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Are Alcohol Trajectories a Useful Way of Identifying At-Risk Youth? A Multiwave Longitudinal-Epidemiologic Study

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Abstract

Objective—Trajectory approaches are a popular way of identifying subgroups of children and adolescents at high risk of developing alcohol use problems. However, mounting evidence challenges the meaning and utility of these putatively discrete alcohol trajectories, which can be analytically derived even in the absence of real subgroups. This study tests the hypothesis that alcohol trajectories may not reflect discrete groups—that the development of alcohol use is continuous rather than categorical.

Method—A multiwave longitudinal-epidemiologic twin study was conducted using 3,762 twins (1,808 male and 1,954 female) aged 11–29 years from the Minnesota Center for Twin and Family Research (MCTFR). Main outcome measures included various assessments of substance use, psychopathology, personality, and cognitive ability.

Results—Although multiple trajectories are derived from growth mixture modeling techniques, these trajectories are arrayed in a tiered spectrum of severity, from lower levels of use to higher levels of use. Trajectories show perfect rank-order stability throughout development, monotonic increases in heritability, and perfect rank-order correlations with established correlates of alcohol use, including other substance use behaviors, psychiatric disorders, personality traits, intelligence, and achievement.

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Conclusion—Alcohol trajectories may represent continuous gradations rather than qualitatively distinct subgroups. If so, early detection and interventions for youth based on trajectory subtyping will be less useful than continuous liability assessments. Furthermore, a continuous account of development counters the notion that individuals are predestined to follow one of a few categorically-distinct pathways and promotes the opposite idea—that development is mutable, and its continuous terrain can be traversed in many directions.

Keywords

alcohol; trajectories; development; longitudinal; early intervention

INTRODUCTION

A major focus of alcohol research is to identify children and adolescents who are at risk of developing alcohol problems. To the extent that such children can be identified, prevention and early intervention efforts have the potential to preclude or mitigate problematic drinking and its associated consequences. These consequences are not only concurrent but also cumulative. That is, beyond the immediate consequences of excessive alcohol use in adolescence—academic problems, poisoning, risky sex, motor vehicle accidents, suicides, and so on—the accretion of these consequences also reduces legitimate avenues to success in adulthood, disrupting key processes of brain development and increasing the likelihood of disability, unemployment, relationship problems, and criminal behavior.^{1–3}

One way of identifying at-risk youth is to posit the existence of distinct developmental trajectories, only some of which lead to problematic alcohol use. Two different approaches are used to identify these trajectories: the rationally-constructed approach and the statistically-acquired approach. The rationally-constructed approach relies on experts who propose distinct developmental trajectories based on patterns drawn from the research literature or their own clinical experiences. Well-known examples include Cloninger's types (Type I Alcoholism/milieu-limited and Type II Alcoholism/male-limited) and Zucker's types (Antisocial Alcoholism, Developmentally Cumulative Alcoholism, Developmentally Limited Alcoholism, and Negative Affect Alcoholism).^{4,5} A more recent example is a study by Hicks et al., who split a sample of young men into four rationally-constructed groups: (1) individuals with at least 2 alcohol use disorder (AUD) symptoms at age 17, "adolescent onset"; (2) individuals with at least 2 AUD symptoms at either age 20 or 24, "early adult onset"; (3) individuals with at least 2 AUD symptoms at age 29 and one previous age, "persistent course"; and (4) individuals with 0 AUD symptoms at age 29 but at least 2 AUD symptoms at a previous age, "desistent course."⁶ The strengths of the rationally-constructed approach include its simplicity, flexibility, and the ability to integrate information gleaned across settings and studies to develop theoretically coherent groups. However, the primary weakness of this approach is the subjective construction of groups. In the Hicks et al. study, for example, one might ask, why four groups? Why an AUD symptom cut-off of 2? Why those specific age permutations?

By contrast, the statistically-acquired approach relies on analytic techniques to uncover the "correct" number of trajectory groups from a dataset.^{7–12} Growth mixture models allow

investigators to estimate these trajectories—which typically vary as a function of intercept (i.e., the initial level of alcohol use), slope (i.e., the magnitude and direction of change), and growth (the linearity or curvilinearity of growth across development)—and examine their distinct relations to predictors and outcomes. Unfortunately, different studies yield different numbers of trajectories with different intercepts and slopes. These problems are due to substantial differences between studies in their sample and methods, their power to detect small classes, their timing and the length of their development window, their number of measurement occasions, their measurement and coding of alcohol use, their application of growth mixture modeling techniques, and statistical overfitting. If discrete trajectory groups do exist in the population, they are not consistently identified across studies^{13–15} or even within the same study.¹⁶

In any case, both approaches assume that most people follow one of a few distinct trajectories of alcohol use. Between these frequently traversed trajectories are developmental gaps—zones of rarity that enable analytic techniques to identify the common trajectories by contrast. The trajectory group approach is appealing because it simplifies, categorizes, and predicts: data are reduced, individuals are classified, and risk is forecasted. If the trajectory group approach reflects real categorical differences in the population, it is an extremely powerful tool for identifying category members and attuning prevention and intervention strategies.

An alternative hypothesis is that there are no discrete trajectory groups to be uncovered. From this perspective, alcohol use is a behavior that fluctuates uniquely for each (non-abstaining) person, and these unique, individual pathways cover the entire developmental terrain. A familiar example is the pediatric growth chart, which shows percentile trajectories for height or weight across the first few years of a child's development. Such charts show the average trajectory of growth—faster at first and then slowing with age—as well as a “rainbow” of percentile trajectories around the average that represent lower and higher rates of growth. Growth charts do not portray development in categorical terms, where children are grouped into one of a few distinct trajectories; rather, growth charts portray a continuous developmental landscape.

However, if the development of alcohol use is continuous and discrete alcohol trajectory groups do not exist, why are they generated by statistical approaches in the first place? Surprisingly, trajectories can be derived from nonnormal data—and even appear optimal—when only one group exists in the population.^{1,2} Growth mixture models require conditional normality, and even small violations of this assumption will lead to the extraction of too many latent classes. If no real population subgroups exist, these classes are invalid; if they do exist, there is little chance that they will be accurately mapped by the estimated trajectories.^{13,17} Because the distribution of alcohol use is nonnormal throughout development, trajectory analyses of alcohol use will violate the normality assumption and may lead growth mixture models to extract artifactual latent classes.

Here we test this alternative hypothesis—that statistically-acquired trajectory classes are best understood as gradations on a developmental continuum. Of course, groups can always be created using the rational-construction approach, even when they do not exist in the

population—one need only chop the continuum into categories according to a compelling or clinically useful rationale. However, if the true state of development is continuous and distinct trajectory groups do not exist, we will attempt to “triangulate” around the absence of such groups using four methods.

First, we expect that analytic fit statistics will continue to indicate that a greater number of trajectories always fit the data better than a lesser number of trajectories (suggesting that each additional trajectory brings the set closer and closer to approximating the underlying developmental continuum). Second, we expect that the distribution of individuals across the trajectory arcs will be relatively normal; that is, the growth mixture modeling will disperse the underlying continuum of alcohol use into a “rainbow” of developmental arcs, ranked from lower levels of use to higher levels of use, with most individuals grouped into moderate trajectories and fewer individuals grouped in higher and lower trajectories. Third, we expect that the rank-order of individuals will be stable throughout development—that trajectory arcs will not cross or show qualitatively distinct patterns of growth. And fourth, we expect that alcohol trajectory rank will change monotonically with heritability estimates and various external correlates of alcohol use, including personality traits, cognitive abilities, and psychiatric disorder symptoms. If trajectory groups represent severity gradations rather than distinct subgroups, then the external correlates of alcohol use should change monotonically with trajectory rank.¹⁸ Similarly, because heritability estimates are higher in more severe alcohol use groups, the heritability of group membership should also increase across the trajectories.¹⁹ On the other hand, if alcohol trajectories are qualitatively distinct, there will be little evidence for this stepwise pattern of genetic and external continuity.

The current investigation tests these ideas using data from a multiwave longitudinal-epidemiologic twin study. This study is large enough for analytic methods to extract the rare, problematic trajectories of alcohol use that are the focus of most research efforts, and long enough to span the developmental arc of normative alcohol use, which increases during adolescence, peaks in early adulthood, and decreases thereafter.²⁰ This study also uses a twin design and includes a wide range of alcohol use correlates, allowing us to assess the genetic and external continuity of extracted alcohol trajectories.

METHOD

Setting and Participants

Participants were 3,762 twins (1,808 male and 1,954 female) from the Minnesota Twin Family Study (MTFS). The MTFS is a longitudinal-epidemiological study examining the development of substance use and related disorders. The current investigation used data from the initial and enriched samples of the MTFS. Detailed information on the recruitment and design of these samples are described elsewhere.^{21,22} Briefly, the initial sample consists of two parallel cohorts of same-sex twin pairs reared by their biological parents, one first assessed at age 11 (Cohort 1) and one at age 17 (Cohort 2). The enrichment sample consists of twins at risk for the development of substance use problems (Cohort 3). All twins were identified using public birth records for the years 1977–1984 (initial cohorts) and 1988–1994 (enriched cohort) and located using public databases. Over 90% of twins born in these periods were located and over 80% of eligible families agreed to participate. Parents were

representative of the Minnesota population of the target birth years in education, socioeconomic status, and history of mental health treatment. Although the samples lack racial and ethnic diversity (96% Caucasian), they are sex balanced (52% female), cover a wide range of the socioeconomic spectrum, and include a mix of families living in urban (65%) and rural settings.²¹

Written informed assent/consent was obtained prior to data collection, and all study protocols were approved by an institutional review board. The twins were invited to participate in follow-up assessments every 3–5 years: Cohort 1 was assessed at ages 11, 14, 17, 20, 24, and 29; Cohort 2 at ages 17, 20, 24, and 29; and Cohort 3 at ages 11, 14, 17, and 20. Retention rates were excellent, with approximately 90% of each sample retained across follow-up assessment. Bias due to attrition on the variables included in this study has been shown to be minimal.^{23–25}

Assessments

Alcohol use—An alcohol use index (AUI) was derived from five measures: frequency of drinking occasions, average number of drinks per occasion, frequency of intoxication, and symptoms of alcohol abuse and dependence. An expanded version of the Substance Abuse Module of the Composite International Diagnostic Interview²⁶ was used to assess alcohol abuse and dependence symptoms. The AUI was composed by setting scores on these five variables on a 0–10 scale and then averaging them. This index is essentially equivalent to a latent variable approach: a factor analysis with all five alcohol measures modeled as indicators of a single latent alcohol use variable had high factor loadings (range .81–.89 across indicators) and explained 70% of their variance. This latent alcohol use variable was very highly correlated with the AUI at all ages, ranging from .98 (age 14) to .99 (ages 17, 20, 24, and 29). However, a latent variable could not be calculated for age 11 because participants have not begun drinking and there is no variance in use. In contrast, the AUI yields a single manifest variable with a meaningful “0” point (no substance use), and scores across development represent absolute rather than relative changes in alcohol use. These AUI data were used to derive alcohol trajectory groups in the growth mixture model analyses.

Psychopathology—Twins were interviewed separately and concurrently by different interviewers, who assessed them for psychiatric disorders according to criteria from the *DSM-III-R*.²⁷ The current analysis uses symptom counts for 11 disorders, including various childhood disruptive disorders, internalizing disorders, and externalizing disorders. Symptoms were assessed by trained staff using structured clinical interviews for *DSM-III-R*.^{26,28,29} Interview data were subsequently reviewed in a case conference where diagnosticians had to reach a consensus regarding the presence or absence of a symptom before it was assigned, referring to audiotapes of the interview when necessary. The consensus process yielded uniformly high diagnostic reliabilities (e.g., .92 or greater for all substance use disorder diagnoses²¹). To simplify our results and represent psychopathology across a span of development, symptoms scores across all ages were averaged into a single score for each disorder.

Personality—Personality was assessed at ages 17 and 24 using the 198-item version of the Minnesota Personality Questionnaire (MPQ³⁰). Alpha estimates for MPQ scales ranged from .78 to .94, with a mean coefficient alpha of .88. MPQ scores at ages 17 and 24 were averaged into a single score for each scale (test-retest intraclass correlation coefficient [ICC] range = .78–.86).

Cognitive ability—Intelligence was assessed at ages 11, 17, and 24 using abbreviated versions of the Wechsler Intelligence Scale for Children–Revised (WISC-R³¹) and the Wechsler Adult Intelligence Scale–Revised (WAIS-R³²). The abbreviated versions consist of 2 verbal (Vocabulary and Information) and 2 performance (Block Design and Picture Arrangement) subtests. These subtests were selected for their high correlation (.90) with total IQ. Achievement was assessed at various ages using the Wide-Ranging Achievement Test–Revised (WRAT-R³³). Reading achievement was assessed in Cohorts 1 and 3 at ages 11, 14, 17, and 20, and in Cohort 2 at age 20. Writing and math were assessed in Cohorts 1 and 3 at ages 14 and 20, and in Cohort 2 at age 20. Cognitive ability scores were also averaged across age (intelligence test-retest ICC range = .82–.90; achievement test-retest ICC range = .84–.88).

Data Analysis

Alcohol trajectories were derived from age 14–29 data. As only 0.1% of participants at age 11 had ever used alcohol, this time point was dropped. Data from all three cohorts were combined in the trajectory analysis because growth mixture modeling techniques are well suited to individual developmental data that start and stop at different times or have missing values. In the current study, data were missing according to cohort length, but all three cohorts had mean AUI scores within 0.1 standard deviations at each age, and the overall pattern of scores across development was comparable (see Figure 1).

We derived trajectories from AUI scores using *Mplus*, Version 7,³⁴ using a 10-point scaling of the AUI for ease of interpretation. An AUI score of 0 represents almost no alcohol use and a score of 10 represents the maximum use—the highest possible alcohol frequency (nearly every day), quantity (10+ drinks), and symptoms of abuse and dependence. Because the distribution of AUI scores changes substantially across age, AUI scores were bundled into discrete units (i.e., scores of 0–.49 were coded as “0,” 0.50–1.49 were coded as “1,” and so on) and treated as count outcomes.³⁵ Bundling the AUI scores into discrete units creates a count variable and allows a Poisson regression approach, which can directly model the distribution of the skewed data as well as accommodate changes in these distributions across age by using a consistent yardstick (thresholds). This is preferable to treating the AUI scores as continuous because doing so involves making erroneous assumptions about the normality of AUI scores—assumptions that invariably produce multiple normally distributed classes to accommodate the skewed data.

Following the procedure outlined in Jung and Wickrama,³⁶ we first specified a single-class growth curve model, which gave the overall growth curve of the sample. This overall growth curve, included in Figure 1, closely matches the sample means for all three cohorts. Next, we derived multiple trajectories using latent class growth analysis (LCGA) and growth

mixture modeling (GMM). In LCGA, individuals within each trajectory group are constrained to have the same intercept and slope, but in GMM, individuals in each trajectory group can have different intercepts and/or slopes. When determining the optimal number of trajectory classes, the usual approach is to start with LCGA, which is less computationally burdensome because within-class variances are fixed to zero, then move to GMM, freeing intercept and/or slope variances for the trajectory classes and then allowing each class to have its own unique variance. Selection of the optimum model can be determined using Lo-Mendell-Rubin Likelihood Ratio Test (LMR-LRT) *p*-values and the Bootstrapped Likelihood Ratio Test (BLRT).

We varied this general procedure, taking a more thorough approach. Specifically, we conducted LCGA for all 1,089 permutations of linear, quadratic, and cubic growth 2-, 3-, 4-, 5-, and 6-class models, stopping only when group size dropped to below 1%. Both LMR-LRT and BLRT tests consistently preferred higher-class models, with the 6-class model fitting best. Next, we conducted 1,089 GMM analyses with intercepts freed for all models, again stopping when group size dropped below 1%. As before, higher-class models were preferred, with the 6-class model fitting best. We then repeated the 1,089 GMM analyses, allowing each class to have its own unique intercept variance, with the same results. To rule out the possibility that solutions were local, the seed values associated with the two best log-likelihood values from each GMM output were used in a subsequent reanalysis. Global solutions from successfully converged models had the best log-likelihood values repeated at least twice.³⁶

Heritability estimates for the resulting GMM trajectories were derived using structural equation modeling in *Mplus*.³⁴ To ascertain the heritability of trajectory group membership, we used the continuous posterior probabilities that each individual belongs to each trajectory group. These posterior probabilities are continuous and available for every person at every time point. For each of the six trajectories, we used a two-group (monozygotic [MZ]–dizygotic [DZ]) twin model for continuous outcomes, where factors represent the additive genetic (A), common environmental (C), and unique environmental (E) components. Finally, mean psychopathology, personality, and cognitive ability values for each trajectory group were examined using rank-order correlations. This approach examines whether the external correlates of alcohol use change monotonically with trajectory rank.

RESULTS

Trajectory Evidence of Developmental Continuity

Presented in Figure 1 is the overall growth curve for our sample, the average trajectory of alcohol use between ages 11–29. Presented in Figure 2 are the best-fitting trajectory group models, which yielded 6 trajectory groups (for both LCGA and GMM). In these models, alcohol trajectories are splayed out in a series of quadratic arcs ranked from lower levels of alcohol use to higher levels of use, with more individuals grouped in center trajectories than in fringe trajectories. From low to high, the percent of participants in each of the six trajectories is 4%, 11%, 39%, 29%, 15%, and 1% (LCGA) or 4%, 11%, 40%, 27%, 16%, and 1% (GMM). The rank order of these trajectories is stable throughout development, and none of the trajectories crosses at any age. Repeating our entire analytic approach in samples

comprised of only one twin replicated these results, ruling out the possibility that genetic dependency between twins affected the results, and providing a strong replication (same method, same sampling, same demographics, 50–100% shared genetics, common environment, etc.).

Genetic and External Evidence of Developmental Continuity

Heritability estimates for the six GMM trajectories are presented in Figure 3. These results suggest that heritability increases in a stepwise fashion up the trajectory ranks—the severity and heritability of the trajectories graduate in tandem. Presented in Figure 3 are these estimates of A, which monotonically increase from 5% to 42%. Conversely, the estimates of E monotonically decrease from 93% to 43%. The estimates of C were low across all trajectory groups, ranging from 0–4%.

Also presented in Figure 3 are the mean psychopathology, personality, and cognitive ability values for each trajectory group. Because the goal of this analysis was to determine whether the external correlates of alcohol use change monotonically with trajectory rank, we only displayed variables that are correlated with alcohol use and of at least modest effect size ($r > .10$). Measures not included were several trait scales from the MPQ, including Social Potency, Achievement, Social Closeness, Well-Being, Stress Reactivity, and Positive Emotionality. As seen in Figure 3, the correlates of alcohol use show perfect rank-order correlation with trajectory group ($r_s = 1.00$). When split into Cohorts 1, 2, and 3, rank-order correlations are .98, 1.00, and .98, respectively.

DISCUSSION

Across four criteria, our results suggest that the development of alcohol use is continuous rather than categorical. First, for all analyses, each added trajectory improved the fit of the model. This finding suggests that the analytic method is trying to model an underlying continuum and gets closer with each successive trajectory. Second, the distribution of individuals across the trajectory arcs was relatively normal, with most individuals grouped into moderate trajectories and fewer individuals grouped in higher and lower trajectories. Third, the rank-order of individuals was stable throughout development—the trajectory arcs did not cross or show qualitatively distinct patterns of growth. And fourth, genetic and external evidence suggests that these arcs reflect ordinal points on a severity continuum—the heritability and external correlates of alcohol use change monotonically across the trajectory ranks. These findings support the developmental continuity of alcohol use and challenge the trajectory group approach. Of course, future research must determine whether such findings generalize beyond our sample of mostly White twins from Minnesota, and whether evidence of developmental continuity extends beyond the age of 29.

The trajectory group approach posits that there are several distinct pathways to alcohol use. But for this to be true, most of the variation in alcohol use would have to be explained by a small number of powerful categorical influences (e.g., having a particular risk allele or experiencing a particular event). These influences would need to be common enough to form sizable groups with a homogenous and predictable developmental course. In this case, numerous small influences would still have some effect on alcohol use, much as they do on

intelligence in people with and without Down syndrome, but most people would follow a course of use within the relatively narrow constraints of their trajectory.

Genetic and environmental evidence does not support this notion. With the exception of an aldehyde dehydrogenase variant (*ALDH2*2*) in East Asian populations, alleles of large effect have not been identified.³⁷ Although a number of common alleles have been identified through genome-wide association methods, these are of very small effect.³⁸ Thus, like other complex diseases such as diabetes³⁹ and traits such as height,⁴⁰ alcohol use is characterized by polygenic inheritance. When genetic influences are weak, numerous, and common, they interact and aggregate to form a quantitative continuum of risk in the population, making it unlikely that qualitatively distinct groups will arise as a function of polygenetic risk.

Strong environmental influences could still segregate individuals into distinct trajectories. However, shared environmental influences are mostly weak,^{41,42} and unique environmental influences, though sometimes strong, are stochastic and therefore often intractable to exact study. Furthermore, the individual differences most strongly correlated with alcohol use—such as externalizing psychopathology, internalizing psychopathology, and traits related to behavioral disinhibition and neuroticism—are themselves continuously distributed and shaped by myriad genetic and environmental influences. Theoretical models may yet explain how small forces aggregate to produce discrete alcohol use trajectories (e.g., dynamic systems theory⁴³), and sophisticated analytic techniques may yet identify them (e.g., free-curve slope intercept models⁴⁴). However, using the most common methods in contemporary alcohol trajectory research, the current study does not provide evidence supporting the validity of distinct trajectory groups.

It may very well be that alcohol trajectory classes are best understood as gradations on a continuum rather than highly disjunctive categories. Epigenetic developmental pathways linking gene products to complex behavior are numerous and distant, and research in this area generally yields evidence of small correlations between such causally distant variables. With many genetic and environmental forces at play—not to mention their nearly innumerable interactions and correlations—it is no surprise that such astonishing complexity should fail to neatly cohere into a small set of distinct developmental trajectories.

Thus, the current analysis serves as a cautionary tale for clinicians and as a call to action for researchers. Regarding the cautionary tale, because alcohol trajectories may represent continuous gradations rather than qualitatively distinct subgroups, early detection and intervention programs based on trajectory subtyping may be less useful than continuous liability assessments. Importantly, moving away from interpretations of trajectory groups as literally distinct entities may help discount the notion that people follow predestined pathways, and promote the hopeful alternative—that development is mutable and its continuous terrain can be traversed in many directions.

Regarding the call to action, much more research in this area is needed, particularly because supporting the absence of distinct trajectory classes requires a lot of work. Our findings are preliminary rather than definitive and subsequent research using high-powered longitudinal studies is needed to replicate our results, expand our range of correlates, generalize our

findings beyond our sample, and rule out various alternatives. Furthermore, the possibility remains that very rare taxa (<1% prevalence) may remain hidden within the broader distribution, eluding attempts to uncover them using trajectory analytic techniques.

Our findings cast some doubt as to the existence of putatively discrete alcohol trajectories. And yet, even in the absence of true population subgroups, trajectories may still be useful in research and clinical practice.^{45,46} Like contour lines on a topographical map, trajectory groups can function as a convenient way of defining elevations (clinical cut-offs) and summarizing changing distributions of alcohol use across development (see Figure 4). However, if trajectories are not capturing literal entities, they should not be reified. In this case, rather than carve nature at its joints, trajectory approaches may carve joints into nature.

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Clinical Guidance

- One way of identifying at-risk youth is to assume there are a few distinct developmental pathways, only some of which lead to problematic alcohol use. Here, we provide evidence that this is not the case. Rather, each individual has a unique trajectory of use shaped by various genetic and environmental influences.
- If alcohol use is fluid across development, it can be changed. Even high-risk individuals are not fatalistically stuck in a problematic trajectory group.
- As with pediatric growth charts, trajectory analyses can be used to visualize the development of alcohol use, identify developmental norms, and create clinical cut-offs (see Figure 4).

Figure 1.

Alcohol Use Index (AUI) sample means for each cohort, and overall growth curve from combined sample. Note: Cohort 1 = ages 11, 14, 17, 20, 24, 29; Cohort 2 = ages 17, 20, 24, 29; Cohort 3 = ages 11, 14, 17, 20.

Figure 2.
Alcohol use trajectory groups

Figure 3. Mean scores for each alcohol trajectory group. Note: “rev.” = reversed; these scales were reversed so that all measures were displayed in the direction of dysfunction (e.g., higher reversed IQ scores indicate lower intelligence). External correlates exhibit perfect rank-order correlation with trajectory group ($r_s = 1.00$). ADHD = attention-deficit/hyperactivity disorder; GAD = generalized anxiety disorder; MDD = major depressive disorder; ODD = oppositional defiant disorder; PD = personality disorder.

Figure 4.
Alcohol trajectories as contour lines on a continuous developmental topography.