

MODULE 7

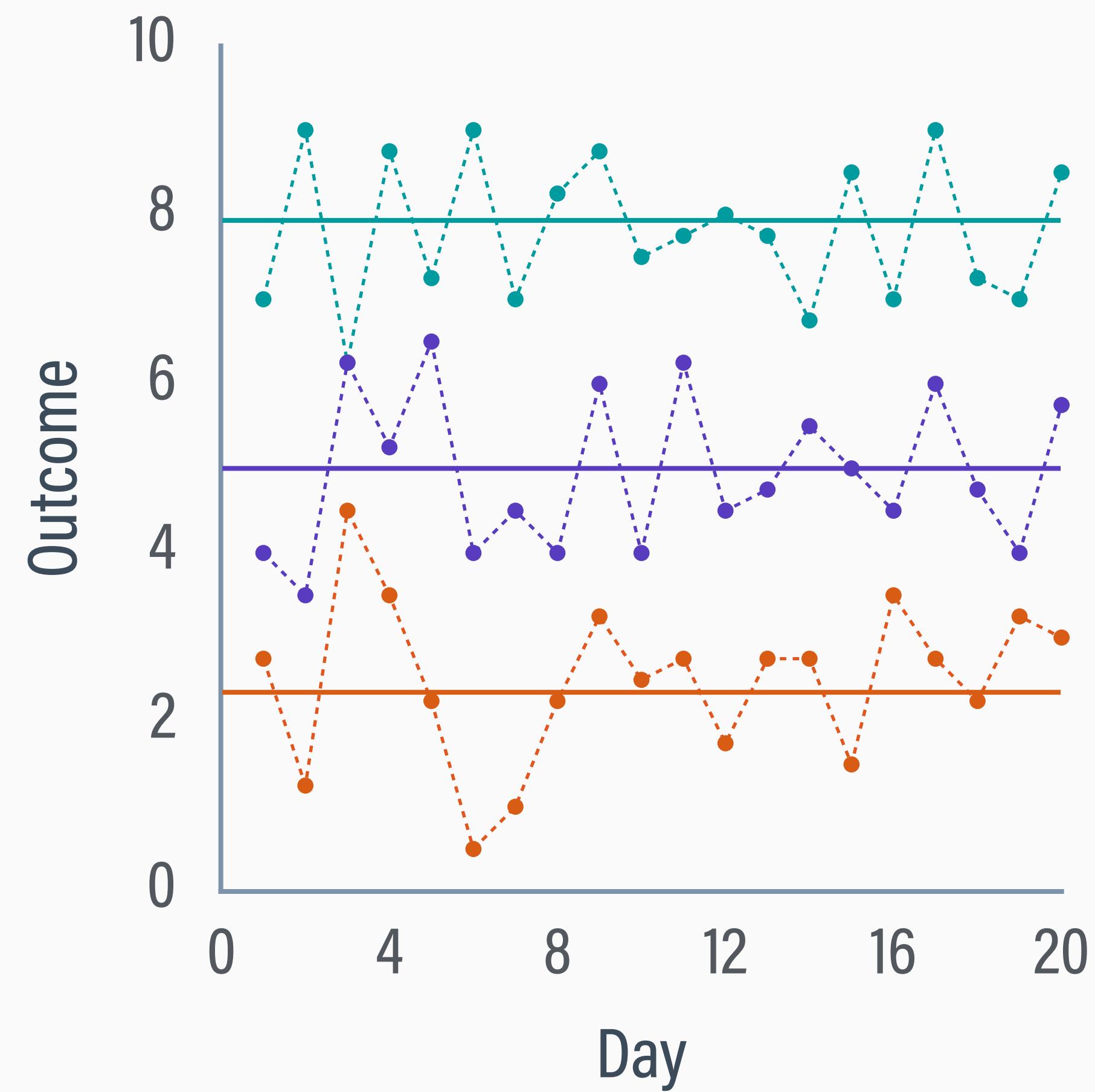
MULTILEVEL GROWTH MODELS

GROWTH MODEL OVERVIEW

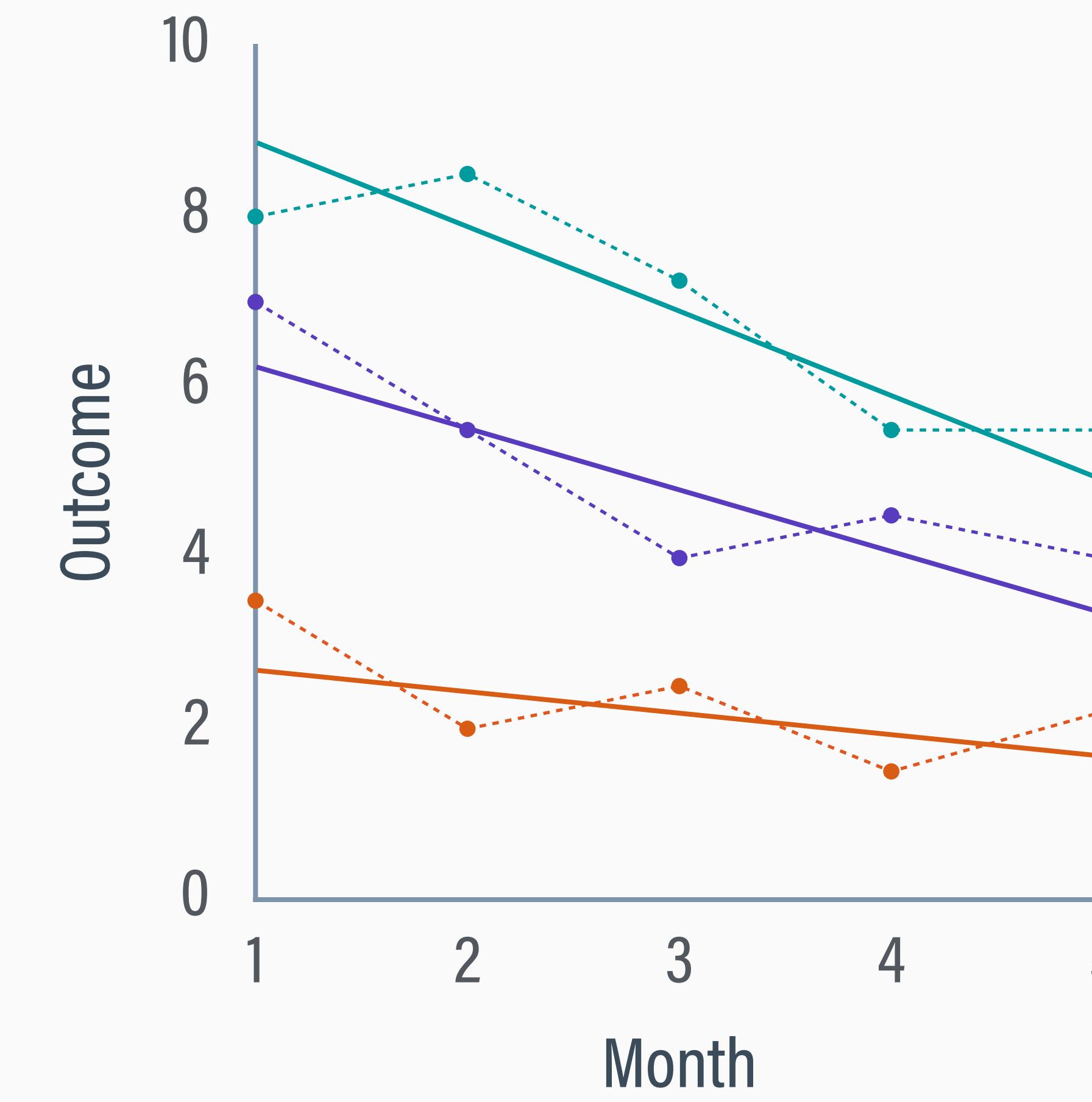
- Intensive repeated measures studies focus on short-term changes that represent adjustments to daily events or experiences (intraindividual variation)
- No systematic change expected
- Growth models differ because they address questions about longer-term time trends or change (intraindividual change)
- Systematic change is the focus

INTRAINDIVIDUAL VARIATION VS. CHANGE

Intensive repeated measures design
(intraindividual variation)

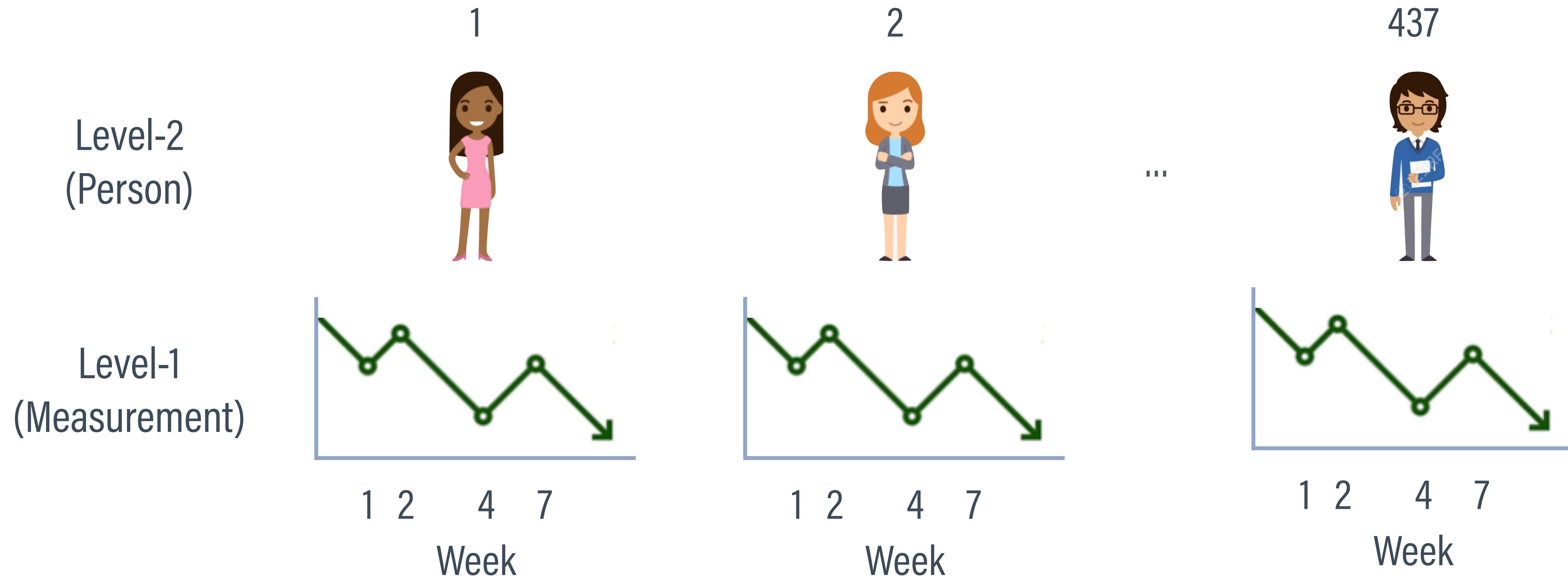


Longitudinal design
(intraindividual change)



CLINICAL TRIAL APPLICATION

- $n_j = 4$ measurements at level-1 nested within $J = 437$ persons at level-2 ($N = 630$ data records in total)



CLINICAL TRIAL DATA

 Predictors
 Outcome

Variable	Definition	Missing %	Scale
Person	Person-level (level-2) identifier	0	Integer index
Time	Measurement occasion	0	1, 2, 4, and 7 weeks
Drug	Medication condition	0	0 = placebo, 1 = medication
Male	Gender dummy code	0	0 = female, 1 = male
Severity	Illness severity rating	10.24	1 = not at all ill to 7 = extremely ill

DATA STRUCTURE

- Stacked or long format data
- Each person has a row of data for every measurement occasion
- i indexes occasions at level-1, and j indexes persons at level-2

Row	i	j	DRUG	WEEK	SEVERE _{ij}
1	1	1	0	1	7.0
2	2	1	0	2	2.5
3	3	1	0	4	5.2
4	4	1	0	7	6.3

5	1	2	1	1	4.0
6	2	2	1	2	4.0
7	3	2	1	4	3.5
8	4	2	1	7	4.4

...
1745	1	437	1	1	3.3
1746	2	437	1	2	4.8
1747	3	437	1	4	...
1748	4	437	1	7	4.8

OUTLINE

- 1 Examine Sample Means
- 2 Define Temporal Predictor (Time Variable)
- 3 Linear Growth Model
- 4 Model Nonlinear Change
- 5 Add Predictors of Change

REPEATED MEASURES ANOVA

- A repeated measures analysis in MLM fixes the average intercept (β_0) to zero and enters time-specific dummy codes as predictors
- β_1 through β_4 are occasion-specific means

$$\text{severity}_{ij} = \beta_1(\text{time}_{1ij}) + \beta_2(\text{time}_{2ij}) + \beta_3(\text{time}_{4ij}) + \beta_4(\text{time}_{7ij}) + u_{0j} + \varepsilon_{ij}$$

- The random intercept captures mean severity differences among persons (ANOVA includes a similar “subjects factor” term)

BLIMP SCRIPT 7.1

DATA: SchizophreniaTrial.dat;

VARIABLES: person week drug male severity;

CLUSTERID: person;

MISSING: 999;

MODEL:

severity ~ intercept@0 (week==1) (week==2) (week==4) (week==7) | intercept; # dummy codes

BURN: 20000;

ITERATIONS: 10000;

SEED: 90291;

RBLIMP SCRIPT 7 (MODEL 1)

```
model1 <- rblimp(  
  data = ClinicalTrial,  
  clusterid = 'Person',  
  model = 'Severity ~ intercept@0 (Week==1) (Week==2) (Week==4) (Week==7) | intercept',  
  seed = 90291,  
  burn = 10000,  
  iter = 20000)  
  
output(model1)  
posterior_plot(model1, 'Severity')
```

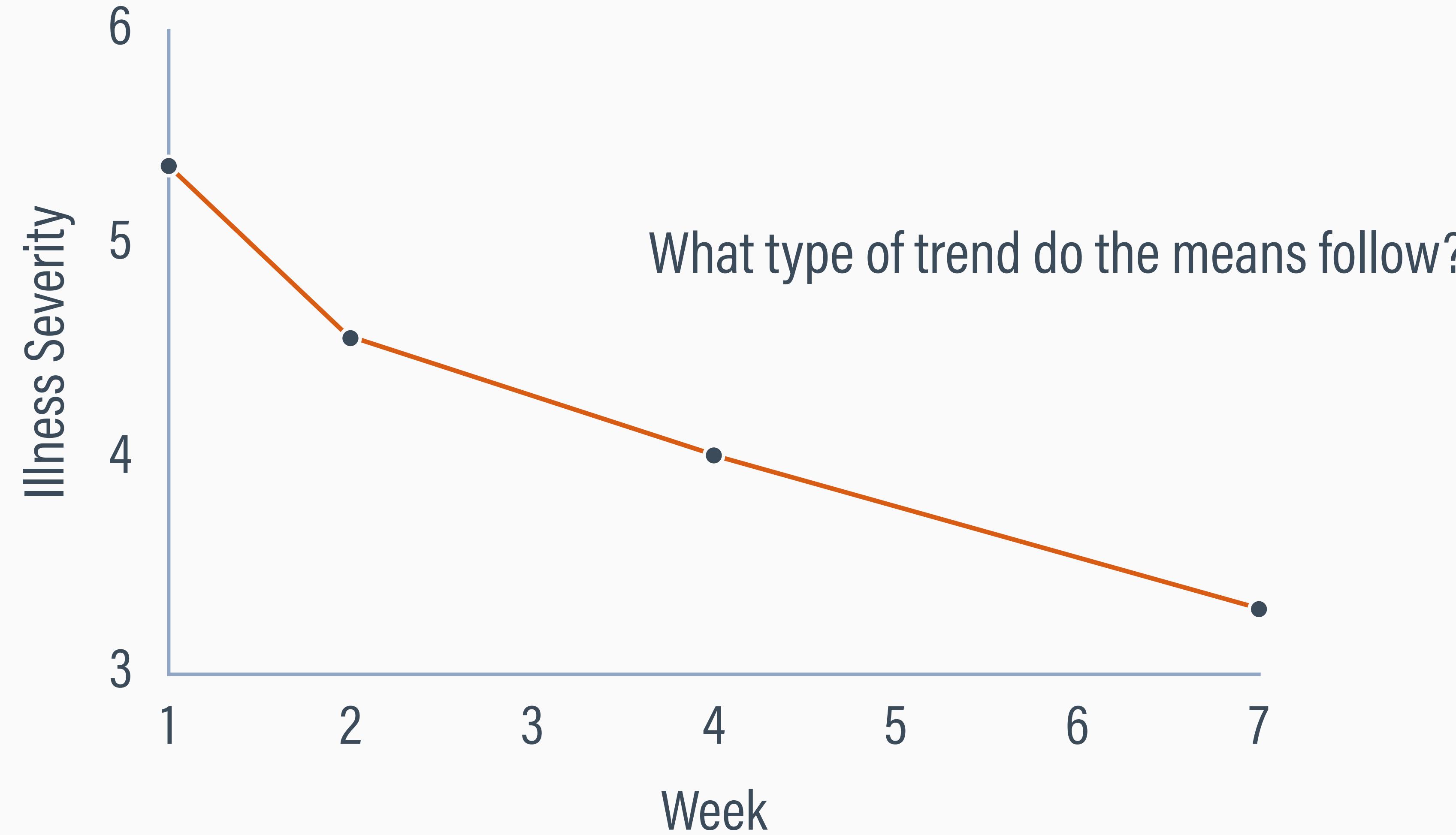
BLIMP OUTPUT

Outcome Variable: Severity

Parameters	Estimate	StdDev	2.5%	97.5%	ChiSq	PValue	N_Eff
<hr/>							
Variances:							
L2 : Var(Intercept)	0.812	0.074	0.679	0.968	---	---	8103.509
Residual Var.	1.024	0.040	0.951	1.107	---	---	11539.996
<hr/>							
Coefficients:							
(Week==1)	5.571	0.064	5.447	5.698	7507.678	0.000	3952.190
(Week==2)	4.783	0.065	4.658	4.910	5489.585	0.000	3920.349
(Week==4)	4.227	0.065	4.098	4.355	4215.678	0.000	3755.119
(Week==7)	3.542	0.065	3.416	3.669	2969.764	0.000	4223.158

...

MODEL-PREDICTED MEANS

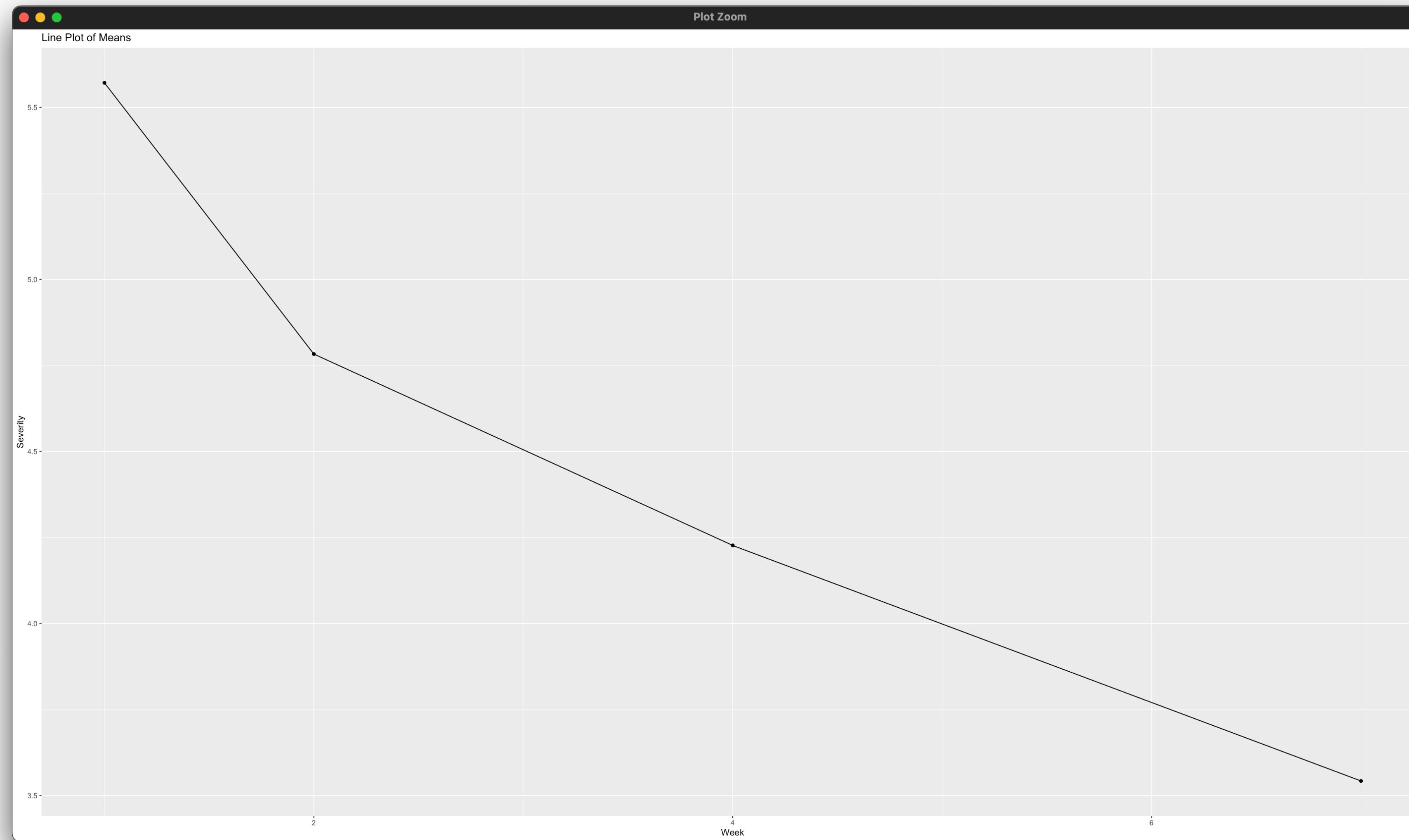


R PLOTTING CODE

```
# extract means from estimates object (always starting in 3rd row and first column)
means <- model1@estimates[3:6,1] # extract means
waves <- c(1,2,4,7) # specify values of the measurement occasions
means <- as.data.frame(cbind(waves,means))

# plot means
ggplot(means, aes(x = waves, y = means)) +
  geom_line() +
  geom_point() +
  labs(x = "Week", y = "Severity", title = "Line Plot of Means")
```

R LINE GRAPH OF MEANS



GROWTH MODELING

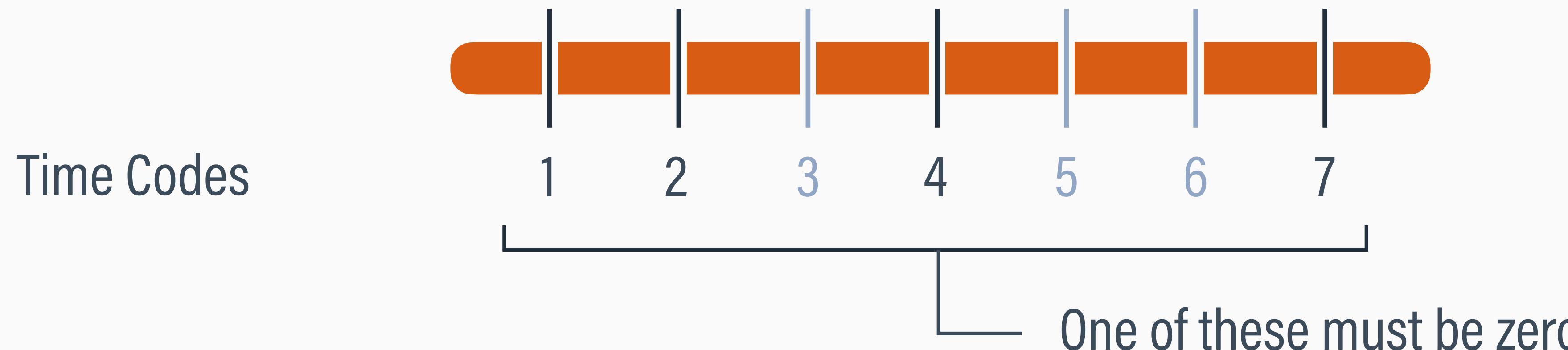
- Growth models apply time trends (linear, curvilinear) to the sample means and individual repeated measurements
- The model features an average change trajectory (fixed effects) and person-specific trajectories (random effects)
- The model incorporates a within-person predictor that captures the passage of time across the study's span (e.g., days, weeks)

OUTLINE

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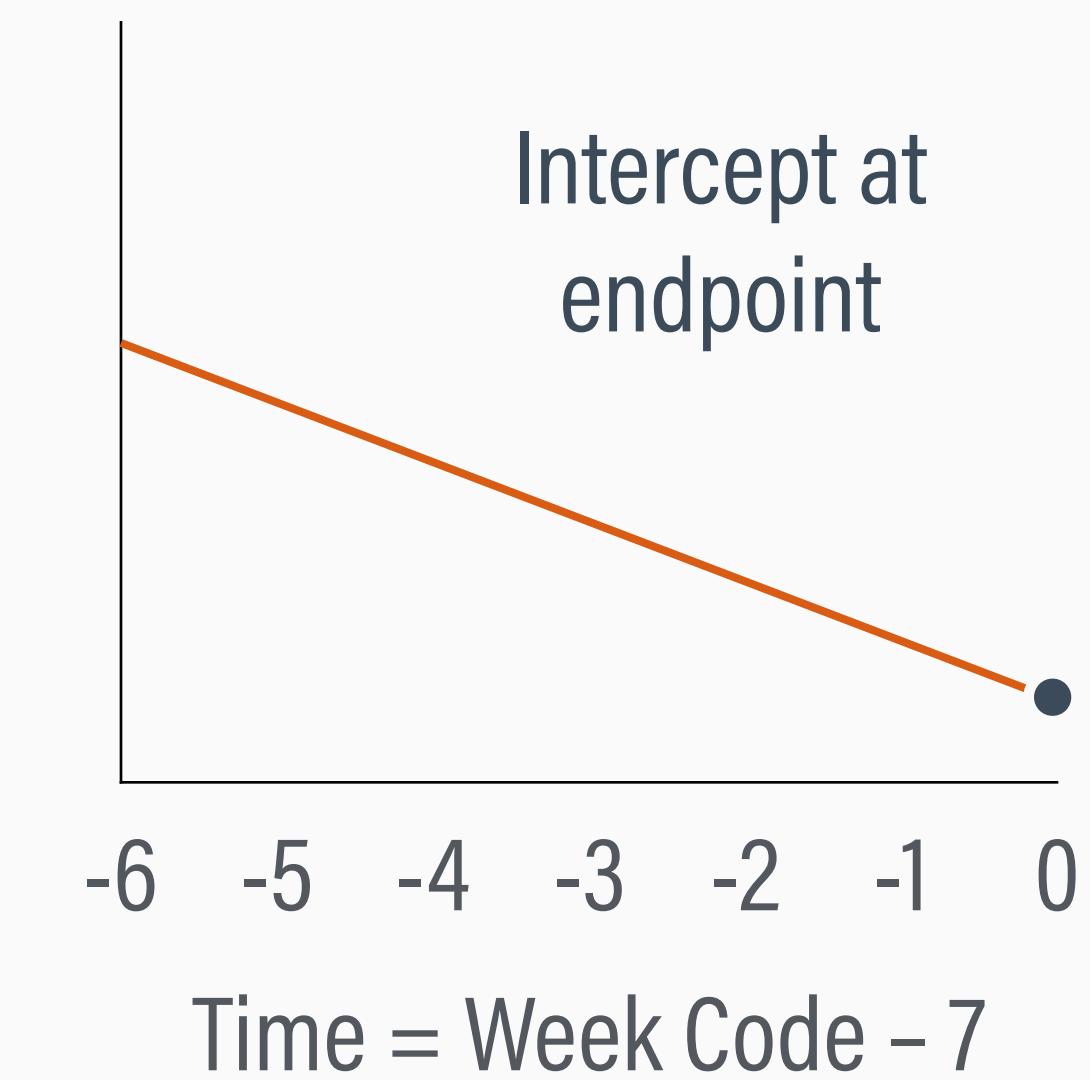
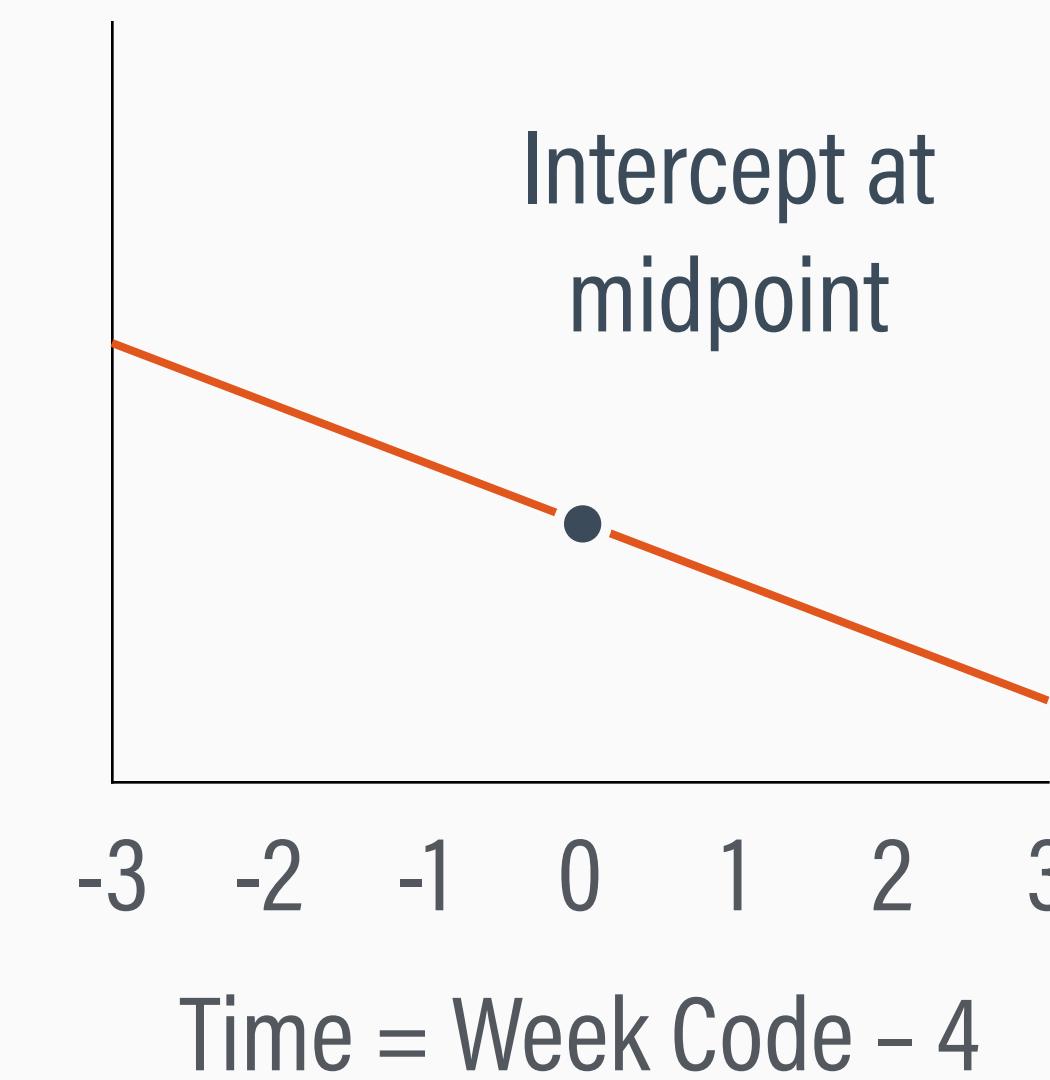
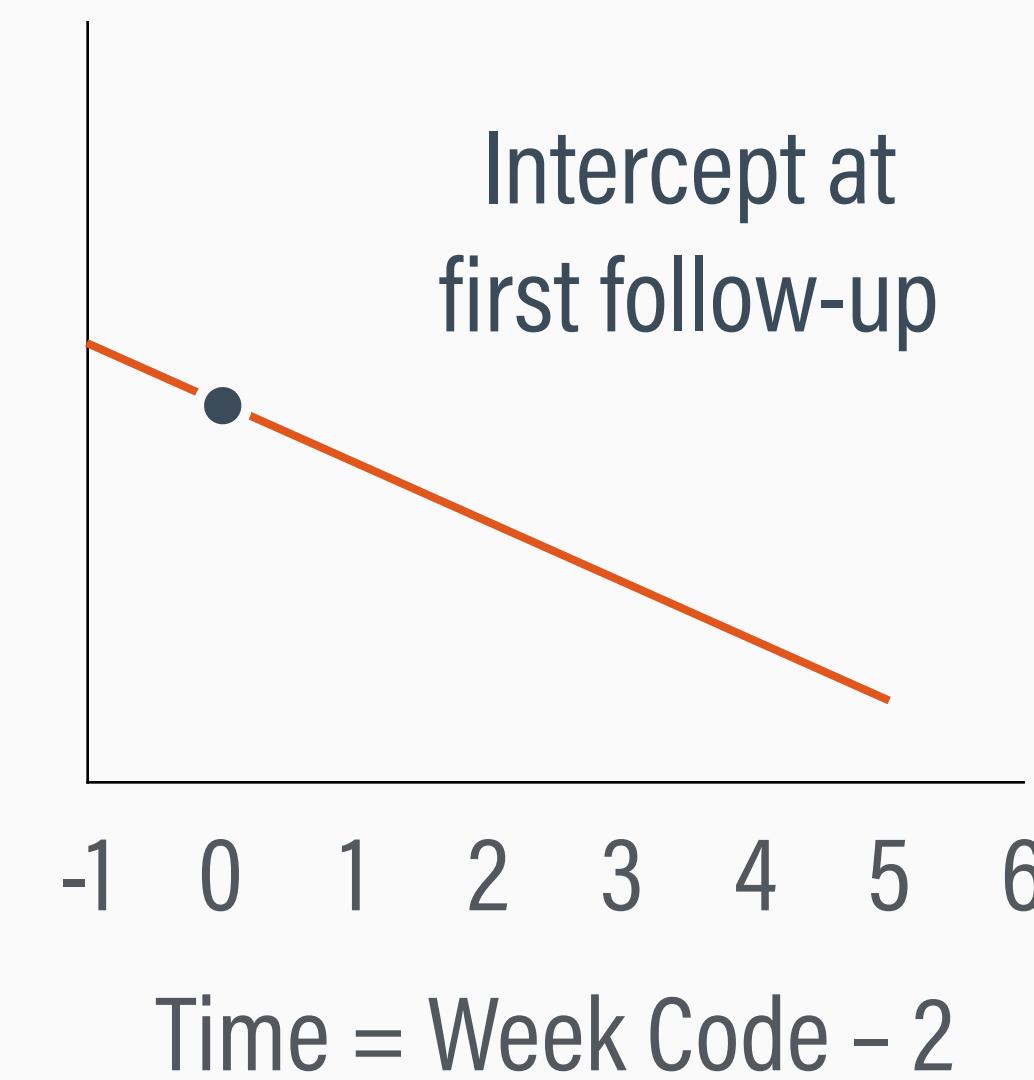
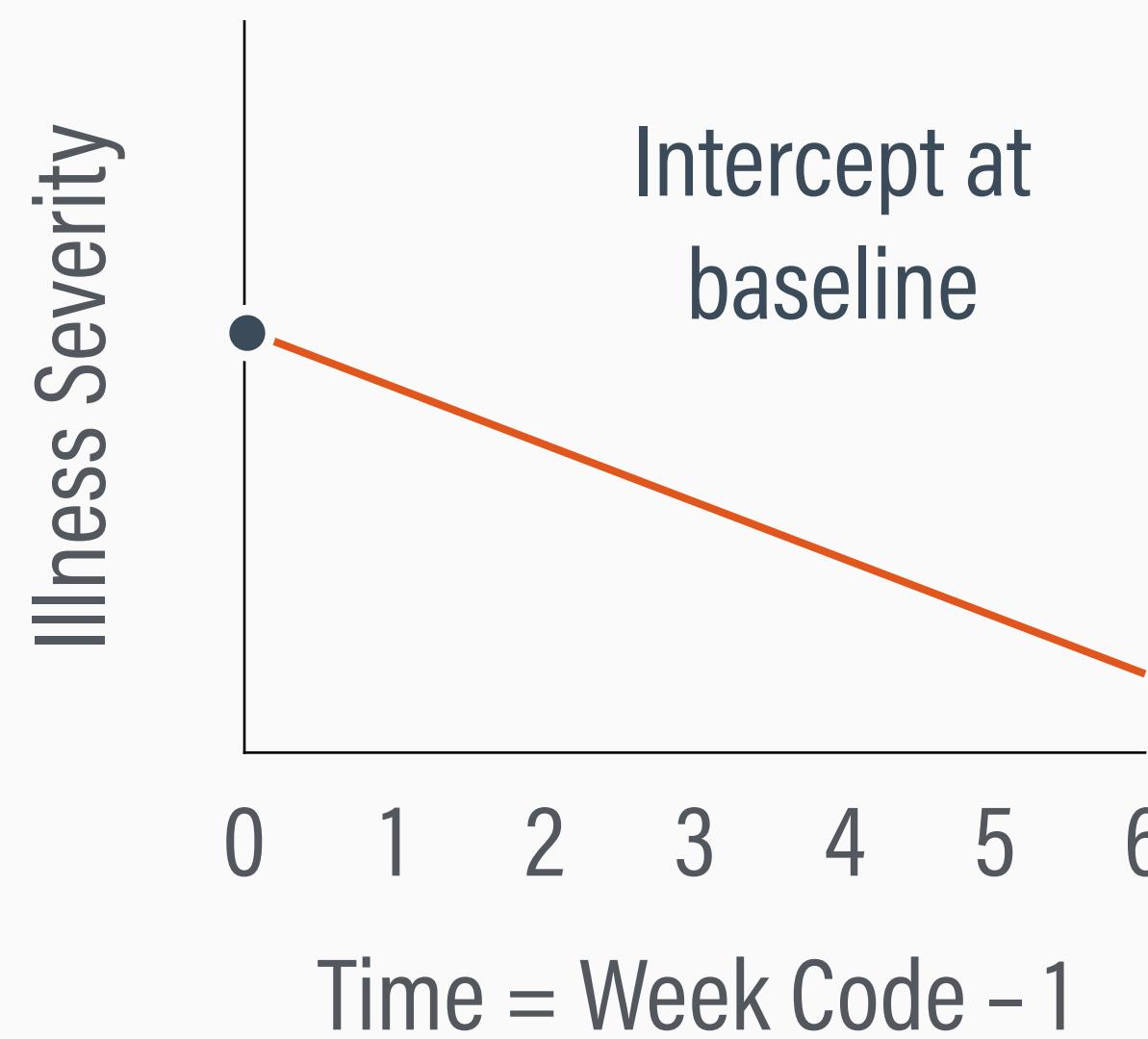
TIME SCORES

- The temporal predictor (*continuous time* in weeks) requires a meaningful zero point in order to define the intercept
- Substantive concerns dictate centering (e.g., assign 0 to an occasion where you will predict between-person differences)



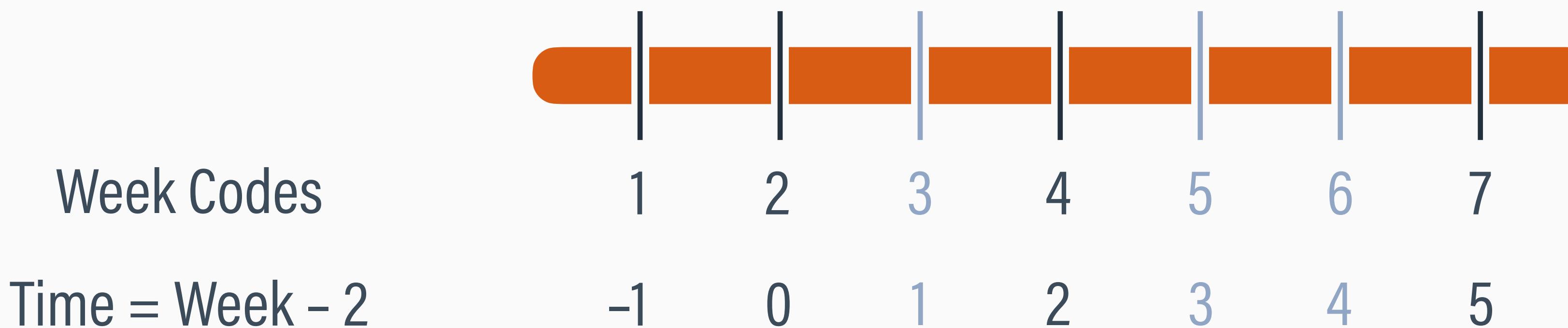
CENTERING AFFECTS THE INTERCEPT

- Centering the week codes changes the definition of the intercept, but model fit and the linear slope are unaffected

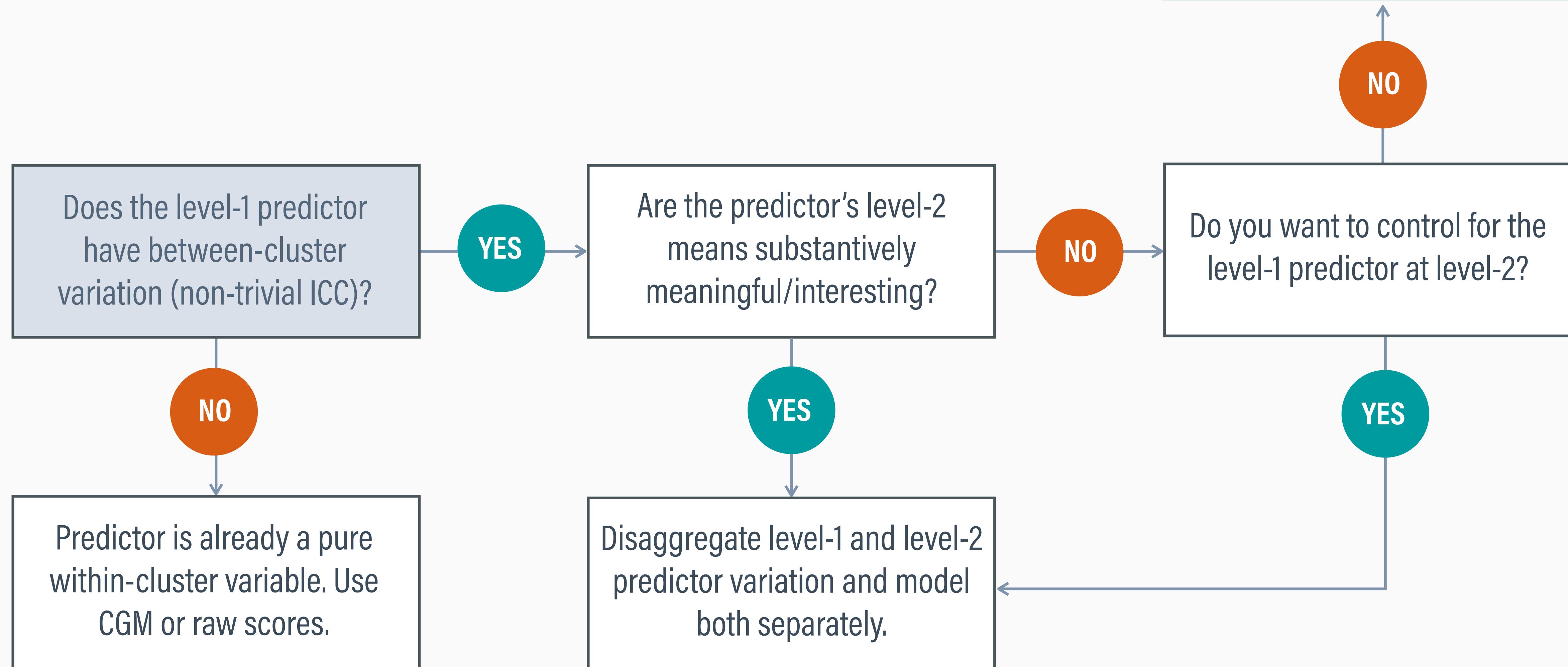


CENTERING FOR THIS EXAMPLE

- Centering the time codes at the second occasion defines the intercept as illness severity at the first follow-up
- Evaluating treatment-related differences at the first follow-up is common in randomized trials



DISAGGREGATION DECISION TREE



TIME SCORE ICC

- Time scores usually have no between-person variation ($ICC = 0$) because their values are similar (or identical) across all people
- No need to disaggregate and use person-specific time averages as a level-2 predictor

Does the level-1 predictor have between-cluster variation (non-trivial ICC)?

NO

Predictor is already a pure within-cluster variable. Use any centering or raw scores.

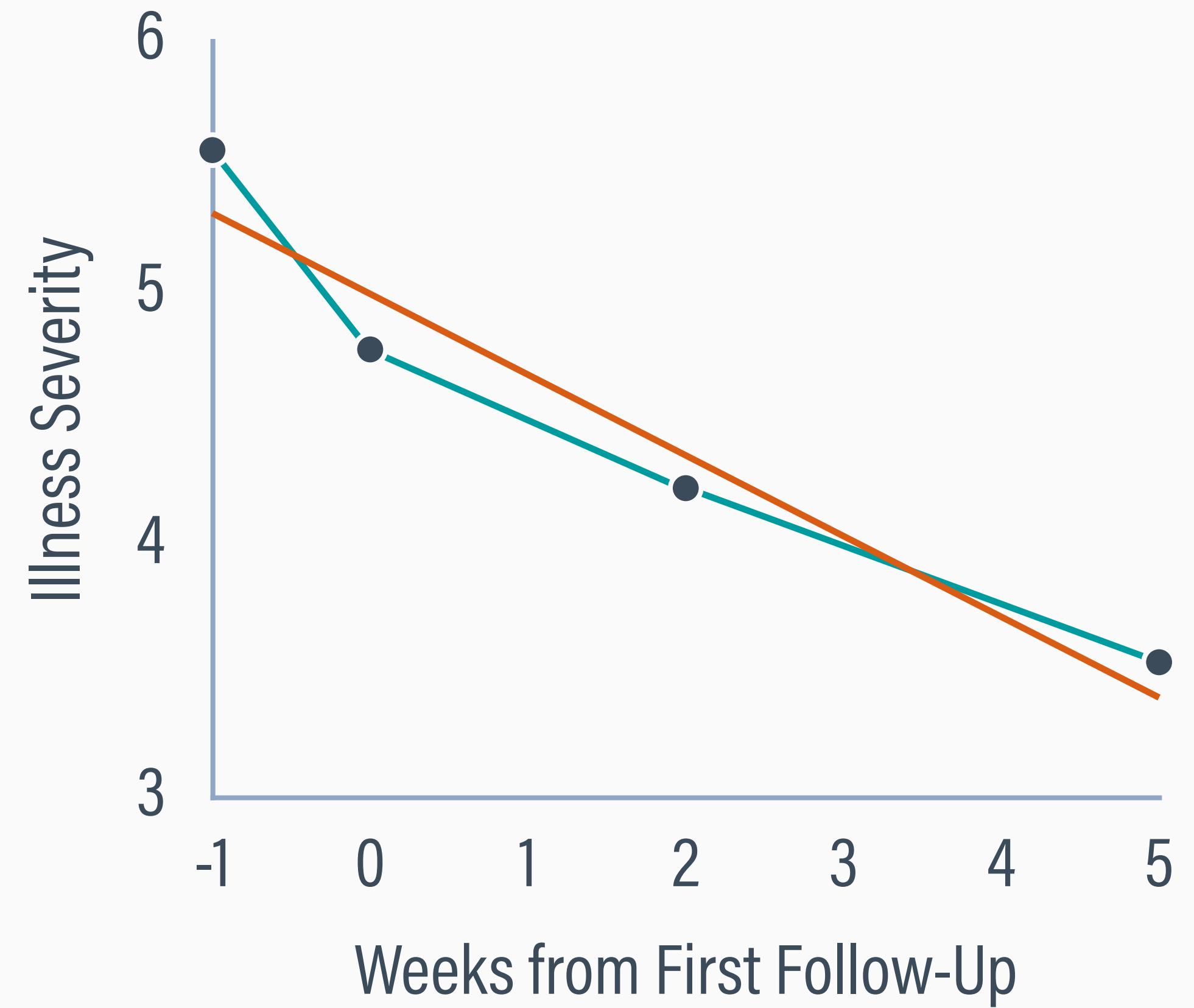
Continuous time scores

OUTLINE

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LINEAR GROWTH MODEL

- Linear growth is often a good starting point
- The amount of change is constant across each time increment
- Nonlinear trends can be added as needed and evaluated against the linear change model



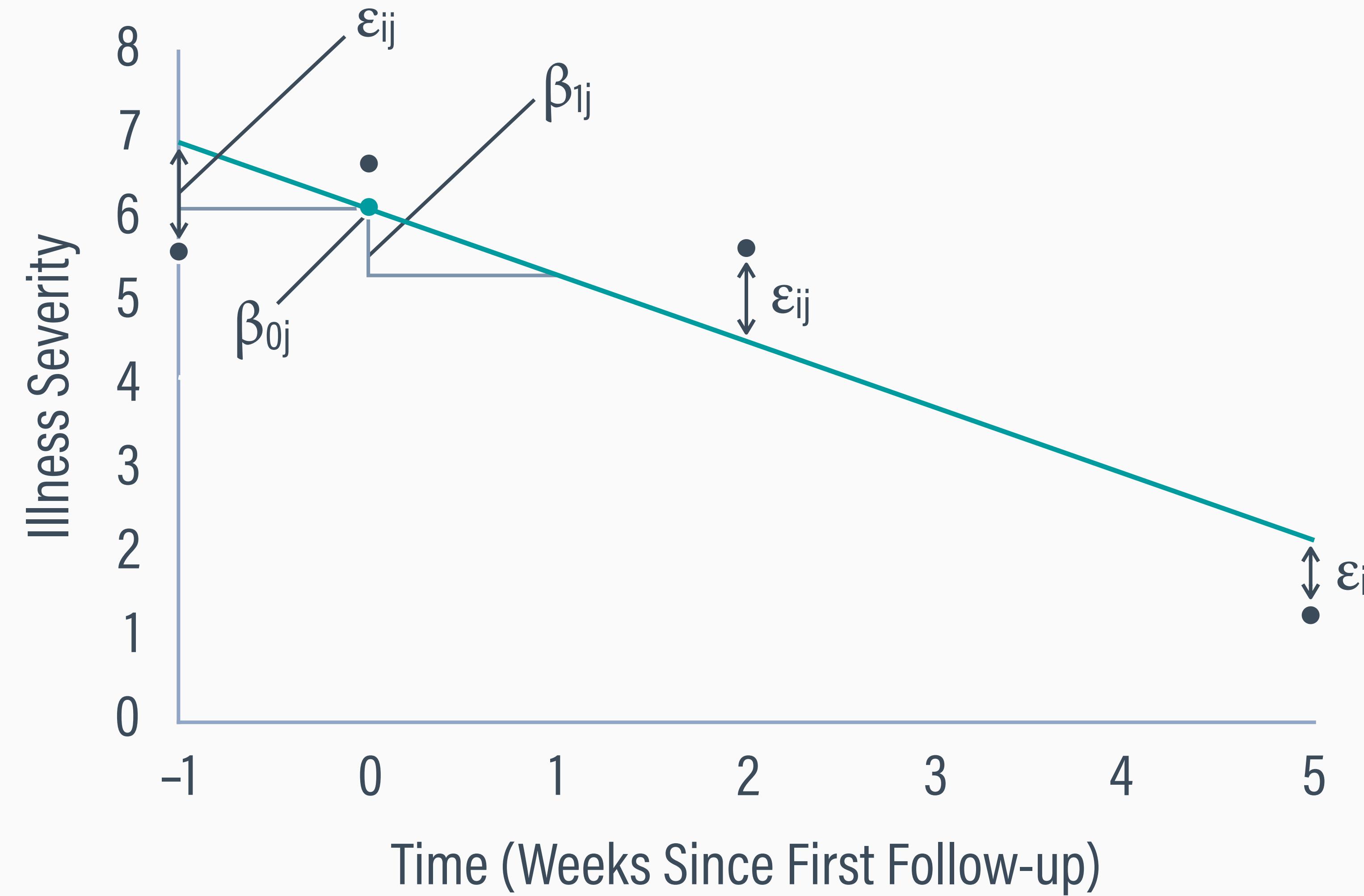
WITHIN-PERSON (LEVEL-1) MODEL

- The severity rating at occasion i for person j is the sum of one's predicted severity at follow-up (β_{0j}), a person-specific weekly change rate (β_{1j}), and a time-specific residual (ε_{ij})

$$\text{severity}_{ij} = \beta_{0j} + \beta_{1j}(\text{time}_{ij}) + \varepsilon_{ij}$$

- Within-person residuals are normal with constant variation across all occasions (level-1) and persons (level-2)

PERSON-SPECIFIC GROWTH TRAJECTORY



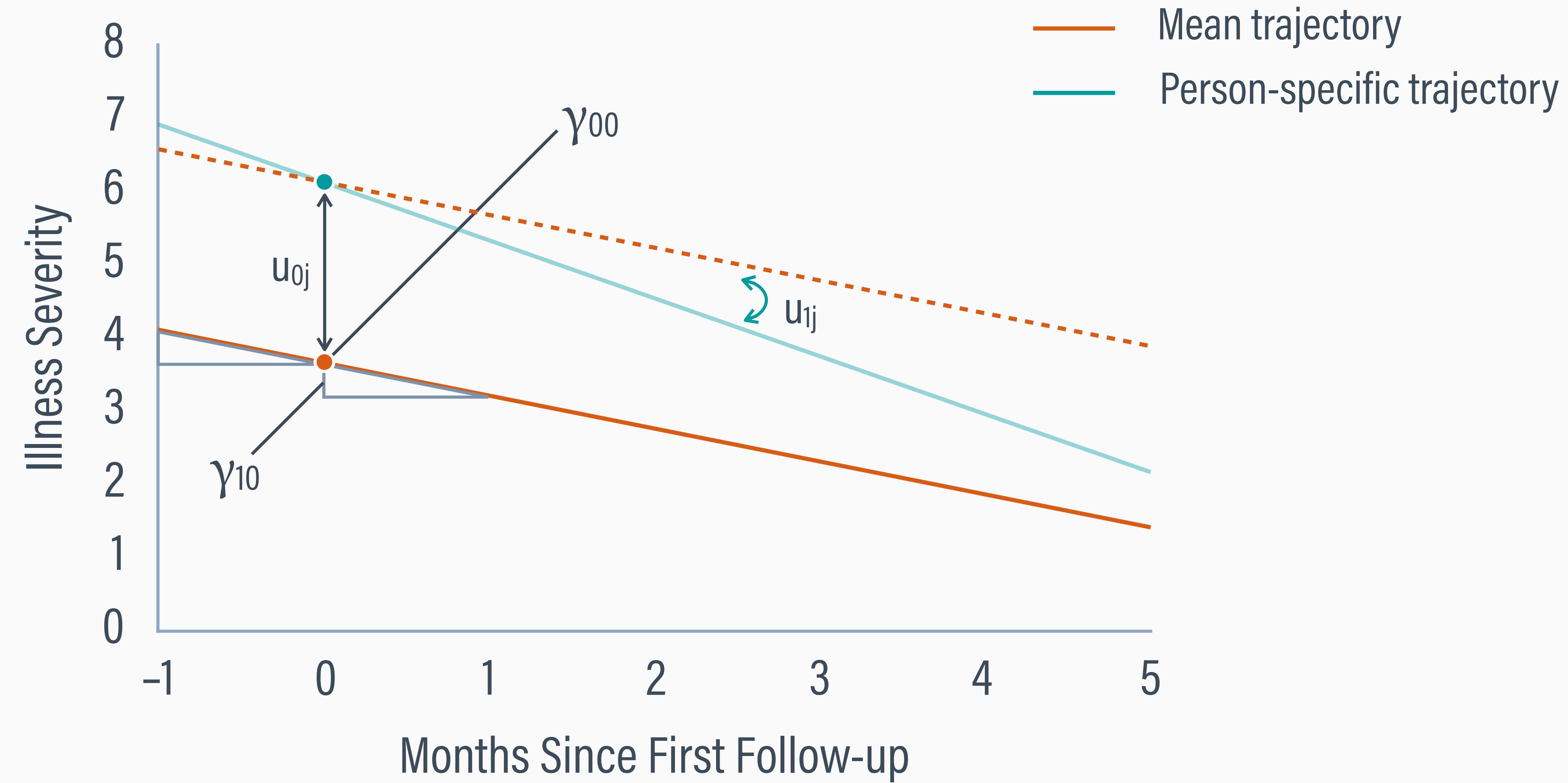
BETWEEN-PERSON (LEVEL-2) MODEL

- Person-specific predicted severity at follow-up and weekly change rates (β_{0j} and β_{1j}) are the sum of grand means (γ_{00} and γ_{10}) and person-level residuals (u_{0j} and u_{1j})

$$\begin{aligned}\beta_{0j} &= \gamma_{00} + u_{0j} \\ \beta_{1j} &= \gamma_{10} + u_{1j}\end{aligned}\quad \begin{pmatrix} u_{0j} \\ u_{1j} \end{pmatrix} \sim N(0, \Sigma_u) \quad \Sigma_u = \begin{pmatrix} \sigma_{u0}^2 & \sigma_{u0u1} \\ \sigma_{u1u0} & \sigma_{u1}^2 \end{pmatrix}$$

- Random intercept and slope residuals are bivariate normal and correlated (their covariance matrix is “unstructured”)

MEAN TRAJECTORY



COMBINED-MODEL EQUATION

Substituting the right sides
of the level-2 equations ...

$$\beta_{0j} = \gamma_{00} + u_{0j}$$
$$\beta_{1j} = \gamma_{10} + u_{1j}$$

into their coefficients
from the level-1 equation

$$\text{severity}_{ij} = \beta_{0j} + \beta_{1j}(\text{time}_{ij}) + \varepsilon_{ij}$$

gives the combined-model regression equation (Raudenbush & Bryk, 2002)

$$\text{severity}_{ij} = \gamma_{00} + u_{0j} + (\gamma_{10} + u_{1j})(\text{time}_{ij}) + \varepsilon_{ij}$$

COMMON NOTATIONAL SYSTEMS

Combined-model equation (Raudenbush & Bryk, 2002)

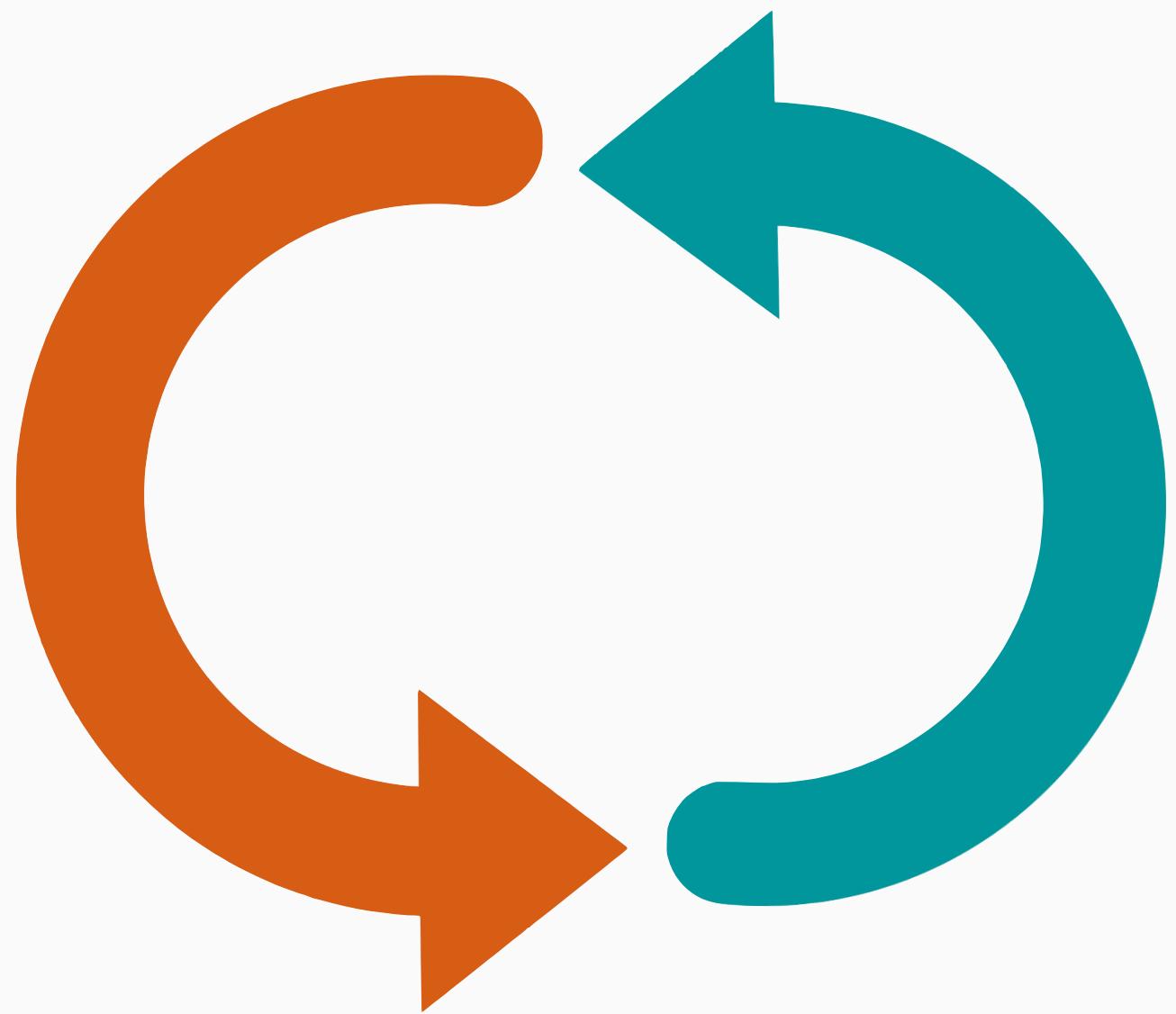
$$\text{severity}_{ij} = \gamma_{00} + \gamma_{10}(\text{time}_{ij}) + u_{0j} + (u_{1j})(\text{time}_{ij}) + \varepsilon_{ij}$$

Standard(ish) regression notation (Scott, Shrout, & Weinberg, 2013)

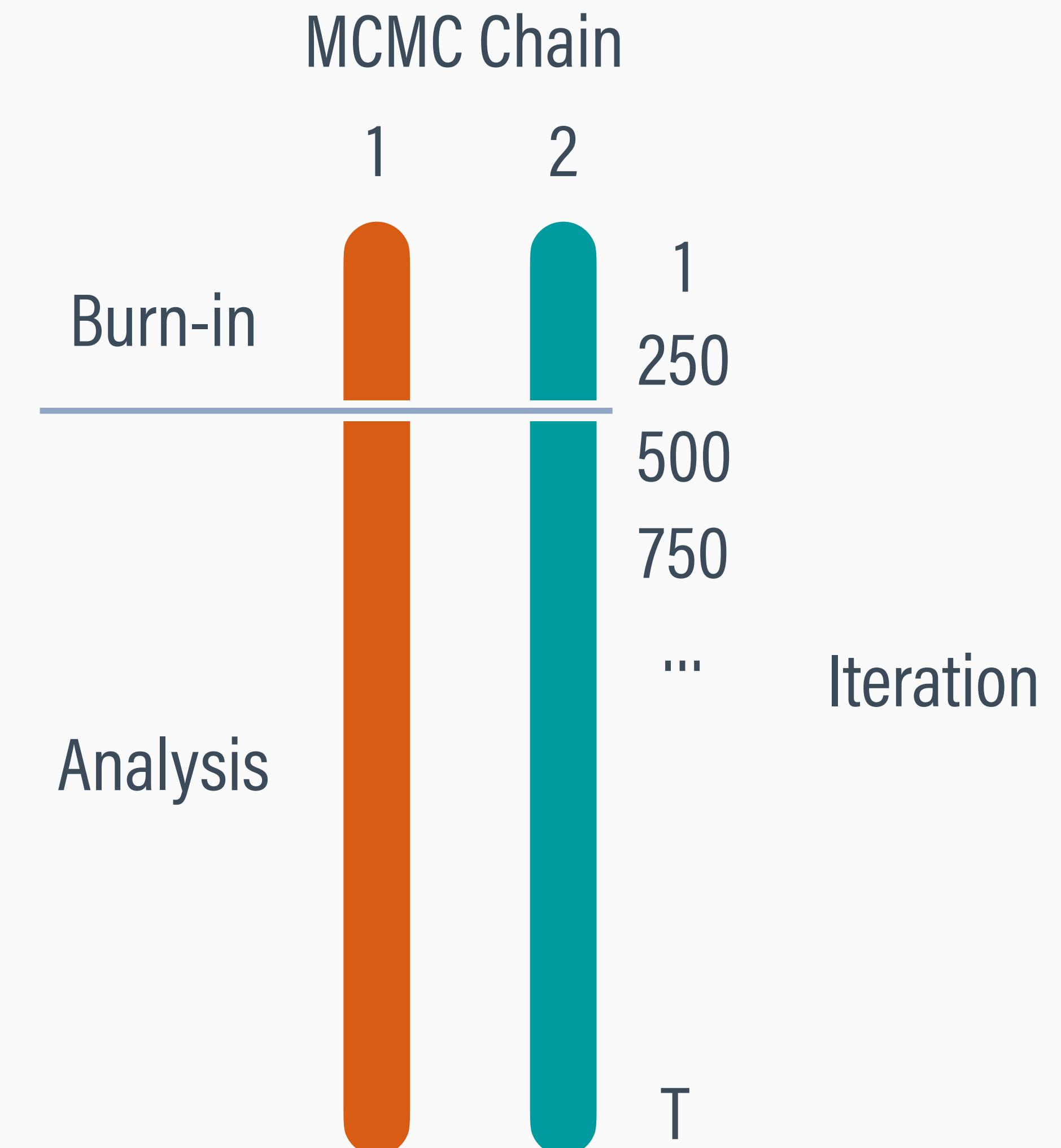
$$\text{severity}_{ij} = \beta_0 + \beta_1(\text{time}_{ij}) + u_{0j} + (u_{1j})(\text{time}_{ij}) + \varepsilon_{ij}$$

MCMC ALGORITHM

Estimate multilevel model

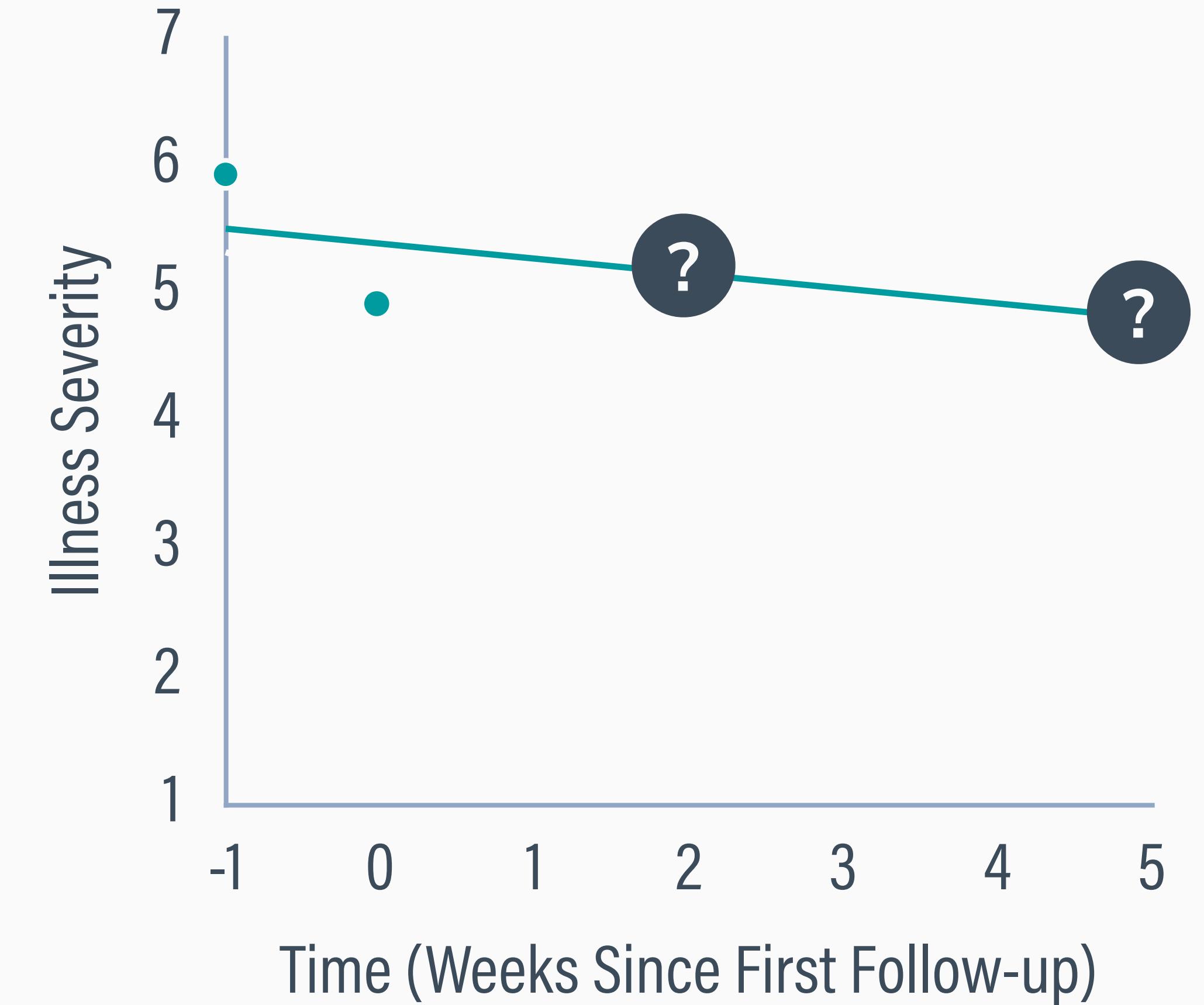


Impute missing values



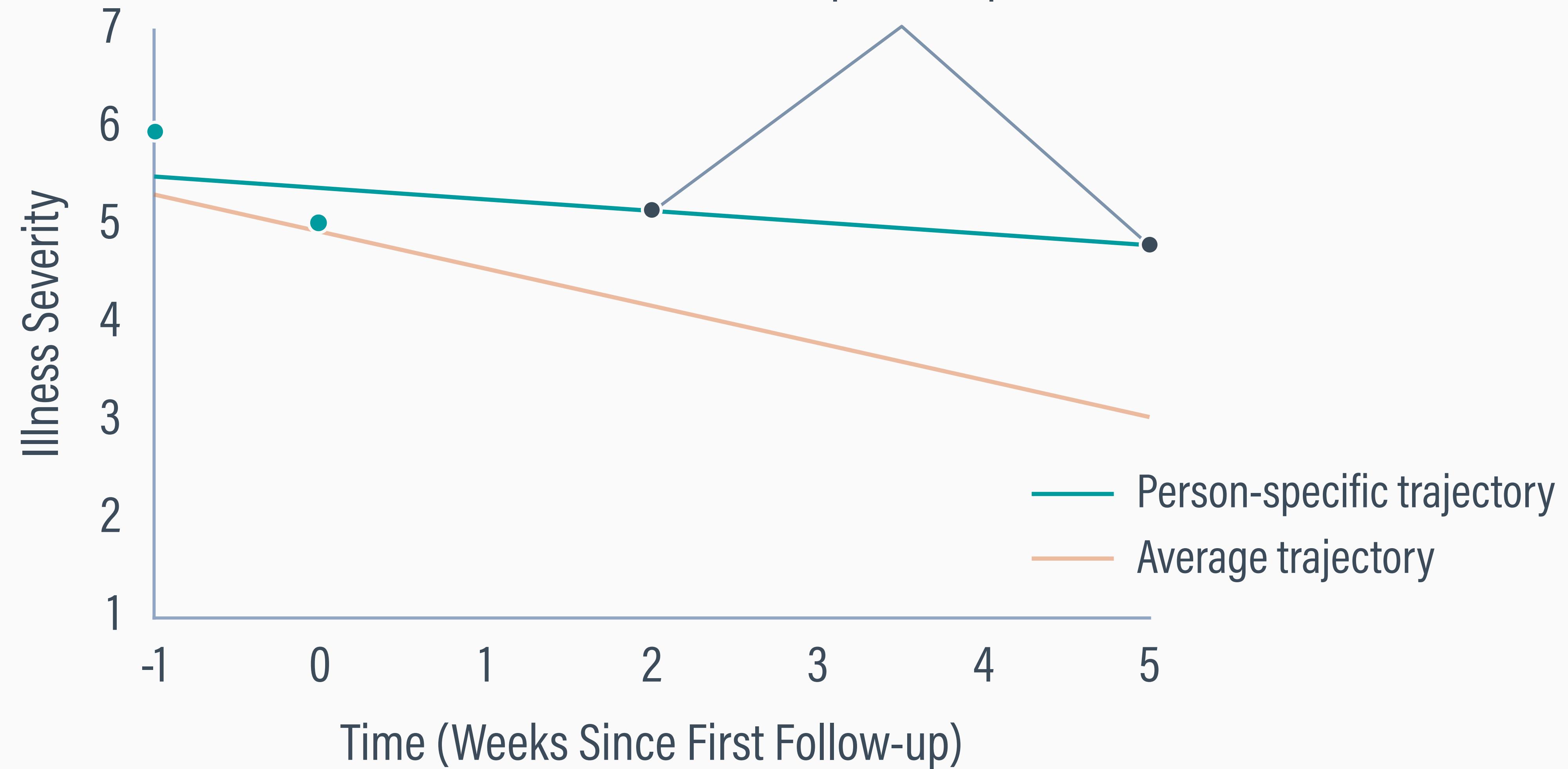
MISSING DATA IMPUTATION

- A participant provides baseline and one-week follow-up scores then drops out
- Missing scores are imputed by sampling from a distribution of plausible values



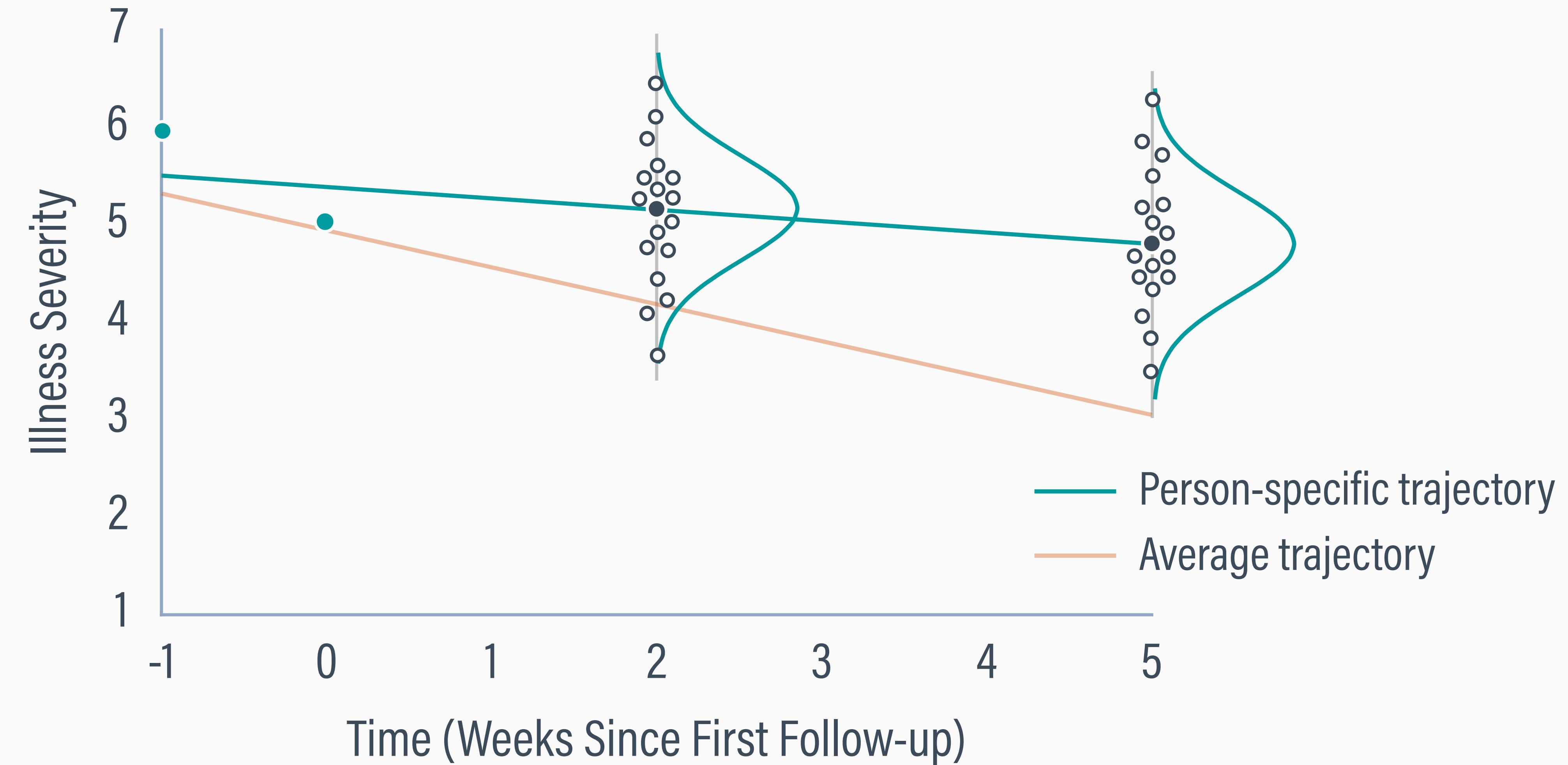
PREDICTED VALUES

Predicted missing scores fall
on person-specific curves

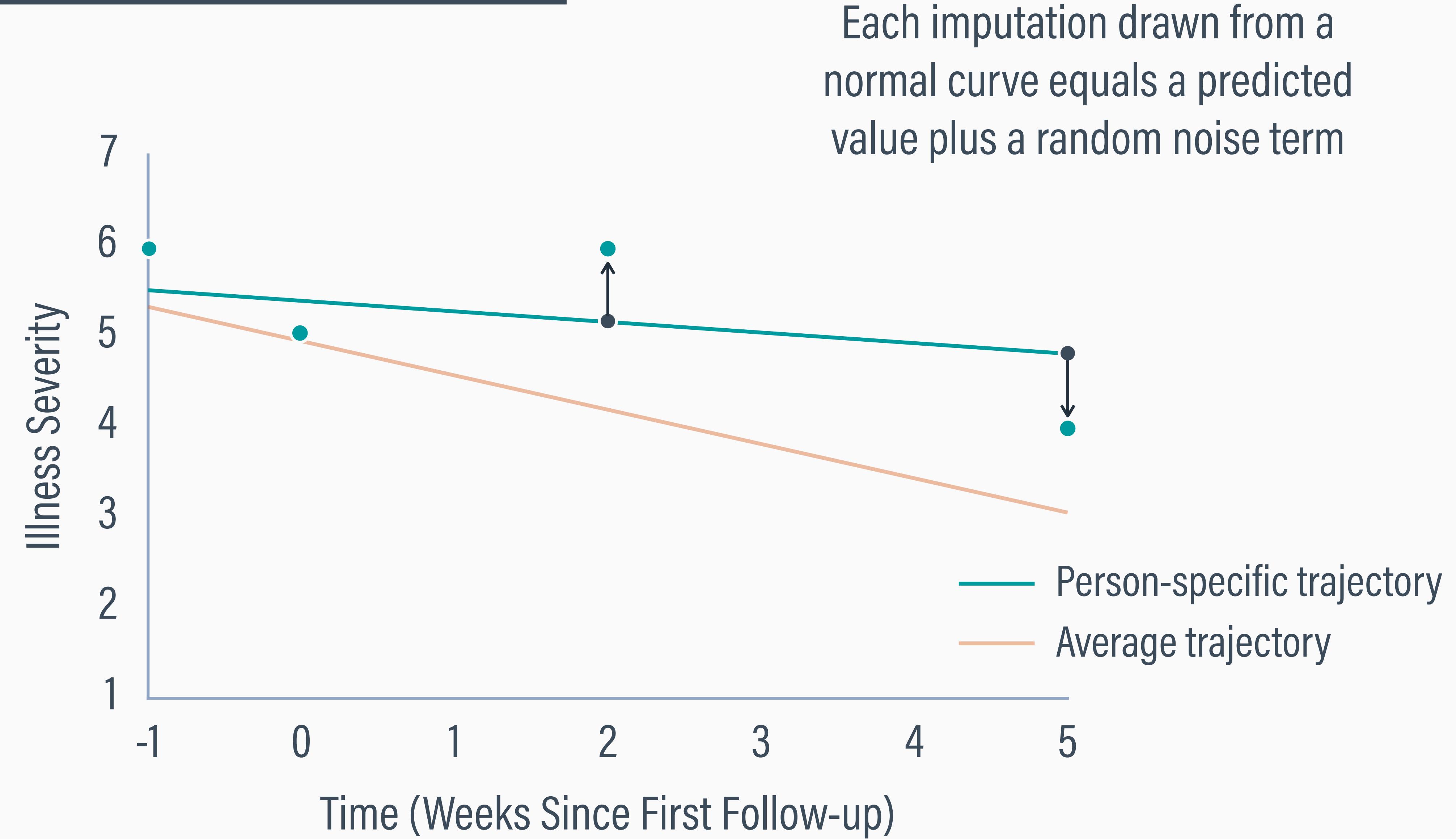


DISTRIBUTIONS OF IMPUTATIONS

Plausible replacement scores are normal around predicted values (within-person variation determines spread)



IMPUTATION = PREDICTION + NOISE



BLIMP SCRIPT 7.2

DATA: SchizophreniaTrial.dat;

VARIABLES: person week drug male severity;

CLUSTERID: person;

MISSING: 999;

TRANSFORM: time = week - 2; # compute temporal predictor

MODEL:

severity ~ intercept time | intercept time;

BURN: 10000;

ITERATIONS: 20000;

SEED: 90291;

RBLIMP SCRIPT 7 (MODEL 2)

```
model2 <- rblimp(  
  data = ClinicalTrial,  
  clusterid = 'Person',  
  transform = 'Time = Week - 2',  
  model = 'Severity ~ intercept Time | intercept Time',  
  seed = 90291,  
  burn = 10000,  
  iter = 20000)  
  
output(model2)  
posterior_plot(model2, 'Severity')
```

PSR DIAGNOSTIC OUTPUT

Quality control check: PSR diagnostics all < 1.05 well before the end of the burn-in period

BURN-IN POTENTIAL SCALE REDUCTION (PSR) OUTPUT:

NOTE: Split chain PSR is being used. This splits each chain's iterations to create twice as many chains.

Comparing iterations across 2 chains	Highest PSR	Parameter #
251 to 500	1.056	10
501 to 1000	1.032	6
751 to 1500	1.040	10
1001 to 2000	1.016	10
...
2501 to 5000	1.004	11
2751 to 5500	1.002	11
3001 to 6000	1.004	10
3251 to 6500	1.007	5
3501 to 7000	1.005	11
3751 to 7500	1.003	2
4001 to 8000	1.002	3
4251 to 8500	1.002	11
4501 to 9000	1.005	3
4751 to 9500	1.005	11
5001 to 10000	1.004	2

EFFECTIVE SAMPLE SIZE DIAGNOSTIC

Quality control check: Number of effective MCMC samples diagnostics all > 100

Outcome Variable: Severity

Parameters	Estimate	StdDev	2.5%	97.5%	ChiSq	PValue	N_Eff
<hr/>							
Variances:							
L2 : Var(Intercept)	0.556	0.058	0.451	0.679	---	---	2586.940
L2 : Cov(Time, Intercept)	0.076	0.013	0.051	0.101	---	---	2184.196
L2 : Var(Time)	0.046	0.006	0.035	0.058	---	---	2066.432
Residual Var.	0.760	0.036	0.693	0.835	---	---	2985.422
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Coefficients:							
Intercept	5.002	0.043	4.918	5.087	13382.537	0.000	2339.636
Time	-0.314	0.014	-0.341	-0.287	524.047	0.000	3386.166
<hr/>							
Standardized Coefficients:							
Time	-0.464	0.018	-0.498	-0.427	655.463	0.000	4037.432
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Proportion Variance Explained							
by Coefficients	0.215	0.017	0.182	0.248	---	---	4039.518
by Level-2 Random Intercepts	0.368	0.021	0.328	0.410	---	---	6365.108
by Level-2 Random Slopes	0.100	0.012	0.078	0.123	---	---	1876.288
by Level-1 Residual Variation	0.316	0.018	0.282	0.352	---	---	2846.117

BLIMP OUTPUT

Outcome Variable: Severity

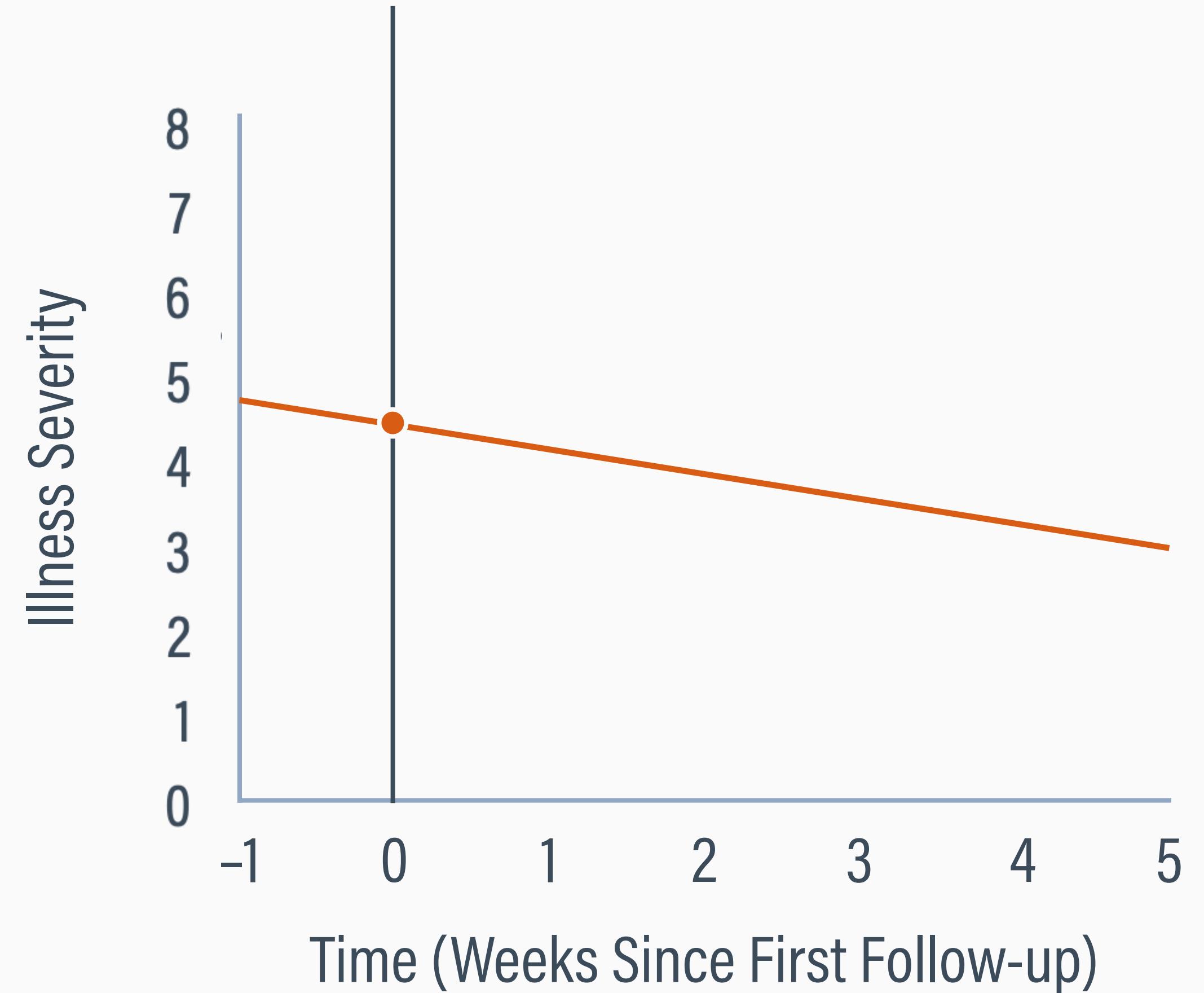
- █ = level-2 estimate
- █ = level-1 estimate
- █ = combined estimate

Parameters	Estimate	StdDev	2.5%	97.5%	ChiSq	PValue	N_Eff
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Variances:							
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MEAN GROWTH TRAJECTORY

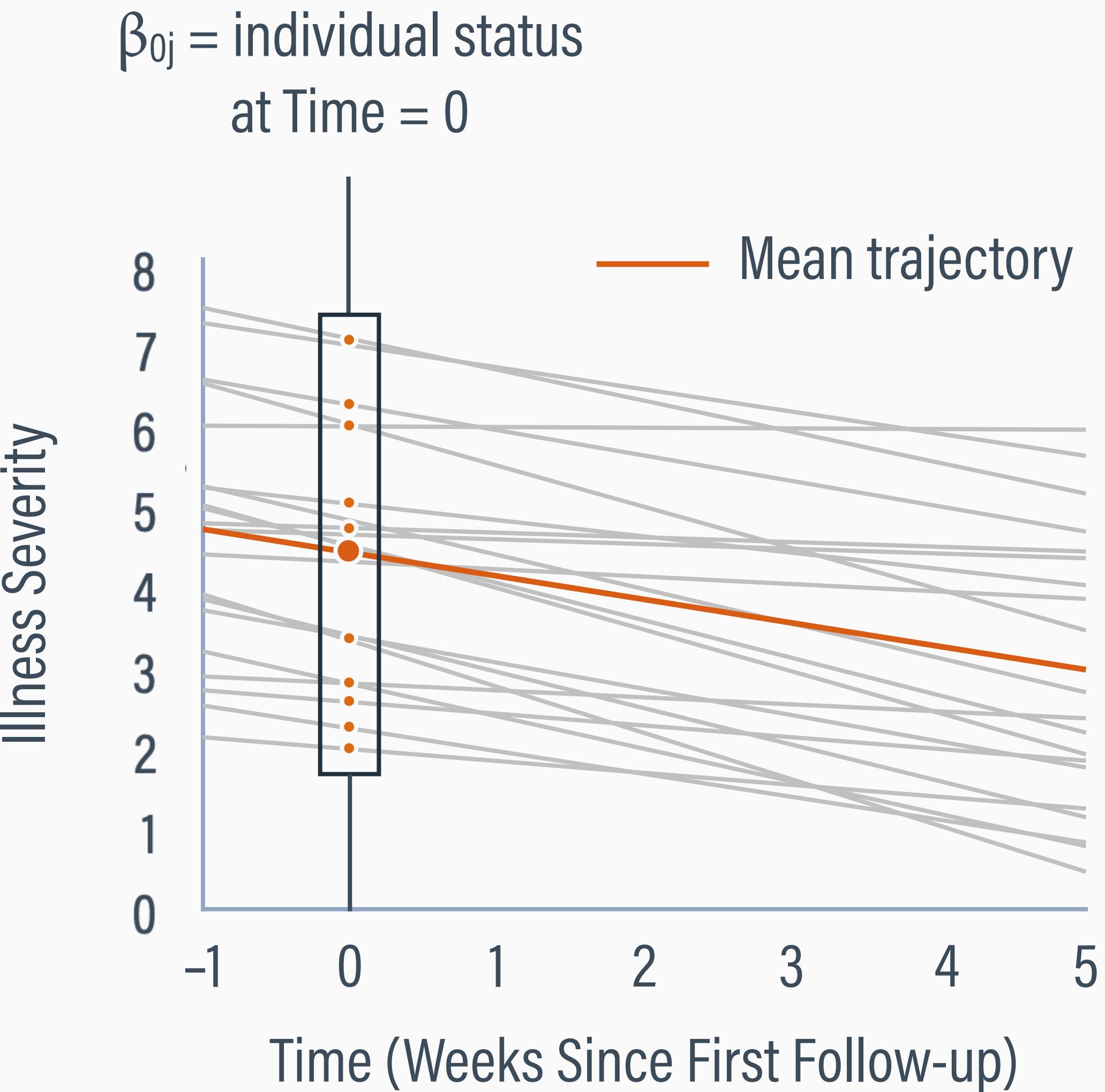
- The intercept ($\beta_0 = 5.00$) is the point on the mean growth trajectory at Time = 0
- $\beta_1 = -0.31$ is the average weekly change rate across all persons
- A linear trend implies that mean change is constant across adjacent weeks

$$\text{severity}_{ij} = \beta_0 + \beta_1(\text{time}_{ij}) + u_{0j} + (u_{1j})(\text{time}_{ij}) + \varepsilon_{ij}$$



SPAGHETTI PLOT

- Random intercept variance ($\sigma_{u0}^2 = 0.56$) quantifies the elevation of the regression lines (person differences) at Time = 0
- Random slope variance ($\sigma_{u1}^2 = 0.05$) quantifies degree to which person-specific growth trajectories deviate from parallel





The covariance between the intercepts and slopes is 0.076, which translates into a correlation of $0.076 \div \sqrt{(0.556 \times 0.046)} = 0.48$. Provide an interpretation of this effect. How does one's status at the first follow-up relate to their change rate?

INTERPRETATIONS

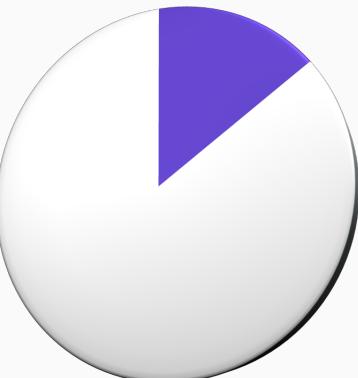
Parameter	Est.	Interpretation
Fixed intercept	5.00	Predicted severity score at the first follow-up
Time (within-person)	-0.31	Expected severity change for every additional week in the study
Between-cluster intercept variance (variance of u_{0j} residuals)	0.56	Average squared distance between a person's predicted severity score and the grand mean at the first follow-up
Between-cluster slope variance (variance of u_{1j} residuals)	0.05	Average squared distance between a person's slope (change rate) and the average slope
Intercept-slope covariance (covariance of u_{0j} and u_{1j} residuals)	0.08	Positive association ($r = .48$) where people with higher intercepts (higher severity at Time = 0) also tend to have higher (more positive or flatter) change rates
Within-cluster residual variance (variance of ε_{ij} residuals)	0.76	Average squared distance between a person's predicted and observed severity score

VARIANCE EXPLAINED MEASURES

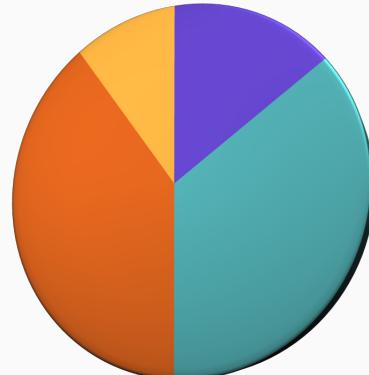
Fixed effects
of predictors

$$R^2_{\text{predictors}} = \frac{\beta^T \Sigma_X \beta}{\sigma_Y^2}$$

Explained ÷ Total



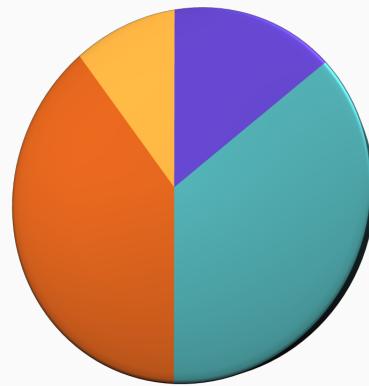
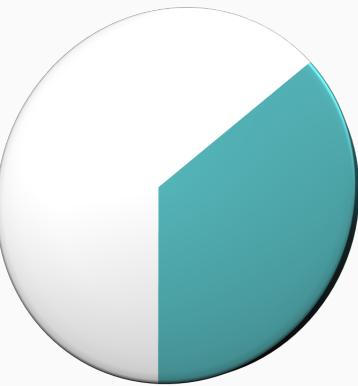
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Level-2 random
intercept residuals

$$R^2_{\text{slopes}} = \frac{\text{tr}(\Sigma_u \Sigma_x)}{\sigma_Y^2}$$

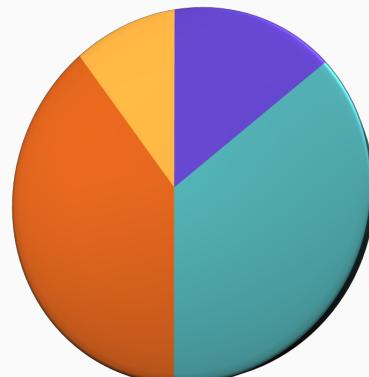
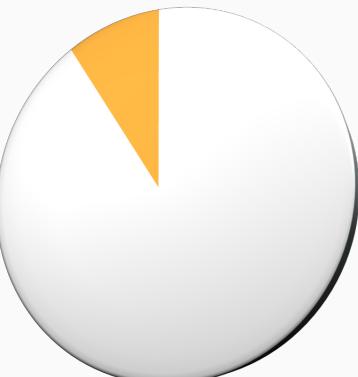
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Level-2 random
slope residuals

$$R^2_{\text{intercepts}} = \frac{\sigma_u^2}{\sigma_Y^2}$$

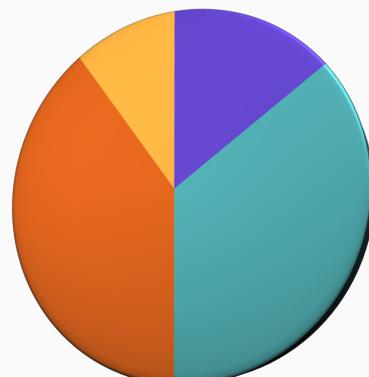
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Level-1 within-
cluster residuals

$$R^2_{\text{residual(within)}} = \frac{\sigma_\varepsilon^2}{\sigma_Y^2}$$

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R² EFFECT SIZE MEASURES

Outcome Variable: Severity

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INTERPRETATIONS

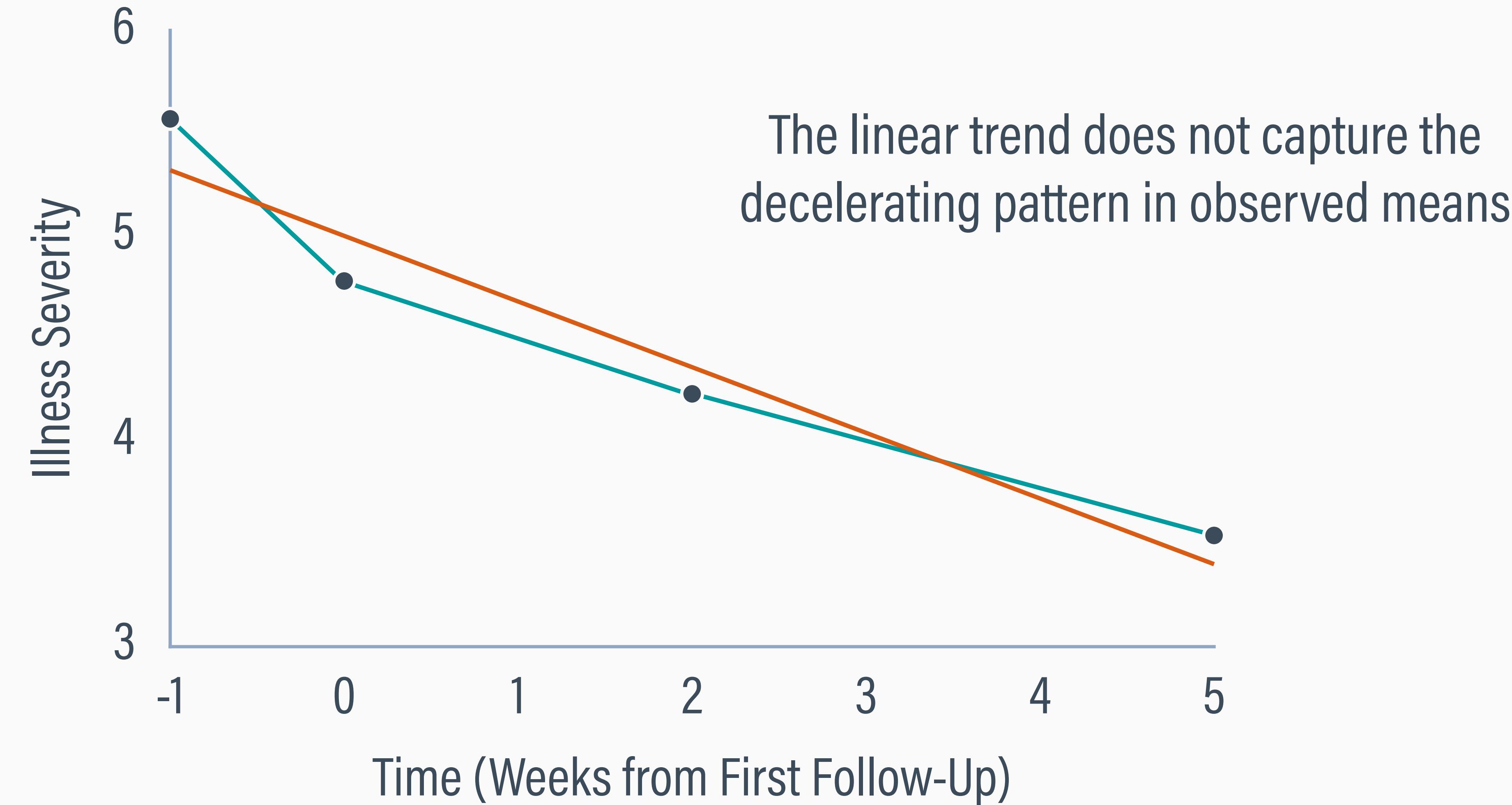
- Effect sizes for the level-1 and level-2 residuals are not explained variance, per se, but rather proportions that convey the size of the residual variation

R ² Effect Size	Est.	Interpretation
Predictors	.22	The level-1 predictor (Time) explains 22% of the total variation in severity
Between-cluster intercept variance (variance of u_{0j} residuals)	.37	Between-person variation in the level-2 residuals (variance of predicted scores at first follow-up) accounts for 37% of the total variation
Between-cluster slope variance (variance of u_{1j} residuals)	.10	Between-person variation in the random slope residuals (variance of the individual change rates) accounts for 10% of the total variation
Within-cluster variance (variance of ε_{ij} residuals)	.32	Within-person variation in the level-1 residuals (variance of scores around person-specific trajectories) accounts for 32% of the total variation

OUTLINE

- 1 Examine Sample Means
- 2 Define Temporal Predictor (Time Variable)
- 3 Linear Growth Model
- 4 Model Nonlinear Change
- 5 Add Predictors of Change

OBSERVED VS. PREDICTED MEANS



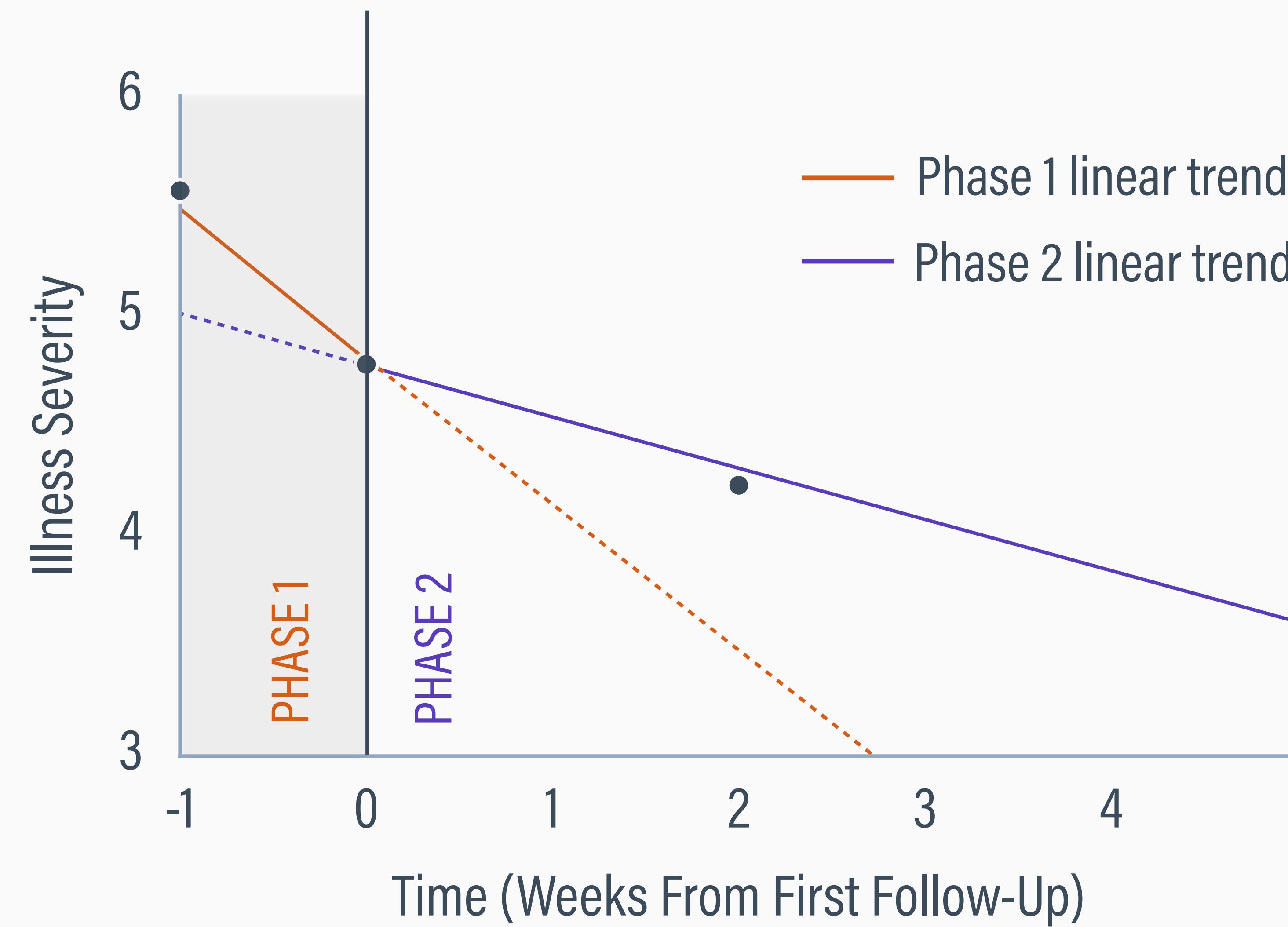
NONLINEAR MODELING OPTIONS

- Transform the time metric (e.g., square root of Time)
- Piecewise growth model (multiple epochs of linear trends)
- Polynomial growth trajectories

PIECEWISE GROWTH MODEL

- A piecewise model divides the study period into multiple epochs or phases (may or may not be a data-driven division)
- The within-person model introduces two time variables, the slopes for which capture linear change rates
- Simple to interpret, but time division may be arbitrary

PIECEWISE MODEL GRAPHIC



QUADRATIC WITHIN-PERSON MODEL

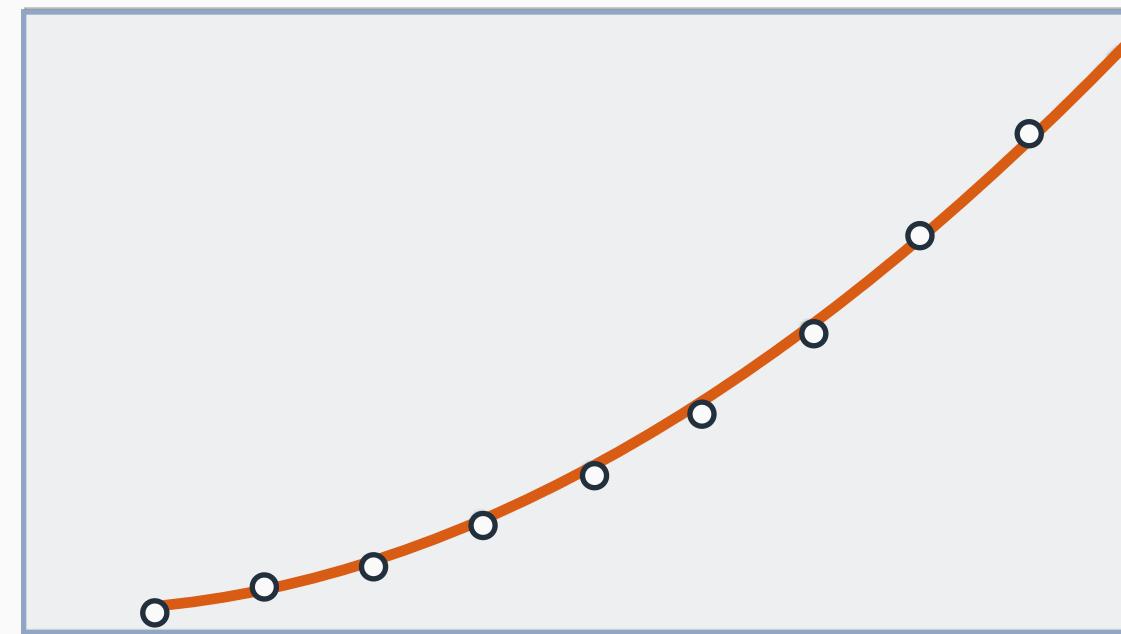
- The linear slope β_{1j} is now the conditional weekly change rate at Time = 0, and β_{2j} represents curvature

$$\text{severity}_{ij} = \beta_{0j} + \beta_{1j}(\text{time}_{ij}) + \beta_{2j}(\text{time}_{ij}^2) + \varepsilon_{ij}$$

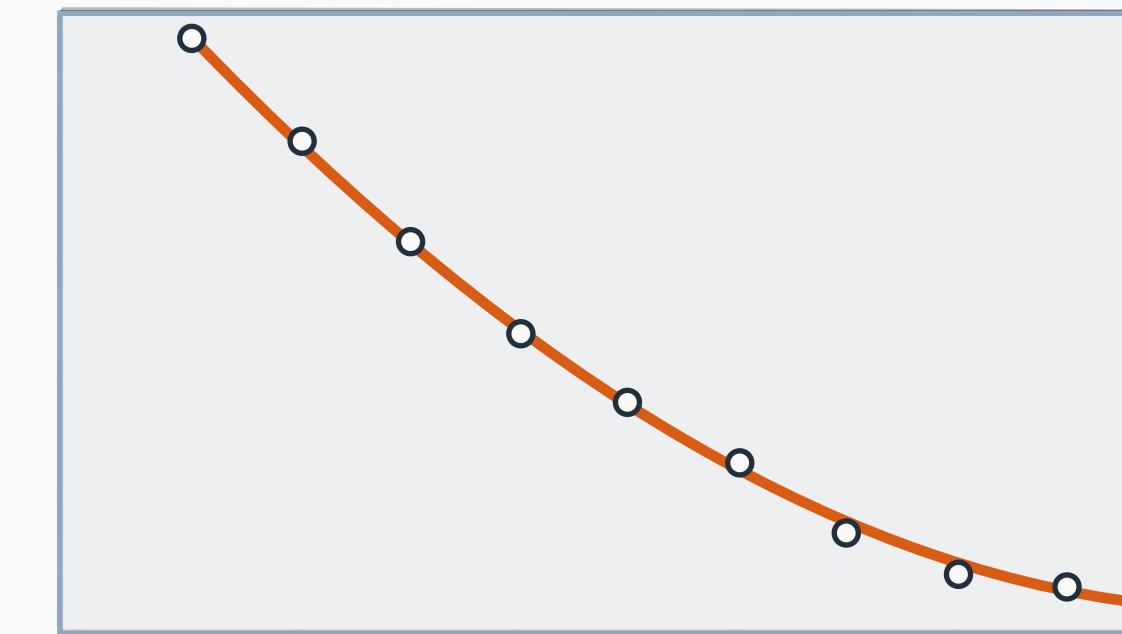
- Within-person residuals are normal with constant variation across all occasions (level-1) and persons (level-2)

POLYNOMIAL COMBINATIONS

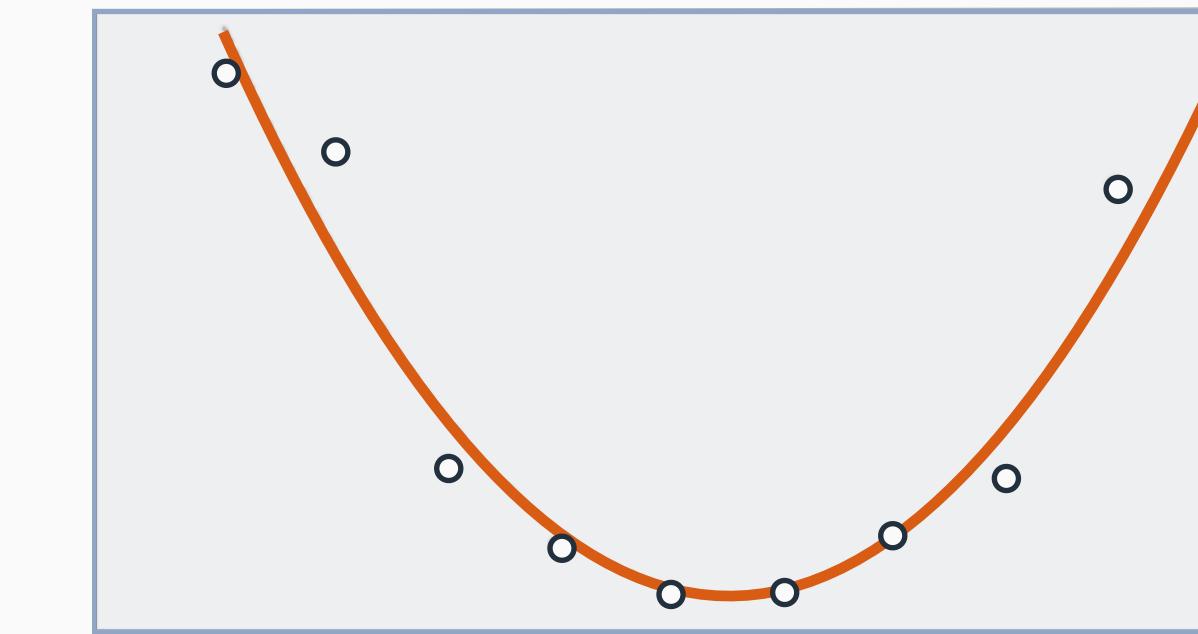
Linear +, Quadratic +



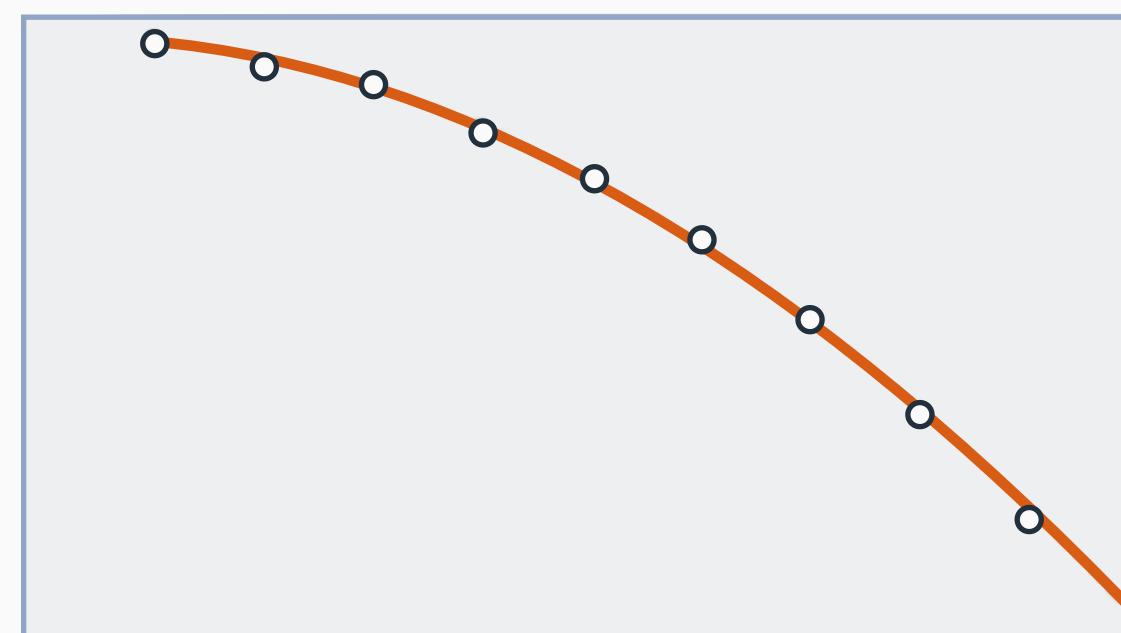
Linear -, Quadratic +



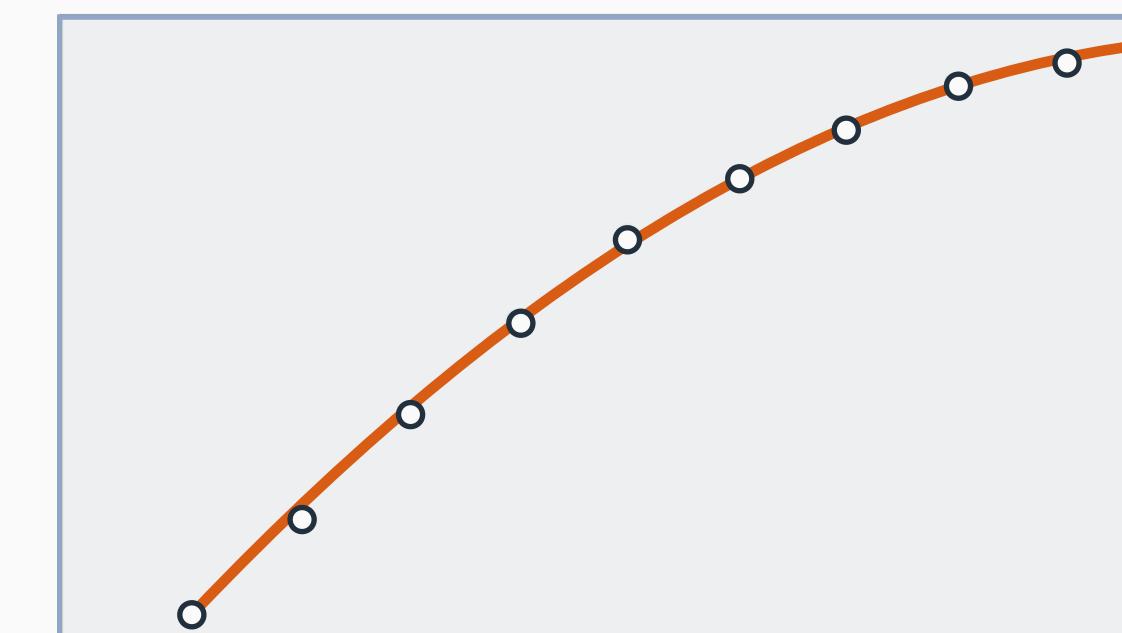
Linear 0, Quadratic +



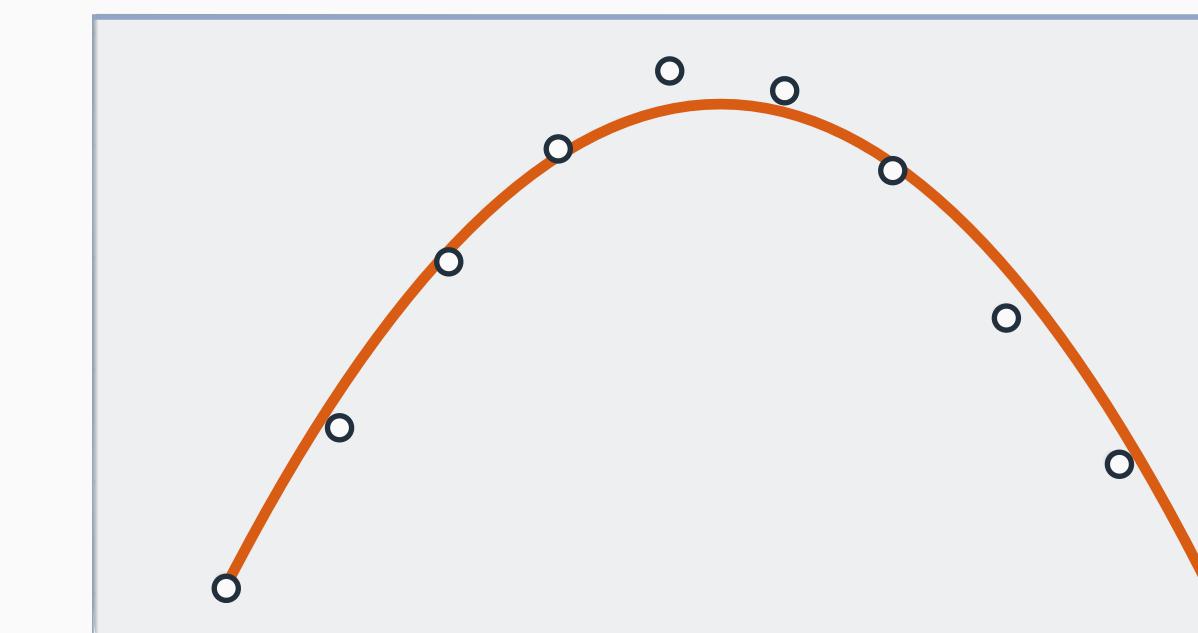
Linear -, Quadratic -



Linear +, Quadratic -



Linear 0, Quadratic -



BLIMP SCRIPT 7.3

DATA: SchizophreniaTrial.dat;

VARIABLES: person week drug male severity;

CLUSTERID: person;

MISSING: 999;

TRANSFORM: time = week - 2; # compute temporal predictor

MODEL:

severity ~ intercept time time^2 | intercept time; # average trajectory with curvature

BURN: 10000;

ITERATIONS: 20000;

SEED: 90291;

RBLIMP SCRIPT 7 (MODEL 3)

```
model3 <- rblimp(  
  data = ClinicalTrial,  
  clusterid = 'Person',  
  transform = 'Time = Week - 2',  
  model = 'Severity ~ intercept Time Time^2 | intercept Time',  
  seed = 90291,  
  burn = 10000,  
  iter = 20000)  
  
output(model3)  
posterior_plot(model3, 'Severity')
```

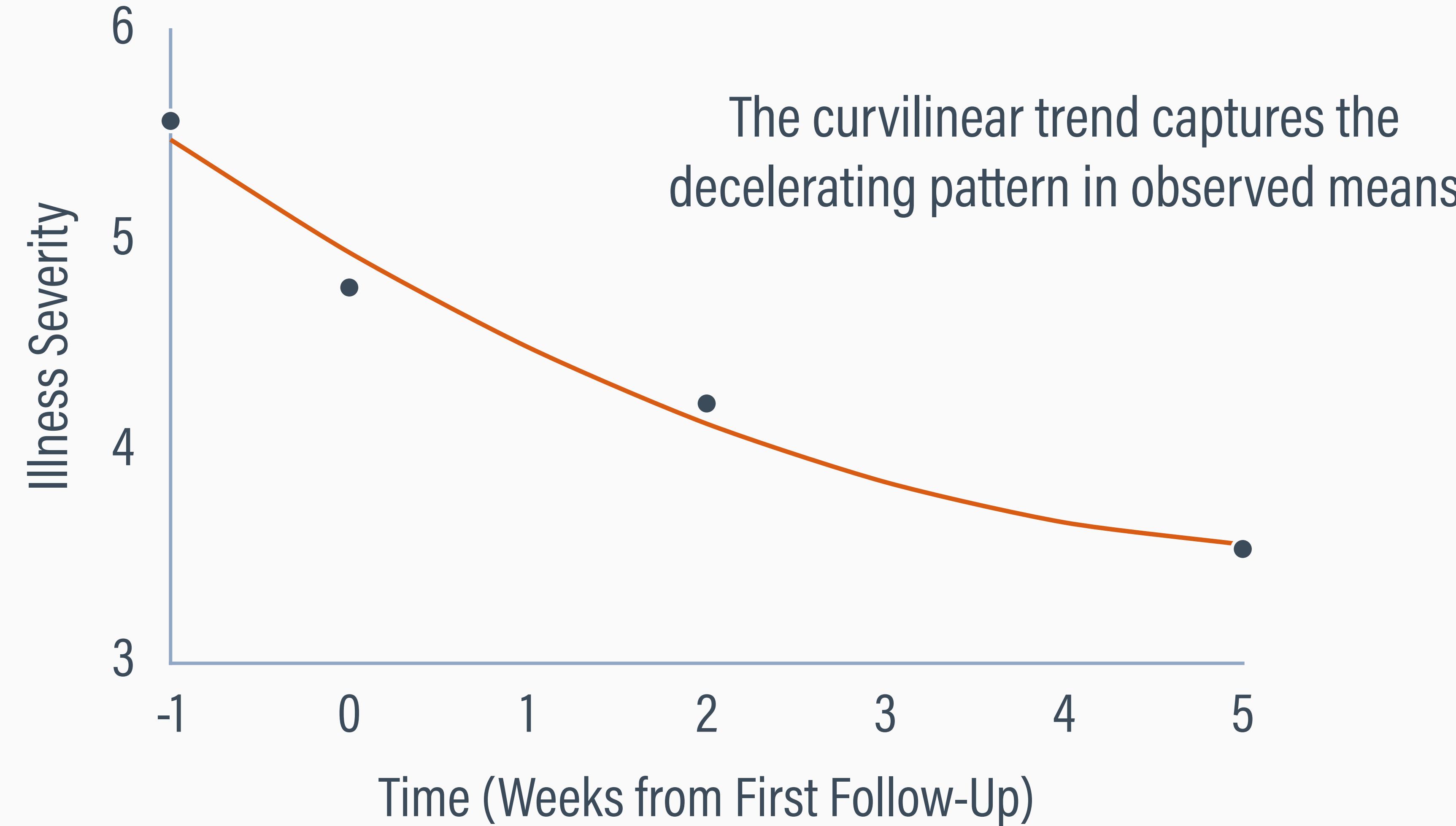
BLIMP OUTPUT

Outcome Variable: Severity

- █ = level-2 estimate
- █ = level-1 estimate
- █ = combined estimate

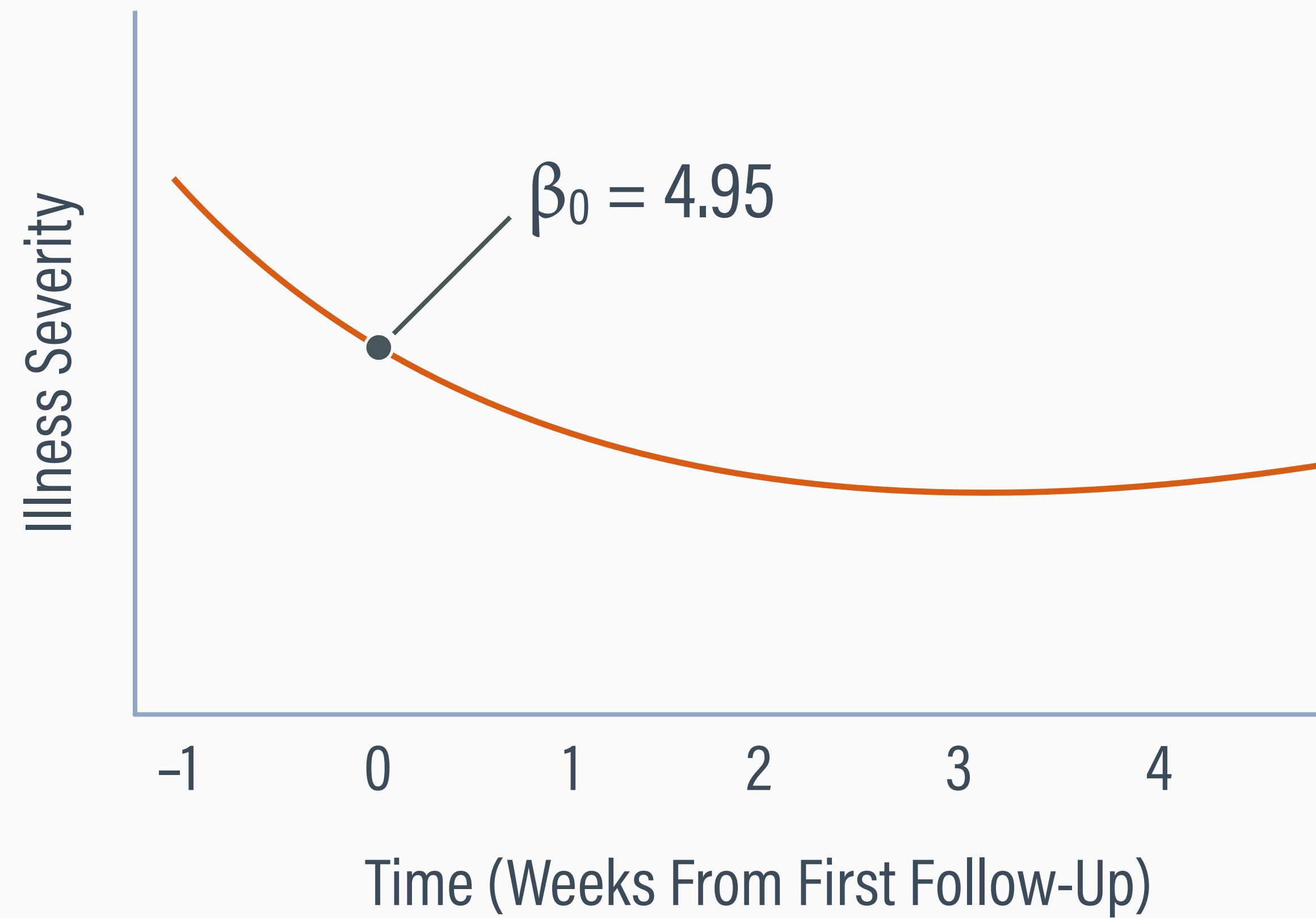
Parameters	Estimate	StdDev	2.5%	97.5%	ChiSq	PValue	N_Eff
<hr/>							
Variances:							
L2 : Var(Intercept)	0.576	0.058	0.472	0.699	---	---	3360.519
L2 : Cov(Time, Intercept)	0.071	0.013	0.047	0.097	---	---	2746.642
L2 : Var(Time)	0.048	0.006	0.037	0.060	---	---	1987.837
Residual Var.	0.709	0.034	0.646	0.779	---	---	3152.210
<hr/>							
Coefficients:							
Intercept	4.946	0.044	4.859	5.033	12442.763	0.000	2123.025
Time	-0.491	0.026	-0.542	-0.440	355.403	0.000	8622.227
Time^2	0.043	0.005	0.032	0.053	63.319	0.000	19556.373
<hr/>							
...							
<hr/>							
Proportion Variance Explained							
by Coefficients	0.226	0.017	0.194	0.259	---	---	3828.158
by Level-2 Random Intercepts	0.374	0.021	0.334	0.415	---	---	6180.673
by Level-2 Random Slopes	0.104	0.012	0.083	0.129	---	---	1952.582
by Level-1 Residual Variation	0.295	0.017	0.263	0.330	---	---	2759.832

OBSERVED VS. PREDICTED MEANS

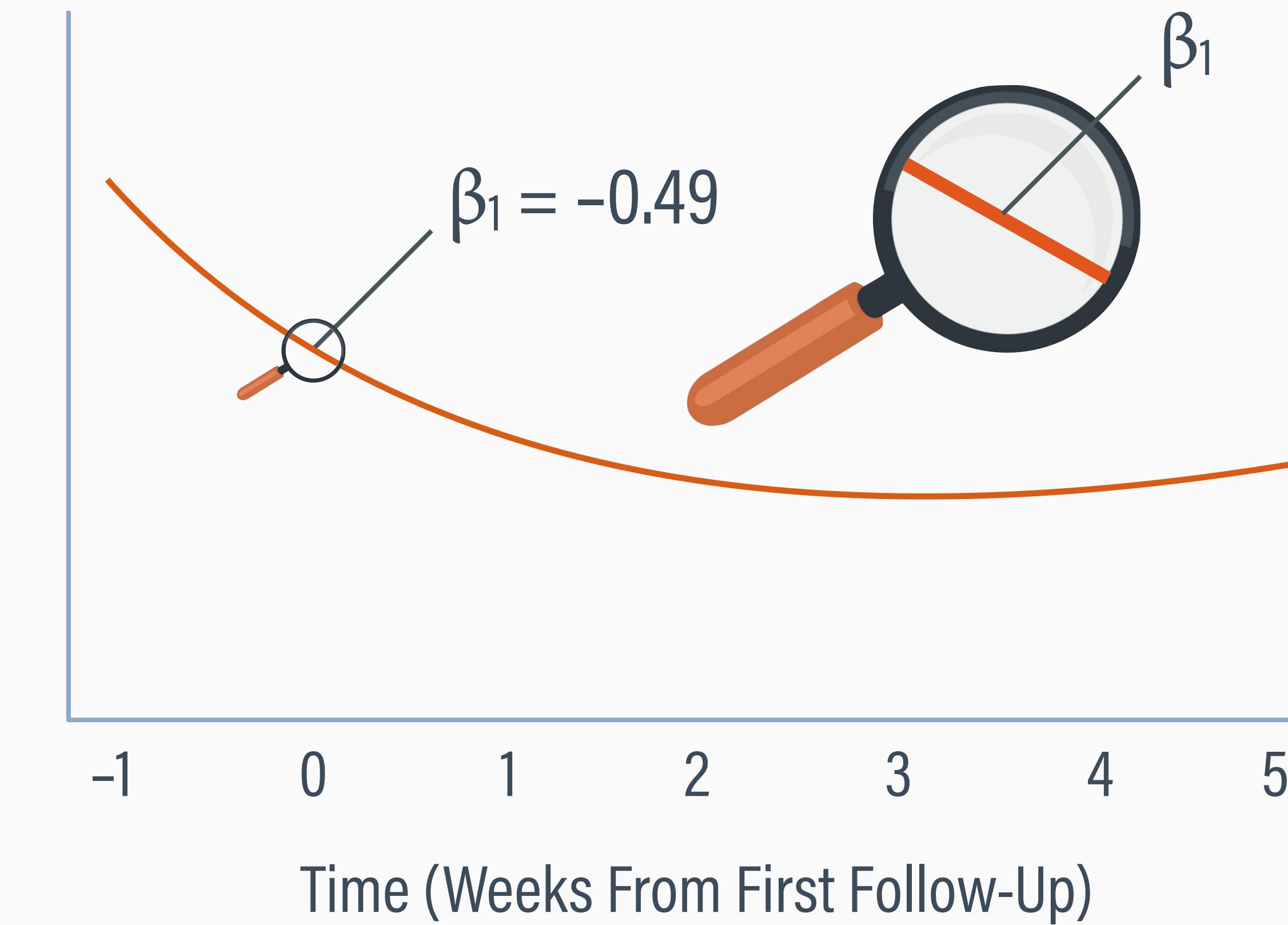


INTERPRETATION OF LINEAR TREND

The intercept is still the predicted outcome at the first follow-up



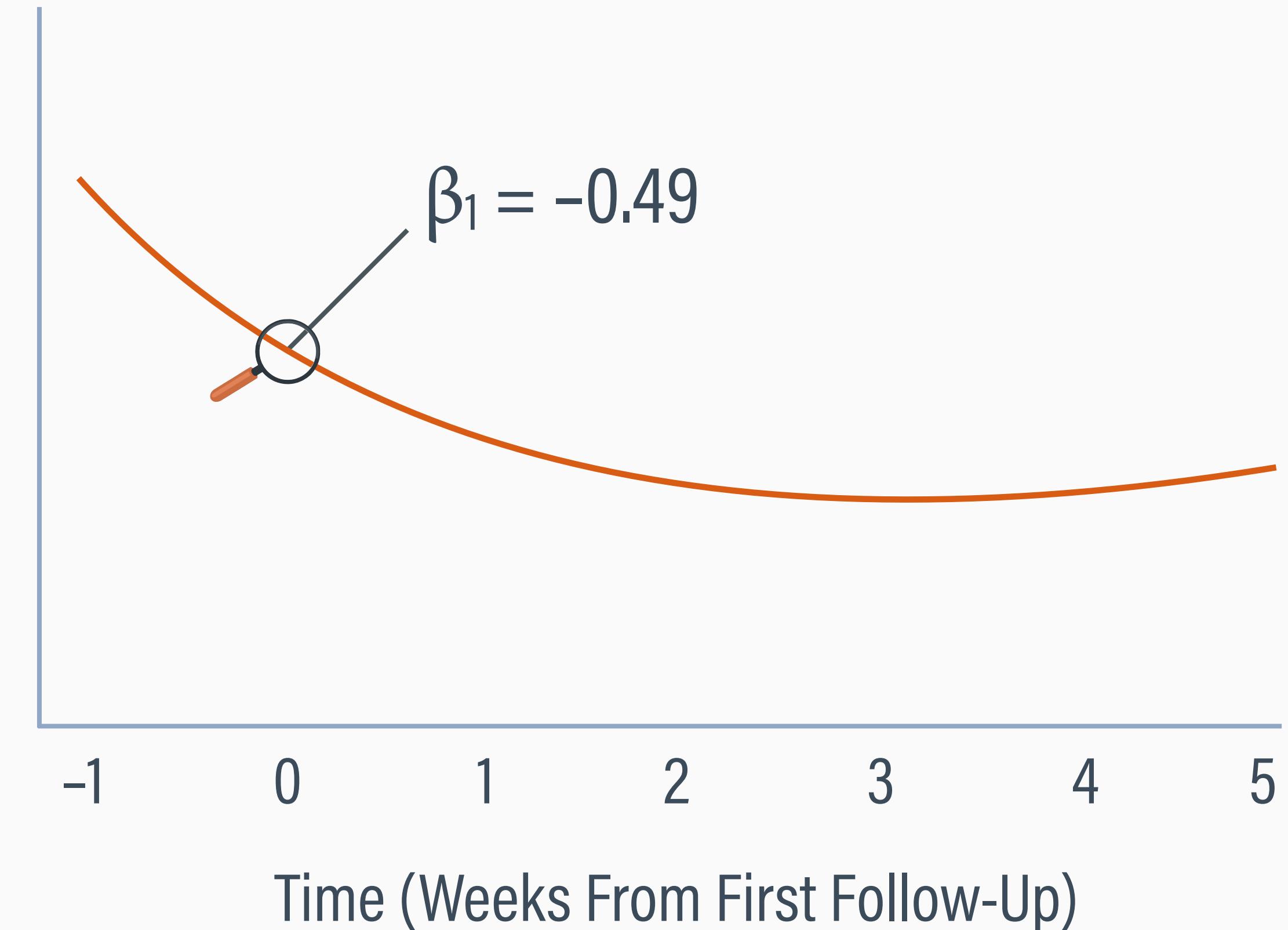
The linear trend is instantaneous (conditional) change at Time = 0



QUADRATIC SLOPE

- The linear trend is instantaneous (conditional) change at Time = 0
- The positive quadratic term ($\beta_2 = 0.04$) conveys that the negative linear trend becomes more positive (flattens) over time

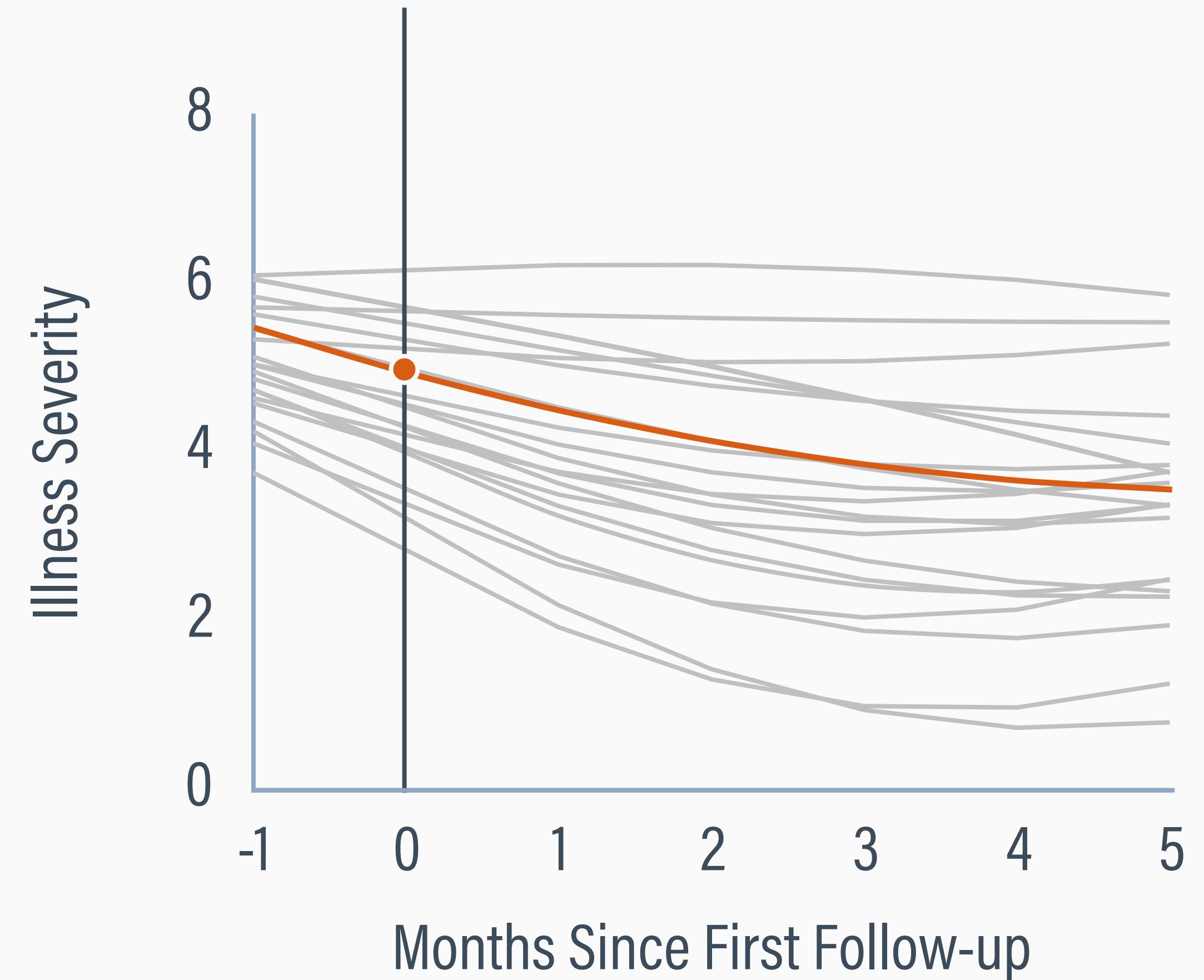
$$\text{severity}_{ij} = \beta_0 + \beta_1(\text{time}_{ij}) + \beta_2(\text{time}_{ij}^2) + u_{0j} + (u_{1j})(\text{time}_{ij}) + \varepsilon_{ij}$$



SPAGHETTI PLOT

- Random intercept variance quantifies vertical elevation of regression lines (person differences) at Time = 0
- Linear slope variance quantifies degree to which person-specific regression lines deviate from parallel at Time = 0

β_{0j} and β_{1j} = vertical elevation and instant linear change at WEEK = 0



See supplemental slides for worked examples
of piecewise and quadratic growth models.

OUTLINE

- 1 Examine Sample Means
- 2 Define Temporal Predictor (Time Variable)
- 3 Linear Growth Model
- 4 Model Nonlinear Change
- 5 Add Predictors of Change

MODELING CAVEAT

- The linear model is a reasonable but imperfect representation of change; the quadratic model may be preferable
- To simplify the example, I add predictors to the linear model
- Additional slides on BruinLearn demonstrate the process for the quadratic and piecewise models

WITHIN-PERSON (LEVEL-1) MODEL

- The severity rating at occasion i for person j is the sum of one's predicted severity at follow-up (β_{0j}), a person-specific weekly change rate (β_{1j}), and a time-specific residual (ε_{ij})

$$\text{severity}_{ij} = \beta_{0j} + \beta_{1j}(\text{time}_{ij}) + \varepsilon_{ij}$$

- Within-person residuals are normal with constant variation across all occasions (level-1) and persons (level-2)

BETWEEN-PERSON (LEVEL-2) MODEL

- γ_{00} is the placebo group mean at first follow-up, γ_{01} is the mean difference for the medication group, γ_{10} is the placebo group's weekly change rate, and γ_{11} is the growth rate difference for the medication condition (the group-by-time interaction)

$$\begin{aligned}\beta_{0j} &= \gamma_{00} + \gamma_{01}(\text{drug}_j) + u_{0j} \\ \beta_{1j} &= \gamma_{10} + \gamma_{11}(\text{drug}_j) + u_{1j}\end{aligned}\quad \begin{pmatrix} u_{0j} \\ u_{1j} \end{pmatrix} \sim N(0, \Sigma_u) \quad \Sigma_u = \begin{pmatrix} \sigma_{u0}^2 & \sigma_{u0u1} \\ \sigma_{u1u0} & \sigma_{u1}^2 \end{pmatrix}$$

- The level-2 residuals (u_{0j} and u_{1j}) now reflect leftover differences

COMBINED-MODEL EQUATION

Substituting the right sides
of the level-2 equations ...

$$\begin{aligned}\beta_{0j} &= \gamma_{00} + \gamma_{01}(\text{drug}_j) + u_{0j} \\ \beta_{1j} &= \gamma_{10} + \gamma_{11}(\text{drug}_j) + u_{1j}\end{aligned}$$

into their coefficients
from the level-1 equation

$$\text{severity}_{ij} = \beta_{0j} + \beta_{1j}(\text{time}_{ij}) + \varepsilon_{ij}$$

gives the combined-model regression equation (Raudenbush & Bryk, 2002)

$$\begin{aligned}\text{severity}_{ij} &= \gamma_{00} + \gamma_{01}(\text{drug}_j) + u_{0j} + (\gamma_{10} + \gamma_{11}(\text{drug}_j) + u_{1j})(\text{time}_{ij}) + \varepsilon_{ij} \\ &= \gamma_{00} + \gamma_{01}(\text{drug}_j) + u_{0j} + \gamma_{10}(\text{time}_{ij}) + \gamma_{11}(\text{drug}_j)(\text{time}_{ij}) + (u_{1j})(\text{time}_{ij}) + \varepsilon_{ij} \\ &= \gamma_{00} + \gamma_{01}(\text{drug}_j) + \gamma_{10}(\text{time}_{ij}) + \gamma_{11}(\text{drug}_j)(\text{time}_{ij}) + u_{0j} + (u_{1j})(\text{time}_{ij}) + \varepsilon_{ij}\end{aligned}$$

COMMON NOTATIONAL SYSTEMS

Combined-model equation (Raudenbush & Bryk, 2002)

$$\text{severity}_{ij} = \gamma_{00} + \gamma_{01}(\text{drug}_j) + \gamma_{10}(\text{time}_{ij}) + \gamma_{11}(\text{drug}_j)(\text{time}_{ij}) + u_{0j} + (u_{1j})(\text{time}_{ij}) + \varepsilon_{ij}$$

Standard(ish) regression notation (Scott, Shrout, & Weinberg, 2013)

$$\text{severity}_{ij} = \beta_0 + \beta_1(\text{time}_{ij}) + \beta_2(\text{drug}_j) + \beta_3(\text{drug}_j)(\text{time}_{ij}) + u_{0j} + (u_{1j})(\text{time}_{ij}) + \varepsilon_{ij}$$

BLIMP SCRIPT 7.2

DATA: SchizophreniaTrial.dat;
VARIABLES: person week drug male severity;
CLUSTERID: person;
ORDINAL: drug;
MISSING: 999;
TRANSFORM: time = week - 2; # compute temporal predictor
MODEL: severity ~ intercept time drug time*drug | intercept time;
SIMPLE: time | drug;
BURN: 10000;
ITERATIONS: 20000;
SEED: 90291;

RBLIMP SCRIPT 7 (MODEL 4)

```
model4 <- rblimp(  
    data = ClinicalTrial,  
    clusterid = 'Person',  
    ordinal = 'Drug',  
    transform = 'Time = Week - 2',  
    model = 'Severity ~ intercept Time Drug Time*Drug | intercept Time',  
    simple = 'Time | Drug',  
    seed = 90291,  
    burn = 10000,  
    iter = 20000)  
  
output(model4)  
posterior_plot(model4, 'Severity')  
simple_plot(Severity ~ Time | Drug, model4)
```

PSR DIAGNOSTIC OUTPUT

Quality control check: PSR diagnostics all < 1.05 well before the end of the burn-in period

BURN-IN POTENTIAL SCALE REDUCTION (PSR) OUTPUT:

NOTE: Split chain PSR is being used. This splits each chain's iterations to create twice as many chains.

Comparing iterations across 2 chains	Highest PSR	Parameter #
251 to 500	1.043	12
501 to 1000	1.051	14
751 to 1500	1.070	14
1001 to 2000	1.039	2
...
2501 to 5000	1.015	2
2751 to 5500	1.004	4
3001 to 6000	1.007	14
3251 to 6500	1.003	4
3501 to 7000	1.005	14
3751 to 7500	1.007	4
4001 to 8000	1.004	14
4251 to 8500	1.007	3
4501 to 9000	1.009	2
4751 to 9500	1.012	2
5001 to 10000	1.007	2

EFFECTIVE SAMPLE SIZE DIAGNOSTIC

Quality control check: Number of effective MCMC samples diagnostics all > 100

Outcome Variable: Severity

Parameters	Estimate	StdDev	2.5%	97.5%	ChiSq	PValue	N_Eff
<hr/>							
Variances:							
L2 : Var(Intercept)	0.533	0.058	0.429	0.656	---	---	2469.231
L2 : Cov(Time, Intercept)	0.056	0.012	0.032	0.079	---	---	1394.422
L2 : Var(Time)	0.033	0.005	0.024	0.043	---	---	1256.715
Residual Var.	0.759	0.036	0.692	0.834	---	---	2543.118
<hr/>							
Coefficients:							
Intercept	5.294	0.086	5.125	5.462	3805.148	0.000	2677.190
Time	-0.117	0.025	-0.167	-0.068	21.517	0.000	4409.698
Drug	-0.387	0.099	-0.581	-0.196	15.306	0.000	2801.395
Time*Drug	-0.262	0.029	-0.319	-0.204	79.349	0.000	4426.365
<hr/>							
...							
Proportion Variance Explained							
by Coefficients	0.291	0.019	0.253	0.328	---	---	3585.375
by Level-2 Random Intercepts	0.321	0.021	0.282	0.363	---	---	5854.762
by Level-2 Random Slopes	0.072	0.010	0.053	0.093	---	---	1209.357
by Level-1 Residual Variation	0.315	0.018	0.282	0.351	---	---	2252.130

BLIMP OUTPUT

- █ = level-2 estimate
- █ = level-1 estimate
- █ = combined estimate

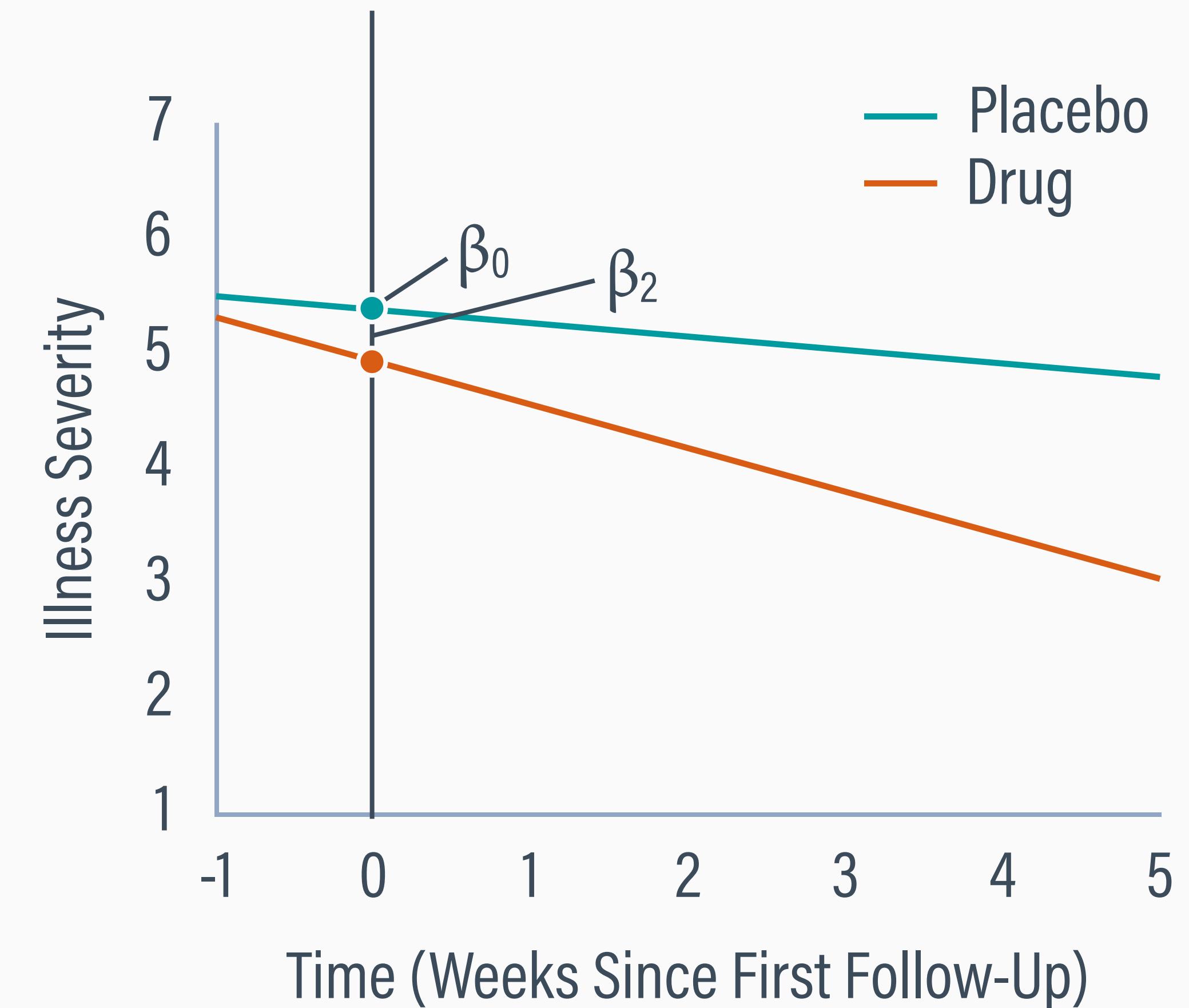
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<hr/>							
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by Level-2 Random Slopes	0.072	0.010	0.053	0.093	---	---	1209.357
by Level-1 Residual Variation	0.315	0.018	0.282	0.351	---	---	2252.130

MEAN GROWTH TRAJECTORIES

- The intercept ($\beta_0 = 5.29$) is the place group mean at Time = 0, and the drug slope ($\beta_1 = -0.39$) is the mean difference at Time = 0
- $\beta_1 = -0.12$ is the average weekly change rate for people in the placebo group
- $\beta_3 = -0.26$ is the additional weekly change for the medication group (i.e., their weekly change rate is -0.38)

$$\text{severity}_{ij} = \beta_0 + \beta_1(\text{time}_{ij}) + \beta_2(\text{drug}_j) + \beta_3(\text{drug}_j)(\text{time}_{ij}) \\ + u_{0j} + (u_{1j})(\text{time}_{ij}) + \varepsilon_{ij}$$

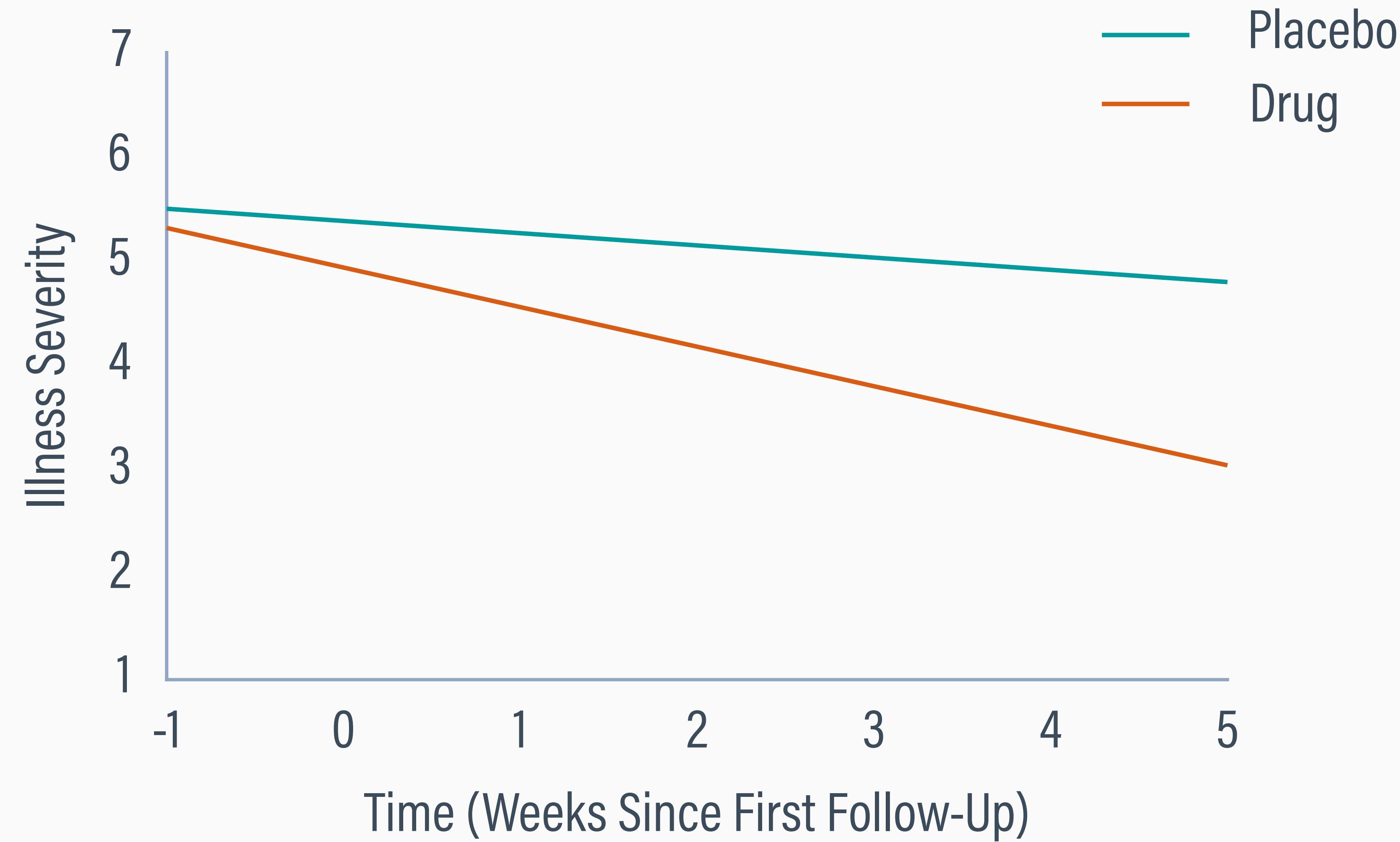


BLIMP CONDITIONAL EFFECTS OUTPUT

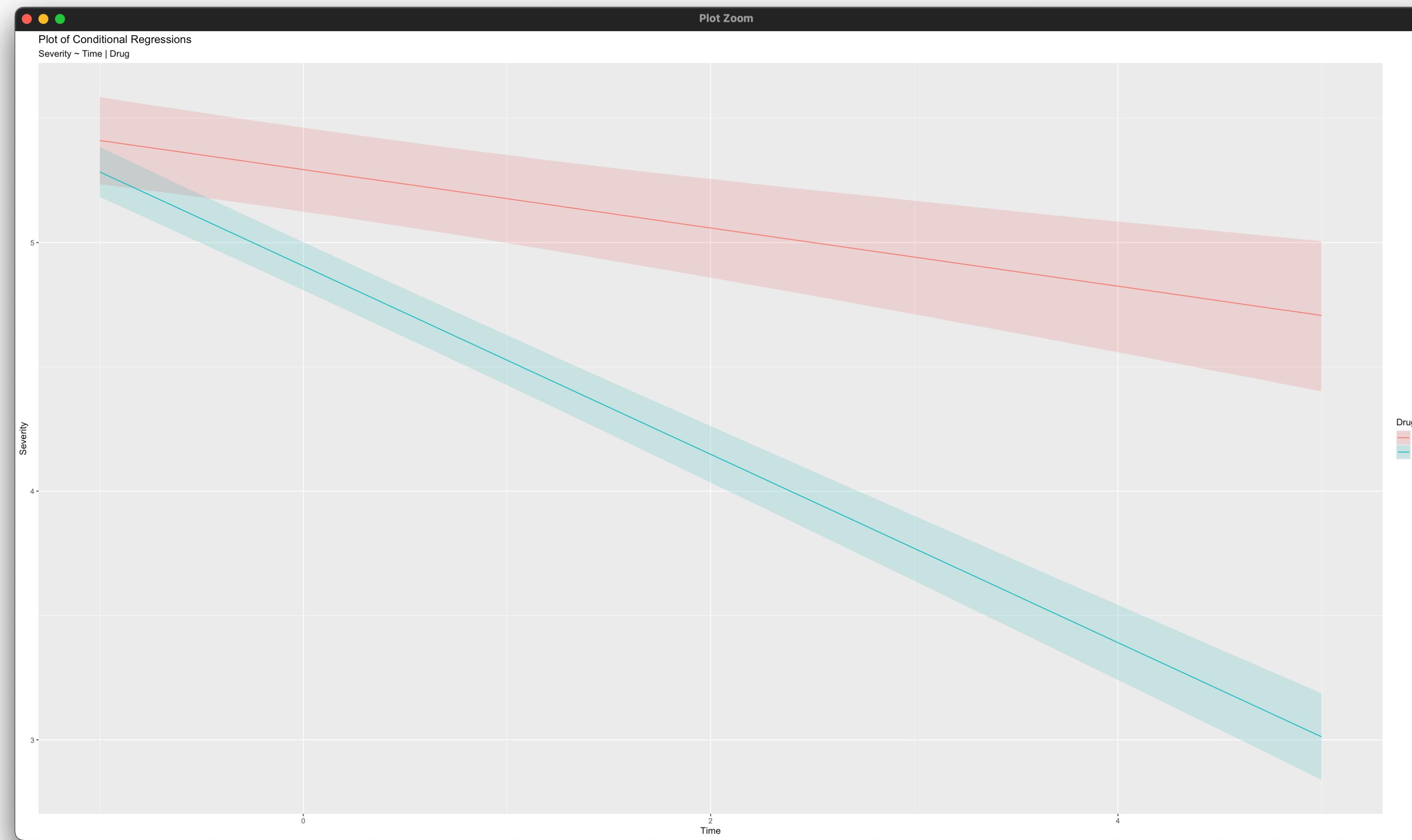
Conditional Effects	Estimate	StdDev	2.5%	97.5%	ChiSq	PValue	N_Eff
<hr/>							
Time Drug @ 0							
Intercept	5.294	0.086	5.125	5.462	3805.148	0.000	2677.190
Slope	-0.117	0.025	-0.167	-0.068	21.517	0.000	4409.698
<hr/>							
Time Drug @ 1							
Intercept	4.906	0.049	4.809	5.002	9834.830	0.000	2912.140
Slope	-0.379	0.015	-0.408	-0.350	671.473	0.000	4604.300
<hr/>							

NOTE: Intercepts are computed by setting all predictors
not involved in the conditional effect to zero.

CONDITIONAL EFFECTS (GROWTH CURVES)



CONDITIONAL EFFECT PLOTS (RBLIMP ONLY)



INTERPRETATIONS

Parameter	Est.	Interpretation
Fixed intercept	5.29	Predicted placebo group severity mean at the first follow-up
Time (within-person)	-0.12	Expected placebo group severity change for every additional week in the study
Drug (between-person)	-0.39	Drug condition mean difference at first follow-up
Time by Drug (cross-level, within)	-0.26	Additional weekly severity change rate for the drug condition
Between-cluster intercept variance (variance of u_{0j} residuals)	0.53	Average squared residual distances at the first follow-up
Between-cluster slope variance (variance of u_{1j} residuals)	0.03	Average squared residual distances in the person-specific slopes (change rates)
Intercept-slope covariance (covariance of u_{0j} and u_{1j} residuals)	0.06	Positive association where people with higher intercepts (higher severity at Time = 0) also tend to have higher (more positive or flatter) change rates
Within-cluster residual variance (variance of ϵ_{ij} residuals)	0.76	Average squared distance between a person's predicted and observed severity score
