# If you're a Bayesian you can do anything that God forbids ( - Willem Heiser)

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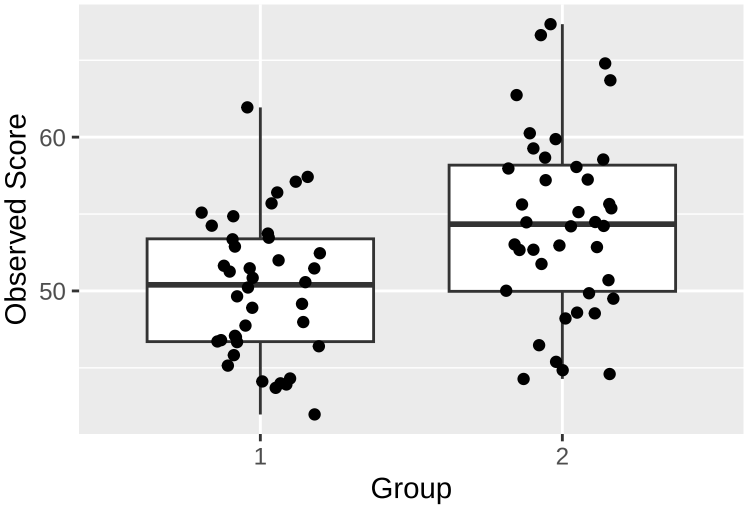
- Say things about means without knowing much about the basic units

# Means without knowing much about the basic units

```r
N <- 80
group <- rep(1:2, each = N/2)
true_score <-
  rnorm(N,
        mean = rep(c(50, 55), each = N/2),
        sd   = 2)  # True scores for each participant
observed_score <- true_score +
  rnorm(N,
        mean =  0,
        sd   =  5)  # Noisy observations
data <- data.frame(participant = 1:N,
                   group = factor(group),
                   true_score, observed_score)
```

## Observed Scores by Group



```r
model_string <- "
model {
  for (i in 1:N) {
    # Likelihood
    observed_score[i] ~ dnorm(true_score[i], tau)
    # Hierarchical model
    true_score[i]     ~ dnorm(mu[group[i]], tau_true)
  }
  diff_mu ~ dnorm(0, 0.001)
  mu[1]   ~ dunif(0, 100)
  mu[2] <- mu[1] + diff_mu
  tau      ~ dgamma(0.1, 0.1)
  tau_true ~ dgamma(0.1, 0.1)
}
"
```

```r
data_list <- list(
  N = N,
  observed_score = data$observed_score,
  group = as.numeric(data$group)
)

# Initial values
inits <- function() {
  list(
    tau        = rgamma(1, 0.1, 0.1),
    tau_true   = rgamma(1, 0.1, 0.1),
    true_score = runif(N, 0, 100)
  )
}
```

```r
jags_model <- jags.model(textConnection(model_string),
                         data     = data_list,
                         inits    =     inits,
                         n.chains =         3 ,
                         n.adapt  =      1000 )
```

```
## Compiling model graph
##    Resolving undeclared variables
##    Allocating nodes
## Graph information:
##    Observed stochastic nodes: 80
##    Unobserved stochastic nodes: 84
##    Total graph size: 250
##
## Initializing model
```

```r
update(jags_model, n.iter = 1000)
samples <- coda.samples(jags_model,
                        variable.names = c("diff_mu",
                                           "true_score"),
                        n.iter = 5000)
```

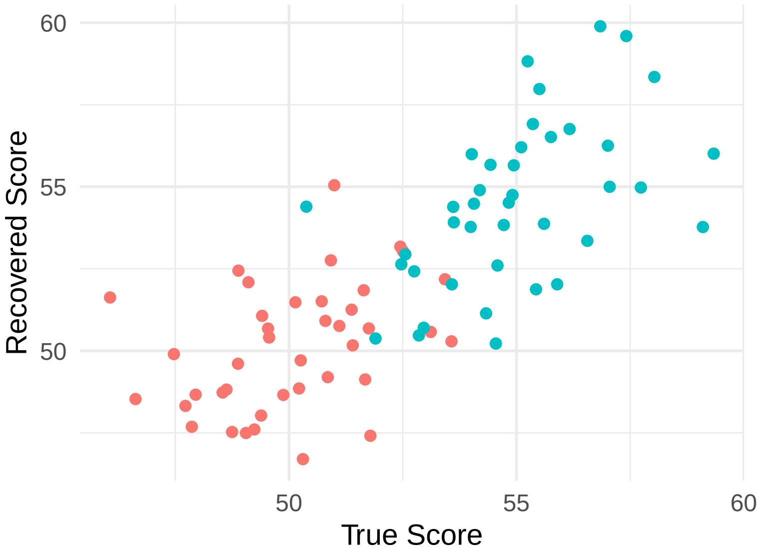
```r
# Summarize the results
summary_diff_mu <- summary(samples)$
  statistics["diff_mu", ]
print(summary_diff_mu)
```

```
##           Mean             SD       Naive SE Time-series SE 
##         4.3799         1.2106         0.0099         0.0642
```

```r
# Extract true scores from the posterior samples
true_scores_posterior <- as.data.frame(as.matrix(samples)) %>%
  select(starts_with("true_score")) %>%
  apply(2, mean)

# Add the recovered true scores to the data frame
data$recovered_true_score <- true_scores_posterior

# Scatter plot of true scores vs recovered true scores
p2 <- ggplot(data, aes(x = true_score, y = recovered_true_score,
                       color = group)) +
  geom_point() +
  labs(x = "True Score", y = "Recovered Score") +
  theme_minimal() +
  theme(legend.position = "none")
```


60
55
50
Recovered Score
50
55
60
True Score

# Hierarchical recovery beats individual recovery

The difference between groups is well recovered as $4.38 \pm 1.21$, even though the true scores within each group are poorly recovered.