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Association between sexes of successive siblings in data from Demographic and Health Survey program

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Abstract

Prediction of future child's sex is a question of keen public interest. Probability of having a child of either sex is close to 50%, although multiple factors may slightly change this value. Some demographic studies suggested that sex determination can be influenced by previous pregnancies, although this hypothesis was not commonly accepted. This paper explores correlations between siblings' sexes using data from Demographic and Health Survey program. In the sample of about 2,214,601 women (7,985,855 children), frequencies of offsprings with multiple siblings of same sex were significantly higher than can be expected by chance. Logistic regression analysis suggested that these deviations of frequencies were driven by positive correlation between sexes of successive siblings (coefficient = 0.065, $p < 0.001$). This correlation could be caused by secondary sex ratio adjustment *in utero* since the effect was decreasing with length of birth-to-birth interval, and birth-to-birth interval was longer for siblings with unlike sex.

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Introduction

A family with multiple children of same sex, say, a family with ten boys and no girls, always draws attention, and speculations are made about possible reasons of such an incident. These may include a lack of either parent's ability to conceive girls, influence of witchcraft, astrology etc.

Surely, large unisex families may emerge simply by chance, when sexes of siblings are completely independent from each other. However, some studies indicate that sex of a child may depend statistically on sexes of other siblings (see references below). There are at least two possible sources of such dependence, that may increase frequency of unisex families. First, some parents indeed may have a predisposition to have children of particular sex. This bias can be caused by chemical compounds, infectious diseases, psychological distress (James 2000) and other conditions specific for given parents. As a result, each couple can be characterized by a probability of male birth p that may differ from proportion of boys in the population. This variation of p among couples was dubbed "Lexian".

Second, the sex of a child could be affected somehow by the sex of immediately preceding sibling, or sexes of several preceding siblings. This effect could be positive (birth of a child with either sex increases chances than next child will be of same sex) or negative. The variation of p within an offspring, dependent on previous birth, was called "Markovian". The unisex families would be in excess in a population with positive Markovian correlation.

Another source of variation in sex ratio is called "Poisson". It refers to random or systematic variation of p within a family, for example a decrease of p with mother's age. Additionally, statistical dependence between siblings' sexes can be caused by parents' sex preferences, e.g. boy preference documented in many Asian cultures, or a preference for mixed-sex offspring.

Since at least 1889[1] the problem was studied using demographic data. Geissler ((Geissler 1889), reviewed in (Gini 1951)) analyzed about 5 million births in 19th century Germany and did not detect significant deviation from expected offspring frequencies. Nevertheless, he noted that in same-

[1] Other aspects of sex ratio variation were studied as early as in 1710, see James, W. H. (2000). "The variation of the probability of a son within and across couples." Human Reproduction **15**(5): 1184-1188.

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sex offsprings probability of birth of one more child of same sex was higher than in other families (a positive correlation). For mixed-sex offsprings the correlation was negative (for instance, probability of female birth increased after many male births).

Gini (Gini 1951) re-analyzed Geissler's data, together with additional datasets from Germany, Italy and Netherlands, and concluded that some couples had a predisposition to have children of particular sex, although this predisposition may reverse with time. For example, a family may start procreation with a tendency to produce one sex, and end with a tendency to produce the opposite sex. He noticed a positive association between sexes of successive siblings in a data from Italy, and interpreted it as an evidence for such predisposition.

Turpin and Schutzenberger (Turpin and Schutzenberger 1949) (reviewed in (Gini 1951)) analyzed a sample from France (14,230 families) and observed positive correlation between sexes of successive siblings. Unlike Gini, they hypothesized that the correlation could be explained by an influence of one birth on the following birth. This idea was supported by the fact that the interval between births of same-sex siblings was on average shorter than for unlike sex siblings (however, Gini interpreted this result in favor of his "reversal of predisposition" explanation).

(Bernstein 1952) analyzed a sample from USA (7,616 families). She reported positive correlation between sexes of first two children in family, and excess of unisexual three-child families.

Malinvaud (Malinvaud 1955) (reviewed in (James 1975)) investigated nearly 4 million births in France. The probability of male birth correlated positively with number of preceding boys and negatively – with number of preceding girls.

Renkonen *et al* (Renkonen 1956, Renkonen, Makela et al. 1961) collected data from 31215 families in Finland. Their dataset was analyzed by several researchers, who reached contradictory conclusions. Original authors confirmed associations reported earlier by Geissler (Renkonen, Makela et al. 1962). First, sex ratio was higher when all previous siblings were boys, and lower when they were girls (positive correlation). Second, for mixed offsprings the sex ratio was decreasing when number of preceding boys increased (negative correlation). The negative correlation was explained by

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possible immunization of mother's organism against male fetal antigens. Edwards (Edwards 1961, Edwards 1962, Edwards 1966) re-analyzed the data using different statistical methods and demonstrated that correlation between sexes of successive siblings was positive (presumably due to some kind of *in utero* adjustment of sex ratio), although it became negative when only two last siblings in a family were concerned (probably due to birth control). Beilharz (Beilharz 1963) analyzed same data and dismissed previous conjectures about biological factors. Instead, he concluded that there is no influence of sex of previous sibling, and apparent positive correlation is caused by heritable tendency of some parents to have same-sex offsprings.

No correlation was found between successive siblings' sexes in 116,458 sibships from Utah, USA (Greenberg and White 1967). Also, interval between births in this sample did not depend on whether the siblings were of like or unlike sex.

In the data from 1970 USA census, with more than 230,000 families, sex ratio increased with number of preceding boys, and decreased with number of preceding girls. The authors suggested that their data provide evidence for both Markovian and Lexian variation (Ben-Porath and Welch 1976).

In another USA sample (649,366 births) the sex of last child in a family was negatively correlated with sexes of preceding siblings (probability of male birth decreased with number of preceding brothers) (Thomas Gualtieri, Hicks et al. 1984).

Mitter *et al* reported an excess of unisexual offsprings in small sample (451 families) from India (Mitter and Anand 1975).

(Maconochie and Roman 1997) reported that sex ratio was not associated with sexes of preceding siblings in 330,088 offsprings from Scotland. (Jacobsen, Moller et al. 1999) used a sample of 815,891 children from Denmark. According to their analysis, neither sex of immediately preceding sibling nor sexes of two or three preceding siblings had significant effect on sex ratio, when the regression model was adjusted for paternal age. (Rodgers and Doughty 2001) analyzed 6,089 families from USA and concluded that sexes of previous siblings had no effect on sex ratio.

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Garenne (Garenne 2009) analyzed over 2 million births in Sub-Saharan Africa. There was no correlation between sexes of successive siblings (although, only the correlation between two last births was tested). The sex ratio was dependent on number of preceding boys (positively) and number of preceding girls (negatively), as it was the case in Malinvaud's sample.

Overall the results of published studies are mixed. Many, but not all of them, report a correlation between sexes of siblings in a family. When the correlation is found researchers disagree about it's possible sources, since it can be attributed to both positive Markovian and to Lexian variation. The situation is complicated by a variety of statistical methods employed. Some authors tested pair-wise correlation between sexes of two successive siblings. Others used a regression of probability of male birth on numbers of preceding boys and girls. Sample size is also an issue, with many studies conducted on only few thousands of families (while others use hundreds of thousands). Few studies explicitly tested for an excess of families with particular composition, such as unisex families.

Recently large scale demographic data, including birth sequences, became available for analysis from Demographic and Health Survey (DHS) program. The DHS is international organization that assists in conducting demographic surveys, mostly in developing countries. I used DHS data from about 7 million births to test (1) if there are significant deviations from expected frequencies of offsprings with various sex compositions, (2) if there is a correlation between sexes of successive siblings, and (3) if this correlation can be attributed to Lexian or Markovian variation.

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Methods

The surveys were carried out in 1985-2014 mostly in developing countries of Africa, Asia and South America. Datasets were downloaded from DHS website (dhsprogram.com) in August-September 2015. Surveys of following types were selected for analysis: Standard DHS, Continuous DHS, Interim DHS, Special DHS. For each survey, the "individual response" dataset was downloaded, in Stata format (.dta). The sequences of siblings sexes were taken from variables b4_01-b4_20. Other variables used in analysis were b11_01-b11_20 (intervals between births), b3_01-b3_20 (child's date of birth), v011 (mother's date of birth), b0_01-b0_20 (indicator of plural birth), v201 (total number of children ever born).

Data handling and statistical analysis were done with Stata/MP 13. Logistic regression used sex of each child (except of first child in an offspring, who doesn't have any preceding sibling) as dependent variable, and sex of previous child – as independent variable. Pairs of successive siblings where at least one of them was from plural birth were excluded. Offsprings with reported total number of children ever born (variable v201) did not match number of children recorded in variables b4_01-b4_20 were excluded as well.

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Results

Large same-sex offsprings were more numerous than expected

Total sample included 7,985,855 children in 2,214,601 offsprings (Table 8). An offspring can be characterized, regardless of birth order, by total number of children *n* and number of boys *k*. If sex of each child is determined independently of siblings, then expected frequency of the offspring can be calculated according to binomial law: $E_{n,k} = \binom{n}{k} r_n^k (1 - r_n)^{n-k}$, where r_n is proportion of boys in all offsprings with size *n*. Expected and observed frequencies were compared using chi-squared test, and deviations were highly significant (Chi2 = 994, df = 178, p < 0.001). The deviations remained significant when offsprings with at least one plural birth were excluded from the analysis (Chi2 = 1071, df = 176, p < 0.001), or when only one proportion of boys *r* for whole sample (instead of specific proportion for each offspring size) was used to calculate expected frequencies (Chi2 = 1700, df = 177, p < 0.001).

Next, chi-squared test was applied to test frequency deviation for each type of offspring (as characterized by *n* and *k*) (Table 1).

Table 1 Odds ratios demonstrating relative abundance of offsprings with various sizes *n* and numbers of boys *k*. Odds ratio above 1 indicates an excess of offsprings with given composition, relative to expected frequency. *p-value < 0.05. For 31 out of 63 chi-square tests performed the p-value was below 0.05. Offsprings with n > 10 are not shown.

	n								
k	*2*	*3*	*4*	*5*	*6*	*7*	*8*	*9*	*10*
0	0.94*	0.95*	0.94*	0.97	0.98	1.08	1.25*	1.27	1.39
1	1.09*	1.01*	0.99	1.01	1.02	1.05*	1.08*	1.18*	1.14
2	0.95*	1.05*	1.04*	1.01	1.01	1.01	1.02	1.05	1.09*
3		0.93*	0.98*	0.98*	0.99	0.97*	0.98	0.99	1.01
4			0.97*	1.01	0.98*	0.99	0.98	0.97*	0.99
5				1.02	1.03*	0.99	0.97*	0.98	0.98
6					1.07*	1.05*	1.02	0.99	0.97
7						1.16*	1.06*	1.05*	0.99
8							1.31*	1.15*	1.06
9								1.08	1.31*
10									1.63*

Deviations from expected frequencies were significant for many offspring compositions. Notably, offsprings with many boys were in excess among large families. For instance, among 30,393

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offsprings with exactly ten children 52 were all-boys, while expected number was only 32 (OR = 1.63, p = 0.037). Similarly, among large offsprings number of those composed mostly with girls tended to be higher than expected. At the same time among small offsprings (<5 children) mixed-sex types were more common. For example, among offsprings with only 2 children those with one boy and one girl were overrepresented (OR = 1.09, p < 0.001).

Sex ratio depended on sex of preceding sibling

The dependence between sexes of successive siblings was tested using logistic regression (male sex was coded as "0" and female as "1"). The sex of preceding sibling had small but significant positive effect on sex of a child (coef = 0.016, p < 0.001, ~0.4%[2] change of sex ratio). Assuming that this effect could depend on offspring size and birth order of a child, the regression was repeated for different offspring sizes *n* and birth orders *i* (Table 2).

Table 2 Correlations between sexes of successive siblings, by offspring size *n* and birth order *i*. Regression coefficients from logit model are presented (sex of *i*'th child as dependent variable, sex of *i-1*'th child – independent variable). Offsprings with more than ten children are not shown. *p-value < 0.05.

	n								
i	*2*	*3*	*4*	*5*	*6*	*7*	*8*	*9*	*10*
2	-0.168*	0.013	0.063*	0.089*	0.075*	0.063*	0.104*	0.081*	0.046
3		-0.11*	-0.002	0.069*	0.08*	0.085*	0.078*	0.094*	0.171*
4			-0.072*	0.011	0.08*	0.077*	0.092*	0.1*	0.116*
5				-0.028*	-0.001	0.093*	0.085*	0.105*	0.093*
6					-0.037*	0.028*	0.075*	0.078*	0.073*
7						-0.016	0.068*	0.072*	0.066*
8							0.005	0.068*	0.035
9								-0.003	0.041
10									0.063*

When dependent variable was the sex of last child in an offspring ($i = n$), the regression coefficients were mostly negative. Meanwhile, for most other combinations of *n* and *i* the coefficients were positive. When the analysis (for all offspring sizes *n* combined) was performed excluding last child of each offspring (i.e. when $i \neq n$, for all *n*), the regression coefficient was 0.067 (p < 0.001).

[2] As a rule of thumb in these models, logistic regression coefficient of 0.1 corresponds to 2.5% increase of probability that the *i*'th child has same sex as preceding sibling.

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Conversely, when only last children were included ($i = n$, for all n), the regression coefficient was -0.083 ($p < 0.001$).

For confirmation of the results obtained in pooled sample the regression was performed in each dataset from DHS website (one dataset per survey), and then random effects meta-analysis was applied to pool estimates of regression coefficients. When all children were included (regardless of birth order) the result was not significant (coef = 0.002, $p = 0.67$, $I^2 = 48.4\%$, $p < 0.001$). When last child of each offspring was excluded, the effect of preceding sibling's sex was positive and significant (coef = 0.065, $p < 0.001$, $I^2 = 68.6\%$, $p < 0.001$). When only last children were included the effect of previous sibling's sex was negative and significant (coef = -0.121, $p < 0.001$, $I^2 = 86.2\%$, $p < 0.001$).

Why does the sign of this correlation depend on whether "dependent" child is last or not last in a family? Is it possible that sex of preceding sibling affects sex of a child via two different mechanisms, depending on whether the next sibling is a last child in the family or not? The negative correlation for last child may be explained by deliberate family planning, namely parents' willingness to have a family with mixed sex composition ("balance preference", discussed by (Gini 1951) and others). Such preference may dictate specific stopping behavior. For instance, if a couple have several daughters they may continue procreation until having a son, and then stop. A couple having a boy and a girl may decide to stop the procreation, while a family with two girls may wish to have one more child in a hope that it will be a boy.

However, the last child recorded in DHS data is not necessary the last child in the family. The respondent woman may continue the procreation after interview date (i.e. the family could be incomplete). The proportion of children who are last in complete families should increase with the interval between date of last birth and date of interview. If the negative correlation between sexes of two last siblings is caused by parents' stopping behavior, the correlation should be stronger when proportion of complete families is higher. Indeed, in logit model including the time since last birth as a covariate, the effect of interaction term was negative and significant (Table 3). The negative sign suggests that coefficient's absolute value is increasing when the time since last birth increases. For instance, when last birth was less than 6 months before interview (bottom 10% of distribution of

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interval values) the effect of previous sibling's sex was not significant (coef = -0.017, p = 0.096). When last birth was more than 167 months before interview (top 10%) the negative correlation was highly significant (coef = -0.24, p < 0.001).

Table 3 Effects of preceding sibling's sex and time since last birth on sex of last sibling in an offspring. Logistic regression coefficients. p-values in italic.

Independent variable	*1*	*2*	*3*
Sex of preceding sibling	-.0979 *< 0.001*	-.0994 *< 0.001*	-0.02 *< 0.001*
Time since last birth, months		-.0006 *< 0.001*	-0.00008 *< 0.001*
Interaction term			-0.0011 *< 0.001*

Alternatively to deliberate family planning, some biological factors behind the correlation between sexes may change their direction from positive to negative, and such a change could be accompanied by the end of procreation.

Was the correlation caused by Lexian or Markovian variation?

If some parents have a tendency to produce children of particular sex, then a correlation should be observed between sexes of siblings regardless their birth order, not only between successive siblings (Edwards 1961). If the association between successive siblings has major role, then little or no correlation should be observed between sexes of siblings separated by other births. In DHS data the correlation was strong between successive siblings, less strong but still significant– between siblings separated by one birth, and negligible when siblings were separated by two or more births (Table 4, column *2*).

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Table 4 Correlations between sexes of siblings separated by various numbers of births. Logistic regression coefficients. Offsprings with more than 10 children are omitted.

Number of births separating the two siblings	1. All pairs of siblings			2. Excluding last children			3. Only last children		
	coef	*P*	*N*	*coef*	*P*	*N*	*coef*	*p*	*N*
0	0.016	<0.001	5540403	0.067	<0.001	3819694	-0.098	<0.001	1720709
1	-0.011	<0.001	3766164	0.021	<0.001	2519485	-0.077	<0.001	1246679
2	-0.019	<0.001	2524926	0.003	0.32	1648152	-0.059	<0.001	876774
3	-0.015	<0.001	1653104	0.004	0.27	1046960	-0.049	<0.001	606144
4	-0.013	<0.001	1051994	-0.008	0.13	638503	-0.022	<0.001	413491
5	-0.014	0.004	643119	-0.006	0.37	370079	-0.026	<0.001	273040
6	-0.003	0.70	373788	0.004	0.62	201079	-0.010	0.28	172709
7	0.001	0.92	203656	-0.006	0.63	101590	0.008	0.54	102066
8	-0.001	0.96	103270	0.004	0.83	46867	-0.004	0.80	56403
9	0.004	0.82	47840	-0.015	0.59	20087	0.018	0.45	27753
10	-0.018	0.52	20606	-0.037	0.42	7770	-0.007	0.85	12836

When only last children were concerned (i.e., last sibling's sex was dependent variable) the negative coefficient remained highly significant even when siblings were separated by up to five births (Table 4, column *3*). This negative correlation with sexes of several preceding siblings is not surprising if the last child's sex is influenced by parents' balance preference (parents take into consideration sexes of several existing children).

When all children, regardless of birth order, were included in the model, the coefficient was positive and significant for successive births, but it was negative and significant when siblings were separated by 1-4 births (Table 4, column *1*). Apparently, this result is caused by combination of two effects: positive correlations in most successive pairs, and negative correlation between sex of last child and sexes of several siblings preceding the last one.

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Effects of birth-to-birth interval on correlation between sexes

If previous sibling's sex exerts it's effect by leaving some kind of temporary chemical mark in mother's organism, then this effect could be stronger for shorter intervals between births (Edwards 1961). The interaction between birth-to-birth (BTB) interval and sex of previous sibling was tested using logistic regression (Table 5).

Table 5 Interaction of preceding sibling's sex and birth-to-birth (BTB) interval. Logistic regression coefficients are shown (p-values in italic).

Independent variable	**1. Excluding last children**			**2. Only last children**		
Sex of preceding sibling	0.062 *<0.001*	0.063 *<0.001*	0.087 *<0.001*	-0.065 *<0.001*	-0.082 *<0.001*	-0.084 *<0.001*
BTB interval, months		.00051 *<0.001*	0.00089 *<0.001*		.00048 *<0.001*	.000489 *<0.001*
Interaction term			-.00077 *<0.001*			.0000325 *0.8*

The effect of BTB interval alone was significant, regardless of whether last children were excluded or not: every additional month since last birth increased chances to have a girl by approximately 0.01%. The interaction term was significant only in the model excluding last children (coef = -0.00077, $p < 0.001$). The negative sign of the coefficient suggests that the effect of preceding sibling's sex is vanishing with time. This interaction can be seen on Figure 1 (the value of regression coefficient is decreasing from 9 to 40-45 months of BTB).

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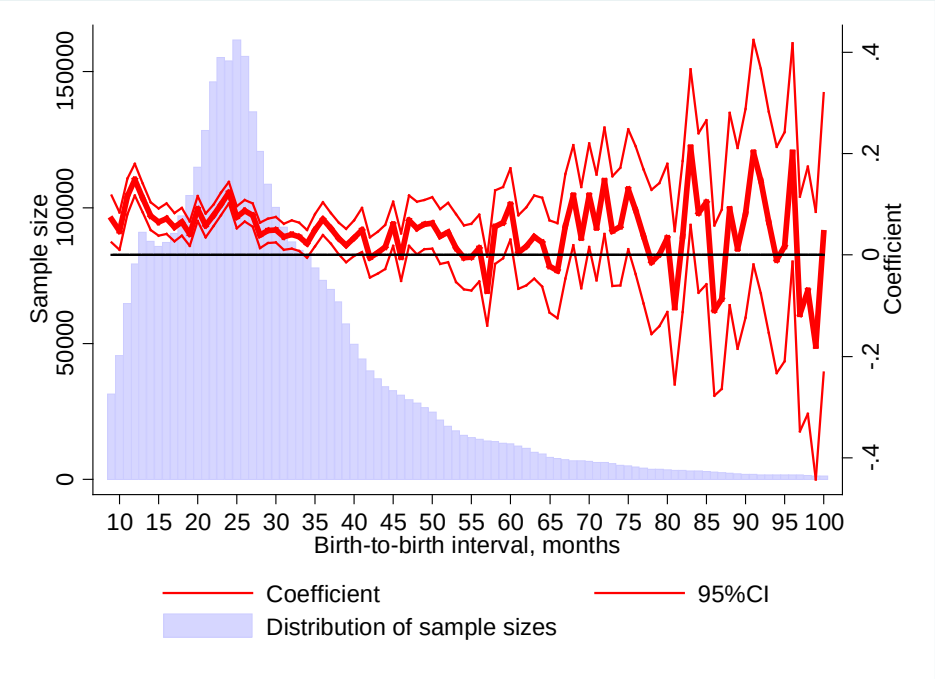

Figure 1 Logistic regression coefficients (effect of preceding sibling's sex) by BTB intervals, with last child of each offspring excluded from analysis. Distribution of sample sizes over BTB values is shown in the background.

When the analysis was limited to last children, the interaction was not significant (coef = -0.00003, p = 0.8), Table 3, Figure 2.

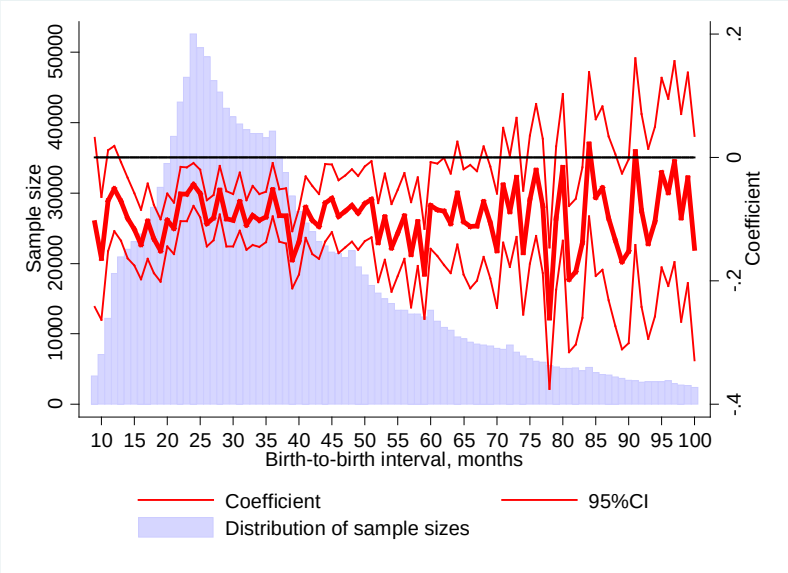

Figure 2 The effect of preceding sibling's sex doesn't change substantially with BTB interval, when only last children are considered. Logistic regression coefficients (effect of preceding sibling's sex) by BTB intervals. Distribution of sample sizes over interval values is shown in the background.

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Edwards (Edwards 1961) suggested also that the correlation between successive siblings' sexes could be mediated by secondary adjustment of sex ratio, namely by lower chances of fetus survival when it's sex is opposite to preceding sibling. In this case the BTB interval could be longer when successive siblings were of unlike sex.

BTB interval between same sex births was significantly shorter than between opposite sex births when excluding last children (linear regression, pair of same sex births coded as "1", opposite sex – "0", coef = -0.135, $p < 0.001$). Results of nonparametric rank sum test were significant as well ($p < 0.001$).

(Greenberg and White 1967) noted that such analysis of intervals should control for birth order or family size (because if their data the interval decreased with family size when birth order was constant). When offspring size and birth order were included into regression model as covariates, the interval still was significantly longer for opposite sex pairs (coef = -0.085, $p < 0.001$). Additionally, the analysis was repeated for each combination of offspring size *n* and birth order *i* (Table 6).

Table 6 Differences between BTB intervals for siblings of same and opposite sex. Linear regression coefficients are shown (the value corresponds to difference of BTB between pairs of opposite sex siblings and pairs of same sex siblings). * p < 0.05. Offsprings with more than 10 children are not shown.

i	**n**							
	3	*4*	*5*	*6*	*7*	*8*	*9*	*10*
2	0.337*	0.03	-0.142	-0.008	-0.263*	-0.124	-0.167	-0.047
3		0.257*	-0.055	-0.127	-0.309*	-0.331*	-0.071	-0.284*
4			0.019	-0.072	-0.11	-0.339*	-0.137	-0.108
5				-0.108	-0.268*	-0.333*	-0.164	-0.24
6					-0.308*	-0.015	-0.278*	-0.367*
7						-0.167	-0.405*	-0.115
8							-0.176	-0.273
9								-0.372*

The difference of BTB intervals was significant for multiple, but not for all, combinations of *n* and *i*. Notably, all coefficients were negative for offsprings with six or more children.

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Additional datasets

Detailed information about siblings sexes and birth order was presented in several published papers ((Renkonen, Makela et al. 1961, Greenberg and White 1967, Maconochie and Roman 1997, Jacobsen, Moller et al. 1999, Rodgers and Doughty 2001)). Logistic regression was applied to these datasets to investigate the reproducibility of results obtained in DHS data (Table 7).

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Table 7 Logistic regressions of child's sex on preceding siblings' sex in datasets from published papers.

Publication		All observations	Excluding last child	Limited to last child
(Renkonen, Makela et al. 1961) (as presented in (Edwards 1962))[1]				
All data				
	coef	.053	.104	-0.017
	p	< 0.001	< 0.001	0.32
	N	123445	71577	51868
< 5 siblings				
	coef	.036	.158	-.049
	p	0.021	< 0.001	0.018
	N	62797	26091	36706
(Greenberg and White 1967)[2]				
All data				
	coef	-.008	.005	-0.044
	p	0.195	0.46	< 0.001
	N	438788	322399	116389
< 7 siblings				
	coef	-.024	.004	-0.073
	p	0.005	0.71	< 0.001
	N	220154	140204	79950
(Maconochie and Roman 1997)				
	coef	-.0009	.0051	-.002
	p	0.7	0.3	0.3
	N	217960	46119	171841
(Jacobsen, Moller et al. 1999)[3]				
	coef		0.078	
	p		< 0.001	
	N		51016	
(Rodgers and Doughty 2001)[4]				
All data				
	coef	-.064	.076	-0.14
	p	0.196	0.372	0.023
	N	6435	2227	4208
< 4 siblings				
	coef	-.153	-.036	-.194
	p	0.007	0.74	0.003
	N	5046	1301	3745

[1] in original report families with five or more children were pooled together. Thus, the analysis limited to last children was informative only for offsprings with four siblings or less. [2] in original report families with seven or more children were pooled. Thus, the analysis limited to last children was informative only for offsprings with six siblings or less.[3] the data were taken from Table V of original report, that lists birth sequences of first three siblings for families with at least four children (sex of fourth child was not shown in original paper). Thus, only the analysis excluding last children (and only in offsprings with three or more siblings) was possible. [4] in original report families with four or more children were pooled. Thus, the analysis limited to last children was informative only for offsprings with three siblings or less.

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In data from Renkonen (Renkonen, Makela et al. 1961) the effect of previous sibling's sex was positive when last children were excluded (coef = 0.158, p< 0.001) and negative when only last children were included (coef = -0.049, p = 0.018), as in the DHS data. In Greenberg's data (Greenberg and White 1967) positive correlation, after exclusion of last children, was not significant, while there was strong negative correlation between sexes of last two siblings in a family. Similar situation was observed in Rodgers data (Rodgers and Doughty 2001) (excluding last children – not significant effect; including only last children, coef = -0.19, p = 0.003). In Maconochie's data (Maconochie and Roman 1997)both kinds of correlation were not significant. In Jacobsen's data (Jacobsen, Moller et al. 1999) the correlation was positive and significant in the model excluding last children (coef = 0.078, p < 0.001).

Thus, positive correlation between sexes of successive siblings (excluding last children) was found in two out of five additional datasets. It should be noted, however, that Jacobsen and Rodgers do not report statistics of birth sequences after excluding plural births. Thus the positive values of coefficients could be overestimated. One should note also that unlike other datasets, Renkonen data don't include children from a previous marriage of each woman.

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Discussion

Current results demonstrate an excess of large offsprings with high (many boys) and with low (many girls) sex ratios, relative to binomial expectation. The overrepresentation of such offsprings was accompanied by correlation between sexes of siblings. Notably, positive correlation was observed between sexes of successive siblings and siblings separated by one birth, but not for those separated by two or more births. This effect is consistent with hypothesis of Markovian variation, but not with Lexian one.

Makela (Makela 1963) noted that even in the presence of Lexian variation, lack of correlation for siblings separated by several births could be observed due to other factors, for example an immunization against male fetal antigens. But in this case it is not clear why such factors do not make correlation between successive siblings negative as well.

Additional evidence for Markovian variation comes from analysis of birth-to-birth intervals. Namely, the correlation between sexes was stronger when births were separated by shorter intervals.

Several published studies reported an absence of Markovian variation. However, negative report doesn't necessarily mean that the correlation is absent. Perhaps it is absent in a subsample selected for testing, or can't be detected using specific methods employed. For example, Garenne (Garenne 2009) performed a test of association between sexes of successive siblings and found it insignificant. However, this test was conducted not on all children of the sample. Instead, from each offspring only two siblings were selected: the last one and second to last in birth sequence. Moreover, the analysis was restricted to women at least 35 years old.

Jacobsen (Jacobsen, Moller et al. 1999) reported that correlation between sexes was not significant, but no distinction was made between last birth in an offspring and all other births. When logistic regression was applied only to non-last births, significant positive association was seen between successive siblings (Table 7).

Regarding samples used in (Greenberg and White 1967) and (Maconochie and Roman 1997) samples, there seems to be no significant Markovian correlation even when non-last births were tested

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separately. The lack of correlation in these (and possibly other) samples might be explained by between-population heterogeneity. Both samples were collected in developed countries (USA and Scotland, respectively), while most of DHS data come from developing countries. Notably, Greenberg and White confirmed that the correlation was present in Renkonen's data.

It is unknown what biological mechanisms could underlie positive Markovian variation. Gini (Gini 1951) stated that "[the] hypothesis may be considered excluded by the mechanism of sex determination in a male heterogametic species like the humans". Other researchers also noted that there is no plausible mechanism for influence of one siblings' sex on the next one (Ben-Porath and Welch 1976) (James 2000).

However, the casual influence is not biologically impossible. Potential mechanism could be based, for example, on fetal microchimerism. During pregnancy fetal cells penetrate into mother's organism and remain there for years. These cells migrate into heart, skin, thyroid and adrenal glands, liver, kidney, lung, and spleen (Bayes-Genis, Roura et al.). Thus, they may migrate into reproductive system as well. They can differentiate into myocardial cells (Bayes-Genis, Roura et al.) and probably into other cell types (Khosrotehrani and Bianchi 2005). In principle, such cells, remaining in the reproductive system after previous pregnancy, may induce an adjustment of sex ratio by influencing viscosity of cervical mucus or embryo mortality. Alternatively, fetal cells may alter activity of adrenal glands (and levels of cortisol), pituitary (and levels of ACTH) and other glands related to sex determination.

A study on Mongolian gerbils demonstrated that females, developed between male embryos *in utero*, had higher sex ratio in their offsprings later on (Clark and Galef 1995). This effect in gerbils could be related to an acquisition of cells by female fetus from adjacent male fetuses. Perhaps this effect is based on same mechanism as Markovian correlation in humans.

One study reported that concentration of fat in human milk depends on sex of a child (Fujita, Roth et al. 2012). The authors noted also "near-significant negative influence of the number of sons living at home on milk fat concentrations". Biological mechanism of these effects is unknown, but it

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is likely that sex of the child causes persistent alterations in mother's physiology, that can be related to both milk production and adjustment of sex ratio.

Future directions. The analysis used simple regression tests to distinguish Lexian and Markovian variation. These sources of variation could be distinguished using more sophisticated modelling, with dedicated parameters for correlation between sexes of successive siblings and parameters for distribution of sex ratios across families (along with other sources). At least two such models were proposed and tested (Crouchley and Pickles 1984) (Astolfi and Tentoni 1995), but, to my knowledge, never employed for analysis of independent samples. Analysis of DHS data using structural modelling would be beneficial.

Among many studies of sex ratios in families only few present raw data. Other papers contain only a summary of data, that isn't sufficient for many kinds of analysis. Presenting full data is essential for replication. In case of sex sequences the data can be made quite compact: it is enough to indicate birth sequence (e.g., Boy-Girl-Boy) and number of offsprings with given sequence. The data used in current paper are available on DHS website (after an approval from DHS).

Biological mechanisms of Markovian variation could be investigated using model organisms. To the best of my knowledge, among animals the Markovian dependence (controlling for Lexian variation) was explicitely tested only in dairy cattle (Astolfi and Tentoni 1995). The variation was not significant, although authors noted weak effect in expected direction: "after a male calf the probability of a male birth was slightly higher than the probability of a female birth". It is not clear if cattle could be good model organism; for example, probability of male birth increased with parity in Astolfi's data, while in humans it is usually decreasing. It would be interesting to see if Markovian variation is present in mice, rats or other species amenable to experimentation.

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Supplementary information

Table 8 Summary statistics

Offspring size (number of children)	Count	Percent	Sex ratio
1	438,612	19.81	0.517
2	467,637	21.12	0.524
3	387,089	17.48	0.520
4	283,323	12.79	0.512
5	202,076	9.12	0.508
6	147,510	6.66	0.506
7	105,567	4.77	0.505
8	74,526	3.37	0.507
9	48,161	2.17	0.507
10	30,393	1.37	0.505
11	15,964	0.72	0.506
12	8,477	0.38	0.510
13	3,110	0.14	0.510
14	1,266	0.06	0.516
15	527	0.02	0.510
16	239	0.01	0.502
17	67	<0.01	0.519
18	30	<0.01	0.509
19	16	<0.01	0.493
20	11	<0.01	0.527
Total	2,214,601		0.512

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