# **Advanced Bayesian modeling**

Joachim Vandekerckhove

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Sum of products vs. product of sums:

$$\sum_{r=1}^{2} \left( \prod_{c=1}^{3} x_{rc} \right) \neq \prod_{c=1}^{2} \left( \sum_{r=1}^{3} x_{rc} \right)$$

In general, order of operations matters:

$$f \circ g(x) \neq g \circ f(x)$$

### Estimating parameters is an operation

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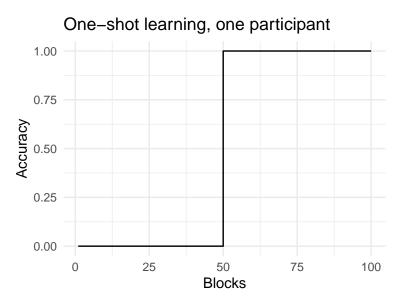
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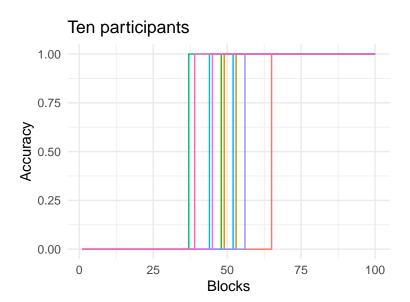
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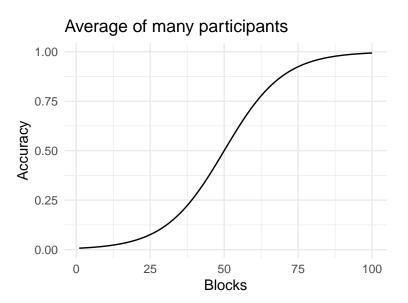
$$\hat{\theta} = f(x)$$

Do we want the average model parameters of the data or the model parameters of the average data?

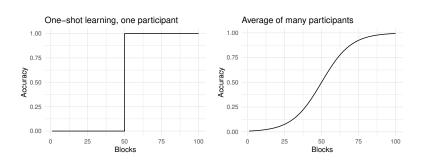
$$\overline{f(x)} \neq f\left(\overline{x}\right)$$







The "average" learning curve looks nothing like the person-specific learning curve!



Instead, what we want here is to acknowledge that each person has their own trajectory, and then say something about the (average) properties of the trajectories.

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We want to make an abstraction of the data, which are something complicated that is generated by a process with parameters  $\theta_p$  (for person p), and instead focus on parameters.

#### Basic hierarchy

$$\mathcal{M}_h: egin{cases} x_p \sim \mathsf{one}\text{-shot}\,(\theta_p) \ \theta_p \sim N(\mu, au) \end{cases}$$

The hierarchical model contains one set of assumptions about the data given the model (the likelihood level), and another set of assumptions about structure among parameters.

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The hierarchical model contains one set of assumptions about the data given the model (the likelihood level), and another set of assumptions about structure among parameters.

Here, the hierarchical parameters  $\mu$  and  $\tau$  tell us something about the population of participants, each with their own change point  $\theta_p$ .

### Population assumptions

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If  $n_t > 2$ , a measurement error may have occurred.

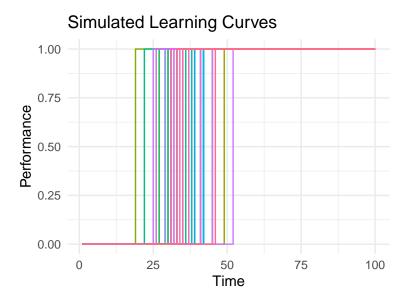
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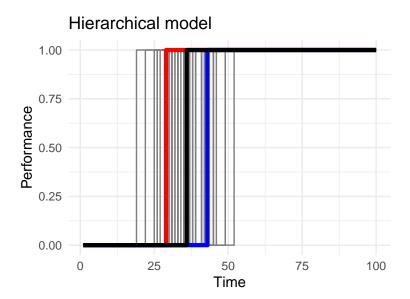
- Let's generate learning curves for a population of n=50 participants, each with a random change point.
- Let's use a step function to represent the learning curves.



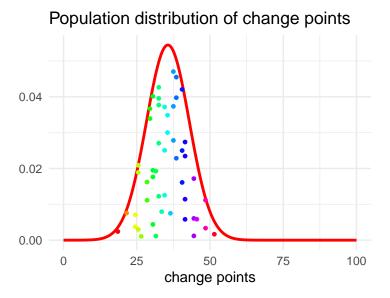
 We define a hierarchical model in JAGS to estimate each participant's change point.

- We define a hierarchical model in JAGS to estimate each participant's change point.
- The change point for each participant is modeled as a uniform distribution between 1 and 100.

```
##
## model {
##
     for (j in 1:P) {
       for (i in 1:N) {
##
         y[i, j] ~ dbern(p[i, j])
##
         p[i, j] <- ifelse(time[i] < theta[j], 0, 1)</pre>
##
##
       theta[j] ~ dnorm(mu, tau)T(0,100)
##
##
##
     mu ~ dnorm(50, 0.05)T(0,100)
     tau ~ dnorm(20, 0.10)T(0,)
##
     sigma <- pow(tau, -0.5)
##
## }
```



## Population results



#### Parameter estimates

```
## Mean SD Time-series SE
## mu 35.625707 1.0286096 0.010823168
## sigma 7.324946 0.7521836 0.007949786
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#### Compare to:

• Simulated  $\mu=35$ 

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## Mean SD Time-series SE
## mu 35.625707 1.0286096 0.010823168
## sigma 7.324946 0.7521836 0.007949786
```

#### Compare to:

- Simulated  $\mu=35$
- Simulated  $\sigma = 8$

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Accumulate evidence for the absence of an effect

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- Accumulate evidence for the absence of an effect
- Draw valid conclusions with almost no data

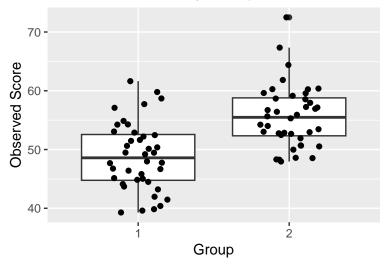
"If you're a Bayesian you can do everything that God forbids."

- ( Willem Heiser)
  - Accumulate evidence for the absence of an effect
  - Draw valid conclusions with almost no data
  - Say things about means without knowing much about the basic units

## Means without knowing much about the basic units

```
N < -80
group \leftarrow rep(1:2, each = N/2) # Make two groups
# True score for each participant depends on group
true score <-
  rnorm(N,
        mean = rep(c(50, 55), each = N/2),
        sd = 2
# Observations are noisy
observed score <- true score +
  rnorm(N, mean = 0, sd = 5)
data <- data.frame(participant = 1:N,</pre>
                    group = factor(group),
                    true score, observed score)
```

# Observed Scores by Group



```
model_string <- "</pre>
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] \leftarrow mu[1] + diff mu
  tau ~ dgamma(0.1, 0.1)
  tau true \sim dgamma(0.1, 0.1)
```

```
data list <- list(</pre>
 N = N.
  observed_score = data$observed_score,
  group = as.numeric(data$group)
# Initial values
inits <- function() {</pre>
  list(
    tau = rgamma(1, 0.1, 0.1),
    tau_true = rgamma(1, 0.1, 0.1),
    true score = runif(N, 0, 100)
```

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

SD

6.84520561 1.30258822 0.01063559 0.10491280

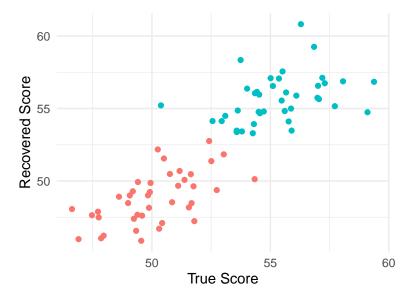
Naive SE Time-series SE

##

##

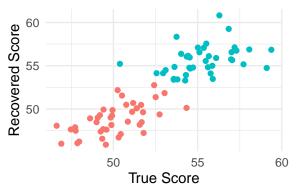
Mean

```
# 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</pre>
# 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")
```



## Hierarchical recovery beats individual recovery

The difference between groups is well recovered as  $6.8452056\pm1.3025882$ , even though the true scores within each group are poorly recovered.



### Perform inference with no actual data

Suppose these were scores from a test (and suppose the two groups are an "on-track" group and an "advanced" group). One student from the advanced group missed class. What do we know about student N+1?

```
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] \leftarrow mu[1] + diff mu
 tau ~ dgamma(0.1, 0.1)
 tau_true ~ dgamma(0.1, 0.1)
 true_score[N+1] ~ dnorm(mu[2], tau_true)
  observed score[N+1] ~ dnorm(true score[N+1], tau)
```

```
data list <- list(</pre>
 N = N.
  observed_score = c(data$observed_score, NA),
  group = as.numeric(data$group)
# Initial values
inits <- function() {</pre>
  list(
    tau = rgamma(1, 0.1, 0.1),
    tau_true = rgamma(1, 0.1, 0.1),
    true score = runif(N+1, 0, 100)
```

```
## Compiling model graph
## Resolving undeclared variables
## Allocating nodes
## Graph information:
## Observed stochastic nodes: 80
## Unobserved stochastic nodes: 86
## Total graph size: 252
##
## Initializing model
```

```
update(jags_model, n.iter = 1000)
samples <- coda.samples(jags_model,</pre>
                        variable.names = c("diff_mu",
                                            "true score",
                                            "observed_score"),
                        n.iter = 5000
# Summarize the results
summary_new <- summary(samples)$</pre>
  statistics[c("true_score[81]", "observed_score[81]"),
             c("Mean", "SD")]
print(summary_new)
##
                          Mean
                                   SD
## true_score[81] 55.67140 4.425973
## observed_score[81] 55.66311 5.762727
```

```
# Extract true scores from the posterior samples
true_scores_posterior_new <- as.data.frame(as.matrix(samples)) %>%
select(starts_with("true_score[81]"))
```

### True score and observed score

