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The clinical course of alcohol use disorders: Using joinpoint analysis to aid in interpretation of growth mixture models

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ABSTRACT

Background: The clinical course of alcohol use disorders (AUD) is marked by great heterogeneity both within and between individuals. One approach to modeling this heterogeneity is latent growth mixture modeling (LGMM), which identifies a number of latent subgroups of drinkers with drinking trajectories that are similar within a latent subgroup but different between subgroups. LGMM is data-driven and uses an iterative process of testing a sequential number researcher-selected of latent subgroups then selecting the best fitting model. Despite the advantages of LGMM (e.g., identifying subgroups among heterogeneous longitudinal data), one limitation is the lack of precision of LGMM to model abrupt changes in drinking during treatment that are often observed by clinicians. Joinpoint analysis (JPA) is a data analysis procedure that is used to identify discrete change points in longitudinal data (e.g., changes from increasing to decreasing or decreasing to increasing).
Method: This study presents a demonstration of using JPA as a post hoc procedure for LGMM to improve accuracy in modeling abrupt changes in clinical course of AUD.
Results: Results from this secondary data analysis of 549 AUD participants participating in the NIAAA sponsored relapse replication and extension project uncovered four latent classes of drinking trajectories.
Discussion: Within these trajectories the addition of JPA improved precision in modeling the clinical course of AUDs.

1. Introduction

Over four decades ago, Subotnik (1972) described variability between and within individuals over time as a general characteristic of behavioral and psychological disorders. Consistent with this observation, alcohol use disorders (AUD) clinical course, defined as changes in alcohol use and related problems following the initiation or completion of an episode of AUD specialty treatment (treatment in which clients present specifically for treatment of AUD in a setting specifically designed to address it rather than initially presenting for another physical or mental health concern say in primary care and AUD is identified and treated in that context), is heterogeneous across individuals (Maisto et al., 2006, 2007; McKay, 2008; Witkiewitz and Marlatt, 2007). Within person variability among problem drinkers is characterized by varying periods of abstinence, non-problem drinking, and problem drinking (Witkiewitz, 2008), as well as intermittent periods of psychological and/or social difficulties. Between-person differences in clinical course may be attributed in part to the multiple biopsychosocial factors that vary in importance between individuals and within individuals over time (McKay et al., 2006). Furthermore, alcohol use following treatment can be characterized by nonlinear, abrupt changes (increases or decreases) in alcohol consumption and related problems (Witkiewitz et al., 2010). Taken together, these data provide one explanation for the modest amount of variance that has been accounted for in longer-term (at least 1 year) clinical course by the application of statistical methods based on the general linear model (Witkiewitz et al., 2010).

In response to the limitations in application of the general linear model, in the last decade alcohol clinical researchers have recently applied advanced methods of analyzing longitudinal data to the investigation of AUD clinical course. One of these methods is latent growth mixture modeling (LGMM), which combines latent growth curve modeling, which is used to model inter- and intraindividual change over time, with a categorical latent trajectory class variable (Witkiewitz et al., 2010). The latent categorical variable is used to identify subgroups or classes of individuals with common patterns of change over time.

Through separating subgroups of participants based on variability in clinical course, latent growth mixture modeling permits insights about AUD clinical course that remain obscured by application of the general linear model. Nevertheless, LGMM results are often limited to describing the entirety of the trajectory for a given

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class. However, it often would be valuable for clinical practitioners and clinical researchers to know of change points in a trend, that is, points of inflection in a growth function. Such information would help in the timing of prevention and treatment interventions at the points of greatest risk of hazardous or harmful alcohol consumption. A method for determining points of inflection in a growth curve function is available and is called Joinpoint analysis (JPA; http://www.surveillance.cancer.gov/joinpoint). JPA has been described in the literature for over 12 years (Kim et al., 2000) but has not been applied by alcohol clinical researchers to our knowledge. Joinpoint analyses offer a longitudinal data analytic strategy for identifying discrete change points in the clinical course of AUD within a latent class.

Using JPA as a post hoc procedure for identifying critical change points in latent trajectories of AUD derived from LGMM has advantages over other longitudinal analytic procedures. For example, latent transition analysis (LTA) examines changes in latent class membership from one time point to another (Muthèn and Muthèn, 2000). LTA can be viewed as a repeated measures latent class analysis (LCA) with latent classes being calculated at each time point and then studying the probability of transitioning from one class to another. Thus, LTA provides all possible clinical course patterns. One disadvantage of LTA is that it is computationally intense, especially in cases with many time points. Another disadvantage is that there may be many unlikely and therefore unpopulated patterns. In contrast, LGMM examines the same outcome (e.g., alcohol use) at each time point then identifies a researcher-selected number of subgroups with similar developmental trajectories across time. The addition of JPA to LGMM provides a finer level of analysis to LGMM by identifying moments in time when a subgroup changes course (e.g., from improving to deteriorating, or deteriorating to improving). Further, JPA is less computationally intensive than LTA and eliminates the examination of unlikely patterns of the outcome data. Moreover, LGMM with JPA is an improvement over LGMM alone, because LGMM only provides linear or quadratic trends for the entire growth trajectory for each subgroup; however, by adding JPA these trends can be divided into periods of improvement and deterioration that may be lost by classifying the trajectory with a single trend.

The purpose of this study was to illustrate the application of LGMM together with JPA in the analysis of AUD clinical course data. The data obtained from the National Institute on Alcohol Abuse and Alcoholism-sponsored Relapse Replication and Extension Project (Lowman et al., 1996) were analyzed in completing this study.

2. Methods

The data from 549 AUD adults participating in the NIAAA sponsored Relapse Replication and Extension Project (RREP; Lowman et al., 1996) were analyzed. Participants were recruited from three sites: Brown University (Providence, RI), the Research Institute on Addictions (RIA; Buffalo, NY), and the University of New Mexico (UNM; Albuquerque, NM). As requested by the NIAAA, the three sites shared design elements, including parallel treatment procedures and identical assessment measures.

2.1. Participants

RREP eligibility criteria required participants to be at least 18 years of age (21 years of age at RIA), to meet diagnostic interview survey criteria for alcohol abuse or dependence within the past 6 months without severe concomitant drug diagnoses, to report no intravenous drug use in the past 6 months, to have no major comorbid psychiatric diagnoses, and to provide informed consent. The total sample was 563 participants who all met DSM-III-R (American Psychiatric Association, 2000) criteria for alcohol dependence and who all reported alcohol dependence symptoms on the alcohol dependence scale (Skinner and Horn, 1984; 549 with complete data on the study variables were included in this study). The breakdown of participant recruitment included 300 from six facilities in the Providence area, 142 from eight programs in the Buffalo area, and 121 from a single outpatient program in the Albuquerque area. Participants in the total combined sample were 41.2% female, aged 18–64 years ($M = 34.33$, SD = 8.72), and 67.3% Caucasian, 16% African American, 8.9% Hispanic, 2.6% Native American, and 5.2% other race/ethnicity.

2.2. Measures

Drinking frequency was assessed using the Form 90 every other month for 1 year (6 assessments in 12 months) following admission to the treatment program. The Form 90 is a structured assessment interview for drinking and related behaviors (Miller, 1996) that gathers self-reported daily alcohol use between each assessment period. For ease of presentation of the analytic methods employed we chose to report on only one alcohol use variable namely, percent days abstinent (PDA). We selected PDA from a number of possible alcohol use outcomes because the AUD specialty treatment that clients in the RREP study received was abstinence focused. Patterns in PDA during each month of treatment were analyzed, providing 12 waves of data to be included in the data analyses. Because alcohol use was assessed on the daily level, aggregating the 6 assessments conducted over 12 months to monthly level data was possible (i.e., PDA = (number of days abstinent during each month/30) × 100).

2.3. Data analysis plan

This study used JPA as a post hoc analytic procedure following LGMM procedures to identify latent classes of individuals of individual's percent days abstinent (PDA). A series of 5 LGMMs were conducted using Mplus version 6 (Muthèn and Muthèn, 1998–2010), and post hoc JPAs were run using Joinpoint Regression Program, Version 3.5 (National Cancer Institute, 2011). The GMMs were run to determine the number of distinct groups of individuals with similar PDA patterns across the 1-year study period. The JPAs were used to aid in interpretation of the best fitting LGMM model.

2.4. Growth mixture model class selection

This sample of 549 AUD adult participants is medium-sized based on the standards for LGMMs (Nylund et al., 2007). The model fit indices used to determine the best fitting model were selected based on recommendations from Nylund and colleagues' (2007) Monte Carlo study designed to determine the most appropriate fit indices for LGMMs across a range of sample sizes, and based on Muthen and Muthen's (2000) recommendations for class selection for LGMMs. Thus, four criteria (i.e., bootstrapped parametric likelihood ratio test (BLRT), sample size adjusted Bayesian information criterion (saBIC), entropy, average latent class probabilities) were used to determine the optimal number of latent growth classes (Muthèn and Muthèn, 2000).

First, the BLRT (McLachlan and Peel, 2000), tests for improvement over a model with one fewer class, designed for smaller samples by extrapolating the data to better represent the true distribution. Second, the saBIC (Sclove, 1987) is a comparative fit index that rewards parsimony while maximizing the model's likelihood ratio statistic. Better model fit is indicated by a lower value; therefore, the value for a single model cannot be interpreted without another model with a known adjustment for comparison. The saBIC helps identify the best in a series of models (Muthèn and Muthèn, 2000) and is well-suited for smaller samples (Lubke and Neale, 2006). Third, model classification quality was assessed using the entropy statistic. Entropy ranges from 0 to 1, with higher values suggesting better classification quality (Celeux and Soromenho, 1996; Ramaswamy et al., 1993) and values greater than 0.80 typically considered to have adequate classification quality (Jung and Wickrama, 2008). Fourth, average latent class probabilities for the most likely latent class membership by latent class discrimination values were evaluated, with good model fit being represented by values close to 1 in the primary diagonal and values close to 0 in all other cells. Once the best fitting LGMM was selected, the latent class sample statistics (i.e., model-estimated means for each timepoint for each class) were transferred to Joinpoint Regression Program for post hoc JPA analyses. The model-estimated means were calculated using the TECH7 feature in Mplus Version 6. The TECH7 feature provides model-estimated means using model-estimated posterior probabilities to produce estimated "sample statistics" for subclasses in mixture modeling. These estimates are imperfect because the means are not observed (B. Muthèn, personal communication, April 22, 2013). Joinpoint software allows for the inclusion of standard errors in addition to the means in calculating the number of joinpoints and the slopes and intercepts for each line segment; however, in the current study we assumed homoscedasticity and estimated the JPA models using only the model-estimated means.

JPA seeks to identify discrete inflection points in longitudinal data (e.g., when a trend changes from increasing to decreasing) through the use of a permutation test (Kim et al., 2000). Joinpoint Regression Program statistically determines the number of change points through a series of permutation tests such that if one more change point is added the resultant model is not an improvement over a model with one fewer change point. This process begins with zero change points and continues to the maximum number of change points defined by the researcher and based on recommendations by Yu and colleagues (2007). Once the number of change points is determined intercepts and slopes for each segment are available for interpretation and comparison.

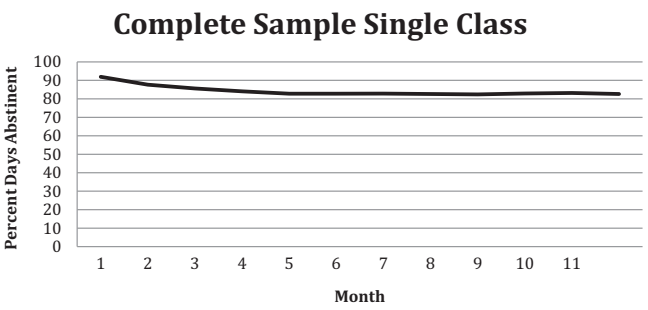

Fig. 1. Single class model for PDA across the study period.

3. Results

3.1. Sample characteristics

Participants considered as a single group maintained a steady and infrequent drinking pattern across the study period (Fig. 1; $M = 84.30$, SD = 28.41). Close examination of the sample revealed extreme heterogeneity and significant variance of PDA at every time point (variance ranged from a minimum at month 1 of 111.48 to a maximum of 289.17 at month 8). As noted in the Method section, we then conducted a series of 5 latent growth mixture models (LGMMs) to determine the number of latent classes of individuals that shared common trajectories of drinking frequency across the study period. Final model selection was based on model fit and interpretability.

3.2. Growth mixture model selection and interpretation

Overall model fit indices for the series of five LGMMs, and the estimated means for each time point along with the intercept, linear and quadratic slopes for the best fitting model are presented in Table 1. The growth factors presented in Table 1 all had significant variances constrained to be equal across classes (intercept variance = 30.39, linear slope variance = 47.96, quadratic slope variance = 0.40, p's < .05). The 4-class model was the best fitting model based on model fit indices and interpretability. Specifically there was a substantial improvement in saBIC from the 3- to 4-class model (decrease of 184 points), but the saBIC did not continue to improve from the 4- to 5-class model (decrease of 4 points). Additionally, the 3 participants in the first class of the 5-class model are likely to be a subset of the 4th class of the 4-class model ($n = 67$) and the 5th class of the 5-class model ($n = 64$). In comparison to the 5-class model, the 4-class model had similar saBIC and entropy values. In addition, although the BLRT suggests that the 5-class model is an improvement over the 4-class model, the 5-class model included a class with only 3 participants (i.e., 0.54% of the total sample), which is not substantively interpretable. Moreover, the 4-class model showed near-perfect average latent class probability for the most likely latent class membership by latent class discrimination, indicating that the 4-class model was a good representation of participant reports.

Qualitatively, the 4-class model had two classes that increased in PDA across the 12-month study period. We named these classes *slightly decreasing frequency drinkers* (SDFD) and *greatly decreasing frequency drinkers* (GDFD) based on the magnitude of the improvement across the study period. One class, which contained the

Table 1
Growth mixture model overall model fit statistics and monthly means for the best fitting model.

	PDA				
	1	2	3	**4**	5
saBIC	54,660	54,160	53,772	**53,588**	53,584
Entropy	1	0.99	0.995	**0.97**	0.97
BLRT improvement	N/A	<0.01	<0.01	**<0.01**	<0.01
# people/class (% of total sample)					
1	549 (100%)	495 (90%)	483 (88%)	**44 (8%)**	3 (<1%)
2		54 (10%)	44 (8%)	**416 (76%)**	22 (4%)
3			22 (4%)	**22 (4%)**	44 (8%)
4				**67 (12%)**	416 (76%)
5					64 (12%)
4 class model	SDFD	SOD	GDFD	IFD	

Month	Mean	Mean	Mean	Mean
1	59.80	98.6	13.17	97.11
2	50.96	96.18	22.76	78.59
3	60.35	94.24	23.97	67.78
4	58.11	92.17	36.97	65.78
5	60.51	91.67	37.12	55.89
6	60.27	90.94	48.64	56.86
7	65.53	91.04	51.6	52
8	65.33	92.29	49.04	42.8
9	68.27	93.51	45.33	30.5
10	69.52	93.41	39.49	28.31
11	69.38	94.77	50.66	25.92
12	71.82	94.05	50.41	25.03
N	44	416	22	67

	M (SE)	*M* (SE)	*M* (SE)	*M* (SE)
I	59.91* (2.04)	98.61** (0.21)	13.13** (2.41)	97.23** (0.79)
S	−0.26 (1.55)	−2.37** (0.31)	8.23** (2.46)	−12.16** (1.825)
Q	0.13 (0.13)	0.19** (0.03)	−0.47* (0.24)	0.50** (0.17)

Note: PDA, percent days abstinent; saBIC, sample size adjusted Bayesian Information Criterion; BLRT, bootstrapped likelihood ratio test; SDFD, slightly decreasing frequency drinkers; SOD, stable occasional drinkers; GDFD, greatly increasing frequency drinkers; IFD, increasing frequency drinkers; I, intercept; S, linear slope; Q, quadratic slope.
* $p < 0.05$.
** $p < 0.01$.

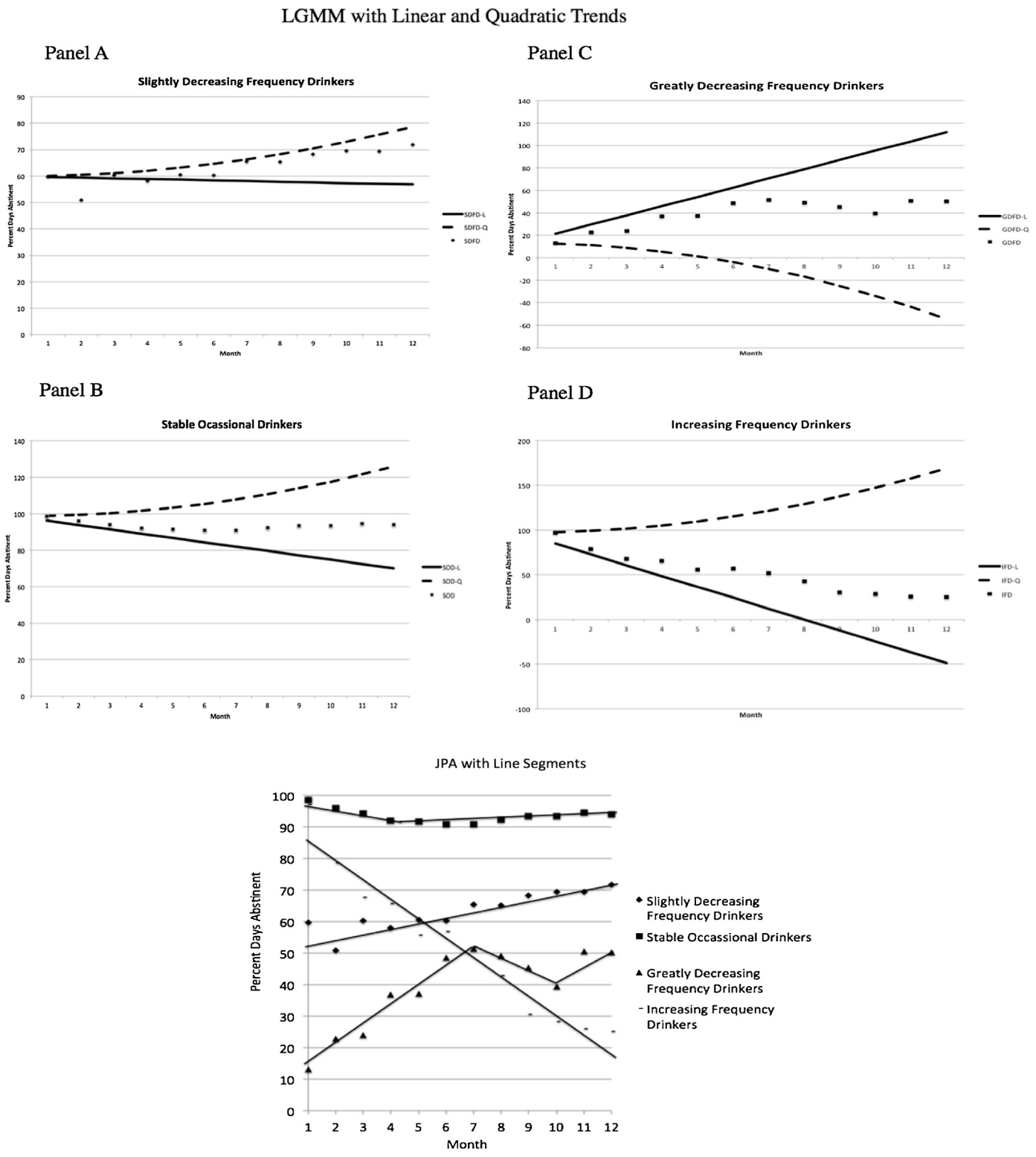

Fig. 2. (a) Latent growth mixture model subclasses with linear and quadratic trendlines. *Note*: Dashed lines indicate quadratic trends and solid lines indicate linear trends. SDFD – slightly decreasing frequency drinkers; SOD – stable occasional drinkers; GDFD – greatly decreasing drinkers; IFD – increasing frequency drinker; Q – quadratic trend; L – linear trend. (b) Joinpoint analysis line segments with latent growth mixture modeling subclasses. *Note*: In (b) JPA, joinpoint analysis.

majority of the sample maintained steady and infrequent drinking levels throughout the study period, and were named *stable occasional drinkers* (SOD). The final class steadily and rapidly deteriorated throughout the 12-month study period and was named *increasing frequency drinkers* (IFD).

Thus the best-fitting LGMM model for PDA had 4 latent classes and is presented in Fig. 2a panels A–D. LGMM analysis estimates linear and quadratic trends for individual subclasses, in conjunction with the intercept for each class. In Fig. 2a panels A–D the dashed lines represent the estimated quadratic trajectories for

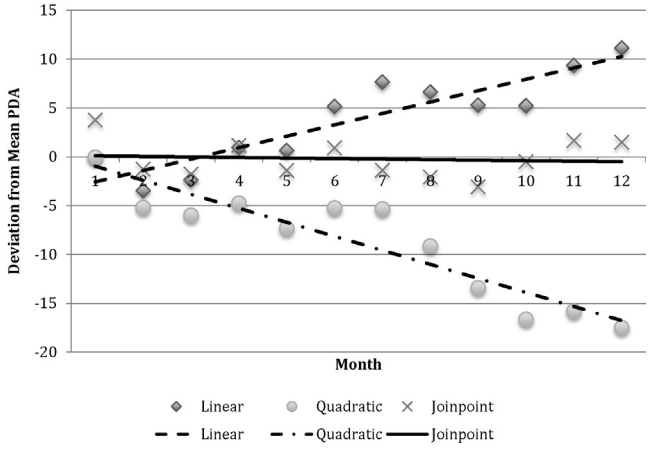

Fig. 3. Comparison of deviation from actual value across time by prediction method. *Note*: PDA, percent days abstinent.

each latent class, and the solid lines represent the estimated linear trends for each latent class based on the parameter estimates produced from the LGMM. These lines extend beyond the data and beyond the limits of percent days abstinent (i.e., 0–100%) because the calculated trend lines begin at the intercept and then change according to the following equations (linear: predicted value = intercept + (linear trend parameter × month); quadratic: predicted value = intercept + (quadratic trend parameter × month^2)) across the study period. This estimation procedure produces increasingly less accurate predictions across time if the true data points do not follow a pure linear or quadratic trend. In this case, because the actual PDA trends are best described by abrupt changes throughout the study period, the LGMM linear and quadratic trend lines become increasingly inaccurate at the later time points. Specifically, in Fig. 2a, it is clear that the projected trends exaggerate the observed changes by assuming constant linear or quadratic change across the study period. If we juxtapose Fig. 2a with Fig. 2b, which presents the same LGMM trajectories with JPA trend lines, it is clear that the JPA regression lines fit much more closely to the data points of the LGMM linear and quadratic trend lines.

Fig. 3 presents the average difference between the estimated means for each group at each time point and the predicted value based on the LGMM linear trend, the LGMM quadratic trend or based on the multiple line segments provided by the JPA. It is clear that while both the linear and quadratic trends provided by the LGMM decrease in precision across time, the precision of the JPA remains stable across time.

The majority of the sample was in the stable occasional drinkers group (SOD; $N = 416$, 76% of the total sample, mean PDA 93.57), which was characterized by a stable pattern of infrequent drinking. The intercept, linear slope, and quadratic slope for the SOD group all significantly differed from 0 (intercept = 98.63, $p < 0.001$; linear slope = −2.37, $p < 0.001$; quadratic slope = 0.19, $p < 0.001$). The negative linear slope implies that over time the SOD group increased their drinking frequency, and the positive quadratic slope implies that at some point the trend in drinking frequency either increased more rapidly than would be expected from a linear trend or changed from increasing to decreasing during the study period. Fig. 2 panel A suggests that the latter interpretation is more accurate.

The next most common group was the increasing frequency drinkers group (IFD; $N = 67$, 12% of the total sample, mean PDA 52.21), which was characterized by a rapid increase in drinking frequency across the study period. The intercept, linear slope, and quadratic slope for the IFD group all differed from 0 (intercept = 97.23, $p < 0.001$; linear slope = −12.16, $p < 0.001$; quadratic slope = 0.50, $p < 0.004$). The negative linear slope implies that the IFD group started with a high percentage of abstinent days and ended with a low percentage of abstinent days, and the positive quadratic slope suggests that this trend is more rapid than would be expected from a linear trend.

Table 2
Joinpoint analysis test for number of segments and segment intercepts and slopes. JP, joinpoint.

#JP	Test for #JP		Segment	Intercept	Slope
	Test	*p*-Value			
Slightly decreasing frequency drinkers					
0	0 vs. 2	0.89[a]	1	53.49	1.51
	0 vs. 1	0.77[a]	2	–	–
			3	–	–
Stable occasional drinkers					
1	0 vs. 2	0.0002[a,**]	1	100.14	−1.89
	1 vs. 2	0.22[b]	2	87.86	.56
			3	–	–
Greatly decreasing frequency drinkers					
2	0 vs. 2	0.004[a,**]	1	7.70	6.44
	1 vs. 2	0.04[b,*]	2	79.25	−3.78
			3	−12.78	5.42
Increasing frequency drinkers					
0	0 vs. 2	0.07[a]	1	92.30	−6.17
	0 vs. 1	0.04[a]	2	–	–
			3	–	–

[a] Tested against $p < 0.025$.
[b] Tested against $p < 0.05$.
[*] $p < 0.05$.
[**] $p < 0.025$.

The third most common group was the slightly decreasing frequency drinkers (SDFD; $N = 44$, 8% of the total sample, mean PDA 63.32), which was characterized by a mild decrease in drinking across the study period. The SDFD group had an intercept that significantly differed from 0 (intercept = 59.91, $p < 0.001$), but neither the linear nor quadratic slopes differed from 0. This implies that the SDFD group maintained a stable level of moderately frequent drinking throughout the study period.

The least common group was the greatly decreasing frequency drinkers (GDFD; $N = 22$, 4% of the total sample, mean PDA 39.10), which was characterized by a rapid decrease in drinking frequency over the 12-month study period. The intercept, linear slope, and quadratic slope for the GDFD group all differed from 0 (intercept = 13.13, $p < 0.001$; linear slope = 8.23, $p = 0.001$; quadratic slope = −0.47, $p = 0.046$). The positive linear slope implies that the GDFD group decreased its drinking frequency (had more abstinent days) across the study period, and the negative quadratic slope in this case implies that at some point in the study period the drinking pattern of participants in this group changed from decreasing drinking frequency to increasing drinking frequency as seen in Fig. 2 panel A.

3.3. Joinpoint analysis results and interpretation

Joinpoint analysis (JPA) was run as a post hoc procedure to aid in the interpretation of the LGMMs by simplifying the trends into a discrete number of line segments describing trends within each class. Joinpoint results are presented in Table 2 and Fig. 2b. The permutation test (http://surveillance.cancer.gov/joinpoint/aapc.html) used by the Joinpoint software uses a correction to control for type I error. The criteria for significance are adjusted to control for type I error using the following procedure. $\alpha(k_a; k_b) = \alpha/(\text{MAX} - k_a)$, where α is 0.05, k_a is the null and k_b is the alternative hypothesis.

For example if the MIN is 0 and the MAX is 2 joinpoints then the test would be

$$P(k > 0|k = 0) = \alpha(0, 2) + \alpha(0, 1)$$
$$P(k > 1|k = 1) = \alpha(1, 2)$$

and the correction would be

$$\alpha(0, 2) = \alpha(0, 1) = \alpha/2$$
$$\alpha(1, 2) = \alpha$$

In other words, for tests comparing 0 to 2 joinpoints or 0 to 1 joinpoint the criteria for significance is $\alpha = 0.05/2 = 0.025$, and for tests comparing 1 to 2 joinpoints the criteria for significance is $\alpha = 0.05$ (see joinpoint regression software users guide for further details). For this study, the recommended range of possible change points is 0, 1, or 2. Up to two joinpoints is recommended for 12 time points based on two criteria (a) a joinpoint cannot occur within 3 data points from the beginning or end of a series, and (b) there must be at least 4 data points between two joinpoints (Kim et al., 2000; joinpoint regression software users guide). If the more complex model (i.e., the model with more change points) fits better than would be expected by chance than the simpler model (i.e., the model with fewer change points), the more complex model is selected.

The JPA results for the SOD group revealed one joinpoint point at month 4 from increasing frequency of drinking to decreasing frequency of drinking. One joinpoint point was selected because although two joinpoints fit better than zero joinpoints, two joinpoints did not fit better than one joinpoint. Examination of the slopes of each line segment reveals that the SOD group began with 100% days abstinent, increased in frequency of drinking from months 1 to 4 to 92.17% days abstinent, and then decreased in drinking frequency to 94.05% days abstinent by month 12. Furthermore, a comparison of the slopes of the line segments descriptively shows that the rate of increased drinking frequency in months 1 to 4 was greater than the subsequent decreased drinking frequency in months 5 to 12 (slope for months 1 to 4 = −1.89 vs. slope for months 5 to 12 = 0.56).

JPA results for the IFD group revealed a single line with zero joinpoints best fit the data. Zero joinpoints were selected because neither the test for two vs. zero nor the test for one vs. zero joinpoints were significant. Interpretation of this line shows a group of participants who steadily increased the frequency of their drinking across the 12-month study period from 92.30% days abstinent at month one to 25.03% days abstinent at month 12, a rate of −6.17% days abstinent change in drinking frequency per month.

Similarly, JPA results for the SDFD group revealed a single line with zero joinpoints best fit the data. Zero joinpoints were selected because neither the test for two vs. zero nor the test for one vs. zero joinpoints were significant. Interpretation of this line shows a group of participants that steadily decreased their drinking frequency across the 12-month study period from 53.49% days abstinent at month 1 to 71.82% days abstinent by month 12, a rate of 1.51% days abstinent change in drinking frequency per month.

Finally, the JPA results for the GDFD group revealed two joinpoints, at months 7 and 10. The two joinpoint models were selected because both the test comparing two joinpoints to zero joinpoints and the test comparing two joinpoints to one joinpoint were significant. Examination of the slopes of each line segment revealed that the GDFD group reported 7.70% days abstinent at month 1 decreased their frequency of drinking at a rate of change of 6.44% days abstinent per month until month 7, at which point they reported 51.60% days abstinent. Then they reported increasing their drinking at a rate of change of -3.78% days abstinent per month until month 10, when they reported 39.49% days abstinent. This trend was followed by a decrease in drinking for the remainder of the study period at a rate of 5.42% days abstinent per month to a frequency of 50.41% days abstinent at month 12.

4. Discussion

This paper provides a demonstration of the application of JPA as a post hoc analytic procedure for LGMM analyses of AUD clinical course data. As expected, the results from this study showed considerable heterogeneity in the clinical course of AUD, which was best represented by a 4-class LGMM. This study also showed that application of JPA allowed the identification of changes in the clinical course of the four subgroups. Therefore, the JPA procedure helped to characterize the changing drinking behavior of a sample of AUD adults with finer detail than LGMM alone. Identifying the rates of change along with the moments in time when groups of people change from improvement to deterioration can help identify critical periods in the change process for AUD individuals. In addition, employing the JPA procedure following LGMM analysis promotes ease of dissemination of results with the final interpretation consisting of a series of linear regression analyses that may be more amenable for communicating to clinicians with less exposure to latent variable modeling interpretation. Further, the JPA provides information about the number of inflection points for a given subset of participants, which might have clinical utility in identifying moments during or after treatment to intervene. Finally, frequently a single intercept, linear slope, and quadratic slope, as provided by LGMM models, is not sufficient to model the complex and often fluctuating clinical course of AUD (see Fig. 3).

This represents a key advantage to using JPA in tandem with LGMM; while the LGMM will break down the sample into subgroups, which are similar to each other and different from one another, the JPA will model longitudinal changes in each of these groups across times identifying the critical inflection points for each group. Further, because JPA is able to model linear trends in segments rather than for a complete trajectory, the results are more accurate across the study period. Indeed, JPA enhances LGMM by providing potentially clinically useful change points in the growth trajectories for each latent class and by providing a more precise description of change over time than is possible from LGMM alone.

For example, examining qualitatively the SOD class (see Fig. 2a and b), one key difference between the LGMM with JPA and LGMM alone interpretations is that the JPA identifies a pattern of increasing and decreasing frequency of drinking that results in overall stability. In contrast, the LGMM alone provides contradictory suggestions that the SOD group will continue to deteriorate across time or that it will continue to improve across time, neither of which represents the actual clinical course of this group. Similarly, the GDFD group appears to greatly decrease its drinking frequency until month seven at which point it begins to fluctuate between increasing and decreasing its drinking frequency between 40% and 50% days abstinent. This nuance in the clinical course for the GDFD group is captured by adding the JPA to the LGMM, unlike the LGMM alone that projects the GDFD group to either continue to improve (linear trend) or continue to deteriorate (quadratic trend) across time. Thus, it is clear that a level of detail is lost with the LGMM alone compared to the LGMM with JPA when the JPA identifies change points in the data. However, even when we examine the two groups with zero joinpoints, namely SDFD and IFD, we can see that the JPA provides a better fit to the data than the trends produced by the LGMM alone. Specifically, for the SDFD group even though the positive quadratic trend from the LGMM alone matches fairly well, the negative linear trend incorrectly projects a slight deterioration across time. And, for the IFD group, the results from the LGMM alone deviate greatly from the data in both the linear and quadratic trends, with the quadratic trend being in the wrong direction. Taken

together, even when the JPA does not identify inflection points in the clinical course the results better match the data then the LGMM alone.

The results of this study should be interpreted with consideration of its limitations. First, although this study used a representative sample of AUD participants, potential predictors of class membership were not included in the model for the purposes of presenting a realistic but simple demonstration of this analytic procedure. Second, we focused our analyses only on PDA even though other alcohol use variables are known to be important indicators of alcohol use severity (e.g., PHDD – percent heavy drinking days and DDD – drinks per drinking day). However, it is worth noting that the advantages of using JPA as a post hoc procedure would hold with other outcomes including PHDD and DDD. Third, we did not test for class differences in psychosocial variables, limiting the substantive interpretability of the class structure. Fourth, we did not map the inflection points in drinking frequency to clinical markers of functioning. Fifth, we assumed homoscedasticity of the model-estimated means included in the JPA.

This illustration of the utility of JPA as a post hoc procedure for LGMMs can provide a starting point for future research aimed at identifying critical change points in the clinical course of AUD and other biopsychosocial phenomena. JPA is a useful tool for analyzing longitudinal data with the goal of identifying non-linear trends. Given the growing body of research employing LGMM and other similar procedures, JPA might help to provide a clearer picture of the dynamic patterns of alcohol use often seen in AUD clinical samples during and following treatment.

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Contributors

Authors Mark A. Prince and Stephen A. Maisto designed the study and wrote the manuscript. Mark A. Prince undertook the statistical analysis, and Stephen A. Maisto wrote the introduction section. All authors contributed to and have approved the final manuscript.

Conflict of interest statement

No conflict declared.

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