Handling Missing Data in Longitudinal Study Design

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Overview of the Session

Handling Missing Data in Longitudinal Study Design
• Importance of Handling Missing Data
• Missing Mechanism in Longitudinal Data
• Methods for Handling Missing Data
  • Maximum Likelihood Methods (Multilevel model and Structural Equation Model)
  • Multiple Imputation
  • Pattern Mixture Model

Handling Missing Data

Why handling missing is important
If not properly handled, missing data can lead to biased, invalid or insignificant results.
The guidelines indicate that methods for dealing with missing data should be predefined in the protocol. The guidelines also point out that methods for dealing with missing data can be refined in the statistical plan during the blind review of the data. This is a very important step to consider, given that it can be difficult to anticipate all potential missing-data problems that could occur. Probably the most important suggestion the ICH guidelines make, however, is to investigate the sensitivity of the results of the analysis to the method of handling missing data.

**Trends of MI used in Publications**

**Missing Mechanism**

Missing Completely at Random (MCAR): There may be no particular reason why some respondents told you their weights and others didn’t. That is, the probability that Y is missing may have no relationship to X or Y. Missing at Random (MAR): One sex may be less likely to disclose its weight. That is, the probability that Y is missing depends only on the value of X. Not Missing at Random (NMAR): Heavy (or light) people may be less likely to disclose their weight. That is, the probability that Y is missing depends on the unobserved value of Y itself.
Missing Mechanism in Longitudinal Data

Example

Based on this plot, we may conclude:
- dropout is not MCAR, because it operates differently in the treatment and control groups.
- dropout is not MAR, because completers and dropouts differ in the (presumably) unmeasured.
- dropout could be MAR or NMAR; it's impossible to tell.

Methods to Handle Missing Data by Missing Mechanism

If data are MCAR or MAR, you can ignore the missing data mechanism and use multiple imputation and maximum likelihood.

If data are NMAR, you can't ignore the missing data mechanism; two approaches to NMAR data are selection models and pattern mixture.
Missing Mechanism

- If the data set is large and a few random points are missing, the problem is not serious.
- In a smaller data set with a non-random distribution of missing values, the problem may be serious.

Maximum Likelihood using multilevel model
Maximum Likelihood using multilevel model

Missing values that are out of scope
There is one additional situation when it is appropriate to not model the DQE when the fact that an observation is missing causes it to have the outcome of interest.

Example
Consider a study involving elderly persons trial where the outcomes are at the subject and random intercepts, and patients “drop-out” because of death. In this case, we can regard death as ignorable.

- In reality, there are no missing data.
- We may use missing-data procedures based on ML (e.g., PROD MIXED), understanding that we are estimating means of quality-of-life for live patients only.
- Population trajectory estimates the average QOL for those who are alive at any given time.

For an interesting perspective on causal inference in the presence of death, see Fong and Rubin (2002), Zhang and Rubin (2002).

Definition of Multi-level Analysis

- Multilevel analysis is a methodology for the analysis of data with complex patterns of variability caused by hierarchical or clustered data structure (Snijders & Bosker, 1999).

Multilevel linear modeling refers to a family of regression estimation techniques applied to data organized into hierarchically structured clusters, such as students (level-1) nested within classrooms (level-2) (Raudenbush and Bryk, 2002).
Examples of Multilevel Data (Hierarchical structure)

Level 1  kids  students  Repeated observations  children
Level 2  peer groups  classes  Patients  families
Level 3  schools  neighborhoods

Why we have to use multi-level analysis?

• Conventional methods for inferential data analyses, including analysis of variance (ANOVA) and general linear regression, assume that observations obtained from each individual are independent.
• Responses are not independent - individuals within clusters share influencing factors

Example of clustering effect:

Children with same biological parents tend to be more alike than children chosen at random from the general population. They are more alike because they share genetics, environment and/or both.

• When conventional methods are applied to data obtained from interacting dyads, the assumption of independent observations may be violated, leading to underestimation of standard errors and invalid inferences (i.e., increased Type I error).

PID  Visit  BMI
J0001  1  32
J0001  2  33
J0001  3  35
J0001  4  37
J0001  5  38
J0002  1  27
J0002  2  24
J0002  3  28
J0002  4  29
J0003  1  20
J0003  2  23
J0003  3  25
J0003  4  26
J0003  5  27
• Longitudinal study design is common in clinical research.
• Most usual approach is to use changed scores (discharge-admission) or last score as an outcome variable.
• This approach does not tell us a complete pattern of change.
• One popular approach to dealing with this type of data is Repeated measure of ANOVA.

• However, RM does not provide us with information on direction of change, change rate, initial value, relationship between initial and change rate, so on.
• It is based on strong assumption (equal same time interval) and balanced (same number of observation) data, so it can not deal with missing.
• A contemporary technique to solve the problem is mixed model.
Simple linear level-1 submodel for individual change

\[
BMI_i = \alpha_i + \beta_i Vnum + \epsilon_i
\]

\(i\) indexes persons (\(i=1\) to \(n\)), \(j\) indexes occasions/periods (\(j=1\) to \(5\)).

BMI

Structural portion, which embodies our hypothesis about the shape of each person's true trajectory of change over time.

Stochastic portion, which allows for the effects of random error from the measurement of person \(i\) on occasion \(j\).

Usually assume

\[
\epsilon_{ij} \sim N(0, \sigma^2)
\]

\(i, j\) are deviations of \(i\)'s true change trajectory from linearity on each occasion (including the effects of measured and unmeasured time-varying predictors).

\(\gamma_1\) is the slope of \(i\)'s true change trajectory, his yearly rate of change in true COG, his true "annual rate of change".

\(\alpha_i\) is the intercept of \(i\)'s true change trajectory. Net result: The individual growth parameters, \(\alpha_i\) and \(\gamma_1\), fully describe person \(i\)'s hypothesized true individual growth trajectory.
Data source: ARIC (4 visits) and JHS (1 visit)

- Research question: What is the time trend of BMI among JHS samples?
  - Within-individual: How does a study subject’s BMI change for 10 years?
  - Between individuals: Do the trajectories for samples differ between males and females? [And, if they do differ, how do they differ?]

**Preparing working dataset**

```sas
prep working dataset

******CONVERTING WIDE TO LONG*****
data combine; set comlong;
array bmiv[5] bmi1-bmi5;
do i=1 to 5;
  bmi=bmiv[i];
  stress=stressv[i];
  output;
drop i bmi1-bmi5 stress1-stress5;
run;
```

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Program data: aric1; set an.aric1 (keep=bmi01 stress01 subjid);
Visitnum=1; Bmi=bmi01; Stress=stress01; run;
data aric2; set an.aric2 (keep=bmi02 stress02 subjid);
Visitnum=2; Bmi=bmi02; Stress=stress02; run;
data aric3; set an.aric3 (keep=bmi03 stress03 subjid);
Visitnum=3; Bmi=bmi03; Stress=stress03; run;
data jhs1; set an.jhs1 (keep=bmi04 stress04 subjid);
Visitnum=4; Bmi=bmi04; Stress=stress04; run;
data comlong; set aric1-aric3 jhs1; run;
proc glimmix data=comlong noclprint noitprint;
class id gender;
model bmi= vnum  /solution ddfm=bw;
random intercept vnum /type=un subject=id;
run;
www.rtrn.net
A baseline model for change over time
\[ \begin{align*}
Y_{ij1} &= \alpha_i + T_1 \beta_i + \epsilon_{ij1} \\
Y_{ij2} &= \alpha_i + T_2 \beta_i + \epsilon_{ij2} \\
\ldots
\end{align*} \]
where \( \alpha_i \sim N(0, \sigma^2_\alpha) \) and \( \epsilon_{ij} \sim N(0, \sigma^2_\epsilon) \)

Level-1 Model:
\[ Y_{ij} = \beta_0 + \beta_1 T + \beta_2 \text{Visit} + \beta_3 \text{Gender} + \epsilon_{ij} \]

Level-2 Model:
\[ \beta_1 = \gamma_1 + \gamma_2 \text{Visit} + \gamma_3 \text{Gender} + \zeta_1 \]

Composite Model:
\[ \beta_0 = \zeta_0 + \zeta_1 \text{Visit} + \zeta_2 \text{Gender} \]

What about the variance components from this unconditional growth model?
Comparison between multilevel and conventional

Result of Multi-level model
Solution for Fixed Effects

| Effect       | Est. | SE    | DF  | t Value | Pr > |t |
|--------------|------|-------|-----|---------|------|
| Intercept    | 29.14| 0.15  | 1617| 193.80  | <.0001|
| vnum         | 0.4241| 0.0218| 6090| 19.50   | <.0001|

Result of conventional regression analysis

<table>
<thead>
<tr>
<th>Parameter Estimates</th>
</tr>
</thead>
<tbody>
<tr>
<td>Variable</td>
</tr>
<tr>
<td>Intercept</td>
</tr>
<tr>
<td>vnum</td>
</tr>
</tbody>
</table>

The unconditional growth model: Interpreting the variance components

Level-2 (between-persons):
- There is between-person residual variance in initial status (but careful, because the definition of initial status has changed)
- There is between-person residual variance in rate of change (should consider adding a level-2 predictor)
- Estimated residual covariance between initial status and change is significant.

Composite Model:

\[ y(t) = \gamma_0 + \gamma_1 t + \delta_0(t) + \epsilon(t) \]

Covariance Parameter Estimates

<table>
<thead>
<tr>
<th>Cov</th>
<th>Subject</th>
<th>Est.</th>
<th>Standard Error</th>
<th>Z Value</th>
<th>Pr Z</th>
</tr>
</thead>
<tbody>
<tr>
<td>UN(1,1)</td>
<td>ID</td>
<td>2.1569</td>
<td>1.2217</td>
<td>26.35</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>UN(2,1)</td>
<td>ID</td>
<td>0.635</td>
<td>0.1239</td>
<td>5.07</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>UN(2,2)</td>
<td>ID</td>
<td>0.5390</td>
<td>0.02732</td>
<td>19.73</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Residual</td>
<td></td>
<td>2.2104</td>
<td>0.04673</td>
<td>47.30</td>
<td>&lt;.0001</td>
</tr>
</tbody>
</table>

Level-1 (within person)
There is still unexplained within-person residual variance.
Analytical Goal: to determine if there is any difference in change rate of BMI between male and female

```r
proc glimmix data=comlong noclprint noitprint;
class id gender;
model bmi= vnum gender age*gender /solution ddfm=bw ;
random intercept vnum /type=un subject=id;
run;
```

For female,

\[ \text{BMI} = 29.82 + 0.39V - 2.12\text{Gen} - 0.15V^*\text{Gen} \]

Gender variable: 0=female, 1=male

For female,

\[ \text{BMI} = 29.82 + 0.39V - 2.12(0) - 0.15V^*(0) \]
\[ = 29.82 + 0.39V \]

For male,

\[ \text{BMI} = 29.82 + 0.39V - 2.12(1) - 0.15V^*(1) \]
\[ = 29.82 + 0.39V - 2.12 - 0.15V \]
\[ = 27.70 + 0.24V \]
Illustrative Example of mixed model: Wheelchair project

- Analytic objective: to determine if there is any difference in change of hip pressure among healthy persons and patients as increasing wheelchair back angle.
- Measure: Hip pressure was measured at every 10 degree from 5 to 55.

<table>
<thead>
<tr>
<th></th>
<th>Mean (SD)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>5 deg</td>
</tr>
<tr>
<td>HEALTHY (n=31)</td>
<td>44(8) 43(8) 42(7) 40(7) 38(6) 36(5)</td>
</tr>
<tr>
<td>PATIENTS (n=20)</td>
<td>45(8) 44(8) 43(8) 41(7) 39(7) 39(6)</td>
</tr>
</tbody>
</table>
mixed
tavg with degree patient patdeg
/METHOD = REML
/fixed = intercept degree patient patdeg | SSTYPES=
/PRINT = descriptive CORR G MATRIX R SOLUTION TEST COV
/random = intercept degree | subject (id1) covtype(un).

proc mixed data=wheel1 covtest;
class id patient;
model tavg=degree patient patient*degree/solution ddfm=bw notest;
random intercept degree /type=un sub=id gcorr;
run;
Intercept and change rate are highly associated with each other. The higher initial pressure, the greater decreasing rate in pressure.

There is no difference in initial pressure (at 5 degree) and change rate among patients and healthy persons. Patients had 45.79 mmHg at initial compared to 43.79 mmHg of healthy persons. Patients had 1.69 mmHg dropping rate per 10 degree compared to 1.43 mmHg of healthy persons.
\[
Apres = 43.79 - 1.43\text{deg} + 2.01\text{pat} - 0.27\text{deg}\times\text{pat}
\]

Pat variable: \(0=\text{healthy}, 1=\text{patients}\)

For healthy,
\[
Apres = 43.79 - 1.43\text{deg} + 2.01(0) - 0.27\text{deg}(0)
\]
\[= 43.79 - 1.43\text{deg}\]

For patients,
\[
Apres = 43.79 - 1.43\text{deg} + 2.01(1) - 0.27\text{deg}(1)
\]
\[= 43.79 - 1.43\text{deg} + 2.01 - 0.27\text{deg}
\]
\[= 45.80 - 1.70\text{deg}\]

Fitting the multilevel model for change to data

Three general types of software options:

- Programs expressly designed for multilevel modeling
- Multipurpose packages with multilevel modeling modules
- Specialty packages originally designed for another purpose that can also fit some multilevel models

Handling Missing Using SEM (FIML)
Convert Long form to Wide form data

data vtd.wide_vaf;
set vtdalli;
by pt;
retain vtd1-vtd5;
array vt(1:5) vtd1-vtd5;
if first.pt then do;
   do i = 1 to 5;
      vt[i] = .; /*initializing to missing*/
   end;
end;
vt(visit) = vitd3; /*looping across values in the variable period*/
if last.pt then output; /* outputs only the last obs in a family*/
keep pt vtd1-vtd5 trtg ;
run;

/* ADD COVARIATES
E1 E2 E3 E4
\\
R1 R2 R3 R4     reading scores
X
X -->   FI1   FS1         growth params (reading)
*/

proc calis noint ucov data = kids method=fiml maxiter=1000;
lineqs
   vtd1 =  FI1 + 0 FS1 + E1,
   vtd2 =  FI1 + 1 FS1 + E2,
   vtd3 =  FI1 + 2 FS1 + E3,
   vtd4 =  FI1 + 3 FS1 + E4,
   FI1 = b00 cons + b01 trtg + D0,
   FS1 = b10 cons + b11 trtg + D1;
std
   D0-D1 = 2 * A: (2 * 1.),
   E1-E4 = 4 * A: (4 * 1.),
   cov
   DD D1 = cov;
run;
quit;
Handling Missing using SEM (FIML)

Insert result tables

Imputation

— Complete Case method
— Last Observation Carried Forward method
— Single Imputation method
— Multiple Imputation method

Complete Case method
• The method is simply to omit all case with missing data at any measurement occasion
• This is a default method in most statistical packages to treat missing data.
• The advantage is that no special computational methods are required and it can be used for any kind of statistical analysis.
• However, the research has already shown the method requires MCAR for unbiased estimation
**Last Observation Carried Forward (LOCF) method**

- The method is for every missing data to be replaced by the last observed value from the same subject.
- Although the assumption of missing values is MAR, a recent research has shown that LOCF method creates bias even in MCAR.
- Additionally, this method does not give a valid analysis if the missing mechanism is anything other than MCAR.

**Single Imputation**

Substitute a single value for each missing value. Some of the ways to choose this value:

- **Mean Imputation**
  - Replace missing data with the mean of non-missing values.
  - Standard deviation and standard errors are underestimated (no variation in the imputed values)

- **Hot-deck Imputation**
  - Stratify and sort by key covariates, replace missing data from another record in the same strata.
  - Underestimation of standard error

- **Predict missing values from regression**
  - Impute value for each independent variable with missing on the basis of other independent variables in the model
  - Produces biased estimates

Disadvantages:

- Single imputation results in the sample size being over-estimated due to underestimated variance and standard errors

**Multiple Imputation**

- The most popular imputation method of handling missing data is Multiple Imputation (MI) method in which replaces each missing item with two or more acceptable values representing a distribution of possibilities.
- The advantage of this method is that once the imputed dataset has been generated, the analysis can be carried out using procedures in virtually any statistical packages.
- However, there are some disadvantages. Missing data individuals are allowed to have distinct probability which indicates that individual variation is ignored.
- Furthermore, the uncertainty inherent in missing data is ignored because the analysis does not distinguish between the observed and imputed values.
Multiple Imputation

- Multiple imputation (Rubin 1987)
- Impute for missing values several (M) times using random draws from the predictive distribution of the missing data given the observed data.
- Analyze each of the M completed data sets using methods designed for complete data; then combine point estimates and estimated variances.
  - Combined point estimate is average of point estimates from M data sets.
  - Total estimated variance is:
    1. Average of variances from M data sets, plus
    2. Variation among point estimates from M data sets.
- Component (2) reflects extra uncertainty due to missing data.

Three steps of multiple imputation

• Impute data.
  - Data is assumed to be multivariate normal.
  - Parameters are first estimated based on complete case. The imputed data is randomly picked from the distribution. Parameters are estimated again, and another imputation follows. Do it until parameter converges. Then multiple sets of data are drawn randomly from the distribution.

• Analyze data.
  - Each set of data is analyzed using any preferred methods.
  - Proc ###; BY _Imputation_; …; Run;
  - Save the parameters in a data sets.
Three steps of multiple imputation

- Combine results
  - Estimate = mean of all estimates.
  - Total variance = (Average within variance) + (1 + 1/m) (Between Variance).
  - Proc MIAnalyze parms =####; Run;

Features of MI

- Works with standard complete-data analysis methods
- One set of imputations may be used for many analyses
- Can be highly efficient, even for very small m

Efficiency of multiple imputation (%)

<table>
<thead>
<tr>
<th>m</th>
<th>0.1</th>
<th>0.3</th>
<th>0.5</th>
<th>0.7</th>
<th>0.9</th>
</tr>
</thead>
<tbody>
<tr>
<td>3</td>
<td>97</td>
<td>91</td>
<td>86</td>
<td>81</td>
<td>77</td>
</tr>
<tr>
<td>5</td>
<td></td>
<td>94</td>
<td>88</td>
<td></td>
<td></td>
</tr>
<tr>
<td>10</td>
<td></td>
<td>97</td>
<td>91</td>
<td>93</td>
<td>92</td>
</tr>
<tr>
<td>20</td>
<td></td>
<td>99</td>
<td>94</td>
<td>97</td>
<td>96</td>
</tr>
</tbody>
</table>

Packages for MI

Multiple Imputation

Available with best Statistical packages
  - Stata
  - SAS

Available with freeware programs that work in conjunction with statistical packages
  - Norm
  - Amelia
  - IVEware
  - Mice
Example Using Proc MI & Proc MIANALYZE

1. Impute values
   /* Proc MI will create sets of data in which missing values are imputed. */
   proc mi data = vtdalli nimpute = 20 seed = 4321567 out = int /* THIS DATASET WILL BE USED FOR NEXT STEP */;
   var vitd3 nvisit trtg;
   /* Include variables used in the analytical model and the other variables if you want */
run;

Example Using Proc MI & Proc MIANALYZE

2. Run your analytical model (Standard SAS procedure: genmod or the other) using the created data by Proc MI.
   proc mixed data = int;
   class pt;
   model vitd3 = nvisit trtg nvisit*trtg / solution covb;
   random intercept / subject = pt;
   by _imputation_; /* THESE DATA WILL BE USED FOR NEXT STEP */
ods output SolutionF = mixparms CovB = mixcovb;
run;

Example Using Proc MI & Proc MIANALYZE

3. Conduct Proc MIAnalyze using the data created by just above step.
   ods html;
   proc mianalyze parms = mixparms covb = mixcovb; /* For LS methods, proc mianalyze data = outcov edf = 30 mult */
   modeleffects intercept nvisit trtg nvisit*trtg;
run;
ods html close;
Example Using Proc MI & Proc MIANALYZE

**Without Imputation**

| Effect   | Estimate | Std Error | DF  | t Value | Pr > |t|  
|----------|----------|-----------|-----|---------|------|    |
| Intercept| 15.72    | 0.33      | 128 | 47.80   | <.001|
| nvisit   | 1.55     | 0.07      | 1.30E+04 | 21.75 | <.001|
| trtg     | 3.97     | 0.47      | 1.30E+04 | 8.53  | <.001|
| nvisit*trtg| 3.24    | 0.10      | 1.30E+04 | 32.42 | <.001|

**Without Imputation**

| Parameter | Estimate | Std Error | DF  | Minimu m | Maxim um | t for H0: | Pr > |t|  
|-----------|----------|-----------|-----|----------|----------|-----------|------|    |
| Intercept | 15.51    | 0.69      | 14.07 | 16.95   | 15.00    | 15.85     | 22.50 | <.001|
| nvisit    | 1.13     | 0.37      | 0.36  | 1.90     | 0.64     | 1.46      | 1.10  | <.001|
| trtg      | 4.42     | 1.00      | 2.32  | 6.32     | 3.33     | 4.45      | 4.41  | <.001|
| nvisit*trtg| 4.05    | 0.52      | 2.86  | 5.14     | 3.14     | 4.61      | 3.81  | <.001|

Pattern-mixture Model: A Nonignorable Missing Data Method

- Both MRMs and most forms of multiple imputation assume that the data are ignorable.
- That is, it is not necessary to take into account the missing data mechanism. However, this assumption may not always hold in research where nonresponse is often related to a participant's mental state and not explained by the observed data.
- Pattern-mixture models are non-ignorable missing data methods that stratify participants based on their missing data pattern. A separate model is fit for each pattern and then typically results are combined across the different patterns to obtain an average estimate of the model parameters. In this way, a model is fit for the joint distribution of the outcome and whether or not the outcome is missing.
- The assumption here is that dropouts are potentially systematically different from participants who are observed at every time point or who only have intermittent missing data.
The first step in applying the pattern-mixture approach to handling missing data is to divide the subjects into groups on the basis of their missing data pattern. For example, suppose that subjects are measured at three time points; then there are eight possible missing data patterns (2^3):

<table>
<thead>
<tr>
<th>Pattern</th>
<th>Time1</th>
<th>Time2</th>
<th>Time3</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>O</td>
<td>O</td>
<td>O</td>
</tr>
<tr>
<td>2</td>
<td>M</td>
<td>O</td>
<td>O</td>
</tr>
<tr>
<td>3</td>
<td>O</td>
<td>M</td>
<td>O</td>
</tr>
<tr>
<td>4</td>
<td>M</td>
<td>M</td>
<td>O</td>
</tr>
<tr>
<td>5</td>
<td>O</td>
<td>O</td>
<td>M</td>
</tr>
<tr>
<td>6</td>
<td>M</td>
<td>O</td>
<td>M</td>
</tr>
<tr>
<td>7</td>
<td>O</td>
<td>M</td>
<td>M</td>
</tr>
<tr>
<td>8</td>
<td>M</td>
<td>M</td>
<td>M</td>
</tr>
</tbody>
</table>

Next step is to figure out how to compare the missing pattern.

Start with completers:

*Completers;
ods html;
proc mixed covtest data = vtdalli ;where com = 1;
class pt;
dl i d 3 ii li b mo mod mode model vi ti td3 = nv is is tt r t gn vi is it tt trtg / sol t on cov b;
random intercept visit/type=un sub=pt;
run;
ods html close;

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Pattern Mixture Model for non-ignorable data

Mixed model for all.

*All;
ods html;
proc mixed
covtest data = vtdalli ;
class pt ;
model vitd3=nvisit trtg nvisit*trtg /solution covb;
random intercept visit/type=un sub=pt;
run;
ods html close;

Pattern Mixture Model for non-ignorable data

Include interaction term of missing pattern with others.

*Pattern mixture;
ods html;
proc mixed
covtest data = vtdalli ;
class pt ;
model vitd3=nvisit trtg nvisit*trtg com com*nvisit com*trtg nvisit*trtg*com/solution covb;
random intercept visit/type=un sub=pt;
run;
ods html close;

Pattern Mixture Model for non-ignorable data

<table>
<thead>
<tr>
<th>Parameters</th>
<th>Completers (N=115)</th>
<th>All (N=130)</th>
<th>Pattern mixture (N=130)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Intercept</td>
<td>17.12</td>
<td>16.82</td>
<td>15.00</td>
</tr>
<tr>
<td></td>
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<td>(0.66, &lt;0.0001)</td>
<td>(1.74, &lt;0.0001)</td>
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<tr>
<td>Time</td>
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<td>0.17</td>
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<td>(0.28, 0.5391)</td>
<td>(1.58, 0.7366)</td>
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<tr>
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<td>2.41</td>
<td>-2.44</td>
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<td>(0.98, 0.0085)</td>
<td>(0.93, 0.0103)</td>
<td>(2.98, 0.0014)</td>
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<tr>
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<td>5.55</td>
<td>5.59</td>
<td>6.80</td>
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<td>(&lt;0.0001)</td>
<td>(2.16, 0.0019)</td>
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<tr>
<td>Dropouts</td>
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<td>0.038</td>
<td>-1.25</td>
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<tr>
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<td>0.038</td>
<td>-1.47</td>
</tr>
<tr>
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<td>0.038</td>
<td>-1.25</td>
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<tr>
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<td>0.33</td>
<td>0.42</td>
</tr>
<tr>
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<td>2874.4</td>
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Thank you for participating!