

Hierarchical (a.k.a. Multilevel) Modeling

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Hierarchical Modeling

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A statistical framework for data with **dependencies** from **group structure**.

- Examples: Students in classrooms, patients in hospitals, trials within participants, stimuli within conditions.
- Observations within the same group are typically correlated (non-independent).
- Standard methods ignore this structure, which can lead to biased estimates and incorrect inferences.

Pooling is a spectrum

Complete pooling (ignore structure)

Analyze all data together.

- × Underestimates errors.
- × Hides true group differences.
- × Doesn't quantify group variability.
- × Unlikely to generalize.

No pooling (separate analyses)

Analyze each group separately.

- × Ignores within-group similarities.
- × Inefficient.
- × Noisy estimates.
- × Impossible to generalize.

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- Each unit contributes, weighted by its precision.
- **“Borrow strength”**: Units within populations inform each other.
- Improves individual unit estimates (especially for noisy/small units) with good prior knowledge.
- Simultaneously estimates population-level effects **and** the extent of variation between participants.

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- **Level 1 (within-group):**

$$y_{i|j} = \alpha_j + \beta x_{i|j} + \epsilon_{i|j}, \text{ with } \epsilon_{i|j} \sim \mathcal{N}(0, \sigma_y^2)$$

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- **Level 2 (between-group):**

$$\alpha_j \sim \mathcal{N}(\mu_\alpha, \sigma_\alpha^2)$$

The group intercepts (α_j) are drawn from a population distribution.

- μ_α : Population average intercept.
- σ_α^2 : Variance of intercepts across participants.

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This structure explicitly models the dependency within populations.

Hierarchical model structure

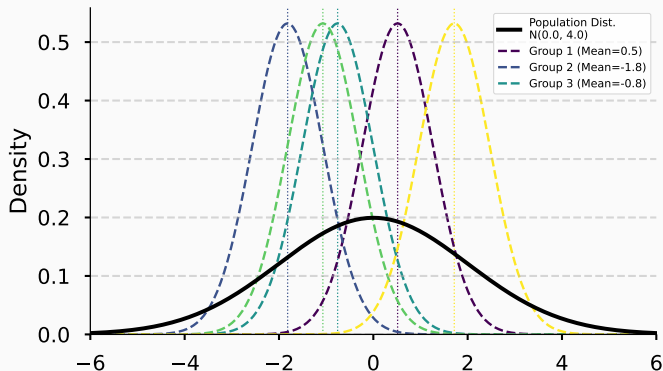


Figure 1: The population distribution (solid black line, representing $N(\mu_\alpha, \sigma_\alpha^2)$) describes the overall tendency for participant means. Person-specific distributions (dashed colored lines, representing $N(\alpha_j, \sigma_y^2)$ for different j) have means (α_j , marked by dotted vertical lines) drawn from the population distribution.

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$$\alpha_j = \mu_\alpha + u_j, \text{ with } u_j \sim \mathcal{N}(0, \sigma_\alpha^2)$$

All together: $y_{i|j} = \mu_\alpha + \beta x_{i|j} + u_j + \epsilon_{i|j}$

This model has a global intercept (μ_α), a global slope (β), a participant-specific deviation (u_j), and a residual error ($\epsilon_{i|j}$).

- **Fixed effects**

Parameters that differ between participants and are estimated independently from one another – they do not share free parameters: $\alpha_1 \sim \mathcal{N}(0, 1), \alpha_2 \sim \mathcal{N}(0, 1), \dots$

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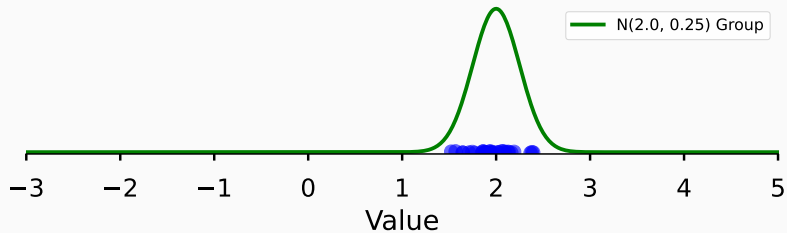
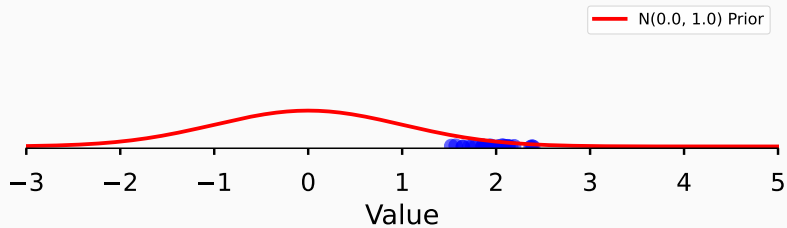
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- **Variance components**

Parameters characterizing variability at different levels:

- Level 1: Residual variance σ_y^2 .
- Level 2: Random effect variances (σ_α^2) quantify the magnitude of inter-individual differences.

Fixed vs. random effects



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$\text{Var}(\hat{\alpha}_{j,\text{no pool}})$ depends on participant sample size n_j and within-participant variance σ_y^2 . Person-specific estimates are **shrunk** towards the population mean.

Adaptive shrinkage

The amount of shrinkage is automatically **adaptive** and data-dependent:

More shrinkage (towards $\hat{\mu}_\alpha$) when:

- Participant has **less data** / noisy estimate (large $\text{Var}(\hat{\alpha}_{j,\text{no pool}})$).
- Participants are very **similar** (small between-participant variance σ_α^2).

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Less shrinkage (estimate closer to participant's own data) when:

- Participant has **more data** / precise estimate (small $\text{Var}(\hat{\alpha}_{j,\text{no pool}})$).
- Participants are very **dissimilar** (large between-participant variance σ_α^2).

Shrinkage visualization

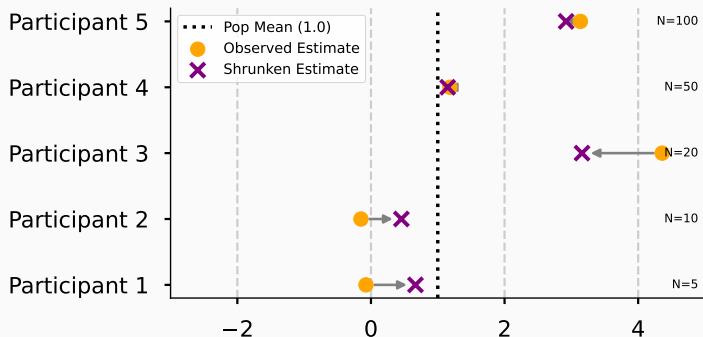


Figure 2: Observed group means (o) are pulled towards the estimated population mean (dashed line). The amount of shrinkage (length of gray arrow) is greater for groups with less data (smaller n_j), resulting in the shrunken estimates (x). The overall population mean estimate itself is informed by all participants.

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- **Coherent uncertainty:** Get full posterior distributions for **all** parameters (fixed effects, random effects, variance components), naturally propagating uncertainty.
- **Computation:** Modern MCMC (e.g., HMC/NUTS in Stan, PyMC) handles complex posteriors effectively.
- **Prior specification:** Requires care!
 - Fixed Effects / Means (μ s): Often weakly informative (e.g., wide Normal).
 - Variance Components (σ s): Crucial! Use weakly informative priors concentrated away from zero (e.g., Half-Normal, Half-Cauchy) to avoid issues.

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Interpretation: Focus on population parameters (μ s, fixed β s), magnitude of variation (σ s), and potentially shrunken group estimates (α_j s, β_j s), always with uncertainty (posterior distributions / intervals).

Crossed vs. nested random effects

- Nested: Students in classrooms, classrooms in schools.

$$y_{i|c|s} = \alpha_{c|s} + \beta x_{i|c,s} + \gamma_s + \epsilon_{i|c,s}$$

- Crossed: Participants respond to multiple stimuli (random effects for participant AND stimulus, not nested).

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- The solution is to add a **constraint**, for example $\mu_\alpha = 0$.

Generalization to cognitive modeling

$$\begin{aligned} y_{ip} &= \alpha_p + \gamma_i + \epsilon_{ip} \text{ with } \epsilon_{ip} \sim N(0, \sigma_{ip}^2) \\ \Leftrightarrow y_{ip} &\sim N(\alpha_p + \gamma_i, \sigma_{ip}^2) \end{aligned}$$

In cognitive modeling, data are rarely normally distributed.

How do we deal with this?

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- Now we handle the **Bernoulli parameter** as a to-be-explained dependent variable:

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- Psychometricians refer to α_p as the **person side** and γ_i as the **item side**.
- We can also handle either of these as a to-be-explained dependent variable:

$$\alpha_p = \beta_0 + \beta_1 z_p + \dots$$

$$\gamma_i = \zeta_0 + \zeta_1 q_i + \dots$$

See the pattern

First, in linear models (with normally distributed data), we did this decomposition:

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Now, in cognitive modeling (with complex distributions), we're going to do this:

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As we go, we'll declare some parameters to be focal (ψ_{ip}) and others nuisance (ς_{ip}).

Hierarchical cognitive models

This is just one way of decomposing model parameters:

$$y_{ip} \sim \text{Cognitive}(\psi_{ip}, s_{ip}) \quad \Leftrightarrow \quad y_{ip} \sim \text{Cognitive}(\alpha_p + \gamma_i, s_{ip})$$

Having a hierarchical structure is optional, but almost always the right call:

$$\alpha_p \sim \text{N}(\mu_\alpha, \sigma_\alpha^2)$$

Maybe $\mu_\alpha = \beta_0 + \beta_1 z_p + \dots$ really the world is your oyster at this point.

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$$y_{ip} \sim \text{SDT}(d'_{ip}, c'_{ip})$$

$$d'_{ip} = \alpha_p + \gamma_i$$

$$\gamma_i = \zeta_0 + \zeta_1 \text{brightness}_i$$

$$\alpha_p \sim \text{N}(\mu_\alpha, \sigma_\alpha^2)$$

... where $\text{SDT}()$ is shorthand for the signal detection theory functions covered earlier.

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The rest is just a lot of typing.

Assignment: Constrain a hierarchical SDT model

Change how group-level sensitivity (d') is modeled across conditions (k) in `full.py`.

Full hierarchical model

(Independent d' per condition)

Group level (per condition k):

- $\mu_{d',k} \sim \mathcal{N}(0, 2^2)$
- $\sigma_{d',k} \sim \text{HalfNormal}(1)$

Individual level (p, k):

- $d'_{pk} \sim \mathcal{N}(\mu_{d',k}, \sigma_{d',k}^2)$

Estimates a separate mean $\mu_{d',k}$ for each condition.

Condition explanatory hierarchical model

(Linear effect of condition on d')

Group level (overall):

- $\mu_{d',\text{intercept}} \sim \mathcal{N}(0, 2^2)$
- $\delta_{d'} \sim \mathcal{N}(0, 1^2)$ (Slope)
- $\sigma_{d',k} \sim \text{HalfNormal}(1)$ (Variance per condition)

Deterministic group mean:

- $\mu_{d',k} = \mu_{d',\text{intercept}} + \delta_{d'} \times k$

Individual level (p, k):

- $d'_{pk} \sim \mathcal{N}(\mu_{d',k}, \sigma_{d',k}^2)$

Estimates intercept and slope; $\mu_{d',k}$ is derived.

Hierarchical (a.k.a. Multilevel) Modeling

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