A cross-national comparison of adolescent risk behavior in post-separation families

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Abstract

Purpose

We (1) examine whether more complex cross-household family structures are associated with higher risk-taking (substance use, bullying, and early sexual onset) in adolescence, (2) identify structural characteristics as potential drivers, and (3) joint physical custody and the frequency (and thus statistical normality) of complex family structures as potential moderators of this association.

Methods

Drawing on representative data from 42 countries or regions from the Health Behaviour in School-aged Children (HBSC) study in 2001, 2006, and 2010 (N = 581’838), we provide detailed analyses on risk behavior even for very rare family constellations, thereby accounting for the complex cross-household structure present in many post-separation families. We combine logistic and count regression models to model risk incidence and intensity.

Results

Controlling for relevant child and family characteristics, our results reveal that (1) risk-taking increases with the complexity of family constellations: The incidence and intensity of risk-taking among adolescents is lowest in two-parent-biological and highest in two-household families with stepparents in both. (2) The thirteen family types can be parsimoniously summarized by just five family structure indicators. (3) Parental care in joint physical custody after parental break-up reduces the association slightly. (4) The association decreases with a higher frequency of the respective family type.

Conclusions

Post-separation family complexity is associated with higher risk-taking in adolescence. We identify five structural indicators that may drive this association, yet future research needs to examine whether this is causal. For policy-makers, our findings on potential buffers against the potential negative consequences of family complexity are relevant.

Keywords

Adolescence, divorce, health, HBSC, joint physical custody, risk behavior, separation, stepfamilies, family complexity,

Implications and Contributions Statement

We demonstrate that higher family complexity is associated with more risk-taking behavior in adolescence and are able to show this for a broader variety of family types than previous studies. Furthermore, we identify potential drivers and moderators of this association, thus providing some leverage for policy-makers.

Risk-taking behaviors among adolescents can lead to negative consequences for mental well-being, physical health and academic achievement that can persist well into adulthood (e.g., Hurrelmann & Richter, 2006). Thus, it is important to identify risk and resilience factors that moderate risk-taking behavior in adolescence. One of those factors that was found repeatedly to have a significant impact is family structure (e.g., Barrett & Turner, 2006; Bjarnason et al., 2003; Brown & Rinelli, 2010; Fomby & Sennott, 2013; Griesbach, Amos, & Currie, 2003; McArdle et al., 2002; Rüütel et al., 2014). Briefly, previous research on the link between family structure and adolescent risk behavior revealed an increased prevalence of risk behavior in single parent and stepfamilies in comparison to adolescents who are growing up in two-parent-biological families.

Findings from the US and Europe have suggested that the heightened risk of tobacco, alcohol, and drug use among adolescents who reside in single parents and stepfamilies is independent of community context (Hoffmann, 2002) but depends heavily on the involvement (Menning, 2006) and the quality of the parent-child relation (Barfield-Cottledge, 2015; McArdle et al., 2002). This is because parental involvement and thus parent-child closeness can buffer adverse effects of family disruption (Booth, Scott, & King, 2010; Van Ryzin, Fosco, & Dishion, 2012). Conflict, on the contrary, either between parents or between parents and adolescents is positively associated with substance use (Kristjansson, Sigfusdottir, Allegrante, & Helgason, 2009; Vanassche, Sodermans, Matthijs, & Swicegood, 2013). Furthermore, findings suggested that adolescents in stepfamilies have a higher prevalence in substance use than adolescents in single parent families, even after controlling for several other risk factors (Griesbach et al., 2003). One study was able to show that a transition from a single-parent to a stepfamily is associated with an elevated risk of initiating alcohol use (Kirby, 2006). In addition, some studies found that adolescents who were residing with a single father showed higher levels of substance use than adolescents who were residing with a single mother (Bjarnason et al., 2003; Hoffmann, 2002; Jablonska & Lindberg, 2007).

Quite similar results as for substance use exist for a variety of outcomes that are more rarely studied: Adolescents from non-traditional families show higher rates of juvenile delinquency (Schroeder, Osgood, & Oghia, 2010), aggression (Hong & Espelage, 2012), problem behavior (Fomby & Sennott, 2013), delinquent behavior (Vanassche et al., 2013), and victimization (Jablonska & Lindberg, 2007). Like for substance use, mobility and thus change of community seemed not to be a relevant explanation (Fomby & Sennott, 2013). However, higher levels of parental communication buffered adolescents against the negative influence of bullying (Ledwell & King, 2015). Conflict between parents as well as between parents has, again, a positive impact on delinquency (Vanassche et al., 2013).

Even fewer results can be found for risky sexual behaviors in adolescence. However, the few existing studies showed that separation and divorce were a risk factor for early sexual onset and activity (Jordahl & Lohman, 2009; Madkour, Farhat, Halpern, Godeau, & Gabhainn, 2010; Poulin & Boislard P., 2011). Adolescents from two-parent families were less likely to have had sex and had fewer partners instead (Haglund & Fehring, 2010). Father involvement, again, proofed to be a protective factor for risky behavior (Jordahl & Lohman, 2009).

At this point, it seems necessary to refer to the interconnectedness and common pathways between substance use, bullying and other risk behaviors like early sexual activity (Espelage, Low, Rao, Hong, & Little, 2014; Madkour et al., 2010; Ttofi, Bowes, Farrington, & Lösel, 2014). However, most of the studies capture only one risk behavior. Another shortcoming of the existing studies is that they all concentrated exclusively on the first or main household where the adolescent lives most of the time and, thus, ignored the complexity of post-separation families with cross-household structures. Our investigation extends previous research by comparing the association of a wider range of complex family constellations across households including stepparents in the first and the second household. According to the stability hypothesis, each family transition creates stress that can accumulate across multiple transitions and negatively affect developmental outcomes in those affected by multiple stressors (Fomby & Cherlin, 2007). A recent review that covers 39 articles published in the last decade shows support for the instability hypothesis. However, it also highlights that mixed results with regard to certain transitions, groups, and outcomes point towards additional explanatory factors that may be at play but that are not yet well understood (Hadfield et al., 2018, p. 20). We argue that a cross-household family structure of an adolescent adds another set of potential stressors.

Navigating family relationships across households may be stressful merely because it is more demanding to organize life across two more or less geographically distant households than it would be to organize in one household. In addition, communicating and negotiating the demands of the parent living in either household may be emotionally taxing, a challenge that arguably becomes more difficult as additional relationships are involved, e.g. towards stepparents and stepsiblings in the main and secondary parental home. We thus propose an extended instability-complexity hypothesis: Multiple family transitions and the degree of complexity of cross-household family structures both provide independent and additive sources of stress that may cumulate and affect developmental outcomes of adolescents.

To disentangle that question further, and to outline potentials buffers against the negative outcomes associated with living in non-traditional, complex, family and household structures, we also look at the role of joint physical custody and of the relative frequency of family forms across countries in our sample. Do they moderate the association between family structure and risk-behavior in adolescents and thus provide leverage for policy-makers? First, independent of the legal custody arrangement, the physical custody arrangement refers to the amount of time the adolescent lives in each parental household. Next to the standard of sole physical custody with mostly mothers providing primary childcare after a parental separation or divorce, a new arrangement emerged recently, that is the joint physical custody (JPC) arrangement. Joint physical custody is a parental care arrangement in which a child lives with each parent about equally after separation or divorce (Steinbach, 2018). Several studies already showed that this certain kind of shared care is able to buffer the stress of a separation or divorce and cross-household family structures (e.g., Carlsund, Eriksson, Löfstedt, & Sellström, 2013; Jablonska & Lindberg, 2007; Sodermans & Matthijs, 2014). However, so far JPC is usually practiced by parents with a low level of conflict, a high level of active paternal parenting prior to separation or divorce, and closer residence to each other (e.g., Fransson, Låftman, Östberg, Hjern, & Bergström, 2017; Melli & Brown, 2008). Second, we assume that the frequency distribution of family types in a country might be a proxy for both family norms and policies in the respective country. Where non-traditional family forms are relatively frequent, this may reflect a regime with fewer normative sanctions against these non-traditional families and family policies may be in place that provide support for the specific needs of these family forms.

Methods

Data

Analyses are based on the cross-national and cross-sectional “Health Behaviour in School-aged Children” (HBSC) study. The HBSC study has been conducted by an international multidisciplinary network of research teams with the World Health Organization (WHO)

Regional Office or Europe (Currie, Gabhainn, & Godeau, 2009). The main aim of the study is to gain insight into young people's well-being, health behaviors and their social context across countries and regions in Europa and North America. The survey was administered to adolescents aged 11, 13, and 15 years, because “these age groups represent the onset of adolescence, a time when young people face the challenges of physical and emotional changes and important life and career decisions are beginning to be made” (Roberts et al., 2009, p. 47). For data collection, standardized questionnaires were administered in school classrooms according to the international protocol. Student selection took place by a clustered sampling design where the initial sampling unit is the school class. The response rate at the level of schools was generally high (majority of countries: 80%) (Richter, 2010, p. 48).

We used data from 2001, 2006, and 2010 waves of the HBSC study, given that the survey captured information on biological mothers and fathers as well as stepmothers and stepfathers across the main home of the focal adolescent and, if existent, the second household. In addition to representative data on health and risk behaviors, the survey includes some information on social context, including family, school, and peers, as well as information on the socioeconomic environment in which young people grow up. For the analysis, we pooled the cross-sectional data of the three waves (2001, 2006, and 2010) across 42 countries or regions[1]. Although in each country, particular family constellations apply only to a small to medium percentage of all families, pooling over these countries and three waves allows us to study the association of

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[1] These include: Armenia, Austria, Belgium (Flemish), Belgium (French), Bulgaria, Canada, Croatia, Czech Republic, Denmark, England, Estonia, Finland, France, Germany, Hungary, Iceland, Ireland, Israel, Italy, Latvia, Lithuania, Luxembourg, Macedonia, Malta, Netherlands, Norway, Poland, Portugal, Romania, Russia, Scotland, Slovakia, Slovenia, Spain, Sweden, Switzerland, Turkey, Ukraine, USA, and Wales.

growing up in a variety of complex family constellations and risk behavior. Altogether, the combined sample includes (N = 581’838) adolescents.

Measures

Risk behavior. For all indicators on risk behavior in the HBSC study, substance use, sexual onset, and fighting/bullying, adolescents were asked to indicate how often they engage in these behaviors or, in the case of bullying and fighting, were victimized. First, we created dummy variables for a variety of risk indicators that were available in all three waves of the HBSC study. These cover nine questions overall on whether the respondent (1) bullied others or (2) was bullied in the two month preceding the interview, (3) got into a physical fight or (4) contracted an injury in the past 12 months, ever tried (5) cannabis, (6) tobacco, or was (7) really drunk, (8) is currently smoking, and (9) ever had sex (“yes” = 1, “no” = 0) (for the same procedure with Add Health data, see Brown & Rinelli, 2010). We provide separate analyses for these nine indicators and for a combined risk indicator that distinguishes adolescents who did not engage in any of these risks (19.7%) from those who engaged in at least one of those risks (80.3%).

Second, we created a count variable on the intensity of risk behavior. This variable takes into account both the intensity of any of a variety of risks and the cumulative engagement in multiple risk behaviors simultaneously. Specifically, the variable is built from five indicators that distinguish the frequency of drinking, smoking, bullying (active), bullying (passive), and lifetime cannabis use, respectively, on various scales that we standardized to range from 0 (no engagement at all) to 3 (frequent engagement). Our aggregate risk count variable sums up the scores from each of these five indicators (see Figure 1 for a histogram).

Family types. In the HBSC data we have information on the household roster for the main household of the adolescent and, if applicable, on a second home. For both homes, information is available on (step-)parents, grandparents, and other persons living there. In addition, there is information on whether the first or second home is a foster home. This leaves many possible cross-household family constellations. We created thirteen family types based on the following inclusions rules: at least one biological parent needs to be present in the focal household of the respondent (home 1); if a second home exists it is considered only if at least one biological parent lives there; and only parents and step-parents are considered for the construction of family types. Although, in our models, we statistically control for the presence of grandparents and other individuals living in either the first or the second home, we did not use this information to inform our choice of family types. This left a total of thirteen family constellations overall, ranging from the two-biological-parent family to complex stepfamilies with two households and a stepparent living in each of the two homes. Selecting only adolescents with a family constellation among these thirteen types left 523’173 of the overall 581’838 respondents. After further removing adolescent with a foster home and respondents who said a second home existed but for which no information was available on who lived there left us with 515’722 adolescents. Table 1 shows the frequency distribution of family types for this remaining sample. The relative frequencies range between 0.2 and 77.9% or 1141 to 401’788 cases. This illustrates that even for very rare family constellations we have relatively large absolute frequencies in the pooled data set. Figure 2 and Figure 3 show the absolute and relative frequencies of family types by country.

In addition to the set of 13 family types we constructed five dichotomous family structure indicators that, we believe, allow to more parsimoniously describe the family and household structures in which adolescents live. The indicators hold information on whether the parents are separated and the adolescent lives with a lone parent in home 1 and no home 2, (2) a second home exists with a biological parent but without a stepparent, (3) a stepparent is present in either the first or second home of the adolescent, (4) a stepparent is present in both homes, and (5) in case of a parental separation the father is the focal parent living in home 1. Whereas the first of these five indicators mainly captures the separation of the parents, indicators two to three serve to capture the degree of complexity present in the family and household structure.

Independent variables. Inclusion of other independent variables led to the further exclusion of cases, leaving a sample size of 506’977 to 511’747 depending on the model. *Age* is operationalized as a categorical variable with the categories 11-, 13-, and 15-years of age. We further controlled for *survey year* (2002, 2006, and 2010), *gender* (“male”, “female”), whether a *grandfather, -mother, or another person* lived in either home 1 or 2 (“yes”, “no”), the *share of specific family types* or indicators by country, whether adolescents spend 50% of the time in the second home (*joint physical custody*) and *socioeconomic status* of the family. The latter was measured based on the Family Affluence Scale (FAS1). We use the same procedure as suggested by Holstein et al. 2009 (p. 268)[2]. To account for differences in levels of risk behavior between

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[2] "We measured SEP by the Family Affluence Scale (FAS) which is simple and easy to answer even for young adolescents. FAS includes four items (assignment of points shown in parentheses): Does your family own a car, van or truck? "No" (0), "yes one" (1), "yes two or more" (2). Do you have your own bedroom for yourself? "No" (0), "Yes" (1). During the past 12 months, how many times did you travel away on holiday (vacation) with your family? "Not at all" (0), "once" (1), "twice" (2), "more than twice" (2). How many computers does your family own? "None" (0), "one" (1), "two" (2,) and "more than two" (2), range 0-7. We categorised the students into high (6-7 points), medium (4-5 points) and low (0-3 points) FAS." (Holstein et al. 2009, p. 268)

countries, we use unconditional fixed effects models that account for the clustering of individuals within countries (cf. Hilbe, 2009).

Regression models

We investigated a series of logistic regression models on the aggregate binary risk indicator and on the nine separate risk indicators. Furthermore, we computed a series of count regression models on the intensity of risk behavior. To account for overdispersion and excess zeros in the count models, we compared different specifications, including Poisson, Negative Binomial and Zero Inflation models[3]. Across specifications we tested for main effects and a number of interaction effects, including the interaction between age and family type, gender and family type, family type and its population share, and the presence of joint physical custody and family type. In both, the count and the logistic regression models, we compared models including a categorical variable to indicate the 13 family types and models including the five family structure indicators instead.

Results

First, we present results from a series of logistic regression models on single risk indicators.

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[3] Results of the zero inflated regression are not yet included in the current version of the paper.

Figure 4 shows the average partial effects (APEs) of family type on any of nine risk indicators. The models include all covariates named above, but no interaction effects. The family types are arranged such that as we move downward on the y-axis, the family types become more complex. We can roughly see that as we move towards more complex family types, the APE of family type on risk incidence gets larger. But the association is not as pronounced for bullying, sex, and injuries. We can also see that in most cases, for two similar family constellations that only differ in whether the father or mother lives in home 1, the APEs are higher if the father is the focal parent. A combined model on the aggregate risk indicator yields a very similar picture as the models with single risk indicators.

Second, in the aggregate model, we tested whether a more parsimonious model with the five family indicators has a similarly good fit as the model with the thirteen family types. Although based on the BIC value the model with five indicators performs slightly worse than the model with 13 family types, Nagelkerke's R^2 is nearly identical for the two models (~.088). Therefore, in order to facilitate more complex models including several interactions terms, we continued with the more parsimonious model. Subsequently we strictly preferred models with lower BIC values, leading to one final logistic regression model on the aggregate risk indicator and one final count model (negative binomial regression) (see Models 1 and 2 in the Appendix). Figure 5 shows the average partial effects for these models. For both risk incidence and risk severity the marginal effects of each family structure indicator increases the values of the dependent variable. The effect on risk incidence or risk severity is lowest for the variable indicating if the father is the focal parent and it is highest for the two variables indicating the existence of a stepparent in one or both homes.

Third, we also tested the buffering role of joint physical custody and the relative frequency of non-traditional family types or family structure indicators that describe these family types. A series of models revealed that only the main effect of joint physical custody, but not the interaction effects with the family-structure indicators were statistically significant and led to improved model fit based on the BIC criterion. As our final models (Models 1 and 2, Appendix) show, the risk-reducing effect of joint physical custody is very small though. We also tested a series of regression models to examine whether the frequency of a family indicator in a given country moderates the association between family structure indicators and risk intensity. It turned out that the model with the best fit includes all interaction effects between the five family structure indicators and their respective population shares. The results are also summarized in Model 1 of the Appendix. Figure 6 shows the average marginal effects of the five family structure indicators on risk intensity by certain values of the variables indicating their respective population shares (these are set to their respective minimum, median, and maximum values). The Figure clear shows that a higher share of the respective family characteristic in the population is associated with a lower average marginal effect on risk intensity, with the exception of the variable indicating that the father is the focal parent. Here, the moderation effect is negligible.

Discussion

Risk-taking behaviors in adolescence has been found to be associated with a range of negative outcomes not only in adolescence but also at later ages and therefore constitutes a risk factor linking family structure and later life outcomes. Our investigation extended previous research on adolescent risk behavior by comparing the association of a wide range of complex family structures across household and compared them with two-biological families.

The results showed that in all family constellations other than the two-biological-parent family, adolescents are of higher risk of risk-taking behavior. As expected, this difference is strongest for the more complex family constellations that involve biological and stepparent-child ties in both the main and the secondary home. Furthermore, in those cases where household ties with both the biological father and the biological mother exist, it makes a differences whether it is the biological father or the biological mother that lives in the main home: generally, the odds for and intensity of risk behavior are higher if it is the biological father who lives in the main home and the biological mother who lives in the secondary home than in the reverse case.

Furthermore, our results show that a more parsimonious model with just five family structure indicators reaches almost the same goodness-of-fit as a model with the 13 family types. This may be interpreted as a sign that the family characteristics these indicators describe may be the driving forces behind the association of family structure and risk behavior. However, our analysis is limited as to the causal implications and future research should further elaborate on this.

In terms of potential moderating factors, our analysis shows that joint physical custody has only a limited risk-reducing effect in the models. This may be due to the fact that our measure of joint physical custody is rather strict due to data limitations: we can only consider joint physical custody if adolescents spend about an equal amount of time in both homes. A stronger moderator is the share of certain family characteristics in the population of a country. This is an aspect that warrants further examination in future research as it might leverage policy-making to reduce the negative association between family structure and risk behavior. Future research should examine whether the moderation is due, for instance, to different norms or different policy structures associated with the statistical distribution of family types.

Given evidence for an advantage of gender-homogeneous parent-child relationships (Lye, 1996), we would have expected an association between gender of the adolescent and gender of the focal parent. Yet, this is not what we found. The model on risk intensity (Model 1, Appendix) shows that it is girls who experience a stronger negative association between family structure and risk behavior.

One limitation of our current study – which is due to data limitations - is that we focus solely on the degree of family complexity that is due to parent-child relationships. An important additional factor, however, is whether half- and/or stepchildren are present in the main or second home. The HBSC data don't allow specifying the type of child present in the household. In addition to limitations in the current data analysis, the HBSC study has several limitations that restrict the kinds of analyses we can do. For example, there is no information on several additional factors that are described as relevant for understanding risk behavior in the research literature. These include child characteristics like genetic factors that make children more prone to engage in substance use (Plomin et al., 2003, chap. 17), birth order which has also been found to be associated with substance use (Argys et al., 2006), or the school track the child is in. Furthermore, information is lacking on parental characteristics like their own substance use habits, their parenting styles (control, warmness), education, and the degree of institutionalization of their partnership (either with the other biological parent or new partner) (cf., Hofferth and Anderson, 2003). Also, in order to describe the complexity of family ties across household in more detail, it would be necessary to assess the quality of parent-child relationships (cf., Skopin et al., 1993) and to include information on the number of (step-)siblings in the main and the second home. These limitations notwithstanding, the data is informative for the analysis of adolescent risk behavior, like substance use, because the potential of the data lies in the high number of cases and the detailed information on family constellations across households.

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Figures

Figure 1: Histogram of risk count variable

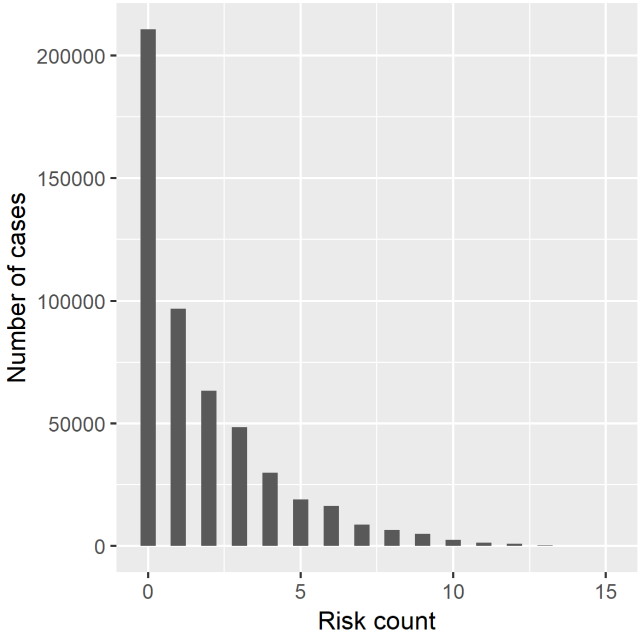


Figure 2: Absolute frequencies of 13 family types, by country/region

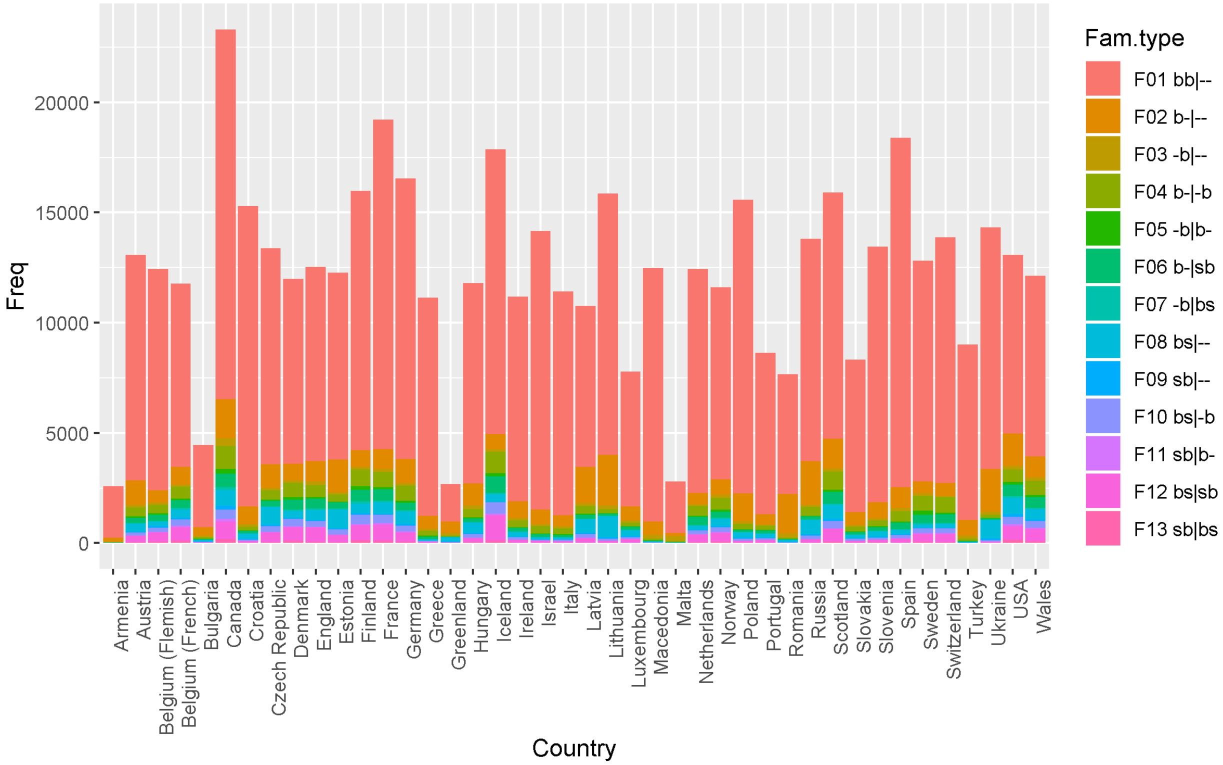


Figure 3: Relative frequencies of 13 family types within countries

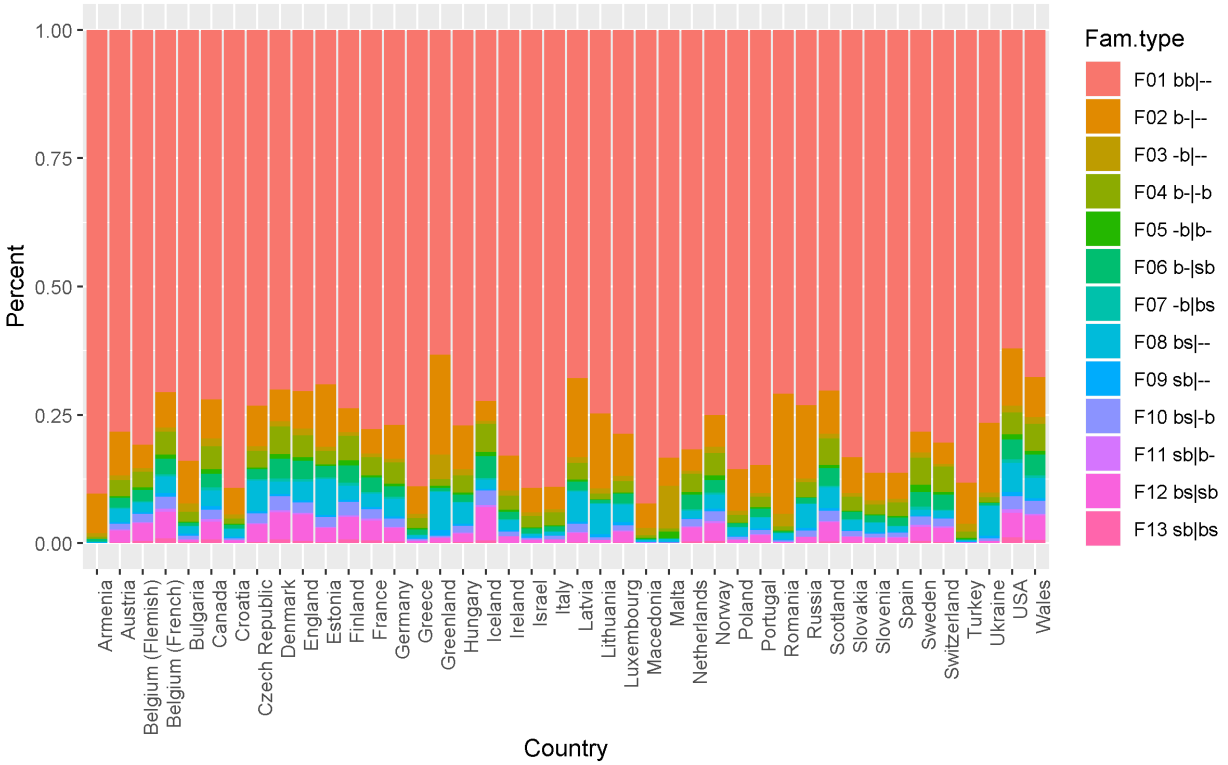


Figure 4: Average marginal (partial) effects of logistic regression on single risk indicators

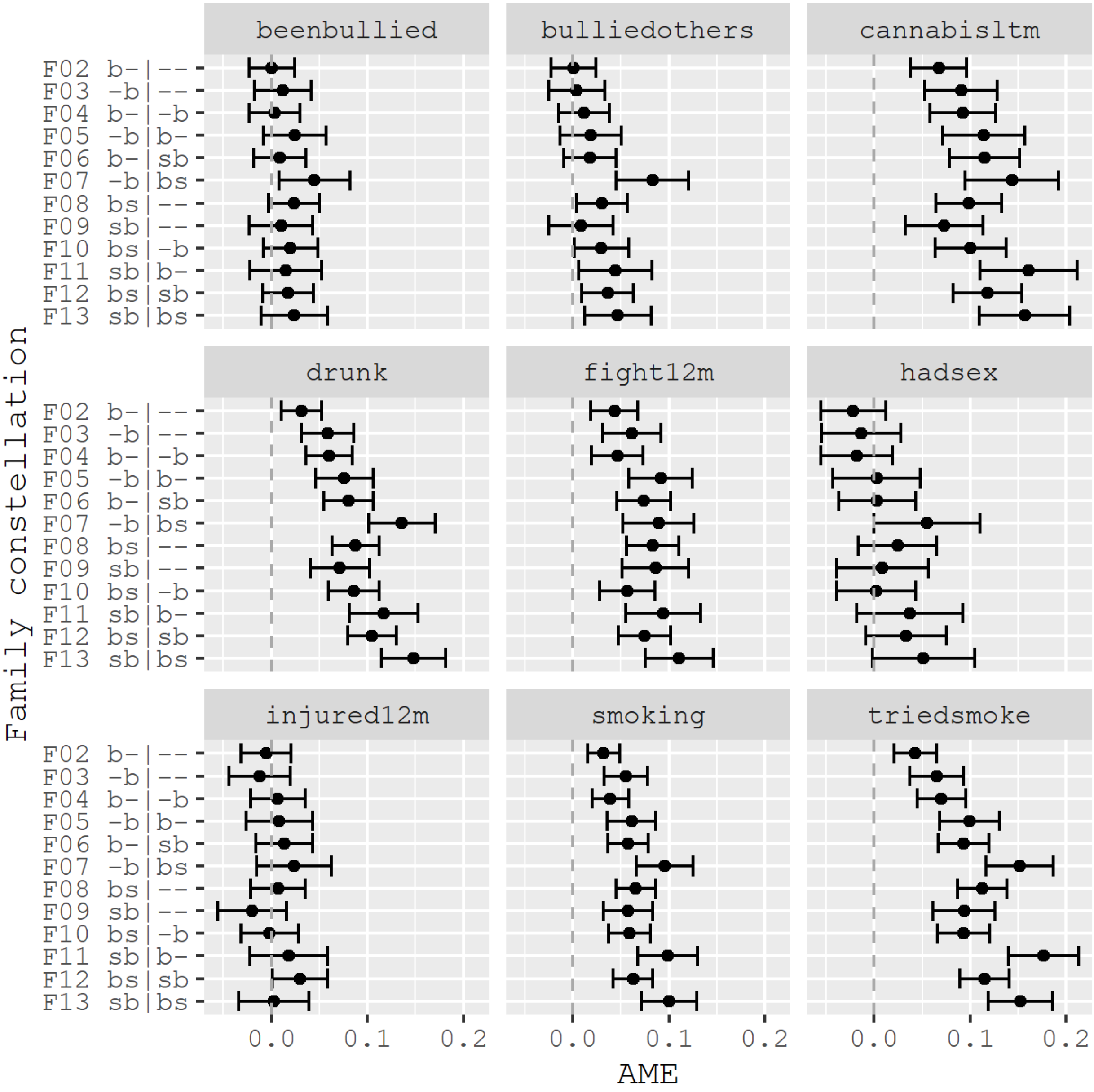


Figure 5: Average marginal (partial) effects from logistic and negative binomial regression on risk incidence and severity (Model 2 and 1 in Appendix)

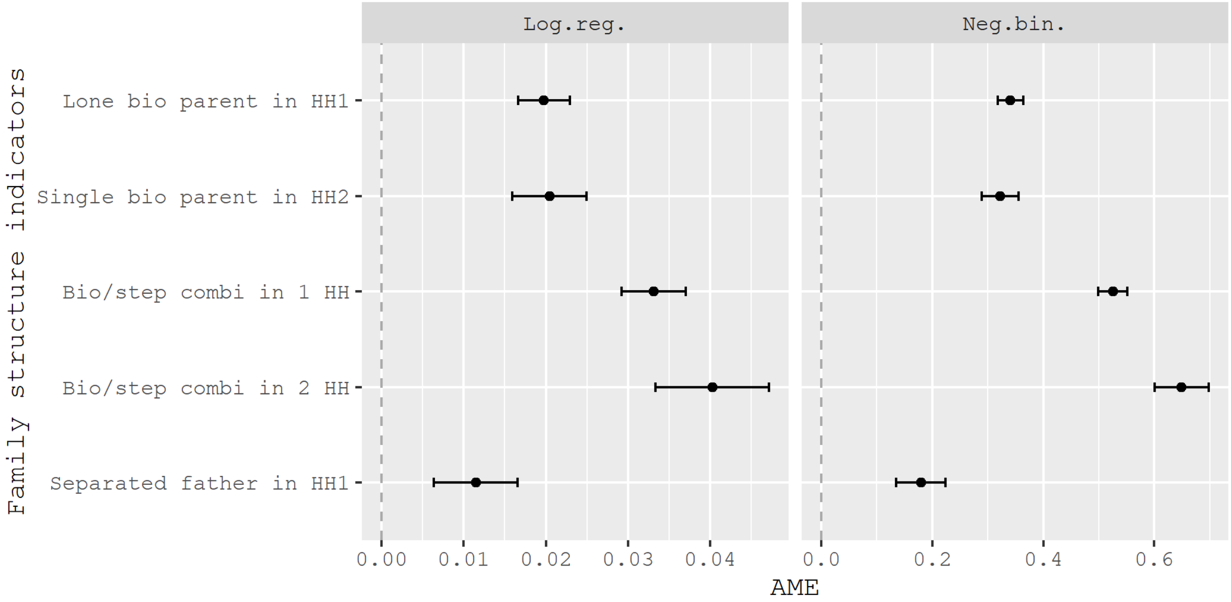
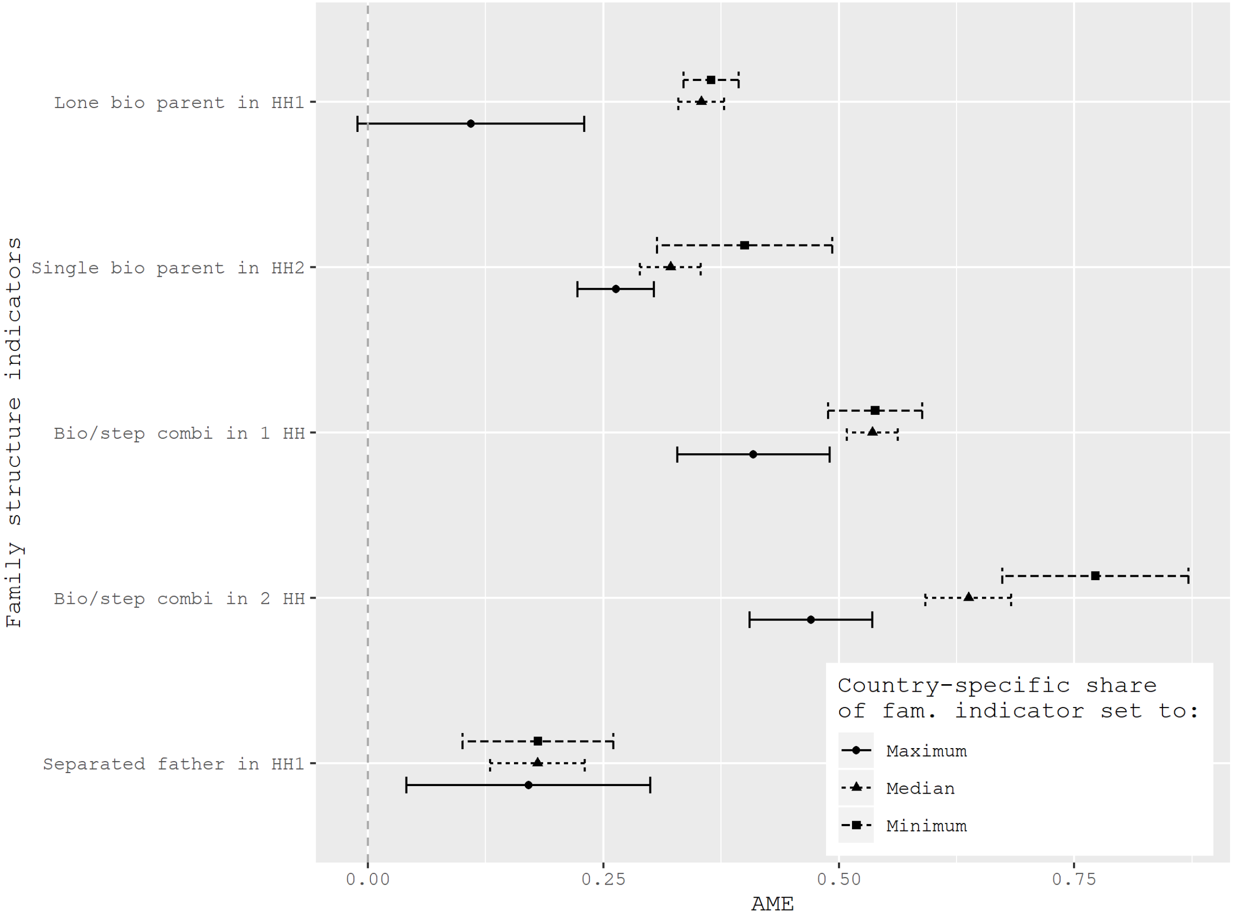


Figure 6: Average marginal (partial) effects of family indicators on risk intensity, by country specific share of family indicator (Model 2, Appendix)



Tables

Table 1: Frequency distribution of the 13 family types

	Family type	Frequency	%
1	F01 bb|--	401788	0,779
2	F02 b-|--	39165	0,076
3	F03 -b|--	5193	0,010
4	F04 b-|-b	16451	0,032
5	F05 -b|b-	2491	0,005
6	F06 b-|sb	10490	0,020
7	F07 -b|bs	1340	0,003
8	F08 bs|--	14565	0,028
9	F09 sb|--	1930	0,004
10	F10 bs|-b	7055	0,014
11	F11 sb|b-	1141	0,002
12	F12 bs|sb	12470	0,024
13	F13 sb|bs	1643	0,003
∑		*515722*	*1,000*

Appendix

	Model 1	**Model 2**
(Intercept)	-0.45***	2.59***
	(0.01)	(0.04)
Age 13 (vs. 11)	0.36***	-0.76***
	(0.00)	(0.02)
Age 15 (vs. 11)	0.91***	-1.60***
	(0.00)	(0.02)
Gender (Male)	0.32***	0.77***
	(0.00)	(0.01)
Family Affluence Scale	0.01***	0.04***
	(0.00)	(0.01)
Survey Year (2006 vs. 02)	-0.15***	-0.12***
	(0.00)	(0.02)
Survey Year (2010 vs. 02)	-0.23***	-0.34***
	(0.00)	(0.02)
Grandmother in HH1 (yes = 1)	0.02*	0.05*
	(0.01)	(0.02)
Grandfather in HH1 (yes = 1)	0.01	0.07*
	(0.01)	(0.03)
Anybody else in HH1 (y=1)	0.10***	0.25***
	(0.01)	(0.04)
Grandmother in HH2	0.08***	0.12
	(0.02)	(0.07)
Grandfather in HH2	0.04*	0.04
	(0.02)	(0.08)
Anybody else in HH2	0.22***	0.47***
	(0.02)	(0.09)
F1 Lone parent in HH1, no HH2	0.33***	0.40***
	(0.02)	(0.06)
F2 Step/bio combi in one HH	0.52***	0.75***
	(0.02)	(0.09)
F3 Step/bio combi in both HH	0.50***	0.69***
	(0.03)	(0.12)
F4 Single parent in HH2	0.24***	0.36***
	(0.03)	(0.10)
F5 Father focal parent	0.11***	0.37***
	(0.03)	(0.10)
F1 country share	3.47***	8.47***
	(0.07)	(0.33)

F2 country share	5.90^{***}	-6.32^{***}
	(0.13)	(0.51)
F3 country share	-1.78^{***}	-21.53^{***}
	(0.29)	(1.00)
F4 country share	-3.87^{***}	27.20^{***}
	(0.21)	(0.73)
F5 country share	-4.50^{***}	-16.33^{***}
	(0.21)	(0.66)
Joint physical custody	-0.08^{***}	-0.08
	(0.02)	(0.07)
F1 x F1 share	-0.97^{***}	-0.78
	(0.12)	(0.54)
F2 x F2 share	-2.10^{***}	-2.31^{*}
	(0.24)	(0.94)
F3 x F3 share	-1.82^{**}	0.94
	(0.60)	(2.47)
F4 x F4 share	-0.13	0.48
	(0.35)	(1.36)
F5 x F5 share	0.39	-6.06^{*}
	(0.68)	(2.39)
Male x F1	-0.08^{***}	-0.05
	(0.01)	(0.05)
Male x F2	-0.12^{***}	-0.17^{**}
	(0.01)	(0.06)
Male x F3	-0.15^{***}	-0.24^{**}
	(0.02)	(0.09)
Male x F4	-0.09^{***}	-0.16^{*}
	(0.02)	(0.06)
Male x F5	-0.04^{*}	-0.02
	(0.02)	(0.09)
AIC	1769685.23	208883.46
BIC	1770075.35	209257.50
Log Likelihood	-884807.61	-104407.73
Deviance	540131.85	208815.46
Num. obs.	512049	442878

$^{***}p < 0.001$, $^{**}p < 0.01$, $^{*}p < 0.05$