EVIDENCE OF A FRATERNAL BIRTH ORDER EFFECT ON MALE AND FEMALE SAME-SEX MARRIAGE IN THE DUTCH POPULATION: A BRIEF REPLY TO BLANCHARD AND SEMENYNA, GÓMEZ JIMÉNEZ & VASEY

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Abstract: In our original manuscript, we provided novel and robust evidence to solidify current understandings of the Fraternal Birth Order Effect (FBOE) and Female Fecundity Effect (FFE) on homosexuality. Specifically, our study set out to achieve three goals: to test the existence of the FBOE and FFE in a remarkably large and representative dataset; to provide a comprehensive account of how these processes operate among women; and to propose methodological refinements to better disentangle between the FBOE and the FFE, and the influence of other sibship characteristics. Our results revealed the presence of an FBOE for both men and women, but no evidence of an FFE. We are pleased that our approach and findings have stirred constructive dialogue about the state of the field and grateful to Blanchard and Semenyna and colleagues for their generous and insightful reflections. In this reply, we briefly respond to three key points raised in their commentaries, namely (i) the potential effect of endogenous stopping rules, (ii) the validity of same-sex marriage as an indicator of same-sex-oriented sexuality, and (iii) the meaning of an FBOE among women. In doing so, we summarize key areas of agreement, as well as avenues for theoretical and methodological refinement identified through this constructive exchange.

Keywords: administrative data; endogenous stopping rules; fraternal birth order effect; female fecundity effect; homosexuality; same-sex marriage.

Introduction

In our original manuscript (Ablaza, Kabátek and Perales, 2021), we aimed to provide novel and robust evidence to solidify our understanding of the Fraternal Birth Order Effect (FBOE) and Female Fecundity Effect (FFE) on homosexuality. Specifically, our study set out to achieve three overarching goals: (i) to test the existence of the FBOE and FFE in a remarkably large and representative dataset; (ii) to provide a comprehensive account of whether and how these processes operate for female homosexuality; and (iii) to propose methodological refinements to better disentangle between the FBOE and the FFE, and the influence of other sibship characteristics. To this end, we leveraged population-level linked administrative data from the Netherlands capturing over nine million records spanning several decades. Our results revealed the existence of an FBOE on homosexuality among both men and women, but no evidence of an FFE.

We are pleased that our study has stirred constructive dialogue about the state of the field and how we can collectively move it forwards, and grateful to Ray Blanchard and Scott Semenyna, Francisco Gómez Jiménez and Paul Vasey for their generous and insightful reflections. Blanchard (2021a) and Semenyna et al. (2021) made important and well-argued remarks about the relative advantages and disadvantages of our data and methodological approach. We take these points well and generally agree with them. In this reply, we briefly respond to three core issues raised in Blanchard's and Semenyna et al.'s commentaries, namely (i) the potential influence of endogenous stopping rules, (ii) the validity of same-sex marriage as an indicator of same-sex-oriented sexuality, and (iii) the meaning and implications of the existence of an FBOE on female homosexuality. In doing so, we summarize key areas of agreement, as well as avenues for theoretical and methodological refinement in the field echoed through this constructive exchange.

Can endogenous stopping rules distort our findings?

In a compelling commentary, Blanchard (2021a) alluded to the existence of endogenous stopping rules in earlier datasets used to test the FBOE (e.g., Blanchard & Lippa, 2007, 2021; Skorska et al., 2020; Zucker, Blanchard, Kim, Pae, & Lee, 2007) and reflected on whether our method can account for any confounding effects stemming from these stopping rules. Similarly, Semenyna and colleagues (2021) mentioned the possibility that our results might represent a spurious relationship attributable to endogenous stopping rules. This raises questions about whether stopping rules are indeed present in our data and whether they might have distorted our findings.

Briefly, endogenous stopping rules emerge when prospective parents exhibit preferences for children of one sex over the other (with a documented predilection for sons in many cultures) or preferences for having children of both sexes (Blanchard, 2021a). Through childbearing choices, these preferences can skew the size and the sex composition of sibships. For example, parents who have two daughters may be more likely to try for another child than parents who already have one daughter and one son. As a result, sex ratios may vary substantially depending on the birth order and the sex composition of older siblings, with potential implications for the estimation of the FBOE and FFE.

Is this phenomenon apparent in the Dutch population-level data leveraged in Ablaza et al. (2021)? To answer this question, we used these data to calculate and plot sex ratios conditional on individuals' position within their sibship (see Figure 1). The sex ratio among eldest siblings was 104.8 (i.e., 104.8 males per 100 females) close to the natural human sex ratio of 106 (Chahnazarian, 1988).¹ We take this ratio (104.8) as a benchmark because it cannot be influenced by endogenous stopping rules. In comparison, the sex ratio among youngest siblings was 104.2, which was marginally yet statistically significantly lower. This suggests

¹ Of note, ours are sex ratios *at the point of observation*. These may be slightly smaller than the sex ratios *at birth* due to higher mortality rates among men up to the point of observation.

that Dutch parents have a slight preference for daughters (an observation previously made by Kabátek and Ribar, 2021). More substantive deviations from the benchmark sex ratio emerged when we split the group of youngest siblings by their sibship composition: the ratio was considerably higher (113.6) if all elder siblings were sisters and considerably lower (95.7) if all elder siblings were brothers. The sex ratio of youngest children with both older brothers and older sisters was nearly identical to the benchmark (104.7). The two deviations from the benchmark (113.6 and 95.7) had similar magnitudes, which suggests that Dutch parents have a relatively strong preference for having children of both sexes (i.e., diversity preferences). Of note, we observed even larger deviations from the benchmark sex ratio among individuals who were the second-youngest siblings within their sibships. Corroborating the results presented by Blanchard and Lippa (2007), the sex ratio of second-youngest siblings was lower (91.7) if all older siblings were brothers.²

The effects of endogenous stopping rules can also be captured by focusing on the youngest siblings of a given gender and quantifying the sex ratios among their older siblings (Blanchard, 2021a; Blanchard & Lippa, 2007). For youngest brothers in our data, the sex ratio among their older siblings was skewed towards females (100.3). For youngest sisters, it was skewed towards males (108.4). In contrast, for males who were the second-youngest sibling, the older-sibling sex ratio was skewed towards males (110.8). For females who were the second-youngest sibling, it was skewed towards females (97.6).

 $^{^2}$ While this pattern may seem counterintuitive, it is also a consequence of endogenous stopping rules. For illustrative purposes, let us assume that all parents follow a strict stopping rule of having at least one son and one daughter (i.e., they will keep having children until the sex composition of their children aligns with the stopping rule). If we observe an individual who is the youngest child and whose older siblings are all brothers, then this individual must be female. In contrast, if we observe an individual who is the second-youngest child and whose older siblings are all brothers, then this individual must be male. In practice, compliance with stopping rules is far from strict. Yet this process is why youngest children whose older siblings are all brothers are more likely to be female, whereas second-youngest children whose older siblings are all brothers are more likely to be male.

Given that stopping rules are unequivocally present in the Dutch population, it is important that we evaluate whether these may have distorted the key findings presented in Ablaza et al. (2021). To this end, we followed Blanchard and Lippa (2007) and Blanchard (2021a) and fitted a version of our preferred model in which we dropped youngest siblings from the data. This reduced the size of our dataset from 9,073,496 to 5,613,917 individuals (i.e., by ~38%). Table 1 compares the results of the principal model specification presented in Ablaza et al. (2021) with the results of this new model excluding youngest siblings. Each model was estimated for both sexes combined, and for men and women separately. The results proved remarkably similar across the two sets of models. In fact, while the coefficients differed somewhat across the two specifications, none of the pairs were statistically significant at the 95% level.³ Altogether, this exercise offers reassurance that the results reported in Ablaza et al. (2021) are unlikely to have emerged due to distortions in the data stemming from endogenous stopping rules.

Given this evidence, we asked ourselves whether (and when) endogenous stopping rules might pose a threat to accurate estimation of the FBOE on homosexuality. Our results suggest that endogenous stopping rules are unlikely to be an issue in Dutch register data. We argue that the scale and representativeness of our data play a crucial role in this regard, because they allow us to produce unbiased estimates of probabilities of same-sex union entry conditional on being in specific sibship configurations. We acknowledge that some sibship configurations may be more common than others because of endogenous stopping rules; yet that fact alone is not sufficient to distort the model estimates. To illustrate this point, men with two older brothers should still face a higher probability of entering a same-sex union than men

³ To formally test whether the model coefficients corresponding to men and women were statistically different to each other we used the same interaction-based procedure applied in Ablaza et al. (2021).

with two older sisters, even though the latter sibship configuration may be more common in the presence of endogenous stopping rules.⁴

At the same time, we note that endogenous stopping rules may pose a potential threat to models relying on smaller and non-representative data. This is because such data are prone to sampling biases that can interact with endogenous stopping rules and, as a result, distort the coefficients of interest. For example, if the dataset oversampled homosexual men who are the youngest siblings in their sibships, then we would expect the FBOE estimate to be biased downwards. While this is a highly specific type of confounding, it is natural to ask how one should account for it. This question goes back to key observations made by Blanchard (2021a) in his commentary. Here, we posit that the practice of excluding observations of youngest siblings does not necessarily address the problem. It can be effective if the sampling biases occur mainly among the youngest siblings, but it can also worsen the situation if the biases occur among older siblings. The key problem here is that the researcher is unaware of the true nature of these distortions, which means that the process of imposing additional exclusions on the estimation sample is prone to heuristic biases, confirmation biases, and specification searching.⁵

Altogether, neither our modelling approach nor the modification proposed by Blanchard and Lippa (2007) and applied in Blanchard (2021a) can reliably account for the

⁴ This reasoning, however, would not apply if the stopping rules themselves had a direct effect on the probability of same-sex union entry (e.g., children whose parents have a diversity preference being more likely to enter a same-sex union). We consider this to be an unlikely situation, both because there is little theoretical ground to expect such an effect and because our coefficients do not change when we exclude youngest children from the estimation sample.

⁵ In the specific case of Blanchard and Lippa (2007) and Blanchard (2021a), we believe that the decision to exclude youngest siblings from the estimation sample was justified. Yet the underlying problem with their data was likely sampling biases unrelated to endogenous stopping rules. The latter becomes apparent when comparing the sibship characteristics of youngest siblings in our data (see Figure 2 below) to those in Blanchard's data (see Figure 1 in Blanchard, 2021a). The comparison suggests that the online survey used by Blanchard and Lippa (2007) and Blanchard (2021a) oversampled homosexual participants with older sisters, which is a likely reason why their full-sample models failed to yield statistically significant estimates of the FBOE.

confluence of sampling biases and endogenous stopping rules. While this limitation is of little consequence in our analyses of a large and representative dataset, it may prove more problematic in analyses of smaller and/or non-probability samples. However, identifying a method that performs well under this type of confounding is challenging, which leads us to advocate for the use of our modelling approach even in smaller and/or non-probability samples.⁶

Is selection into marriage likely to affect our results?

One of the distinctive aspects of our analytical approach is the use of population-level linked administrative data. These data offer several significant advantages, including a very large number of cases and a near-perfect representativeness of the Dutch population. These factors constitute a significant improvement over most samples used in earlier studies of the FBOE and FFE, which were typically small, non-representative and highly selective in nature (e.g., many comprised transgender, gender-dysphoric, and paedophilic individuals). However, as acknowledged in our initial piece, the administrative data used in our study also come with certain limitations and imperfections (Ablaza et al., 2021).

One such imperfection is that the expression of homosexuality can only be approximated through an indicator variable identifying individuals who entered a same-sex union (either a marriage or a registered partnership). Semenyna and colleagues (2021) offered reflections about the value of representative samples for analyses of the FBOE and FFE, and on the extent to which selection into marriage may threaten representativeness and influence

⁶ Of note, Blanchard and Lippa's (2021) extension of the Khovanova (2020) method yielded significant FBOE estimates in the sample used by Blanchard and Lippa (2007) and Blanchard (2021a). This led the authors to speculate that the new procedure may bypass potential biases caused by endogenous stopping rules. While we find much to like about this procedure, we cannot think of a sound methodological argument that would support its superior performance under endogenous stopping rules. Rather, we believe that the performance of this procedure will depend heavily on the nature of sampling biases present in the data. Overall, we expect our modelling approach to perform better, because it operates with an unrestricted estimation sample that should be less vulnerable to small-sample biases.

our findings. Their arguments are persuasive. For example, we fully agree with their observation that population representativeness is not a necessary pre-condition to obtain scientifically valid findings. We will nevertheless point out that representativeness can help overcome problems with model inference (as discussed in the previous section) and dismiss potential concerns about the external validity of findings based on non-probability samples.⁷

Semenyna et al. (2021) are also correct to point out that same-sex union entry is an imperfect proxy measure for homosexuality and that, by using this measure, we likely miss a sizable fraction of individuals who may identify as homosexual, report same-sex attractions, and/or engage in same-sex sexual behaviour. The imperfect nature of same-sex union formation as an indicator for homosexuality is indeed well-recognised in the literature (see e.g., Carpenter & Gates, 2008; Durso & Gates, 2013; Perales & Baxter, 2018; Wolff et al., 2017). Nevertheless, we have several reasons to believe that the incomplete coverage of our measure is unlikely to invalidate our results.

First, the share of individuals who never form a union—either a marriage or a registered partnership—in our data is 28.5%, which is much lower than the share of never-married individuals reported by Statistics Netherlands and alluded to by Semenyna and colleagues (~47%). This is because the latter takes the stock of the full population on a given day and quantifies the share of never-married individuals within this stock (thus classifying children, teenagers, and the majority of young adults as "never married"). In contrast, our longitudinal measure assigns a status of "never married" only to those individuals who were not married at any point in time before December 2019—when even the youngest cohort in our data was ~30 years old.

⁷ As explained in our initial piece, the deficiencies of many earlier FBOE and FFE studies also encompassed a small sample size. For instance, a third of the studies reviewed in Blanchard (2018) included less than 100 homosexual participants. The larger size of our data enables us to detect associations that would be difficult to identify in such samples.

Second, as noted in our initial manuscript, selection into same-sex unions would only distort the associations of interest in highly specific circumstances. For example, artificially observing an FBOE due to such selection would require remarkably strong correlations—net of birth cohort and maternal age at birth—between individuals' birth order and/or the sexes of their older siblings and their propensity to enter same-sex unions. We are aware of no prior theoretical or empirical literature documenting such patterns of association.

Third, the Netherlands is one of the most progressive countries in the world in terms of their attitudes and legislation towards same-sex relations (Andersen & Fetner, 2008; Kabátek & Perales, 2021; Smith et al., 2014). For example, in 2012, 92% of Dutch people agreed with the statement "*Homosexual individuals should be free to live their lives as they wish*" (Smith et al., 2014). Hence, the share of homosexual individuals remaining 'in the closet' due to stigma and social pressures should be lower than in other countries.

Finally, while we acknowledge that entering a same-sex union is not a perfect measure of homosexuality, we will note that the measures used in earlier studies of the FBOE and FFE have their own issues. For example, many such studies rely on sexual-identity measures of homosexual identification (see e.g., Bogaert, 2003; Ellis & Blanchard, 2001; Gomez-Gil et al., 2011); yet many gay men and lesbian women choose not to disclose their true sexual identity in observation studies (Ferlatte et al., 2017; Stange et al., 2018). Further, many men who experience sexual attractions towards other men, or who engage in sexual behaviour with other men, do not identify as homosexual (Durso & Gates, 2013; Wolff et al., 2017).

While we are optimistic about our results not being meaningfully distorted by the aforementioned selection issues, we encourage further scholarship using representative datasets that contain more accurate measures of sexuality. Our inability to measure sexual orientation directly in the administrative data at hand also resonates with voices calling for sexual orientation to be routinely included as an additional socio-demographic variable in government data collections—e.g., data held by government agencies and collected in population censuses (Lyons et al., 2021; Perales, 2021; Waite & Denier, 2019). Given their other advantages, the availability of sexual-orientation information in population-level administrative datasets could go a long way in enabling researchers to move this—and other cognate fields—forwards.

What are the meaning and implications of the existence of an FBOE among women?

A novel finding emerging from our analyses was the presence of an FBOE not only among men, but also among women. In fact, in our data, the FBOE was similar in strength and magnitude for both men and women. For example, replacing one older sister by one older brother increased the odds of same-sex union entry by 11.5% among men and 13.3% among women (Ablaza et al., 2021). This finding is intriguing, as it goes counter to findings from studies documenting an FBOE among men but not women (see e.g., Blanchard, 1997, 2021b; Bogaert, 2000). Further, it can be perceived as being inconsistent with existing explanations for this phenomenon—including the Maternal Immune Hypothesis (MIH) (Blanchard & Bogaert, 1996). Both Blanchard (2021a) and Semenyna et al. (2021) reflected on the meaning and implications of the existence of an FBOE among women in our data, yet the two research teams approached this finding from different angles.

Blanchard (2021a) suggested that the dominant explanation for the FBOE among males, the MIH, could be expanded to explain the presence of an FBOE among women. Briefly, the MIH attributes male homosexuality to a progressive maternal immune response against a Y-linked antigen (i.e., NLGN4Y) responsible for sexual differentiation in the male brain (Bogaert et al., 2018). Blanchard (2021a) argued that the same mechanism may also affect women due to the presence of an X-linked homolog (i.e., NLGN4X) in the female brain. In our

study, we also speculated about the possibility that maternal antibodies may target proteins that are not sex-specific through 'determinant spreading' (Nielsen et al., 2007; Nielsen, 2011).

On the other hand, Semenyna et al. (2021) cautioned against unilateral theoretical approaches that seek to explain male and female homosexuality simultaneously. This is because, evidently, homosexuality manifests differently in men and women: as androphilia among men but gynephilia among women. Instead, Semenyna and colleagues (2021) called for the development of alternative theories for female homosexuality, including explanations based on biological factors (e.g., testosterone) and social factors (e.g., fast life history).

We remain neutral observers in this interesting debate as, admittedly, the data used in our initial study is not sufficient to fully disentangle these competing views and/or the underlying social or biological processes that may underpin the FBOE and FFE. A point of collective agreement though is that the answer to these questions lies in the data and that further research is needed to identify the processes leading to an FBOE among women. The suggestions offered by both Blanchard (2021a) and Semenyna et al. (2021) provide a helpful starting point for future studies in this field. Some of these suggestions require different and specific data types. For instance, Blanchard (2021a) called for a replication on a sample of women of Bogaert et al.'s (2018) study, which used laboratory assays to compare anti-NLGN4Y antibodies between mothers of homosexual and heterosexual men. The results of such a study could inform debates as to whether the MIH could also underpin female homosexuality.

Other avenues for future inquiry could however be pursued using observational or administrative datasets, akin to the linked register data deployed by Ablaza et al. (2021). For instance, Semenyna and colleagues (2021) suggested a research design similar to that in Bogaert (2006), who examined whether adopted and biological siblings—particularly, older brothers—exerted a similar effect on male homosexuality. Applying the same research design to women could help illuminate whether female homosexuality is influenced by biological factors. Administrative data could also be deployed to compare the reproductive histories of homosexual and heterosexual men's maternal aunts. As explained by Semenyna et al. (2021), this could provide a more accurate test of the FFE—given that homosexual men share genes with their maternal aunts. These data could also be leveraged to test the role of certain social factors, as put forwards by Semenyna et al. (2021). This may involve assessing different markers of women's 'fast life-histories' (Alley & Diamond, 2021) on which information may be available in administrative records, including abortion, young or teenage pregnancy, emergency-room visits, general-practitioner visits, gynaecologist visits, and incarceration.

Concluding remarks

Through the application of population-level administrative data and a novel regression parameterization, Ablaza et al. (2021) offered new evidence in support of the existence of an FBOE on male and female homosexuality. The alignment between our findings and those of previous studies conducted using other data types and methodologies—and with different strengths and weaknesses—is crucial. Indeed, the accumulation of evidence of the FBOE from multiple analytic sources and angles adds credibility to its existence.

We hope to have demonstrated that—while not a panacea—administrative data represent a valuable addition to the data sources traditionally used to identify associations between sibship characteristics and human sexuality. The superior scale and representativeness of these data contribute to mitigating any scepticism on the FBOE motivated by the shortcomings of the datasets used in many previous studies. Further, as discussed before, these data may open new avenues for scholarly inquiry. As recognized by Blanchard (2021a) and Semenyna et al. (2021), our results also serve to reinforce the view that the FBOE, FFE and the effects of other sibship characteristics on the propensity for homosexuality need to be jointly evaluated, and that more attention to female homosexuality and its possible biological and/or social basis is warranted.

Ultimately, we are grateful to Ray Blanchard, Scott Semenyna, Francisco Gómez Jiménez and Paul Vasey for their insights on Ablaza et al. (2021) and pleased to have arrived at converging conclusions about the study's strengths and weaknesses. Most importantly, we hope that this constructive exchange serves to delineate the next steps for scientific research into the social and biological causes of human sexual preferences.

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Tables and figures

| Table 1. Coefficients from binary logistic regression models of same-sex union entry, base |
|--------------------------------------------------------------------------------------------|
|--------------------------------------------------------------------------------------------|

| Variables | Original model | | | Model dropping the youngest siblings | | |
|-------------------------------------|----------------|---------------|----------------|--------------------------------------|---------------|---------------|
| | Full sample | Men | Women | Full sample | Men | Women |
| Coefficients | | | | | | |
| Number of siblings | -0.138*** | -0.134*** | -0.140^{***} | -0.125*** | -0.118*** | -0.131*** |
| | (0.006) | (0.009) | (0.008) | (0.007) | (0.011) | (0.010) |
| Number of older siblings | 0.079^{***} | 0.098^{***} | 0.062^{***} | 0.076^{***} | 0.089^{***} | 0.055^{***} |
| | (0.008) | (0.012) | (0.012) | (0.011) | (0.015) | (0.015) |
| Number of older brothers | 0.125*** | 0.115^{***} | 0.133*** | 0.121*** | 0.133*** | 0.126*** |
| | (0.007) | (0.011) | (0.010) | (0.011) | (0.016) | (0.016) |
| Number of younger brothers | 0.012 | 0.016 | 0.009 | 0.012 | 0.016 | 0.009 |
| | (0.009) | (0.013) | (0.012) | (0.009) | (0.013) | (0.012) |
| Birth-cohort fixed effects | Yes | Yes | Yes | Yes | Yes | Yes |
| Maternal-age-at-birth fixed effects | Yes | Yes | Yes | Yes | Yes | Yes |
| Number of individuals | 9,073,496 | 4,634,327 | 4,439,169 | 5,613,917 | 2,868,754 | 2,745,163 |

Notes: The models use linked population register data from the Netherlands. Robust standard errors in parentheses. Columns 1 to 3 list coefficient estimates from binary logistic regression models of entry into same-sex unions using the full analytical dataset. Columns 4 to 6 list coefficient estimates from the same models using an adjusted sample that excludes the youngest siblings. Statistical significance: **p < 0.001, *p < 0.01, *p < 0.05.



Figure 1. Population-level sex ratios, conditional on individual's position within a sibship

Notes: Population shares are extracted from linked population register data from the Netherlands. Whiskers denote 95% confidence intervals.



