Supplementary Material: Description of Models

Models Overview

Both models were implemented via non-centered parametrThis supplementary material provides a detailed explanation of the two models used in the study: the **Growth Model** and the **Mechanisms Model**. Each model is described through mathematical equations. Weakly informative priors were assigned to the variables to regularize the results. Both models were implemented using a non-centered parameterization approach.ization.

Growth Model

The growth model was used both to evaluate the changes in symptom severity and functional impairment over time across different intervention groups, and to investigate changes in proposed mechanisms.

 $R_{itg} \sim \text{Ordered-logit}(\phi_{itg}, \kappa)$

Measurement model:

$$\begin{array}{lll} \phi_{itq} = \alpha_q \cdot (\theta_{it} - \beta_q) & (\text{IRT model}) \\ \kappa \sim \operatorname{Normal}(0, 1.5) & (\operatorname{cutpoints}) \\ \alpha_q \sim \operatorname{Log-Normal}(0, 0.5) & (\text{IRT discrimination}) \\ \beta_q \sim \operatorname{Normal}(0, 1) & (\text{IRT location}) \\ \text{Change model:} & (baseline) \\ & + (\bar{b}_{1,\operatorname{condition}} + u_{2i}) \cdot \min(t-1, \ 3) & (\Delta \ \operatorname{at intervention}) \\ & + (\bar{b}_{3,\operatorname{condition}} + u_{3i}) \cdot 1_{\{t \geq 5\}} & (\Delta \ \operatorname{at FU}_1) \\ & + (\bar{b}_{4,\operatorname{condition}} + u_{4i}) \cdot 1_{\{t = 6\}} & (\Delta \ \operatorname{at FU}_2) \\ & + G \cdot \gamma & (\operatorname{gender}) \\ & \bar{b}_{1,\operatorname{condition}} \sim \operatorname{Normal}(0, 1.5) & (\theta \ \operatorname{intercept}) \\ & \bar{b}_{[2,3,4],\operatorname{condition}} \sim \operatorname{Normal}(0, 0.5) & (\theta \ \operatorname{slopes}) \\ & \gamma \sim \operatorname{Normal}(0, 0.5) & (\operatorname{gender} \ \operatorname{effect}) \\ & \sigma_{1...4} \sim \operatorname{Exponential}(1) & (\operatorname{scale} \ \operatorname{for} \ u) \\ & \rho \sim \operatorname{LKJcorr}(4) & (\operatorname{correlation} \ \operatorname{matrix}) \\ & \Sigma = \operatorname{diag}(\sigma) \cdot \rho \cdot \operatorname{diag}(\sigma) & (\operatorname{covariance} \ \operatorname{matrix}) \\ & \begin{bmatrix} u_{1i} \\ u_{2i} \\ u_{3i} \\ u_{4i} \end{bmatrix} \sim \operatorname{MVNormal} \begin{pmatrix} \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix}, \Sigma \\ & 0 \end{pmatrix} & (\operatorname{person} \ \operatorname{effects}) \\ \end{array} \right.$$

(likelihood)

Here's a breakdown of the variables used in the model:

- R_{itq}: This represents the observed response for individual i at time t on item q. This is the actual
 measured value.
- ϕ_{itq} : This is the linear predictor in the ordered logit model. It links the latent trait (θ_{it}) to the observed response (R_{ita}) .
- κ : These are the cutpoints (thresholds) in the ordered logit model. They define the boundaries between the ordered categories of the responses.
- α_q : This is the discrimination parameter for item q in the IRT model. It indicates how well an item differentiates between different levels of the latent trait. A higher α_q means the item is more sensitive to changes in the latent trait.
- β_q : This is the difficulty (or location) parameter for item q in the IRT model. It represents the level of the latent trait at which a person has a 50% chance of endorsing a particular item.
- θ_{it} : This is the latent trait score (e.g., symptom severity) for individual i at time t. This is the unobserved variable that the model is trying to estimate.
- $b_{1,condition}$: This is the population-level baseline intercept for a given condition. It represents the average starting level of the latent trait.
- $\bar{b}_{2,\text{condition}}$: This is the population-level slope representing the change during the intervention for a given condition.
- $\bar{b}_{3,\text{condition}}$: This is the population-level slope representing the change at the first follow-up (FU1) for a given condition.
- $\bar{b}_{4,\text{condition}}$: This is the population-level slope representing the change at the second follow-up (FU2) for a given condition.
- u_{1i} , u_{2i} , u_{3i} , u_{4i} : These are the individual-level random effects for baseline, intervention change, FU1 change and FU2 change respectively. They capture individual deviations from the population average trajectories. Note that u_{1i} is the random intercept, u_{2i} is the random slope for the intervention period, u_{3i} is the random slope for the change between the end of intervention and FU1, and u_{4i} is the random slope for the change between FU1 and FU2.
- t: Represents time (wave) or measurement occasion.
- $\min(t-1,3)$: This ensures that the intervention effect is only applied up to time point 4 (the end of the intervention period).
- $1_{\{t \geq 5\}}$: This is an indicator function (also known as an Iverson bracket). It equals 1 when t is greater than or equal to 5 (i.e. at FU1 and FU2) and 0 otherwise, thus modeling the change specifically at the first follow-up and beyond.
- $1_{\{t=6\}}$: This is an indicator function. It equals 1 when t=6 (FU2) and 0 otherwise, thus modeling the additional change specifically at the second follow-up.
- G: Represents gender (coded as -0.5/0.5).
- γ : Represents the effect of gender on the latent trait.
- $\sigma_{1...4}$: These are the standard deviations of the random effects (baseline, intervention slope, FU1 slope and FU2 slope). They quantify the variability of individual trajectories around the population average.
- ρ: This is the correlation matrix of the random effects. It describes the relationships between the individual-level deviations in baseline, intervention response, FU1 response and FU2 response.
- Σ : This is the covariance matrix of the random effects, derived from the standard deviations (σ) and the correlation matrix (ρ). It fully describes the variance and covariance structure of the random effects.

Mechanisms Model

The mechanisms model explores the processes underlying symptom changes, identifying potential mediators of the intervention's effects.

Measurement model for Symptoms:

$$R_{x,itq} \sim \text{Ordered-logit}(\phi_{x,itq}, \kappa_x)$$
 (likelihood)
 $\phi_{x,itq} = \alpha_{x,q} \cdot (\theta_{x,it} - \beta_{x,q})$ (IRT model)
 $\kappa_x \sim \text{Normal}(0, 1.5)$ (cutpoints)
 $\alpha_{x,q} \sim \text{Log-Normal}(0, 0.5)$ (IRT discrimination)
 $\beta_{x,q} \sim \text{Normal}(0, 1)$ (IRT location)

Measurement model for Mechanisms:

$$R_{m,itq} \sim \text{Ordered-logit}(\phi_{m,itq}, \kappa_m)$$
 (likelihood)
 $\phi_{m,itq} = \alpha_{m,q} \cdot (\theta_{m,it} - \beta_{m,q})$ (IRT model)
 $\kappa_m \sim \text{Normal}(0, 1.5)$ (cutpoints)
 $\alpha_{m,q} \sim \text{Log-Normal}(0, 0.5)$ (IRT discrimination)
 $\beta_{m,q} \sim \text{Normal}(0, 1)$ (IRT location)

Change model for Symptoms:

$$\theta_{x,it} = (\bar{b_{x1,\text{condition}}} + u_{1i}) \qquad \text{(baseline)}$$

$$+ (\bar{b_{x2,\text{condition}}} + u_{2i}) \cdot \min(t - 1, 3) \qquad (\Delta \text{ at intervention})$$

$$+ (\bar{b_{x3,\text{condition}}} + u_{3i}) \cdot 1_{\{t=6\}} \qquad (\Delta \text{ at FU_2})$$

$$+ G \cdot \gamma \qquad \text{(gender)}$$

$$\bar{b_{x1,\text{condition}}} \sim \text{Normal}(0, 1.5) \qquad (\theta \text{ intercept})$$

$$\bar{b_{x[2,3],\text{condition}}} \sim \text{Normal}(0, 0.5) \qquad (\theta \text{ slopes})$$

$$\gamma \sim Normal(0, 0.5) \qquad (\text{gender effect})$$

Change model for Mechanisms:

$$\theta_{m,it} = (\bar{b_{m4,\text{condition}}} + u_{4i}) \qquad \text{(baseline)}$$

$$+ (\bar{b_{m5,\text{condition}}} + u_{5i}) \cdot \min(t-1, 3) \qquad (\Delta \text{ at intervention)}$$

$$\bar{b_{m4,\text{condition}}} \sim \text{Normal}(0, 1.5) \qquad (\theta \text{ intercept)}$$

$$\bar{b_{m5,\text{condition}}} \sim \text{Normal}(0, 0.5) \qquad (\theta \text{ slopes)}$$

Shared dynamics

$$\sigma_{1...5} \sim \text{Exponential}(1) \qquad \qquad \text{(scale for } u)$$

$$\rho \sim \text{LKJcorr}(5) \qquad \qquad \text{(correlation matrix)}$$

$$\Sigma = \text{diag}(\sigma) \cdot \rho \cdot \text{diag}(\sigma) \qquad \qquad \text{(covariance matrix)}$$

$$\begin{bmatrix} u_{1i} \\ u_{2i} \\ u_{3i} \\ u_{4i} \\ u_{5i} \end{bmatrix} \sim \text{MVNormal} \begin{pmatrix} \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}, \Sigma \end{pmatrix} \qquad \text{(person effects)}$$

Here's a breakdown of the variables used in the model:

- $R_{x,itq}$ and $R_{m,itq}$: These represent the observed responses for individual i at time t on item q for symptoms (x) and mechanisms (m), respectively. These are the actual measured values.
- $\phi_{x,itq}$ and $\phi_{m,itq}$: These are the linear predictors in the ordered logit models for symptoms and mechanisms, respectively. They link the latent traits (θ) to the observed responses (R).
- κ_x and κ_m : These are the cutpoints (thresholds) in the ordered logit models for symptoms and mechanisms, respectively. They define the boundaries between the ordered categories of the responses.
- $\alpha_{x,q}$ and $\alpha_{m,q}$: These are the discrimination parameters for item q in the IRT models for symptoms and mechanisms, respectively. They indicate how well an item differentiates between different levels of the latent trait. A higher α means the item is more sensitive to changes in the latent trait.
- $\beta_{x,q}$ and $\beta_{m,q}$: These are the difficulty (or location) parameters for item q in the IRT models for symptoms and mechanisms, respectively. They represent the level of the latent trait at which a person has a 50% chance of endorsing a particular item.
- $\theta_{x,it}$ and $\theta_{m,it}$: These are the latent trait scores (e.g., symptom severity, mechanism level) for individual i at time t. These are the unobserved variables that the model is trying to estimate.
- $\bar{b_{x1,condition}}$ and $\bar{b_{m1,condition}}$: These are the population-level baseline intercepts for symptoms and mechanisms, respectively, for a given condition. They represent the average starting level of the latent trait.
- $\bar{b}_{x2,\text{condition}}$ and $\bar{b}_{m2,\text{condition}}$: These are the population-level slopes representing the change during the intervention for symptoms and mechanisms, respectively, for a given condition.
- $\bar{b}_{x3,\text{condition}}$ and $\bar{b}_{m3,\text{condition}}$: These are the population-level slopes representing the change at follow-up 2 for symptoms and mechanisms, respectively, for a given condition.
- $u_{x,1i}$, $u_{x,2i}$, $u_{x,3i}$, $u_{m,1i}$, $u_{m,2i}$, $u_{m,3i}$: These are the individual-level random effects for baseline, intervention change, and follow-up 2, respectively, for symptoms and mechanisms. They capture individual deviations from the population average trajectories.
- t: Represents time (wave) or measurement occasion.
- $\min(t-1,3)$: This ensures that the intervention effect is only applied up to time point 4 (the end of the intervention period).
- $1_{\{t=6\}}$: This is an indicator function (also known as an Iverson bracket). It equals 1 when t=6 (FU2) and 0 otherwise, thus modeling the change specifically at the second follow-up.
- G: Represents gender (coded as -0.5/0.5).
- γ : Represents the effect of gender on symptom change.
- $\sigma_{1...3}$: These are the standard deviations of the random effects (baseline, intervention slope, and FU2 slope). They quantify the variability of individual trajectories around the population average.
- ρ: This is the correlation matrix of the random effects. It describes the relationships between the individual-level deviations in baseline, intervention response, and follow-up response.
- Σ : This is the covariance matrix of the random effects, derived from the standard deviations (σ) and the correlation matrix (ρ). It fully describes the variance and covariance structure of the random effects.