),
    color="blue",
    linewidth=1.5)
```



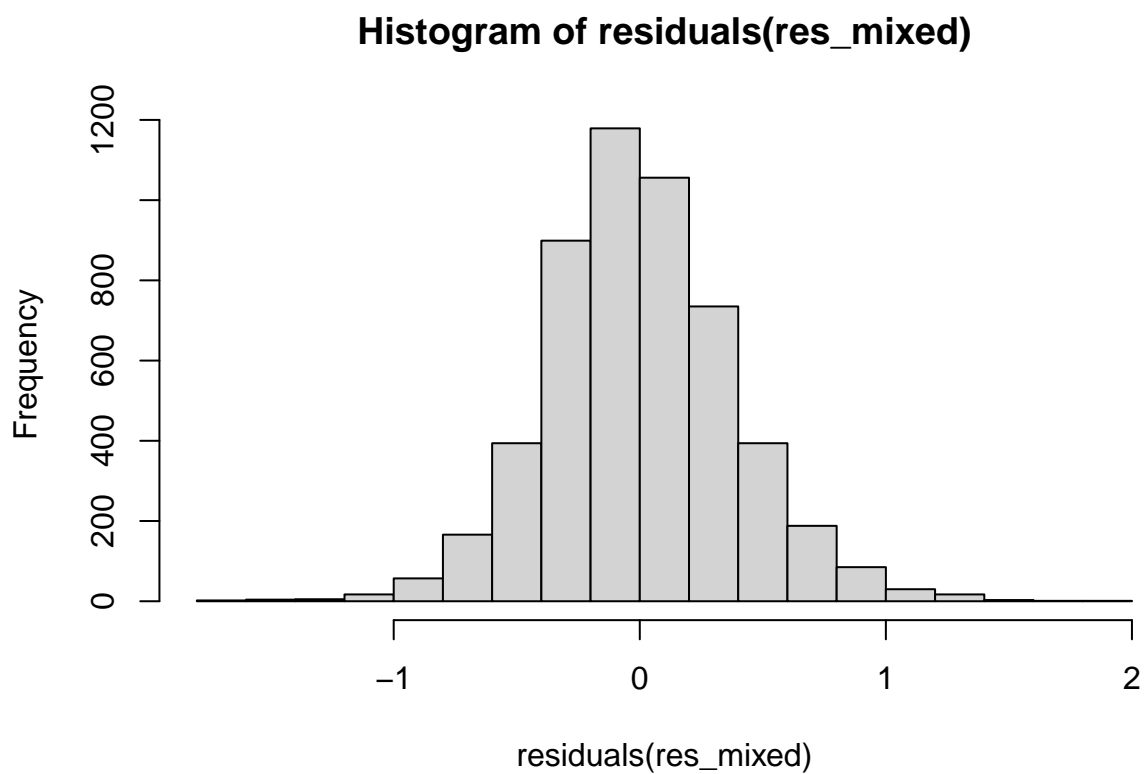
Residuals analysis

```
qqnorm(residuals(res_mixed))  
qqline(residuals(res_mixed))
```

Normal Q-Q Plot



```
hist(residuals(res_mixed))
```



```
ks.test(x=residuals(res_mixed), y='pnorm')
```

```
##  
## Asymptotic one-sample Kolmogorov-Smirnov test  
##  
## data: residuals(res_mixed)  
## D = 0.23004, p-value < 2.2e-16  
## alternative hypothesis: two-sided
```