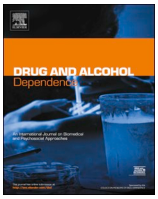
Drug and Alcohol Dependence 201 (2019) 58–64

Contents lists available at ScienceDirect

Drug and Alcohol Dependence

journal homepage: www.elsevier.com/locate/drugalcdep



Full length article

A comparison of longitudinal modelling approaches: Alcohol and cannabis use from adolescence to young adulthood

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ARTICLE INFO

Keywords:
Substance use
Latent curve model
Growth mixture model
Latent class growth analysis
Negative binomial

ABSTRACT

Background: Modelling trajectories of substance use over time is complex and requires judicious choices from a number of modelling approaches. In this study we examine the relative strengths and weakness of latent curve models (LCM), growth mixture modelling (GMM), and latent class growth analysis (LCGA).
Design: Data were drawn from the Australian Temperament Project, a 36-year-old community-based longitudinal study that has followed a sample of young Australians from infancy to adulthood across 16 waves of follow-up since 1983. Models were fitted on past month alcohol use (n = 1468) and cannabis use (n = 549) across six waves of data collected from age 13–14 to 27–28 years.
Findings: Of the three model types, GMMs were the best fit. However, these models were limited given the variance of numerous growth parameters had to be constrained to zero. Additionally, both the GMM and LCGA solutions had low entropy. The negative binomial LCMs provided a relatively well-fitting solution with fewer drawbacks in terms of growth parameter estimation and entropy issues. In all cases, model fit was enhanced when using a negative binomial distribution.
Conclusions: Substance use researchers would benefit from adopting a complimentary framework by exploring both LCMs and mixture approaches, in light of the relative strengths and weaknesses as identified. Additionally, the distribution of data should inform modelling decisions.

1. Introduction

There is continued debate about how to appropriately model population heterogeneity in individual-level substance use over time. Growth modelling methodologies have provided several approaches and have been used regularly in the substance use literature (e.g. Chen and Jacobson, 2012; Nelson et al., 2015; Tucker et al., 2005). However, the suite of growth modelling options available can lead to uncertainty when selecting a modelling approach. This is additionally complicated because substance use data are rarely normally-distributed, which is a common assumption, requiring additional statistical adjustments. Whilst previous research has provided a robust examination of growth modelling approaches with categorical ordinal data (Feldman et al., 2009), the field's knowledge may be significantly advanced through better understanding of the variation arising in modelling approaches when utilising continuously scaled substance use data.

1.1. Latent curve models

Latent curve models (LCMs) offer one method of quantifying substance use over time. Generally, LCMs are a specific application of structural equation modelling. In LCMs, the observed variables are repeated measures of the same variable (e.g., substance use frequency), and latent (unobserved) variables (e.g., intercept and slope) describe

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https://doi.org/10.1016/j.drugalcdep.2019.05.001
Received 19 September 2018; Received in revised form 13 May 2019; Accepted 26 May 2019

the trajectory of change over time in the observed variables. Importantly, the mean of any latent growth variable represents the average growth for the sample, whilst the variance of the latent variable is a measure of individual variability around this mean growth over time (Preacher et al., 2008). Consequently, LCMs of substance use data identify both the average trajectory of the sample and how each individual differs from this average. This is often considered as a variable-centred approach (Laursen and Hoff, 2006), as variation in substance use trajectories is provided for each aspect of growth (e.g., intercept and slope latent variables) within each person. A common assumption underlying LCMs is that the estimated growth parameters are normally distributed. When the observed data are highly skewed, as in substance use, it is important to address the potential violation of this assumption.

1.2. Mixture models

Mixture models, which can be viewed as an extension of LCMs, are another method of quantifying change over time. Two of the most common mixture models are growth mixture modelling (GMMs) and latent class growth analysis (LCGA). These models are generally considered as person-centred analyses (Laursen and Hoff, 2006), as they assume that there are unobserved, qualitatively distinct sub-populations or classes within a larger population, whose members share a similar pattern of growth over time (Nagin, 2005). Consequently, mixture models are able to identify trajectory patterns of substance that putatively reflect taxonomic distinctions.

GMMs have gained substantial attention, particularly because they may address concerns regarding the non-normally distributed growth parameter variation expected within substance use data (Feldman et al., 2009). Specifically, GMMs relax assumptions of normality by using a number of normal distributions to characterise a larger, potentially non-normal, distribution. However, GMMs still require within-class normality (Feldman et al., 2009), for which even mild violations can result in the extraction of too many classes (Bauer, 2007). More specifically, the population distribution of growth is represented as a discrete number of latent classes, each with their own trajectory of growth over time represented by latent growth parameters. Given that each class in a GMM is represented by its own trajectory of growth, decisions must be made about how to model these separate trajectories. While at the most basic level the variance of any latent growth variables is held equal across classes this can be relaxed and the variability can be estimated separately within each class.

LCGA is a restricted application of GMM, specifying that all individuals within the same class follow the same trajectory (Nagin, 1999). In practice, this equates to restricting the variance of latent growth parameters within each class to zero, and thus only the mean growth over time for each class is estimated (Jung and Wickrama, 2008). Since no within-class variance is estimated, the assumption of within-class normality which applies to GMMs does not apply to LCGA; however, local independence is instead assumed, such that the indicators are independent conditional on class membership (Bollen, 2002). In comparison to GMMs, LCGAs generally identify a greater number of classes (Feldman et al., 2009).

1.3. Applicability of models

Some concerns have been raised about the use of mixture approaches such as GMM or LCGM. Specifically, it has been noted that while some populations are comprised of distinct groups, most populations contain a continuous distribution of individual levels (Nagin et al., 2005). It has therefore been argued that mixture models run the risk of overfitting and identifying sample-specific qualitative structures when none truly exists in the population (Bauer, 2007). This is not to say that a class solution cannot fit the data; but rather *"latent trajectory classes are, in most cases, nothing more than artificial categories rendered from the true continuum of change"* (Bauer, 2007; p. 777). It is therefore critical to consider how research questions may drive approach selection. Specifically, for research questions related to qualitative speculation, mixture approaches are necessary to examine the presence of subgroups. However, for questions that seek to estimate population heterogeneity both LCMs and mixture methods may be useful. Researchers therefore need to consider not only the underlying assumptions of data and models, but also how the choice of modelling method may impact on the interpretation of population heterogeneity (i.e., continuous versus groups).

1.4. Distribution specification

Common forms of the models discussed above assume to some extent a normal distribution in the estimation of growth parameters. Mixture approaches soften this assumption by utilising several normal distributions (GMM) or purely discrete classes (LCGA). Concerns have been raised that these approaches may extract too many classes, as additional classes are needed to represent skewed parts of the distribution (Bauer, 2007; Macia et al., 2018). However, these models can be further adjusted to specifically allow for non-normal distributions. For example, observed data can be specified as counts (as opposed to continuous data) and more suitable growth parameter distributions can be assumed. Models that assume a negative binomial distribution can be appropriate for substance use count data as they handle both overdispersion and an excess number of zeros (Zeileis et al., 2008). Statistical programs such as Mplus allow for these accommodations.

1.5. Current study

The purpose of this study is to facilitate informed decision making around model selection. Specifically, the aim is to demonstrate the process and impact of applying commonly used growth modelling methodologies to the quantification of substance use growth over time. We additionally explore the importance of specifying the data's distributional form as normal (continuous) or negative binomial (counts). To exemplify these methods, we utilise alcohol and cannabis use data from a large Australian population-based cohort study.

2. Method

Participants were from the Australian Temperament Project (ATP), a large multi-wave longitudinal study (16 waves) tracking the psychosocial development of young people from infancy to adulthood. The baseline sample consisted of 2443 infants aged between 4–8 months from urban and rural areas of Victoria, Australia. Attrition in the ATP has been sustained at approximately 1% per annum, with a bias toward loss to follow-up of parents from lower socio-demographic and non-Australian-born backgrounds (Letcher et al., 2012). Further information regarding sample characteristics are available elsewhere (Vassallo and Sanson, 2013).

To be included in the study, participants needed to provide self-report survey responses relating to alcohol or cannabis frequency for at least one of the six time points (ages 13–14, 15–16, 17–18, 19–20, 23–24, and 27–28 years). For alcohol use, this resulted in a sample size of 1468 (745 female), of which 71.39% completed four or more waves. For cannabis use, this resulted in a sample size of 549 (270 female), of which 62.66% completed four or more waves.

2.1. Measures of substance use

The number of days per month that participants used alcohol was assessed at all six waves, whilst cannabis use was assessed at five waves (i.e., not at age 13). Scores could range from 0 to 30 days for each substance type.

2.2. Statistical analysis

Mplus Version 8 (Muthén and Muthén, 2010) was used for all analyses (Mplus syntax available in the supplementary material and https://osf.io/2ytfa/). All models were estimated separately for each substance type. We first estimated LCMs. We next estimated the GMMs, for which the variance of growth parameter was estimated for each class, although these were held equal across classes. Finally, we estimated the LCGAs, where the variance of each growth parameter is restricted to zero across all classes. Each analysis was run by both specifying the data as continuous and assuming a normal distribution (models referred to as continuous) and as counts and assuming a negative binomial distribution (models referred to as NegBin). In all models we estimated four parameters (intercept, linear, quadratic, and cubic growth) that characterise growth over time. We attempted to estimate the variance of all growth parameters in applicable models (i.e., LCM and GMM). If this resulted in a model that was not-well identified, we restricted the variance of the highest polynomial (e.g., first cubic, then quadratic, etc.). Additionally, the residual variance of cannabis frequency at age 27–28 years was set to zero. Constraints imposed on the LCMs were applied to the GMMs. Missing data were accounted for using a full information maximum likelihood (FIML) approach. We employed the maximum likelihood estimator with robust standard errors (MLR), which is appropriate to handle non-normal continuous and count data (Muthén and Muthén, 2010).

We estimated GMM and LCGA models with an increasing number of classes until models were not well identified or the addition of another class did not improve model fit. The suitability of each solution was evaluated based on several statistical and observational criteria. A number of fit criteria were used to evaluate model selection: the Log Likelihood value (LL), the Bayesian Information Criterion (BIC), the Consistent Akaike's Information Criterion (CAIC), the Approximate Weight of Evidence Criterion (AWE), the adjusted Lo-Mendell-Rubin likelihood ratio test (LMR), and the Vuong-Lo-Mendell Rubin likelihood ratio test (VLMR). For the BIC, CAIC, and AWE, smaller values indicate better fit (Little, 2013). For the LMR and VLMR a p-value less than 0.05 indicates better fit for that class solution (k) compared to the previous class solution (k-1). Additionally, while entropy was not used to select a class solution, it is useful in interpreting class solutions. Entropy with values closer to 1 indicate clear delineation of classes (Celeux and Soromenho, 2006), and 0.80 is often used as an acceptable level (Nájera Catalán, 2018).Upon deciding the most suitable class solution, participants were assigned to the trajectory class for each substance type for which they had the highest probability of membership.

3. Results

Detailed information regarding class selection for the GMM and LCGA solutions is presented in the supplementary material. Fit indices for the selected models are presented in Table 1. Estimates of the mean and variance for the intercept, linear, quadratic, and cubic growth parameters for the selected models are additionally presented in Table 1.

3.1. Latent curve models

Fig. 1 presents the mean growth trajectories for alcohol, binge drinking, tobacco, and cannabis use, for both the continuous and NegBin LCMs. The NegBin LCMs had better fit across all indices for alcohol and cannabis models.

The continuous LCMs indicated that for both alcohol and cannabis, use had initiated at baseline. For cannabis, there was evidence for linear, quadratic, and cubic growth; however, for alcohol, there was evidence of only linear and cubic growth. There was evidence to suggest subject-specific variation in the intercept as well as linear and quadratic growth parameters (cubic not estimated). For the NegBin LCMs, in both alcohol and cannabis there was evidence that use had initiated at baseline and of linear, quadratic and cubic growth. There was evidence to suggest subject-specific variation in the intercept as well as linear and quadratic growth parameters (cubic not estimated).

3.2. Growth mixture model

Fig. 2 presents the mean growth trajectory classes for alcohol and cannabis use for the selected continuous and NegBin GMMs. The NegBin GMMs had better fit across all indices for alcohol and cannabis models.

The selected GMM (continuous) solutions identified a single trajectory class (LCM results above) for alcohol and two cannabis classes (1 - low use: 89.80%; 2 - high use: 10.20%). For cannabis, there was evidence to support variation in the intercept as well as linear and quadratic growth parameters (but not cubic). Entropy values were high for the cannabis (0.96) model, suggesting good separation amongst the classes. The selected GMM (count) solution identified two alcohol trajectory classes (1 - low use: 87.47%; 2 - high use: 12.53%) and two cannabis classes (1 - low use: 83.61%; 2 - high use: 16.39%). For alcohol use there was evidence to support variation in the intercept and linear growth parameters (quadratic and cubic not estimated) and for cannabis use there was evidence to support variation in the intercept (linear, quadratic, and cubic growth parameters not estimated). Entropy was low for alcohol (0.67) and slightly below the acceptable cut-point (0.76) for cannabis, suggesting that the classes may not be well delineated.

3.3. Latent class growth analysis

Fig. 3 presents the mean growth trajectory classes for alcohol and cannabis use for the selected continuous and NegBin LCGAs. For each analysis, the variance of all growth parameters was set to zero. The NegBin LCGAs had better fit across all indices for alcohol and cannabis models.

In the continuous LCGAs, we identified four alcohol trajectory classes (1 - low use: 80.93%; 2 - high use: 13.28%: 3 - low-high-low-high use 3.54%; 4 - high-low-high-low use: 2.25%) and two cannabis classes (1 - low use: 88.89%; 2 - high use: 11.11%). For the alcohol and cannabis models, entropy values of 0.86 and 0.95, respectively, indicated good separation of classes. In the NegBin LCGAs, we identified two alcohol classes (1 - low use: 43.19%; 2 - high use: 56.81%) and two cannabis classes (1 - low use: 73.95%; 2 - high use: 26.05%). Entropy values however were low for both the alcohol and cannabis models (0.57 and 0.70, respectively), suggesting poor separation amongst the classes.

4. Discussion

In this comparative study we examine the relative strengths and weakness of three common growth modelling methodologies (latent curve models, growth mixture models, and latent class growth analysis) to quantify change in alcohol and cannabis use from ages 13–14 to 27–28. For each model we specified the data as both continuous (assumed normal distribution) and as counts (assumed negative binomial distribution). Our goal was to illustrate how modelling approaches influence the depiction of population growth in real substance use data. Broadly, our results suggest that substance use researchers would benefit from: (1) adopting a complementary framework incorporating both LCMs and mixture models to balance both the strengths and weakness of both approaches; and (2) modelling distributions appropriate to the data.

Our results highlight that interrogating substance use data and considering the distribution should occur prior to any modelling procedures. Specifically, in comparing the continuous and NegBin models, the selected NegBin models provided better fitting solutions across the

Table 1
Fit statistics of the selected Latent Curve Models, Growth Mixture Models, and Latent Class Growth Analyses (continuous and count models) with the mean and variance estimates of growth parameters for alcohol and cannabis use frequency data

	Model	Npar	LL	BIC	CAIC	AWE	LMR	VLMR	Entropy	Classes	Class Size(%)	Intercept M (V)	Linear M (V)	Quadratic M (V)	Cubic M (V
									Alcohol (N = 1468)						
LCM	Cont	16	−18796.30	37709.27	37725.27	37873.94	–	–	–	–	–	**0.896** (**3.136**)	**0.960** (**0.863**)	0.018 (**0.005**)	**-0.003** (n.e.)
	NegBin	16	−15330.53	30777.07	30793.73	30942.40	–	–	–	–	–	**-0.693** (**1.761**)	**0.755** (**0.058**)	**-0.070**(**< 0.001**)	**0.002** (n.e.)
GMM	Cont	2-class solution did not fit better than the 1-class solution (Cont LCM)													
	NegBin	18	−15306.38	30744.02	30762.02	30929.27	0.037	0.034	0.67	1	87.47%	**-0.378** (**0.789**)	**0.642** (**0.005**)	**-0.052** (n.e.)	**0.001** (n.e.)
										2	12.53%	−0.593 (**0.789**)	**0.636** (**0.005**)	**-0.082** (n.e.)	0.003 (n.e.)
LCGA	Cont	25	−18029.73	36241.74	36266.74	36499.04	0.025	0.023	0.86	1	80.93%	**0.380** (n.e.)	**0.843** (n.e.)	−0.012 (n.e.)	−0.001 (n.e.)
										2	13.28%	**0.858** (n.e.)	**0.509** (n.e.)	**0.391** (n.e.)	**-0.025** (n.e.)
										3	3.54%	**2.876** (n.e.)	**10.360** (n.e.)	**-1.916** (n.e.)	**0.088** (n.e.)
										4	2.25%	**13.704** (n.e.)	**-4.614** (n.e.)	**0.848** (n.e.)	**-0.038** (n.e.)
	NegBin	15	−15482.19	31073.74	31088.75	31228.12	0.001	0.001	0.57	1	43.19%	**-1.585** (n.e.)	**0.828** (n.e.)	**-0.071** (n.e.)	**0.002** (n.e.)
										2	56.81%	**0.504** (n.e.)	**0.517** (n.e.)	**-0.046** (n.e.)	**0.001** (n.e.)
									Cannabis (N = 549)						
LCM	Cont	14	−6449.82	12987.95	13001.95	13118.26	–	–	–	–	–	**1.755** (**14.448**)	**1.043** (**3.005**)	**-0.140** (**0.014**)	**0.005** (n.e.)
	NegBin	12	−3736.87	7549.44	7561.44	7661.14	–	–	–	–	–	−0.180 (**1.680**)	**0.490** (**0.022**)	**-0.076** (n.e.)	**0.003** (n.e.)
GMM	Cont	19	−6095.03	12309.92	12328.92	12486.77	0.005	0.004	0.96	1	89.80%	**1.328** (**12.115**)	**0.736** (**1.637**)	**-0.139** (**0.009**)	**0.006** (n.e.)
										2	10.20%	**5.461** (**12.115**)	**3.644** (**1.637**)	−0.130 (**0.009**)	−0.003 (n.e.)
	NegBin	15	−3710.84	7516.293	7531.29	7655.92	0.002	0.002	0.76	1	83.61%	0.016 (**0.461**)	**0.665** (n.e.)	**-0.195** (n.e.)	**0.012** (n.e.)
										2	16.39%	**0.701** (**0.461**)	**0.639** (n.e.)	**-0.061** (n.e.)	0.002 (n.e.)
LCGA	Cont	14	−6140.33	12368.97	12382.97	12499.28	0.030	0.027	0.95	1	88.89%	**1.234** (n.e.)	**0.810** (n.e.)	**-0.184** (n.e.)	**0.010** (n.e.)
										2	11.11%	**5.138** (n.e.)	**3.126** (n.e.)	0.143 (n.e.)	−0.026 (n.e.)
	NegBin	14	−3687.66	7526.71	7540.71	7657.03	< 0.001	< 0.001	0.70	1	73.95%	**-0.394** (n.e.)	0.235 (n.e.)	−0.057 (n.e.)	0.003 (n.e.)
										2	26.05%	**1.378** (n.e.)	**0.505** (n.e.)	**-0.070** (n.e.)	**0.003** (n.e.)

Note: Cont = Continuous model; NegBin = negative binomial count model; Npar = number of parameters; LL = Log-likelihood value; BIC = Bayesian Information Criterion; CAIC = Consistent Akaike's Information Criterion; AWE = Approximate Weight of Evidence Criterion; LMR = adjusted Lo-Mendell-Rubin likelihood ratio test; VLMR = Vuong-Lo-Mendell Rubin likelihood ratio test; M = mean; V = variance; n.e. = specified as not estimated in the model; bolded values indicate $p < 0.05$.

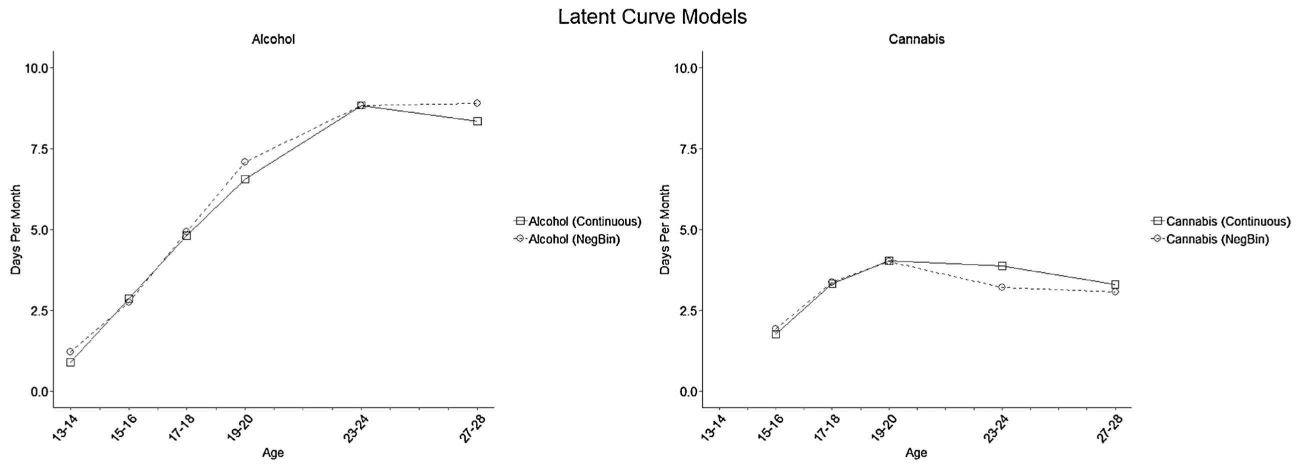

Fig. 1. Estimated latent curve model trajectory for alcohol and cannabis use frequency when data were modelled as continuous (solid lines) and counts (dashed lines).

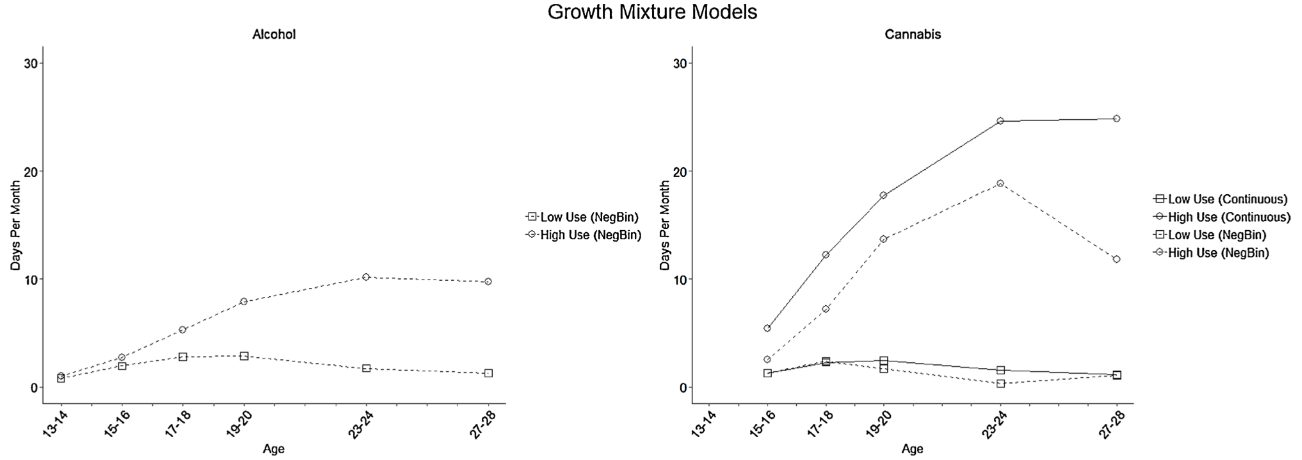

Fig. 2. Estimated growth mixture model trajectory classes for alcohol and cannabis use frequency when data were modelled as continuous (solid lines) and counts (dashed lines).

range of indices (i.e., lower values) across all approaches. This was apparent for both alcohol and cannabis use, suggesting that correctly specifying the data distribution was critical to better fit growth modelling solutions for a range of response patterns. This finding provides general support for previous simulation work which stressed the importance of correctly specifying count data distributions (Macia et al., 2018).

Despite the improvements in fit, the estimated mean trajectory of the continuous and NegBin LCMs was relatively similar. Previous work has also suggested that incorrectly specified distributions may result in the incorrect number of classes being extracted form mixture models (Macia et al., 2018). While this was notable in the alcohol use models,

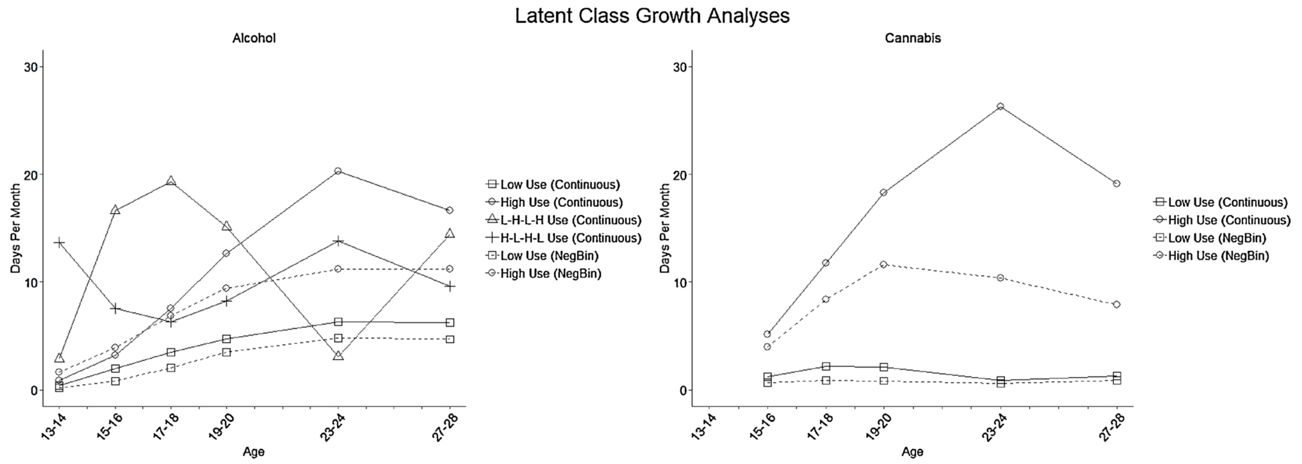

Fig. 3. Estimated latent class growth analysis trajectory classes for alcohol and cannabis use frequency when data were modelled as continuous (solid lines) and counts (dashed lines).

the same number of classes were identified in both the continuous and NegBin cannabis models. There were however differences in the estimate mean solutions. Together this suggests that in order to achieve well-fitting solutions and accurate trajectory shapes, substance use researchers should carefully interrogate their data before use and ensure selected models estimate solutions in which appropriate distributions have been assumed (such as negative binomial).

Within the NegBin approaches our findings suggested that the GMM solutions were the best fitting for both alcohol and cannabis use. However, there were additional issues requiring consideration for these models. First, the variance of numerous growth parameters had to be restricted to zero to enable model estimation. For example, for cannabis use we were only able to estimate the variance of the intercept (almost a LCGA). Consequently, while it has been suggested that GMMs should be preferred over LCGA, as they provide further information regarding individual variability (King et al., 2017), analytic limitations mean that estimating the variance in growth parameters of interest may not always be possible. This means that researchers may run into inadmissible solutions when estimating the variance of high polynomial growth parameters (e.g., cubic growth), and may thus be analytically restricted to simpler GMMs than may be customary in continuous models. These considerations apply similarly to LCMs, as illustrated by the cannabis model.

Second, the entropy values were below the recommended cut-off of 0.80, although only slightly below for the cannabis models. This issue was also apparent in the LCGAs. While entropy is not a measure of fit (i.e., NegBin models still fit better than continuous models), low entropy suggests that the model may not be useful in identifying homogenous groups (Celeux and Soromenho, 2006). This makes the utility of such models uncertain and entreats researchers to be cautious in interpreting the most-likely classes for solutions, despite the improvement in fit.

In light of these concerns, LCMs present as an enticing complementary solution for several reasons. First, in terms of fit, while the LCMs were not the best fit, fit indices were only slightly higher than those observed in the GMMs and even better than those in the LCGAs for alcohol, suggesting relatively good fit. Second, LCMs estimated the variance of more growth parameters yielding more detailed information about the individual variability of growth trajectories. Third, the LCMs do not suffer from limitations imposed by low entropy values. Finally, LCMs quantify the population variability on a continuum, aligning with representations of population variability as innately continuous rather than categorical (Bauer, 2007).

The current findings highlight further considerations for researchers. Studies have suggested that although a decision to restrict growth parameter variation may be a quick and effective solution, they require careful consideration. For example, when growth parameter variation is restricted, an autoregressive structure that distorts the nature of the mixtures may emerge; although this may be handled by explicitly modelling this structure (Gilthorpe et al., 2014). Others have suggested that issues modelling the variance of growth parameters may be indicative of structural misspecification, of which several tests have been proposed (see Kolenikov and Bollen, 2012), although these are not yet provided as default outputs in common SEM packages. Furthermore, decisions made to constrain growth parameter variance to be equal across classes, while resulting in simpler models to estimate, may mean that parameters of greater interest (i.e., class mean estimates) are biased (Enders and Tofighi, 2008). Additionally, low entropy values are of concern when wanting to analyse the most-likely class membership status, like in the alcohol mixture models. However, methods such as the 3-step approach (Asparouhov and Muthén, 2014), allow the incorporation of measurement error when using the most-likely class variable.

In summary, mixture models consistently provided solutions that were statistically better fitting than LCMs. On the other hand, the LCMs were not substantially worse in terms of fit than the mixture approaches, were able to estimate the variance of more growth parameters, and were not limited by issues of entropy. Additionally, NegBin models were consistently of better fit than their continuous counterparts. These findings demonstrate that researchers would be able to achieve the most robust results by utilising these methods in unison and examining whether there is consistency in interpretation of findings. There are however, some key limitations are of note. First, the use of real data is valuable in demonstrating how models may look, but these findings may not necessarily generalise to other populations. Second, we were unable to explore all growth modelling methods that could be applied to substance use data (i.e., zero-inflated models). Of particular relevance to substance researchers, Muthen and Asparouhov (2015) suggest the use of growth modelling approaches that employ the skew-t distribution. The skew-t distribution includes model parameters that capture the skew of scores. As such these models are suggested to capture non-normality without increasing the risk of extracting an increased number of latent classes.

In conclusion, this paper demonstrated the strengths and weaknesses of several common growth models. Our results suggest that substance use researchers would benefit from adopting a complementary framework, by modelling both LCMs and mixture models, to capitalise on the strengths and weakness of each approach. Modelling assuming appropriate distributions for substance use data was also critical. Future substantive work should endeavour to provide both a comprehensive understanding of substance use growth by utilising multiple methods and an accurate estimation of growth by focusing on the distribution of data.

Role of funding source

Data collection for the ATP study was supported primarily through Australian grants from the Melbourne Royal Children’s Hospital Research Foundation, National Health and Medical Research Council, Australian Research Council, and the Australian Institute of Family Studies. Funding for this work was supported by grants from the Australian Research Council [DP130101459; DP160103160; DP180102447] and the National Health and Medical Research Council of Australia [APP1082406]. CJG was supported by a Deakin University PhD Scholarship.

Contributors

CJG conceptualized and designed the study, prepared data for analysis and carried out the analyses, interpreted results, wrote the manuscript, and critically reviewed and revised the manuscript for important intellectual content. GJY conceptualized and designed the study, prepared data for analysis, interpreted results, and critically reviewed and revised the manuscript for important intellectual content. KSB conceptualized and designed the study, and interpreted results, and critically reviewed and revised the manuscript for important intellectual content. PL, JAM, JM, DMH conceptualized and designed the study, contributed to the collection of data, and critically reviewed and revised the manuscript for important intellectual content. LJH and ES interpreted results and critically reviewed and revised the manuscript for important intellectual content. AS conceptualized and designed the study, coordinated the collection of data, and critically reviewed and revised the manuscript for important intellectual content. CO and JT conceptualized and designed the study, contributed to the collection of data, and critically reviewed and revised the manuscript for important intellectual content. All authors read and approved the final manuscript.

Conflict of interest

No conflict declared.

Acknowledgements

The ATP study is located at The Royal Children's Hospital Melbourne and is a collaboration between Deakin University, The University of Melbourne, the Australian Institute of Family Studies, The University of New South Wales, The University of Otago (New Zealand), and the Royal Children's Hospital (further information available at www.aifs.gov.au/atp). The views expressed in this paper are those of the authors and may not reflect those of their organizational affiliations, nor of other collaborating individuals or organizations. We acknowledge all collaborators who have contributed to the ATP, especially Professors Margot Prior, Frank Oberklaid, and Ms Diana Smart. We would also like to sincerely thank the participating families for their time and invaluable contribution to the study.

Appendix A. Supplementary data

Supplementary material related to this article can be found, in the online version, at doi:https://doi.org/10.1016/j.drugalcdep.2019.05.001.

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