





Exploring Genetic Contributions to News Use Motives and Frequency of News Consumption: A Study of Identical and Fraternal Twins

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ABSTRACT

Prior research conducted within the Uses and Gratifications paradigm has considered the contribution of numerous background social and psychological characteristics to motives for media use and media consumption patterns. In this study, we explore the extent to which far more fundamental characteristics—genes—explain, in part, motives to use news media and frequency of news use. Utilizing original data collected on identical and fraternal twins ($n = 334$), we find that latent genetic traits explain a nontrivial amount of variance in two unique news use motives, surveillance and entertainment, as well as frequency of consumption across multiple news sources. Genetic traits were particularly influential in explaining the frequency of using sources commonly characterized as ideological, such as *Fox News* and *CNN*.

User background characteristics are a central feature of audience-centered theories of media effects (Knobloch-Westerwick et al., 2020; Oliver & Krakowiak, 2009). The Uses and Gratifications (U&G) theoretical model, for example, begins with individual media users and assumes that their psychological and social differences guide media selection, shape patterns of consumption, and ultimately condition perceptual and behavioral outcomes of media use. More fundamentally, because U&G assumes that differences in background characteristics influence needs that manifest in motives to select media, in virtually any U&G study links between background characteristics, media use motives, and consumption must be examined.

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While past U&G research has focused on the psychological and social characteristics of users, *biological* characteristics also have been recognized, though seldom studied. This represents an important gap in the research first identified by Rosengren (1974) over 40 years ago. Rosengren (1974) argued that the U&G theoretical model is rooted in a “biological and psychological infra-structure that forms the basis of all human social behavior” (p. 270). He said that “We all carry with us a bundle of biological and psychological needs that make us act and react” to stimuli in our environment, including media stimuli (p. 270). What may motivate media use, in other words, are more fundamental, biologically based mechanisms.

The difficulty in studying biological mechanisms, in Rosengren’s (1974) view, was that U&G researchers at the time did not have the theoretical and methodological tools needed “to clarify the human need structure at this underlying level ... ” (p. 270). Yet, Rosengren emphasized that any “relevant findings [from] biology, psychology, and social psychology ... should be incorporated into the theoretical argument and related to variables of a more social character” (p. 270). Although biological factors could hardly be studied by communication scholars at the time, that is, they were still relevant factors that should be incorporated in U&G.

Since the time of Rosengren’s writing, several methodological tools have been developed that can be used to explore biologically based influences on variables integral to the U&G theoretical framework. For instance, one methodological tool that has become more widely accessible and applied throughout the social sciences is the twin study. Twin studies use levels of genetic relatedness among identical and fraternal twins to estimate the degree to which variation in observed behaviors (e.g., media use) can be traced to variation in latent genetic traits. In this article, we use a twin study to put Rosengren’s conjectures to an empirical test. Specifically, we use original twin study data to explore whether differences at the genetic level influence distinct motives for news media use and frequency of news consumption ($n = 334$). Our results reveal striking patterns of genetic influence on news use for surveillance and entertainment motives, frequency of news consumption across a variety of channels and platforms, as well as relationships between motives and consumption. We argue our findings are theoretically significant considering user background characteristics are a driving force of the U&G paradigm.

Media user background characteristics

Communication researchers generally agree that media influence is not uniform and that individual differences among media users can alter content selection, consumption, and ultimately effects (Knobloch-Westerwick et al., 2020; Oliver & Krakowiak, 2009). Audience-centered theories of

media influence, in particular, emphasize the role and characteristics of the individual audience member in media use and effects relationships. For example, Uses and Gratifications (U&G), a preeminent audience-centered theoretical perspective guiding communication research for over half a century, focuses attention on the role of media users' individual characteristics, goals, purposiveness, motives, and volition in shaping media behavior. As originally suggested by Katz (1959), U&G represented a paradigm shift in communication from perspectives that focused more on what media do to people, to one that focused on what people do with media. Fleshing out the theoretical framework, Katz et al. (1974) outlined an array of relationships for which U&G accounts. These include:

- (1) the social and psychological origins of
- (2) needs, which generate
- (3) expectations of
- (4) the mass media or other sources, which lead to
- (5) differential patterns of media exposure (or engagement in other activities), resulting in
- (6) need gratifications and
- (7) other consequences, perhaps mostly unintended ones. (p. 20)

Thus, the U&G perspective seeks to explain a complex web of relationships among and between user background characteristics, needs manifested in motives for using media, media consumption, and effects. A major assumption of the theory is that people actively use media to satisfy their needs and desires (Haridakis, 2013) and that their psychological and social background characteristics shape their motives (in which their needs and desires are manifested) to use media. As Katz et al. (1973) explained, "the selection of media and content, and the uses to which they are put, are considerably influenced by social role and psychological predisposition" (p. 165). Similarly, Rubin (2009) suggested that individual "predispositions ... " including, and most essentially, "social and psychological factors ... " act as foundational background characteristics that compel and constrain motives to select media. It is, therefore, no surprise that U&G research over the years has concentrated on how individual differences in psychological attributes (e.g., personality traits), social attributes (e.g., roles), and demographic attributes (e.g., age) serve as the "origins" of differences in media use and effects.

Not all background characteristics, however, can possibly be accounted for in a single U&G study. Researchers have instead generally examined characteristics of users deemed relevant to the subject of inquiry. For example, U&G researchers have examined the role of perceived self-efficacy in adoption and use of new media technology (LaRose & Eastin, 2004); gender, disinhibition, and personal experience with crime in selection of violent television programs (Haridakis, 2002, 2006); voyeurism in a study of reality television viewing (Baruh, 2010); and political efficacy, interest, and ideology in political information use (Lin et al., 2016). Across studies of various media, links between social and psychological background characteristics, media use motives, media

consumption, and effects consistently have been found, confirming the U&G assumption that differences in individual user characteristics are critical to how people select and are affected by media (see Haridakis, 2013).

We are interested in this article about whether far more essential, biologically based characteristics can influence media use motives and media consumption patterns. Although few studies have addressed this possibility empirically, a body of research outside the U&G context has emerged in which scholars have posited theoretical relationships between genes, neurobiological traits, and communication. This “communibiological” research program provides a theoretical basis for understanding the etiology of media use motives and behavior.

The communibiological perspective

Communibiology is a research program that positions communication traits and behaviors as originating in heritable differences in neurobiological systems. These systems establish, promote, and modify more explicit psychological characteristics that directly impact communicative expressions. Accordingly, the communibiological perspective proposes that communication behaviors result from “a manifestation of [psychological] traits [such as personality characteristics] that are manifestations of neurobiological systems, which are mostly *heritable*” (Beatty et al., 2009, p. 8, emphasis ours). Under the logic of this perspective, a decision to select media content to satisfy a particular need may be as much an indirect product of genetically grounded individual differences in neural structure and functioning as it is a direct product of psychological attributes such as personality traits.

Consider motivations for watching television. U&G has long posited that motives for watching television should arise from and be guided by differences in psychological traits and social circumstances (Rubin, 2009). Yet, Sherry (2001) demonstrated that motives for watching TV emerge from more fundamental differences in the biologically based construct of temperament, which is largely established at birth, prior to environmental experience. As Sherry suggested, “heritable individual differences in neural processing ...” alter temperament, which in turn guides motives for media consumption and “an individual’s decision to use media” (p. 284). Genetic traits, in other words, are a root source of variation in media selection motives and use. Genes do not control media behavior, but they do lay the foundation for and partially regulate it.

Results from studies that investigate behavioral patterns among identical and fraternal twins lend further support to the communibiological perspective. Used frequently throughout the social sciences and especially in the psychology subfield of behavior genetics, twin studies are designed to estimate the extent to which behavioral differences in human populations

can be accounted for by genetic differences. They do so, in part, by capitalizing on well-known levels of genetic similarity among twin dyads. While twin studies do not allow researchers to identify specific genes or neurobiological mechanisms that shape behavior at the molecular level, they can provide broad estimates of genetic contributions to behavioral variation (see York, *in press*). Consequently, twin studies can be used to explore the communibiological proposition that genetic differences exert an indirect influence on communication traits and behaviors.

In what was perhaps the earliest twin study of a communication trait, Horvath (1995) found that genetic variation among a convenience sample of identical and fraternal twins accounted for significant individual variation in self-reported communicator style. Similarly, latent genetic differences among twins have been shown to explain differences in communicative adaptability (Beatty et al., 2001). One other early twin study found that differences in interpersonal affiliation are heritable (Beatty et al., 2002).

More recent twin studies have supported basic propositions of communibiology and extended them to the domain of media consumption. These more recent studies have shown an array of media-related behaviors and orientations are grounded in heritable genetic differences. For instance, recent twin studies have shown that latent genetic traits explain variation in problematic internet use (Deryakulu & Ursavaş, 2014), frequency of mobile phone use (Miller et al., 2012), frequency of social media use (Ayorech et al., 2017; York, 2017), online and traditional political discussion (York, 2019), and frequency of television and internet use (Kirzinger et al., 2012).

Kirzinger et al.'s (2012) twin study is particularly informative to the present effort. Kirzinger et al. used secondary twin survey data to examine the genetic foundations of various communication and media behaviors. Included in their twin study was a single item that captured how important respondents thought it was "to keep informed about national news" (p. 164). The authors found that latent genetic traits accounted for approximately 35% of the total variance in responses to the "keep informed about national news" item. This result suggests that genes are one mechanism responsible for individual differences in orientations to news content. Yet, it is unclear whether genetic traits may also influence more specific news use motives and behaviors.

Given the communibiological perspective as well as results from twin studies of media behavior, it seems plausible that genetic influence could extend to motives for news use and frequency of consumption. We believe that exploring genetic explanations for these more specific variables is important for several reasons. One reason is that the frequency of news consumption is related positively to political knowledge and participation (e.g., Beaudoin & Thorson, 2004; Shah et al., 2001), though the ideological slant of a news source can alter gains in knowledge and participation

(Stroud, 2011). As such, exploring genetic explanations for news use motives and frequency of consumption may yield important implications for the origins of normatively desirable news use effects.

General predictions and questions

That genes can indirectly shape human behavior through neurobiological pathways is by now widely established through the use of twin studies, adoption studies, and molecular genetic research (see Plomin, 2018; Plomin et al., 2016). For example, nearly two decades of research has shown genes explain differences in a wide array of political phenotypes such as self-reported ideology and voter turnout (e.g., Hatemi et al., 2014; Ksiazkiewicz & Friesen, 2019; Lockyer & Hatemi, 2018). Accordingly, we are not interested in making predictions about *whether* we will find genetic effects on specific news behaviors. The communibiological view assumes such effects. In addition, behavior genetics research shows almost all human psychological orientations and behaviors are at least partly informed by genes (Plomin, 2018). We would, therefore, posit a general prediction that *latent genetic traits will explain a non-zero amount of variance in motives for using news and frequency of news use.*

A more pertinent question is not *if* genetic traits account for differences in behavior, but rather *to what degree?* News use motives are qualitatively distinct (e.g., news for surveillance, for escape), which suggests that latent genetic traits may explain different levels of variance in each motive. Further, research in evolutionary psychology suggests that the surveillance motive may be particularly unique in this respect, as the human brain has evolved to monitor the environment for threats (Neuberg et al., 2011) raising the possibility that news helps fulfill this goal (Shoemaker, 1996). A similar logic could apply to the frequency of using specific news sources. It is important to note that because political ideology is heritable (e.g., Hatemi et al., 2014), genetic traits could contribute to greater variation in the frequency of using sources commonly characterized as slanting coverage to favor ideological extremes (e.g., *Fox News*, *CNN*). Notably, one study has already uncovered links between psychobiological traits, political ideology, and the use of ideological news sources (Keene et al., 2017). We would consequently ask: *To what extent do genetic traits explain individual differences in specific news use motives and frequency of using distinct sources?*

Given U&G research that shows news use motives are related to the frequency of news use (Diddi & LaRose, 2006), it is also plausible that relationships between variables are explained in part by latent genetic traits. For example, if genetic traits explain news media use to relieve boredom, it seems likely that these same traits subsequently explain the frequency of

use. This is a totally unexplored possibility, and we, therefore, ask: *To what degree is the association between news use motives and frequency of overall news use explained by genetic traits?*

Method

To explore our general prediction and questions, we collected original survey data from identical and fraternal twin respondents ($n = 334$).¹ These data were collected purposively by the first author and a trained research assistant at the 2017 Twinsburg, Ohio “Twins Days Festival” (TDF), which is one of the largest annual gatherings of fraternal and identical twin siblings in the world. Survey data from the TDF have often been utilized in prior twin study research (e.g., Cesarini et al., 2008; Horvath, 1995; Settle et al., 2009; York, 2019). While these data present a number of limitations, they were necessary for the present study due to the unique genetic properties of the respondents and because items assessing media behaviors are not commonly available in secondary twin datasets.

Procedure and sample characteristics

The TDF offers a dedicated research space where academic and private research teams can conduct survey, taste testing, facial recognition, and a variety of other biometric studies with twin participants. Due to the outdoor setting of the research site, we used a simple pencil-and-paper questionnaire to record responses about news media motives and frequency of use. Questionnaires were one front-and-back page. Twins over 18 years old and who volunteered to take the study were provided with the questionnaire and asked to complete it concurrently, but independently from each other. This rule was implemented to prevent biased responding. For example, this prevented a twin from discussing their survey answers with their co-twin prior to completing the study. As an incentive, twins who took the study were entered into three random drawings for two 75 USD Amazon gift cards. The survey could only be taken once.

The study questionnaire began by asking respondents to identify whether they were part of an identical or fraternal twin dyad. Respondent e-mail addresses were also collected so that twins could be contacted at a later date regarding the results of the incentive lottery and a study debrief. The questionnaire then asked respondents a series of Likert-type items about their news habits, motives for consuming news, political discussion habits, and

¹The first author obtained approval for human subjects research from the Kent State University Institutional Review board in July 2017 (#17-016).

perceptions of national issues in the news. On the back page of the questionnaire, respondents were provided with a brief experimental stimulus that was part of the broader data collection effort. The questionnaire concluded with three demographic items that help describe the sample. These items indicated that, of the total sample ($n = 334$), 76.65% of respondents were female, the average age was 37.43 years ($SD = 16.73$), and 57% had earned a bachelor's degree or higher. For exact question wording from the study questionnaire as well as the raw data see York (2020).

Measures

Zygosity

Twins' zygosity indicates how related they are genetically. Identical or "monozygotic" twins emerge from the same fertilized egg, or zygote, and ultimately share 100% of their DNA in common. Fraternal or "dizygotic" twins come from separate zygotes and share roughly 50% of their DNA as do full siblings. In this study, we used a simple self-report indicator of zygosity to determine whether twin respondents were identical or fraternal. All twins were asked "Are you (check one) ... "identical" ($n = 276$) or ... "fraternal" ($n = 58$).

News use motives

We adapted question wording from Diddi and LaRose (2006, p. 207) to develop items tapping four motives for news consumption: for relieving boredom, surveillance, escape, and entertainment. To supplement, we adapted items from a television gratifications scale to measure the degree to which respondents used news for its perceived social utility (Rubin et al., 2009, p. 177). In total, we used 10 Likert-type response items to measure five distinct motives for news consumption. Respondents were asked to indicate their agreement (0 = strongly disagree; 4 = strongly agree) with each of the 10 items. Descriptive statistics and dyadic correlations for each motive are shown in Table 1.

Relieve boredom. This motive was assessed using two items for attending to the news "When I have nothing better to do" and "Because it passes the time, especially when I'm bored." Responses to the boredom items were strongly related regardless of twin zygosity ($r_{IDENT} = 0.76$; $r_{FRAT} = 0.65$). We averaged these items in a single measure tapping the relieve boredom motive.

Surveillance. News for surveillance was assessed using items that asked respondents about using news "So I can understand the world" and "To find out things I need to know about daily life." Responses to these items were moderately correlated ($r_{IDENT} = 0.54$; $r_{FRAT} = 0.42$) and were averaged in a single measure of the surveillance motive.

Table 1. Descriptive statistics and within-pair correlations.

	Fraternal twins			Identical twins		
	Y_{FRAT}	SD_{FRAT}	r_{FRAT}	Y_{IDENT}	SD_{IDENT}	r_{IDENT}
News Use Motives						
Relieve Boredom	2.07	0.84	0.15	1.70	0.98	0.22
Surveillance	2.79	0.66	0.00	2.77	0.82	0.38
Escape	0.78	0.69	0.30	0.95	0.86	0.32
Entertainment	1.47	0.98	0.24	1.74	0.97	0.27
Social utility	2.28	0.92	0.40	2.28	0.96	0.26
Frequency of News Use						
Local TV news	1.48	1.37	0.49	1.64	1.49	0.43
News on comedy shows	1.03	1.20	0.22	0.92	1.17	0.41
Online news (USAToday.com)	1.24	1.37	0.03	1.36	1.46	0.46
Social media news	2.28	1.59	0.35	2.45	1.53	0.36
Mobile news use	1.59	1.59	0.15	1.52	1.61	0.30
Liberal news (<i>CNN, MSNBC, NYT</i>)	1.14	1.28	0.19	1.30	1.43	0.52
NPR	0.67	1.22	0.38	0.67	1.21	0.56
Conservative nNews (<i>FOX, WSJ</i>)	0.97	1.20	0.03	0.93	1.36	0.51
Conservative talk radio (<i>Hannity</i>)	0.43	1.01	0.18	0.33	0.89	0.33
Overall news use	1.20	0.61	0.27	1.24	0.66	0.50

$n = 334$, 167 pairs (29 fraternal; 138 identical). All news items were measured on 5-point Likert scales coded 0 to 4. For the news use items, this scale ranged from use the source “Less Often or Never” (0) to “Several Times Per Day” (4).

Escape. Two items were used to assess news use “To help me get away from everyday worries” and “To help me when I want to be cheered up.” These items were positively correlated ($r_{\text{IDENT}} = 0.67$; $r_{\text{FRAT}} = 0.46$) and were averaged to form a single item tapping news for escape.

Entertainment. To assess news use for entertainment, respondents were asked to report the extent to which they used news “Because it’s entertaining” and “Because it’s enjoyable.” Responses on these items were strongly related ($r_{\text{IDENT}} = 0.70$; $r_{\text{FRAT}} = 0.74$). We averaged these two items in a single measure prior to analysis.

Social utility. The social utility motive consisted of items that assessed the degree to which respondents used news “To give me interesting things to talk about” and “So I can pass the information on to other people.” Responses on these items were related ($r_{\text{IDENT}} = 0.73$; $r_{\text{FRAT}} = 0.64$), and, like other items, were averaged in a single measure prior to analysis.

Frequency of news use

Respondents were asked how frequently they used nine news sources across traditional and online platforms (see Table 1). Each news use item was measured on a 5-point Likert scale from “Less Often or Never” (coded 0) to “Several Times a Day” (coded 4). These items asked respondents how often they used “local television news,” “news on comedy shows such as *The*

Daily Show,” “online news sources such as *USAToday.com*,” “news on social media sites such as Facebook and Twitter,” and “mobile phone news apps.”

Respondents also were asked how frequently they used “news from national organizations typically characterized as liberal such as *MSNBC*, *CNN*, or *The New York Times*” as well as “*NPR*.” Additionally, respondents were asked how often they used news from “national organizations typically characterized as conservative such as *Fox News Channel* or *The Wall Street Journal*” and how frequently they “listened to conservative talk radio sources such as Rush Limbaugh or Sean Hannity.” Our classification of these sources as liberal-Democrat leaning and conservative-Republican leaning, respectively, is supported by research assessing their ideological slant and the ideological orientation of the audiences to which they appeal (Budak et al., 2016; Flaxman et al., 2016; Pew Research Center, 2020; Stroud, 2011).

Overall news use

We created a combined measure of overall news use to explore possible genetic influences on the relationship between motives and frequency of consumption. This measure was an averaged index of all nine frequency of news use items described above. Prior to creating the index, we ran a principal component factor analysis that demonstrated all nine news use items loaded on a single factor (eigenvalue = 1.47). This factor explained 70.18% of variance in the construct. The overall news use index demonstrated adequate internal consistency on par with news use indices created in the past research ($\alpha = 0.59$).

Analysis plan

Estimating the effects of unobserved genetic traits on observed behaviors requires novel analytical approaches. One common analytical approach used in twin research involves structural equation modeling using latent variables to represent the genetic and environmental attributes of twin dyads. This approach is known as *ACE* twin modeling.

An *ACE* model is designed to decompose the amount of total variance in an observed trait—in our case, observed motives for and frequency of news consumption—that is attributable to just three latent factors. These latent factors represent, very broadly, the degree of additive genetic similarity among fraternal and identical twin pairs (notated *A*), aspects of the social and physical environment that twins are assumed to share in common, such as a shared upbringing and culture (*C*), and any aspect of the environment unique to one twin in the pair (*E*). We show the classic conceptual illustration of a univariate *ACE* model in [Figure 1](#).

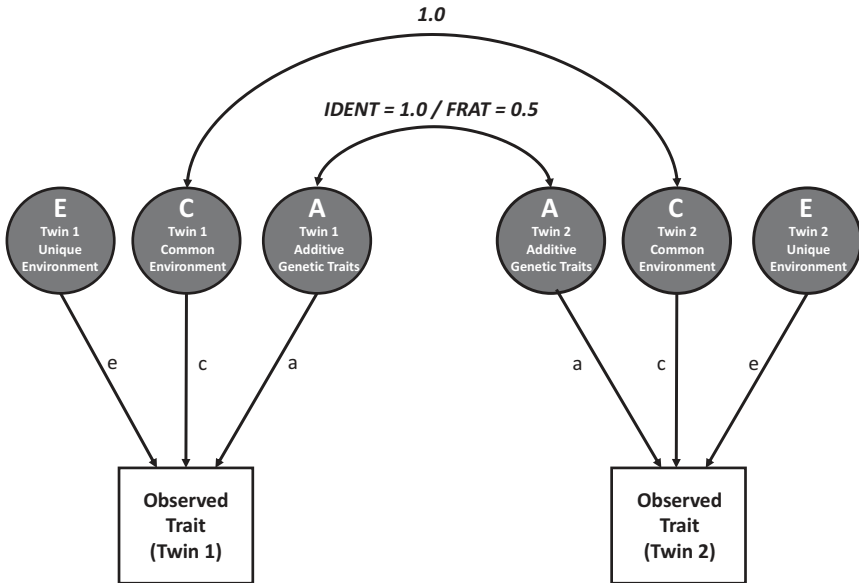


Figure 1. Conceptual illustration of a univariate ACE twin model.

The illustration shows a univariate *ACE* model in which three latent factors account for the total variance in one observed trait measured for each twin in a pair. There are a number of technical specifications and assumptions that must be met to estimate a univariate *ACE* model. For more information, see Medland and Hatemi (2009) and York, *in press*.

In principle, the latent factors in a univariate *ACE* model can decompose the variance in any observed trait by explicitly accounting for two known pieces of information about twins. First, *ACE* models require that the covariance for the additive genetic (*A*) factor be constrained at 1.0 for identical twins who share 100% of their DNA in common and 0.5 for fraternal twins who share roughly 50% of their DNA in common. This constraint approximates known degrees of genetic similarity among fraternal and identical dyads. Second, the covariance for the common environment (*C*) factor is constrained at 1.0 for all twins to account for aspects of the environment that all twins are assumed to share, such as being raised by the same parents in the same household. The unique environment (*E*) factor is freely estimated and represents any aspect of the environment that may affect one twin but not the co-twin, such as a childhood trauma, a spouse, or idiosyncratic psychological reactions to events. Because the unique environment factor is freely estimated, it also acts as an error term, capturing variance in the observed trait not explained by additive genetics (*A*) and the shared environment (*C*). *ACE* estimates of trait variance should thus always sum to 1.0 and are intended as estimates of behavioral

variability in populations due to genetic and environmental variability among respondents in the sample.

It is important to note that *ACE* models rely on model fit tests for interpretation. Specifically, likelihood ratio tests are used to determine if the fit of the *ACE* model to the data is superior to two nested models: the *AE* and *CE* models. These latter models drop the common environment or additive genetic parameter, respectively. If either the *AE* or *CE* model provides an equivalent fit to the data, the reduced model should be preferred as it is more parsimonious.

We proceed by estimating a series of univariate *ACE* twin models using the *OpenMx* package for R. These models are “univariate” in the sense they compare each twin and co-twin’s scores on the same observed trait (e.g., frequency of using online news). We created each univariate model using *OpenMx* syntax adapted from Maes (2016a, 2016b). Full specifications for univariate *ACE* models as well as mathematical proofs are widely available for interested readers (see Medland & Hatemi, 2009; Neale, 2009; York, *in press*).

In the final part of our analysis, we use a multivariate model to examine the genetic influence on the relationship between news use motives and overall news use. That is, we use a common multivariate twin model called a Cholesky decomposition to determine the degree to which the covariance between news use motives and overall news use is explained additive genetic (*A*), common environment (*C*), and unique environment (*E*) factors. Multivariate models like the Cholesky “draw their explanatory power from the information contained in the variances, cross trait (within individual phenotypic covariance), cross twin (identical and fraternal co-twin) and cross twin-cross trait covariances” (Medland & Hatemi, 2009, p. 206). Variables should be entered in a Cholesky model in a logical order of presumed influence from left to right, such that news use motives are entered first followed by the overall frequency of news use. As with univariate models, multivariate models are interpreted on the basis of model fit using likelihood ratio tests. The most parsimonious multivariate model with the fewest parameters should be interpreted.

Results

Table 2 shows the univariate *ACE* model estimates for news use motives. This table provides estimates for variance explained in each news motive variable by latent genetic traits (*A*), which are notated a^2 . Estimates for variance explained by the common environment (*C*) are notated c^2 . Estimates for the unique environment (*E*) are notated e^2 . Only bolded models are interpreted as these are best-fitting models based on likelihood ratio tests.

What is immediately notable about the overall pattern of results shown in Table 2 is that genetic traits explained a non-zero amount of variance in the surveillance motive and to a lesser extent the entertainment motive.

Table 2. Univariate ACE estimates – news use motives.

Variable	Model	a^2	c^2	e^2	AIC	-2LL	χ^2	p
Relieve boredom	ACE	0.00	0.23	0.77	254.50	914.50	Base	—
	AE	0.23	—	0.77	253.10	915.10	0.60	0.44
	CE	—	0.23	0.77	259.23	914.50	0.00	1.00
Surveillance	ACE	0.35	0.00	0.65	111.10	771.10	Base	—
	AE	0.35	—	0.65	109.10	771.10	0.00	1.00
	CE	—	0.33	0.67	110.42	772.42	1.32	0.25
Escape	ACE	0.00	0.32	0.68	148.85	808.85	Base	—
	AE	0.32	—	0.68	148.13	810.13	1.28	0.26
	CE	—	0.32	0.68	146.85	808.85	0.00	1.00
Entertainment	ACE	0.04	0.23	0.73	258.82	918.82	Base	—
	AE	0.28	—	0.72	257.25	919.25	0.43	0.51
	CE	—	0.26	0.74	256.84	918.84	0.01	0.92
Social Utility	ACE	0.00	0.27	0.73	244.53	904.53	Base	—
	AE	0.27	—	0.73	244.04	906.01	1.51	0.22
	CE	—	0.27	0.73	242.53	904.53	0.00	1.00

$n = 334, 167$ pairs (29 fraternal; 138 identical). $a^2 =$ additive genetic traits, $c^2 =$ common environment, $e^2 =$ unique environment. Values for a^2 , c^2 , and e^2 represent the proportion of variance in each outcome variable explained by additive genetic, common environmental, and unique environmental factors. AIC = Akaike Information Criteria. -2LL is -2 times the loglikelihood. The ACE model for each variable is followed by nested AE and CE models. χ^2 values are associated with LR tests of model fit that result from dropping A or C. Models shown in bold are the best-fitting models based on chi-square tests and p -values shown at right. We adapted R syntax from Maes (2016a) to estimate each model treating observed variables as continuous.

Latent genetic traits explained an estimated 35% of the total variance in news use for surveillance, but only 4% of the variance in entertainment. The remainder of variance in both motives was explained by the common and unique environmental factors.

In three other models, the additive genetic factor accounted for 0% of the variance in the observed trait. Take the relieve boredom model for example. Here, the estimate of latent genetic influence in the ACE model is null. The CE model, not coincidentally, is preferred because it fits these data as well as the ACE model, but with one less parameter. Further, the CE model estimates suggest the common environment factor accounted for 23% of the total variance in using news to relieve boredom, while 77% of the variance was accounted for by the unique environment. Genes, therefore, played no role in explaining individual differences in the relieve boredom motive. Rather, aspects of one’s environment as well as idiosyncratic attributes and experience accounted for variance in the motive. The same pattern of environmental effects emerges in the news use for escape and social utility models. The common environment factor explained 32% of variance in escape and 27% in social utility while the estimate of the unique environment explained 68% of the total variance in the escape motive and 73% of variance in the social utility motive. Latent genetic traits appeared to play a null explanatory role in both cases.

Conversely, there was a far more consistent pattern of genetic influence in the frequency of news use models. In terms of frequency of news

Table 3. Univariate ACE estimates – frequency of news use.

Variable	Model	a^2	c^2	e^2	AIC	-2LL	χ^2	p
Local TV news	ACE	0.00	0.52	0.48	334.55	990.55	Base	—
	AE	0.52	—	0.48	335.82	993.82	3.27	.07
	CE	—	0.52	0.48	332.55	990.55	0.00	1.00
News on comedy shows	ACE	0.34	0.15	0.51	189.71	845.71	Base	—
	AE	0.50	—	0.50	187.85	845.85	0.14	.71
	CE	—	0.46	0.54	188.43	846.43	0.73	.39
Online news	ACE	0.54	0.00	0.46	291.85	947.85	Base	—
	AE	0.54	—	0.46	289.85	947.85	0.00	1.00
	CE	—	0.49	0.51	292.78	950.78	2.93	.09
Social media news	ACE	0.15	0.28	0.57	338.05	994.05	Base	—
	AE	0.44	—	0.56	336.50	994.50	0.45	.50
	CE	—	0.41	0.59	336.20	994.20	0.15	.70
Mobile news use	ACE	0.35	0.01	0.64	302.65	958.65	Base	—
	AE	0.36	—	0.64	300.65	958.65	0.00	.99
	CE	—	0.33	0.67	301.18	959.18	0.54	.46
Liberal news (MSNBC, CNN)	ACE	0.59	0.00	0.41	268.66	924.66	Base	—
	AE	0.59	—	0.41	266.66	924.66	0.00	1.00
	CE	—	0.55	0.45	269.68	927.68	3.01	.08
NPR	ACE	0.47	0.18	0.35	-23.26	632.75	Base	—
	AE	0.66	—	0.34	-25.11	632.89	0.14	.71
	CE	—	0.61	0.39	-24.04	633.96	1.21	.27
Conservative news (FOX)	ACE	0.58	0.00	0.42	138.38	794.38	Base	—
	AE	0.58	—	0.42	136.38	794.38	0.00	1.00
	CE	—	0.54	0.46	138.94	796.94	2.56	.11
Conservative talk radio	ACE	0.45	0.07	0.48	-238.61	417.39	Base	—
	AE	0.48	—	0.52	-240.60	417.40	0.01	.91
	CE	—	0.48	0.52	-240.10	417.90	0.50	.48
Overall news Use (9-item index)	ACE	0.35	0.14	0.51	-39.07	620.93	Base	—
	AE	0.50	—	0.50	-40.93	621.07	0.14	.71
	CE	—	0.47	0.53	-39.98	622.02	1.09	.30

$n = 334, 167$ pairs (29 fraternal; 138 identical). a^2 = additive genetic traits, c^2 = common environment, e^2 = unique environment. Values for a^2 , c^2 , and e^2 represent the proportion of variance in each news variable explained by additive genetic, common environmental, and unique environmental factors. AIC = Akaike Information Criteria. -2LL is -2 times the loglikelihood. The ACE model for each variable is followed by a nested AE and CE model. χ^2 indicates change in model fit as a result of dropping A or C parameter from the base model. Models shown in bold are the best-fitting models based on chi-square tests (p -values at right). For overall news use, we adapt R syntax for ACE models for continuous outcomes from Maes (2016a). We use liability threshold models to produce estimates for ordered categorical outcomes (Maes, 2016b; see Neale, 2009).

consumption, perhaps the most remarkable result shown in Table 3 is the explanatory power of genetic traits (a^2) relative to that of environmental influences twins should theoretically share in common (c^2). In almost every analysis, the AE or ACE model was preferred and when the ACE model was selected as the most parsimonious, the common environment factor had relatively little explanatory utility.

Across the news consumption models, latent genetic traits explained from approximately 15% of the variance in the frequency of using news on social media item to 54% of the variance in frequency of using online news sources such as *USAToday.com*. In only one news use model—local television news—did latent genetic traits have no impact on the observed variable, resulting in preferring a more parsimonious CE model with the genetic factor dropped.

Genetic traits were a particularly influential explanatory factor in the ideological news consumption models. The factor capturing latent genetic traits explained approximately one- to two-thirds of the variance in frequency of using liberal (59%) news sources such as *MSNBC* and conservative sources (58%) such as *Fox News*. Similarly, almost half the variance in the *NPR* (47%) and conservative talk radio items (45%) were explained by genes. The remaining variance in each of these models was largely explained by the unique environment.

A full *ACE* model was also preferred for the overall frequency of news use index (see [Table 3](#)). In the overall news use model, 35% of the variance was explained by latent genetic traits. Another 14% of the variance in the index was explained by the common environment. An estimated 51% of the variance in overall news use was explained by the unique environment factor.

Taken together, the univariate models suggest latent genetic traits account for a nontrivial amount of variance in the majority of variables explored. Do genes also account for relationships between variables? Because genes were shown only to influence the surveillance and entertainment motives, and the latter only marginally so, we were primarily interested in whether underlying genetic traits explained covariation between the surveillance motive and the overall frequency of news use index. Results from our multivariate analysis are shown in [Figure 2](#).

This figure shows that the relationship between news use for surveillance and frequency of overall news use, which was correlated in the full sample and among identical dyads but not fraternal dyads ($r = 0.37$; $r_{IDENT} = 0.43$; $r_{FRAT} = -0.02$), was explained in large part by underlying genetic traits. Specifically, the results shown in [Figure 2](#) suggest that the same latent genetic component that explains news use for surveillance purposes accounts for approximately 21.02% of the variance in overall news use. The common environment component explained 1.75% and the unique environment explained 1.51% of the variance in news use. In other words, the relationship between the surveillance motive and overall news use variables in the full sample ($r = 0.37$) is driven mainly by latent genetic factors and not environmental experience.

Discussion

The results of this study support, in part, a central tenet of U&G, that user background characteristics shape motives for media use and consumption patterns. Yet, the results presented here, insofar as they demonstrate the influence of genetic traits on media use motives and frequency of consumption, point to important implications for the role of more fundamental background characteristics in the U&G paradigm. Our main finding, that variation at the genetic level explains a nontrivial amount of variance

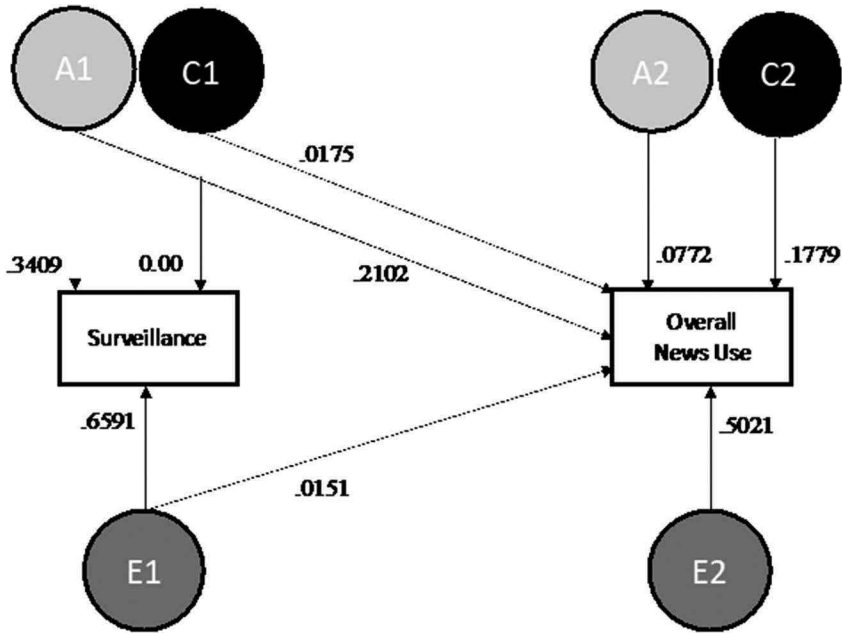


Figure 2. Results from a multivariate Cholesky model.

Image shows results from a bivariate Cholesky decomposition model. Cholesky models are designed to estimate the degree to which the covariance between observed variables is explained by genetic traits (*A*), the common environment (*C*), and unique environment (*E*). For more details and technical specifications see Medland and Hatemi (2009) and Neale (2009). Syntax for this model was adapted from Maes (2016c). Standardized path estimates shown. Results are from the best-fitting ACE model ($-2LL = 1348.69$) and not the AE model ($-2LL = 1349.20$, $\chi^2 = 0.50$, $p = .92$) or CE model ($-2LL = 1350.13$, $\chi^2 = 1.43$, $p = .70$).

in two news use motives and frequency of news use across multiple sources suggests that accounting for user genetic traits may lend considerable explanatory value to U&G studies, particularly those focused on the first legs of the U&G model dealing with links between background characteristics, media use motives, and media selection.

Recall that standard U&G theorizing posits “predispositions [and] the environment ...” including, and most essentially, “social and psychological factors ...” as the mechanisms that “guide, filter, or mediate” needs for content and ultimately media use and effects (Rubin, 2009, p. 167). However, as Beatty et al. (2009) and Sherry (2001) have argued, the root source of communication-related needs and resulting behaviors is likely “heritable individual differences in neural processing” that guide psychological traits, psychological states, and felt needs (Sherry, 2001, p. 284). The results of this study support the latter, communibiological argument for more fundamental explanations for media behavior. The results suggest, at

the very least, that to U&G's "social and psychological factors" that constrain and motivate media behavior should be added another source from which media behaviors originate: genes.

Importantly, and consistent with our general prediction, latent genetic traits explained a nontrivial amount of variance in 11 of 15 univariate ACE models (see Figure 3 for a summary). The largest estimates of genetic influence involved the use of individual news sources often characterized as ideologically liberal (*CNN* and *MSNBC*) or conservative (*Fox News Channel*). We find these results especially compelling in that they dovetail with research that has shown links between psychobiological traits, ideology, and ideological news use (Keene et al., 2017) as well as twin studies that have shown political ideology to be a heritable trait (Hatemi et al., 2014; Ksiazkiewicz & Friesen, 2019; Lockyer & Hatemi, 2018). For example, in an analysis of a combined sample of twins from nine studies conducted over four decades in five countries, Hatemi et al. (2014) found evidence of the genetic influence on political ideology notwithstanding differences in how ideology was measured. Possibly, genetic traits that impact ideology also motivate selection of news that could be characterized as appealing to ideological extremes. This is

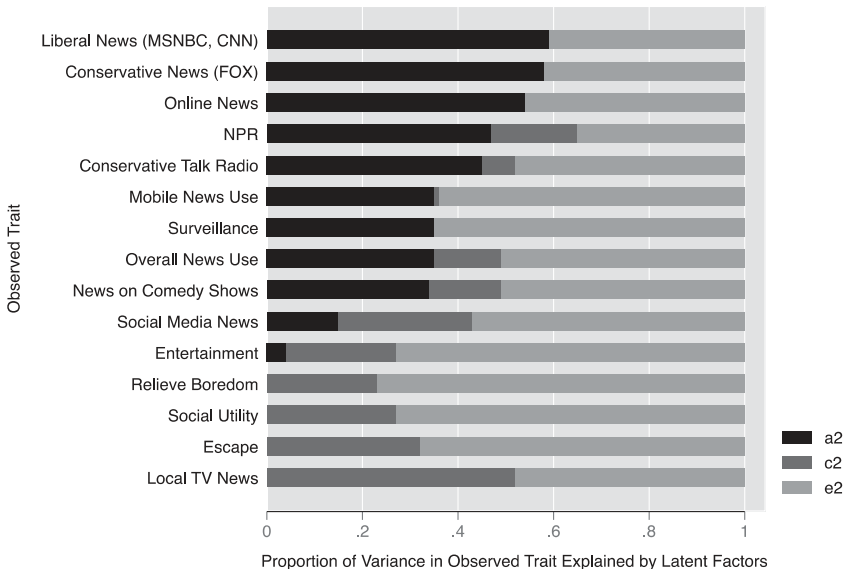


Figure 3. Summary illustration of univariate ACE model results.

Illustration generated using the estimates for a^2 , c^2 , and e^2 shown in Tables 2 and 3.

We graph these estimates here to allow for easier comparisons across observed traits. The black bars represent estimates of latent genetic influence (a^2). The dark gray bars represent estimates for the common environment (c^2). And the light gray bars represent estimates for the unique environment (e^2). Bars are sorted in descending order by estimates of a^2 . See Tables 2 and 3 for exact estimates.

speculative but could be tested using twin study data with variables capturing self-reported political ideology and use of ideological news sources.

We should reiterate here that while the majority of the univariate models showed non-zero genetic effects, we found only a sporadic pattern of genetic influence on news use motives. While our results showed genetic traits explained 35% of the variance in the surveillance motive and 4% of the variance in the entertainment motive for news consumption, they explained approximately 0% of the variance in the remaining motives. These results are unexpected considering, for one, communibiology's central proposition that explicit differences in almost all communication traits should be able to be traced back to heritable variation in neural pathways (Beatty et al., 2009). However, there are several reasons why latent genetic traits may explain substantial variance in the surveillance motive while accounting for few or no differences in other motives.

The simplest explanation is that surveillance is the most salient motive in the context of news use. It has long been recognized that surveillance of the environment is one of the primary functions for which people attend to news (Lasswell, 1948). That is, it is more likely that individuals attend to other types of media content such as situation comedies and dramas to relieve boredom or to escape. As such, these motives for using news may not be prevalent in the population to begin with. Combine this with a lack of statistical power owing to our small twin sample, and it may be next to impossible to detect genetic effects on these news use motives.

An alternative, theoretical explanation might be that genetic traits operate differently on motives based on their relative biological functions. For instance, Shoemaker (1996) theorized that millions of years of biological evolution led to selection for a heightened need to survey the environment for threats (e.g., predators, natural disasters). This process would have provided successive generations with an evolved psychological mechanism that enhanced their survival. In the modern world, Shoemaker suggested this mechanism would manifest in using news media to keep watch over one's environment for distant threats such as disease and catastrophe (see also Ng & Zhao, 2020). Thus, there may be reason to believe genetic variation may more readily explain individual differences in news for surveillance given its proposed evolutionary basis. We find the results of our multivariate model (see Figure 2), which demonstrated that the covariance between surveillance and overall news consumption is mainly explained by the same underlying genetic traits to be compelling in this regard. Though again, communibiology and behavior genetics suggest almost all phenotypes should be rooted in heritable differences in neurobiology. We suspect null genetic effects in univariate models more likely owe to lack of power.

While our results provide preliminary evidence of genetic influence on specific motives for news use, frequency of news consumption, and the relationship between the surveillance motive and overall news consumption, we should emphasize that our findings also highlight the importance of idiosyncratic experience in explaining motives and use. Across our analysis of news motives, the latent factor capturing unique environmental features that presumably impact one twin and not the other (e.g., attending different colleges, having a unique spouse) consistently explained the majority of variance in the observed variables. These findings suggest that totally unique life events explain considerable individual differences in news use motives and frequency of use. To us, the impact of the unique environment factor implies a need to reevaluate what the “social and psychological origins” (Katz et al., 1974, p. 20) described in the first leg of U&G entail. The results suggest random experience may play a relatively larger role in explaining individual variation in media use than does parenting, culture, and social forces commonly invoked as antecedents to media selection in the U&G paradigm.

Limitations

Twin studies are based on several assumptions (see Medland & Hatemi, 2009). Perhaps the most important assumption is called the equal environments assumption or EEA. The EEA supposes between-dyad differences in an observed trait or behavior do not stem from identical twins being treated more similarly than fraternal twins simply because they are identical. If there is reason to suspect, for example, that identical twins are treated more similarly than fraternal twins due solely to their identical status, then the EEA is violated. Violations of the EEA may result in inflated estimates of additive genetic influence in *ACE* models. However, we have no direct reason to suspect an EEA violation here. Further, tests of the EEA suggest it is a reasonable assumption to make unless there are concrete reasons to suspect a violation (e.g., Littvay, 2012).

A more pressing limitation relates to our purposive sampling method. Twins are part of a much smaller population than are “singletons” or non-twins, making opportunities to study twin behavior far rarer. The annual TDF provides an extraordinary chance to survey twins, and thus, the TDF data have been used often in the past (e.g., Cesarini et al., 2008; Horvath, 1995; Settle et al., 2009; York, 2019). Yet, these data come with many caveats. For one, as with any convenience sample, a point estimate for an observed variable may be biased and it is impossible to correct for this bias. It could be the case, for example, that means for media variables are skewed relative to those among the population. Estimates of heritability could also thus be biased. Certainly, caution in interpretation of estimates is warranted on these grounds alone.

A related limitation deals with the TDF study setting. The TDF is billed as a celebration of what makes twins similar. Twins that participate in the events at the TDF may, therefore, attempt to answer survey questions in ways that are similar due partially to the event context. We cannot rule out this possibility, and, given this potential limitation, we further caution readers to treat the results of this study as preliminary evidence subject to additional testing.

Low statistical power poses another limitation. As noted above, it is difficult to detect genetic contributions to traits and behaviors among small samples of twins, particularly if the traits and behaviors are not prevalent in the population to begin with (Medland & Hatemi, 2009). Future research could employ large probability samples of twins to address these limitations. In addition, future research could use advanced analysis techniques to test sex and age differences and gene-environment (GXE) interactions. We eschewed such tests given the exploratory nature of the study, which we view as sufficient first step and basis for future inquiry.

Conclusions and directions for future research

Our results indicate a need to reexamine the psychological and social characteristics assumed to motivate patterns of media use within the U&G framework (Rubin, 2009) and in other audience-centered theories of media effects (Knobloch-Westerwick et al., 2020; Oliver & Krakowiak, 2009). In the U&G paradigm, for example, the psychological and social background characteristics assumed to guide media behavior could be repositioned within a larger framework that accounts for antecedent biological and neurological variation among users, extending the chain of causal precursors that ultimately inform how individuals “act and react” to media stimuli (Rosengren, 1974, p. 270). Future U&G research could continue to use twin studies to examine the role of genetic traits in selection and use of other types of media content (e.g., entertainment television). DNA studies investigating links between genetic polymorphisms that regulate neurotransmitters in the brain (e.g., serotonin), media use motives, consumption, and media effects may also be instructive in future audience-centered theory building.

Our results also suggest a need to revisit the foundations of news effects. News use motives and consumption patterns have been linked to increases in political knowledge and engagement (e.g., Beaudoin & Thorson, 2004; Shah et al., 2001). The antecedents to these outcomes, however, may be fundamentally rooted in variation in genetic as well as social traits. This does not suggest certain individuals are “predisposed” to use news media content. There is no “news gene.” However, our results suggest individuals may have genetic *propensities* for patterns of news use given the right environmental conditions. Such propensities may, in turn, be linked to

higher levels of political knowledge and participation, though we should again note that not all news consumption results in gains in knowledge and participation. Use of ideological sources may lead to key differences and even declines in such outcomes (Stroud, 2011).

Finally, our findings imply researchers should anticipate competing—and likely conflated—influences of shared genetics and shared environments in studies of parent socialization of news behaviors. A considerable body of research has documented positive associations between how frequently parents and kids use news (e.g., Edgerly et al., 2018; York & Scholl, 2015), consistently attributing associations to parent–child socialization processes. Yet, few have attempted to disentangle whether such behavioral associations are due to aspects of social learning, genetic traits shared by parents and children, or both, though the evidence presented here suggests “nature,” in addition to “nurture,” plays a role.

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