



A regression approach to testing genetic influence on communication behavior: Social media use as an example



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ABSTRACT

A behavior genetics perspective suggests both social and biological forces influence human behavior, including highly specialized media and communication behaviors. In this paper, I use a behavior genetics framework and twin study data from the 2013 Midlife in the United States (MIDUS III) survey to examine how both environmental and genetic factors contribute to social media use. By applying a straightforward—and easily replicable—analytical extension to linear regression called DeFries-Fulker (DF) regression, I demonstrate that approximately one-to two-thirds of variance in social media use is attributable to additive genetic traits; unique and shared environmental factors account for the remainder of variance. In addition to showing social media use is partially motivated by underlying genetic traits, this paper, more importantly, provides an analytical blueprint for using DF regression in future investigations of genetic influence on communication behaviors and media effects.

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Behavior genetics research suggests complex human characteristics—from political ideology to cigarette smoking—are motivated by heritable biological traits *in addition* to the environmental forces of culture, parents, peers, and institutions (e.g., Do et al., 2015; Plomin, DeFries, & Fulker, 1988; Plomin, DeFries, Knopik, & Neiderheiser, 2013). From a behavior genetics perspective, sophisticated human beliefs, attitudes, and behaviors are byproducts of a rich interplay between genes underpinning human neurological function and exposure to the social environment, between our biological nature and the nurture we receive from the world around us, not one influence exclusive of the other. This theoretical logic—that both genes and environment play an interactive role in shaping observable human activity—has been applied to a broad spectrum of behaviors investigated throughout the social sciences (Polderman et al., 2015), including human communication and media consumption patterns (Cappella, 1991, 1996; Sherry, 2001, 2004; Shoemaker, 1996), and while a handful of empirical studies have borne out its theoretical postulates in observable detail (e.g., Kirzinger, Weber, & Johnson, 2012), the extent to which genes influence the use of newer information and communication technologies such as social network sites (e.g., Facebook) remains unclear.

In the past, motivations for social media exposure have been

primarily investigated through a uses and gratifications (U&G) framework that proposes individuals actively seek media content to fulfill goal-oriented psychological needs, such as the need to obtain new information and to escape from reality (Katz, 1959; Katz, Blumler, Geurovitch, 1973; Katz, Haas, & Gurevitch, 1973). U&G research on social media suggests users indeed turn to sites like Facebook and Twitter to seek news, establish and maintain social relationships, and for personal amusement, among other reasons (Chen, 2011; Krause, North, & Heritage, 2014; Park, Kee, & Valenzuela, 2009; Quan-Haase & Young, 2010; Raacke & Bonds-Raacke, 2008; Sheldon & Bryant, 2016; Tosun, 2012; Zhang, Tang, & Leung, 2011), although it is unclear the extent to which such consciously articulated motivations are guided by antecedent genetic variation that is foundational to neuroanatomical structure and cognitive processing, and thus, perceived psychological needs satisfied by using social media.

In this article, I apply a behavior genetics framework to a novel set of online communication activities: frequency of using social media sites such as Facebook to communicate with friends and family. Using survey data from the University of Wisconsin's Midlife in the United States (MIDUS) Longitudinal Study of Health & Well-Being collected on identical and fraternal twin pairs and a simple extension of linear regression called DeFries-Fulker (DF) regression, I demonstrate that individual genetic traits explain a non-trivial amount of variance in frequency of social media use; the impact of a person's environment, including shared experiences (e.g.,

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parent-child socialization) and unique individual experiences (e.g., peer influence) account for the remainder. Taken together, the results of this study suggest that social media use is at least partially influenced by genetic traits, which is a result consistent with previous research linking genetic traits to communication and media consumption patterns (Kirzinger et al., 2012). In the Discussion section, I examine the implications of the study for U&G theory as it pertains to social media use. I also discuss the application of the behavior genetics perspective and DF regression to other areas of communication and media effect research. As I later suggest, DF regression offers communication researchers a straightforward approach to analyzing the relative impact of genes and environment on communication behaviors compared to the highly specialized structural equation and Bayesian approaches that are largely taught in research methods courses outside the social sciences.

1. Literature review

1.1. The quantitative behavior genetics approach

Quantitative behavior genetics has foundations in the work of R.A. Fisher (1919) and Sewall Wright (1921), both of whom highlighted a basic principle on which the behavior genetics perspective rests, which is that “If genetic factors affect a quantitative trait, phenotypic [observable] resemblance of relatives [on that trait] should increase with increasing degrees of genetic relatedness” (Plomin et al., 2013, p. 34). Put simply, as the amount of genetic variation shared in common with kin increases (from first-degree cousins, to half siblings, to full siblings, and so on) the greater the amount of behavioral similarity can be attributed to genetics as opposed to the environment (socialization, enculturation, etc.). Because the degree of genetic relatedness between fraternal twins is already known to be 0.5 and identical twins 1.0, researchers can leverage survey data collected on twin pairs and established degrees of genetic affiliation to “assess the relative contributions of nature [genetic relatedness set at 0.5 or 1.0] and nurture” (p. 85). Specifically, by using a *variance components approach* to twin survey data, behavior geneticists attempt to decompose or partition the variance of an observed behavioral, perceptual, or attitudinal trait possessed by fraternal and identical twin respondents “into the constituent parts of genetic and environmental sources of variation” (p. 377).

The variance components approach commonly used in behavior genetics twin study research assumes an observable human trait or phenotype (P), such as news-reading or voting, is comprised of just three components: genetic relatedness or “heritability” (notated A), exposure to the shared environment (C), and exposure to the unique environment (E). Mathematically, then, any observed trait, including any empirically assessed communication behaviors, can be explained by the simple equation: $P = (A + C + E)$. Put another way, this logic suggests the degree to which a twin and their co-twin vary on an observed communication variable (P) is a function of genetic resemblance, exposure to the same shared environment (e.g., parent socialization of both twins in the same household), and an array of unique events that are experienced by one twin and not the other (having a different first-grade teacher,

being involved in different sports, interacting with distinct peer groups, etc.). The overarching goal of behavior genetics research is thus to assess the extent to which individual beliefs, attitudes, and behaviors are attributable to aspects of the individual's environment and to genetic traits.¹

For almost a century, the behavior genetics approach has yielded analytically consistent results across the social sciences. Using adoption, sibling, and twin study survey designs, quantitative behavioral geneticists have shown that genes influence a wide range of complex human traits, including strength of political ideology, political affiliation, political participation, risk-taking, schizophrenia, depression, cigarette smoking, psychological temperament, cognitive ability, cognitive function, IQ, Machiavellianism, empathy, social attitudes, anxiety, neuroticism, height, weight, and anatomical variation, among many others (Bouchard, Lykken, McGue, Segal, & Tellegen, 1990; Do et al., 2015; Ferguson, Munoz, Winegard, & Winegard, 2012; Hatemi, Smith, Alford, Martin, & Hibbing, 2015; Hatemi et al., 2010; Hibbing, Smith, & Alford, 2013; Polderman et al., 2015; Smith & Hatemi, 2013). In fact, Polderman et al. (2015) meta-analysis of over 17,000 human traits studied across over 2700 twin studies estimated that the average heritability of any observed human trait is 49%, leaving environmental factors such as parent socialization an enculturation to explain the remainder of variation in individual characteristics.² Results such as these suggest that while childhood socialization and conscious, goal-oriented decision-making play key roles in guiding human behavior, unarticulated, latent genetic influence is just as crucial to neuroanatomical composition, personality, and specific cognitions that guide performance of complex behaviors such as consuming media content. From a behavior genetics perspective, then, it is likely that the satisfaction of psychological needs through media use is at least partially rooted in the antecedent variables of genetic variation and neuroanatomy, although it is not within the scope of this study to directly explore such associations. Here I simply rely on the basic theoretical premise of quantitative behavior genetics: Genes, in addition to the environment, guide individual thoughts and actions, and there are analytical means by which the relative contribution of each can be assessed. Such an approach does not infringe on the utility or function of traditional media selection theories such as uses and gratifications (U&G); instead, as I argue, behavior genetics approach can contextualize U&G in a broader model of media choice and effects.

² Additionally, the authors showed that the majority of traits (69%) are best explained “with a simple and parsimonious model where the observed variation is solely due to additive genetic variation” (p. 1, italics mine). This is a striking finding, but it is important to note that the behavior genetics approach argues that genes influence rather than determine human characteristics (see Plomin et al., 2013). As Cappella (1996) suggests, “The fallacy that biological approaches to social behavior determine an individual's actions is based on naïve and long-outmoded theories” (p. 5, italics mine). Perhaps it could be argued that behavior genetics is “deterministic” in cases of physical anatomy, where a purely genetic model that omits environmental influence may best explain phenotypic variation. In twin studies of social behavior, however, such characteristics are often better explained by models possessing both genetic and environmental components. It is worth noting again, in other words, that the behavior genetics paradigm does not suggest that explicit, observable behaviors such as cigarette smoking are literally and directly passed through genes from parent to child; an individual does not, for instance, inherit the specific behavior of cigarette smoking from their parents. Rather, parents contribute genes to their children that form the neuroanatomical foundations of certain psychological and physiological characteristics (e.g., a propensity for addiction) that, combined with environmental stimuli (access to cigarettes and peer pressure to smoke), result in a measurable behavior like frequency of cigarette smoking (Plomin et al., 2013; Weber et al., 2008). Genes may, in this sense, be drivers of neuroanatomy, cognition, personality, temperament, and even specific psychological needs that individuals report seeking to satisfy through interpersonal communication and exposure to media content.

¹ It should be noted that the behavior genetics perspective does not assume that observed variation on a given trait analyzed in a twin study directly affects the behavior. There is no “news gene” that can be directly assessed in a twin study, for example. Behavior genetics research assumes, rather, that the impact of genetic variation captured in a twin survey study underpins neuroanatomy, cognition, and personality differences that more explicitly influence the observed perceptual, attitudinal, and behavioral variables (Sherry, 2004, p. 98; Weber et al., 2008).

1.2. Uses and gratifications of social media use

Uses and gratifications (U&G) is an approach to media behavior that investigates *reasons why* individuals select media content. Unlike the “direct” or “hypodermic needle” media effects theories of the early 20th century that suggested individuals had little control over media’s powerful persuasive influence, the U&G framework states that “people bend the media to their needs more readily than the media overpower them” (Katz, Haas, et al., 1973, pp. 164–165). Rather than acting as passive vessels through which media exerts persuasive influence, the U&G paradigm hypothesizes that individuals actively and consciously select media content—including newspaper, radio, television and internet content—with expectations that these materials will satisfy specific psychological needs, such as needs for information, entertainment and escape, and socializing with peers (see Katz, 1959; Katz, Blumler, et al., 1973).

A variety of more recent U&G studies have examined psychological needs satisfied by using social media sites such as Facebook. Using self-reported survey data typically collected on conveniently sampled college students, these studies find users seek social media content to satisfy peer interaction and relationship needs, including establishing and maintaining romantic associations (Tosun, 2012). Similar studies have found that users turn to social media sites “to thank people,” “to show others encouragement,” “because [they] need to talk about [their] problems sometimes,” and “to make friends of the opposite sex,” among other needs such as entertainment and escape (Quan-Haase & Young, 2010, p. 356; see also; Raacke & Bonds-Raacke, 2008). Additionally, individuals have reported using social media sites to engage in unobserved “social surveillance” of friends’ activities (Zhang et al., 2011), document their lives through photographs (Sheldon & Bryant, 2016), listen to music via platform applications (Krause et al., 2014), experience “camaraderie” among weak social ties (Chen, 2011), and obtain information about real-world events (Park et al., 2009).

Drawing on the U&G literature, McAndrew and Jeong (2012) suggested that patterns of social media use may also be influenced by an evolutionary psychology mechanism involving the unconscious desire to transmit one’s genes to the next generation. Specifically, McAndrew and Jeong (2012) hypothesized that individuals might frequently, if unconsciously, use social media to “gossip” about same-sex and same-age friends because of a need to “keep tabs on ... competitors for status and mates” who are typically “those in our own age and sex cohorts” (p. 2360). The authors found that women, younger individuals, and those not currently in a committed relationship were among the most active users surveyed about their social media habits, which are findings consistent with public opinion data on the demographics of social media use (Perrin, 2015) and suggest that differences in perceived needs to use social media could have as much to do with the basic biological drives to maximize inclusive fitness—the spread of one’s genes via reproduction (Williams, 1966)—as they do with sex- and gender-based differences in parent-child socialization of social media behavior, for example. Genetically motivated and unarticulated needs, in other words, may be among those crucial needs that influence how—and how frequently—individuals use social media.

1.3. Genetic and environmental foundations of social media use

The notion that genetic traits influence communication behavior is not new, and has in fact been fleshed out theoretically in several essays. For instance, Shoemaker (1996) suggested that genetic traits may play a key role in the modern production and consumption of news media content because individuals have been

naturally selected to pay close attention to deviant events in their surroundings that may “pose potential threats” to human survival and reproduction, whether these events are observed in the immediate surroundings or, now, via news media (p. 32). Likewise, Cappella (1991) argued automated patterns of interpersonal interaction are embedded in biological traits; specifically, Cappella (1991) suggested that two types of automated patterns in interpersonal communication—stimulation regulation and emotional responsiveness—are rooted in increasing “inclusive fitness of the species” (p. 18); in other words, genetic motivations are central to factors underpinning interpersonal communication.

Similar work by John Sherry, Michael Beatty and colleagues has shown that individual personality traits, especially psychological temperament, are shaped by genetic variation underlying differences in neuroanatomy, which in turn motivate a wide range of communication and media behaviors, including verbal aggressiveness (Beatty & McCroskey, 1997), communication apprehension (Beatty, McCroskey, & Heisel, 1998), communication adaptability (Beatty, Marshall, & Rudd, 2001), interpersonal affiliation (Beatty, Heisel, Hall, Levine, & France, 2002), tolerance for disagreement (McCroskey, Heisel, & Richmond, 2001), communicator style (Horvath, 1995), willingness to communicate (Hazel, Wongprasert, & Ayres, 2006), television use (Sherry, 2001) and a broad assortment of other communication and mass media consumption behaviors (Sherry, 2004). Summarizing this work, McCroskey and Beatty (2000) suggest, “The view is that while nurture certainly has some effects (via cultural influences, formal education, experience, etc.) nature has set forth in one’s genetic code most of what one will become and do ...” with “... inborn, neurobiological structures [being] responsible for communication behavior and associated processes” (p. 2; see also Weber, Sherry, & Mathiak, 2008).

As was mentioned above, a common methodological and analytical approach researchers use to examine the degree to which communication and media behaviors are indeed “inborn” or heritable involves the use of twin and adoption surveys. One such study examining how frequently adoptive and nonadoptive sibling pairs used television found that “that 34% of the variance in television viewing at [age] 4 and 30% of the variance at 5 is due to genetic influences” (Plomin, Corley, DeFries, & Fulker, 1990, p. 375). Other twin studies of media and communication behavior have found that genetics influence individual levels of computer self-efficacy (Deryakulu, McIlroy, Ursavaş, & Çalışkan, 2016), problematic internet behavior (Deryakulu & Ursavaş, 2014), frequency of talking and texting on mobile phones (Miller, Zhu, Wright, Hansell, & Martin, 2012), the effects of television use on aggressive behavior in adolescents (Rowe & Herstand, 1986), and the relationship between TV viewing and antisocial behaviors (Schwartz & Beaver, 2015). In one other twin study, the authors demonstrated that genes, in addition to environment, were primarily responsible for how frequently respondents engaged in interpersonal discussion and how frequently they used computers, video games, television, the internet, and news media (Kirzinger et al., 2012). Across all behaviors studied, the authors found that “one fifth to one third of the variance in media consumption and communication behaviors [were] explained by additive genetic factors” (p. 159). Additionally, for many of the communication behaviors studied, a model including only genetic (A) and unique environmental (E) factors provided more parsimonious explanation of variance than did models also including an indicator of shared environmental influence (C) (pp. 156–158).

1.4. Hypotheses

Based on literature applying behavior genetics to communication and media behavior, a broad theoretical expectation is that

genetic traits should also influence social media use. This theoretical logic should apply to all types of social media use, including use for communicating with (1) friends, and (2) family members living outside the nuclear family's household.

Formally, based on the literature, I would predict,

Hypothesis 1a. *Genetic similarity will explain a nonzero proportion of variance in frequency of using social media for contacting friends.*

Hypothesis 1b. *Genetic similarity will explain a nonzero proportion of variance in frequency of using social media for contacting family living outside the household.*

2. Method

2.1. Data collection and sample

I tested my hypotheses by analyzing nationally representative panel survey data from the University of Wisconsin's Midlife in the United States (MIDUS) Longitudinal Study of Health & Well-Being (<http://midus.wisc.edu/>). These data were applicable to this study because an initial wave of data collection in 1995 and 1996 (nicknamed MIDUS I) contained a representative subsample of $n = 1914$ monozygotic (MZ) identical and dizygotic (DZ) fraternal twins who were interviewed by phone and mail survey as part of a larger data collection effort.³

MIDUS researchers contacted the same twin respondents for a second wave of data collection beginning in 2004 (nicknamed MIDUS II). Of the original $n = 1914$ twins originally contacted by the research team, $n = 1484$ completed the MIDUS II telephone survey, generating a 78% response rate.⁴ The MIDUS III data used in the present study was collected from 2013 to 2014. A total of $n = 1018$ of the original MZ and DZ twins completed the MIDUS III telephone survey, which resulted in a response rate of 69%.⁵

Because a nominal variable assessing twin zygosity was available in the MIDUS I dataset, I merged the zygosity variable with the MIDUS III dataset using a unique identifier variable and a family-level identifier from MIDUS I. After merging these data, it was possible to identify whether twin respondents were fraternal or identical. I then reshaped the dataset from long to wide format so that observations on the criterion variables would be repeated across columns—one observation for the first twin, and one observation on the variable for the co-twin. This process resulted in a total of $n = 94$ MZ pairs and $n = 134$ DZ pairs used in the analysis after accounting for twin pairs that were missing at least one observation on a criterion variable.

2.2. Variables

As is the case with numerous secondary datasets that contain

³ For a full explanation of the MIDUS I sampling design, see the "Sample Description" on the MIDUS website: <http://www.midus.wisc.edu/midus1/index.php>. Respondents were compensated \$50 for completing the telephone interview and \$20 for the mail-in questionnaire. According to the MIDUS I "description of samples" report, 45% of twin respondents were male; ages ranged from 25 to 75 years, with a mean age of 45 ($sd = 12.0$); 11% of the sample had less than 12 years of education, 32% had a high school education; 31% had some college experience or a two-year degree; 27% had a bachelor's degree or higher.

⁴ Again, refer to "sample description" on the MIDUS website: <http://www.midus.wisc.edu/midus1/index.php>. The twin subsample of the MIDUS II study had a mean age of 54 ($sd = 11.6$) after adjusting for respondent mortality.

⁵ For an in-depth discussion of sampling methods and sample composition, refer to the documentation and codebook on the Interuniversity Consortium for Political and Social Science Research (ICPSR) website: <http://www.icpsr.umich.edu/icpsrweb/NACDA/studies/36346>.

communication measures, the MIDUS study was designed mainly to assess outcomes not associated with media use. In fact, the stated purpose of the MIDUS study is "to investigate the role of behavioral, psychological, and social factors in understanding age-related differences in physical and mental health" (see <http://www.icpsr.umich.edu/icpsrweb/NACDA/studies/36346>). While survey items were included to assess social media use, these ordered categorical items were few in number and likely ancillary to the researchers' main interests. Consequently, the two single-item measures available to use as criterion variables in this study may easily possess measurement error associated with a variety of response biases (Prior, 2009), a caveat I discuss in detail in the Discussion section of this article while noting here that single-item measures have been used to study the genetic foundations of communication behavior in previously published research (Kirzinger et al., 2012), and are widely considered adequate, if inexact indicators of psychological or behavioral constructs (e.g., Bergkvist & Rossiter, 2007; Cuny & Perri, 1991; Wanous & Reichers, 1996; Wanous, Reichers, & Hudy, 1997; Zimmerman et al., 2006).

2.2.1. Frequency of social media use for communicating with friends

The first criterion variable asked respondents about frequency of using social media sites for contacting friends. To assess this item, each respondent received the following prompt: "This question asks about social media, which includes Facebook, Twitter, MySpace, Skype, text messages, chat rooms, etc. How often are you in contact using social media with any of your friends using social media?" Respondents could answer "never or hardly ever," "less than once a month," "about once a month," "2 or 3 times a month," "about once a week," "several times a week," "about once a day," or "several times a day." Table 1 describes the study's variables in greater detail.

The point estimate on this item for fraternal (DZ) twins was 2.79 (95% CI = 2.54 to 3.04); the mean for identical twins was 2.92 (95% CI = 2.57 to 3.27). Notably, the correlation between DZ twin pairs on this variable was small and insignificant ($r = 0.06$, $p = ns$); conversely, MZ twins were moderately correlated on this item ($r = 0.59$, $p < 0.001$).

2.2.2. Frequency of social media use for communicating with family

A second criterion variable assessed how often respondents used social media sites to contact family members. This survey item prompted respondents by saying: "This question asks about social media, which includes Facebook, Twitter, MySpace, Skype, text messages, chat rooms, etc. How often are you in contact using social media with any members of your family, that is, any of your brothers, sisters, parents, or children who do not live with you using social media?" As with the first item, respondents could answer "never or hardly ever," "less than once a month," "about once a month," "2 or 3 times a month," "about once a week," "several times a week," "about once a day," or "several times a day."

Table 1 shows the point estimate for the family-related social media use item was 3.01 for DZ twins (95% CI = 2.75 to 3.27) and 3.19 for MZ twins (95% CI = 2.85 to 3.54). Again, the correlation on this variable was not significant for fraternal twin pairs ($r = 0.12$, $p = ns$) while the correlation for identical twins was moderate ($r = 0.43$, $p < 0.001$).

2.2.3. Frequency of social media use (combined index)

For comparison purposes, Table 1 also lists point estimates and confidence intervals for a combined index of the two frequency of social media use items ($r = 0.73$, $p < 0.001$). The overall mean on the social media use index for DZ twins was 2.90 (95% CI = 2.66 to 3.13) while MZ twins scored 3.05 (95% CI = 2.72 to 3.37). The correlation

Table 1
Descriptive statistics for MIDUS III data.

	Y_{DZ}	Y_{MZ}	r_{DZ}	r_{MZ}
Social Media Use for Friends	2.79 (2.54, 3.04)	2.92 (2.57, 3.27)	0.06	0.59***
Social Media Use for Family	3.01 (2.75, 3.27)	3.19 (2.85, 3.54)	0.12	0.43***
Social Media Use (combined items)	2.90 (2.66, 3.13)	3.05 (2.72, 3.37)	0.12	0.52***

Note: *** $p < 0.001$. The 95% confidence intervals in parentheses. DZ = dizygotic fraternal twin pairs; MZ = monozygotic identical twin pairs. Pearson correlations (r) are for MZ and DZ pairs. Variable range = 0 to 7, where 0 = use social media “never or hardly ever” and 7 = use social media “several times a day.”

between DZ twin pairs on the combined criterion measure was small ($r = 0.12$, $p = ns$) while the correlation for MZ twin pairs was moderate (0.52 , $p < 0.001$).

2.3. Statistical procedure

The goal of twin heritability studies is to decompose the variance of some observable behavior, or phenotype. This is often performed mathematically by accounting for how much variability in target phenotypic traits—in this case, frequency of social media use for contact with friends and family—can be accounted for by an additive genetic component that is based on the level of genetic relatedness between identical and fraternal twins (A), the common social environment (home, school, neighborhood, etc.) experienced by both twins (C), and unique environmental influences (e.g., a teacher, friend, coworker) that is specific to one twin but not the co-twin (E). By decomposing how much variance is attributable to genes, shared environmental influences, and unique environmental influence (social or psychological characteristics or events that are unique to each twin), ACE modeling can be used to determine how much a certain behavior can be explained by genetic and social forces.⁶

There are several appropriate statistical approaches used to model ACE influences on phenotypes, including specialized structural equations (Neale & Cardon, 1992), a Pearson-Aitken approach (Hawke, Stallings, Wadsworth, & DeFries, 2008), and Bayesian approaches (Fowler, Baker, & Dawes, 2008), all of which are less likely to be included in standard research methods training in the social sciences broadly and the communications disciplines specifically. A relatively more straightforward analytical approach—and one that is likely to be more familiar to communication researchers—involves a simple extension of linear regression and is called DeFries-Fulker (DF) regression. DF regression was developed as an alternative approach to ACE modeling that produces unbiased estimates of genetic and environmental parameters equivalent to those generated by the maximum likelihood structural equation approach commonly used in behavior genetics (see DeFries & Fulker, 1985; for a technical proof, see; Rodgers & McGue, 1994), with a major advantage being its relative accessibility to social sciences researchers. I outline a standard DF regression model below, in Equation (1):

$$Y_1 = a + b_1 Y_2 + b_2 R + b_3 (R * Y_2) + e \quad (1)$$

Here Y_1 represents a phenotypic measure for one twin, Y_2 represents the measure on the same variable for the co-twin, and R

⁶ ACE modeling, it should be noted, relies the “equal environments assumption” (EEA). The EEA states that identical (MZ) twins and fraternal (DZ) twin pairs experience roughly the same level of similarity in their shared environments (e.g., the childhood home). If, for instance, MZ twins have more shared environmental experiences than do DZ twins, it is possible that the EEA is violated, which could result in biased estimates of genetic influence on behavior (A). Tests of the EEA, however, have confirmed it is a generally valid assumption (e.g., Kendler, Neale, Kessler, Heath, & Eaves, 1993), and that any biases in estimates are “modest” (Felson, 2014).

represents the coefficient of genetic relatedness (1.00 for MZ twins who share 100% of their structural DNA and 0.5 for DZ twins who share 50%).⁷ Note that the DF regression approach thus accounts for variance reflecting genetic influence ($R * Y_2$) and shared environmental influence (Y_2), the latter of which is captured by mathematically isolating the latent component of the model that makes twins similar on the phenotype. In fact, b_1 operates as an unbiased estimate of (C) and b_3 is an unbiased estimate of (A) (proofs can be found in Rodgers & McGue, 1994; see also Turkheimer, D’Onofrio, Maes, & Eaves, 2005, p. 1223). Given estimates of (A) and (C) it is possible, then, to also determine an estimate of (E) assuming that a phenotype (P) such as frequency of social media use is comprised of those components: $P = A + C + E$, where $P = 1.0$. The coefficient for R (b_2), it should be noted, captures the difference in Y between MZ and DZ pairs after accounting for the impact of (A) and (C), but it is rarely reported or interpreted since b_1 and b_3 provide the information necessary to account for the primary variance components of Y and (b_2) is frequently insignificant (Smith & Hatemi, 2013, p. 391). The constant term has its usual interpretation, operating as an estimate of the criterion variable when all other predictors are set to their lowest values.

To the DF regression model it is also possible to add a linear regression component (Equation (2)), which can account for items such as demographic predictor variables (e.g., age):

$$Y = a + \sum b_i X_i + e \quad (2)$$

Equation (2) should have a familiar interpretation. Here Y is simply the criterion variable and X is a vector of theoretically or conceptually specified predictor variables. Coefficients of X represent, for instance, the individual effects of survey respondent sex, age, race/ethnicity, years of education and so forth on a criterion variable of interest (Y), controlling for all other predictor variables in the model. Importantly, genetic heritability is rarely assumed to play an explicit role in such linear models. As Smith and Hatemi (2013) note, from a social scientific perspective, “ Y is [often] viewed as a function of environmental forces (education, socioeconomic status and so forth) and the handful of biologically based variables that do make a regular appearance in the vector X (notably sex) are interpreted through an environmental lens” (Smith & Hatemi, 2013, p. 392). In the field of communication

⁷ In practical terms, it is possible to estimate a DF model using the following procedure: (1) obtain twin survey data (see footnote ¹³); (2) if needed, reshape the dataset from long to wide format such that observations on the criterion variable (e.g., social media use) is on the column—one column for social media use by each twin; (3) double-enter the data by adding a copy of the data at the bottom of the rows, but with observations on the criterion reversed for the co-twin; (4) recode the zygosity variable that indicates whether twins are monozygotic (identical) equal to 1.0 and dizygotic (fraternal) equal to 0.5 to reflect differences in genetic relatedness; (5) standardize (z -score) the recoded zygosity variable along with the criterion observation for twin 2; (6) create an interaction term for the zygosity and twin 2 criterion variables (this variable will provide an estimate of b_3); (7) run a standard linear regression model using twin 2’s scores on the criterion (b_1) the measure of zygosity (b_2) and the interaction term (b_3) followed by any relevant demographic variables, while making sure to; (8) cluster standard errors by twin pair or otherwise adjust standard errors to account for double entry of data.

research, for instance, the influence of sex (X) on frequency of social media use (Y) might be explained in the context of differing patterns of media socialization among adolescent males and females, not sex-based biological differences.⁸ However, by combining the DF model (Equation (1)) with a standard multiple regression model (Equation (2)), into a third model (Equation (3); an extended DF model), the researcher explicitly operationalizes criterion variables as an outcome of both biological and environmental variation as well as specific genetically and environmentally relevant covariates (e.g., sex, education):

$$Y_1 = a + b_1 Y_2 + b_2 R + b_3 (R * Y_2) + \sum b_i X_i + e \quad (3)$$

What is perhaps most novel about Equation (3) is that, given the appropriate twin data, any model formulated within Equation (2) regression framework can be added to Equation 1's biometric model decomposing ACE variance (DeFries & Fulker, 1985; Smith & Hatemi, 2013) to create an extended DF model. In other words, any model of communication behavior or media effects—for instance, a model estimating the effects of news media use (X) on political knowledge scores (Y) or exposure to violent video games (X) on aggressive behavior (Y)—can be combined with the standard DF model (Equation (1)) such that genetic and environmental ACE components can be assessed simultaneously with the influence of relevant predictors. In the models employed below, I present results from both a standard and an extended DF model to demonstrate the relative influence of genetic and environmental components as well as observed demographic variables on target phenotypes.⁹

Finally, it should be noted that to estimate the DF models an important analytical question must be addressed prior to investigation: Which twin's score should be entered as the criterion (Y_1) and which as the predictor (Y_2)? One common solution to this problem recommended by Smith and Hatemi (2013) is to simply double enter twin data such that twin 1's scores on the phenotype are regressed on twin 2's scores and vice versa. Double entry thus doubles n number of twin pairs used to estimate the DF models in Equations 1 and 3, which also requires that standard errors be adjusted for inflated degrees of freedom.¹⁰

3. Results

H1a and H1b predicted associations between respondent genetic traits and frequency of social media use for contacting friends (H1a) and family members not living the household (H1b). Importantly, the unstandardized beta coefficients shown in Table 2, Model 1 are interpreted as the *amount of variance explained* in frequency of social media use for contacting friends by respondent genetics (A) and common environmental influences (C), such as

⁸ Thus, models of communication behavior and effects implicitly assume genetic influence is $A = 0$ even though empirical research has repeatedly shown that $A > 0$ for many communication-related outcomes, raising the possibility that A should be modeled along with standard blocks of relevant predictors.

⁹ A standard block of demographic variables was used to estimate how sample respondents varied on the criteria, and to contrast the effects of generic environmental and genetic predictors (described below) with more specific measures. Because females and younger respondents are more likely to use social media than males who are older (e.g., McAndrew & Jeong, 2012; Perrin, 2015), I included specific measures of respondent sex (59% female) and age ($M = 62.60$, $sd = 9.93$). Dummy variables measuring the race and ethnicity of black (2.7%) and Hispanic respondents (1.80%) were also included. Respondents' level of formal education was measured in years ($M = 14.69$, $sd = 2.45$, range = 10.00–20.00 years).

¹⁰ I accomplished this by using the *robust cluster* option in Stata 13.0, with observations clustered within twin pair entries. See Smith and Hatemi (2013, p. 392) for a full discussion. See also Kohler and Rodgers (2001) and Rodgers and Kohler (2005).

Table 2
Determinants of frequency of social media use for communication with friends.

	Model 1 [Eq. (1)]		Model 2 [Eq. (3)]	
	<i>b</i>	(SE)	<i>b</i>	(SE)
A (Genes)	0.67***	(0.14)	0.61***	(0.14)
C (Common Environment)	0.26***	(0.06)	0.20***	(0.06)
Female			0.61**	(0.21)
Age			−0.04***	(0.01)
Black			−0.27	(0.42)
Hispanic			0.56	(0.75)
Education			0.08†	(0.05)
Constant	1.50***	(0.33)	2.98*	(1.20)
<i>N</i>	448		445	

Note: *** $p < 0.001$, ** $p < 0.01$, * $p < 0.05$, † $p < 0.10$. Unstandardized coefficients and standard errors reported. R is not significant and is therefore not reported (as should be the case; see Smith & Hatemi, 2013, p. 401). E for model 1 is 0.07 or (1 − (0.67 + 0.26)).

being raised in the same household. The remainder of the variance in social media use for contacting friends is explained by the excluded (E) term, which accounts for unique environmental influences. Note that, mathematically, the DF model allows us to make “variance explained” interpretations for coefficients (A), (C), and (E) that would normally be reserved for interpretation of R^2 values. Coefficients generated from a structural equation approach to ACE modeling employ the same type of interpretation because the primary emphasis in any ACE model, whether using SEM or DF regression, is on decomposing the variance of Y (the phenotype, or P) under the assumption $P = (A + C + E)$. Coefficients for demographic predictors employed in combined linear and DF regression models retain their usual interpretation: *a one-unit change in X results in a b-unit change in Y*.

Table 2, Model 1 shows that approximately 67% of the variance in frequency of using social media to communicate with friends is determined by additive genetic traits ($b = 0.67$, $SE = 0.14$, $p < 0.001$, 95% CI = 0.39 to 0.96). Approximately 26% of the variance is accounted for by the shared environment ($b = 0.26$, $SE = 0.06$, $p < 0.001$, 95% CI = 0.14, 0.38), which leaves an estimated 7% of the variance being explained by unique environmental factors such as novel events or peer interactions that apply to one twin, but do not apply to the co-twin.¹¹

The second model in Table 2 shows the impact of adding demographic predictors to the basic DF model. Importantly, the amount of variance in the criterion variable explained by the influence of genes and common environmental influences decrease to 61% and 20%, respectively. Specific covariates assessing respondent sex ($b = 0.61$, $SE = 0.21$, $p < 0.01$), age ($b = -0.04$, $SE = 0.01$, $p < 0.001$), and level of formal education ($b = 0.08$, $SE = 0.05$, $p < 0.10$) predict frequency of social media use for contacting friends, and in ways we might expect. For example, previous research shows that women, younger, and educated individuals tend to spend more overall time using social media sites (e.g., McAndrew & Jeong, 2012; Perrin, 2015); all of these findings are consistent with the results shown in Table 2, Model 2.

It is noteworthy that after adding controls to the model the explanatory power of the genetic (A) term decreases, suggesting that biologically based demographic predictors could at least partially explain the heritable component of the criterion variable. The variable measuring respondent sex, for example, could easily

¹¹ Because linear regression assumes a continuous criterion variable, I ran an alternative ordered logistic regression using Stata 13.0's “GSEM” program. For the basic DF model, treating the criterion as an ordered categorical variable resulted in substantively identical estimates of (A) genetic influence ($b = 0.51$, $p < 0.001$), as well as (C) shared environmental affects ($b = 0.20$).

Table 3
Determinants of frequency of social media use for communication with family.

	Model 1 [Eq. (1)]		Model 2 [Eq. (3)]	
	<i>b</i>	(SE)	<i>b</i>	(SE)
A (Genes)	0.40*	(0.17)	0.30†	0.17
C (Common Environment)	0.24***	(0.07)	0.19**	0.07
Female			0.86***	(0.24)
Age			−0.04**	(0.01)
Black			−0.48	(0.60)
Hispanic			0.85	(0.82)
Education			0.06	(0.05)
Constant	1.98***	(0.38)	3.88**	(1.29)
<i>N</i>	452		449	

Note: *** $p < 0.001$, ** $p < 0.01$, * $p < 0.05$, † $p < 0.10$. Unstandardized coefficients and standard errors reported. *R* is not significant and is therefore not reported (as should be the case; see Smith & Hatemi, 2013, p. 401). *E* for model 1 is 0.36 or $1 - (0.40 + 0.24)$.

be exerting both environmental and genetic on the criterion variable through both a socialization mechanism associated with one's sex-related gender identity (e.g., adolescent girls being encouraged by parents to spend more time relative to boys communicating with peers and developing relationships) as well as a purely biological mechanism (females possessing a genetic predisposition to be more relationship- and communication-oriented than males), with the former socialization mechanism weakening the explanatory power of (*C*) and the latter biological mechanism weakening the explanatory power of (*A*). The DF approach, however, does not allow the researcher to isolate the degree to which a demographic predictor like sex saps the explanatory power from the (*A*) estimate relative to (*C*) and the excluded (*E*) term. In addition, the interpretation of demographic predictors in Table 2, Model 2 is problematic because it is unclear whether estimates of (*A*) and (*C*) reflect clean partitions in genetic and common environmental variance components (see Smith & Hatemi, 2013, p. 402). This possibility could be explored using models that account for interactions between variables tapping genetic traits and specific environmental factors, although such interactions are beyond the scope of the present analysis. What is critical to H1a, is that term (*A*) measuring genetic influence accounts for a non-zero proportion of variance in the criterion variable, social media use for staying in touch with friends. H1a is supported.

The standard DF model shown in Table 3, Model 1 demonstrates that genetic traits likewise account for a non-zero proportion of variance in social media use for contacting family living outside of the respondent's household. Genes account for an estimated 40% of variance in the criterion ($b = 0.40$, $SE = 0.17$, $p < 0.05$, 95% CI = 0.06, 0.73), the common environment accounted for 24% ($b = 0.24$, $SE = 0.07$, $p < 0.001$, 95% CI = 0.11, 0.37), and the unique environment 36%. As was the case with the previous criterion variable, we again see that genes account for a larger proportion of variance in media behavior than do environmental factors.¹²

Adding demographic variables to the model decreases variance explained by the genetic component to about 30% ($b = 0.30$, $SE = 0.17$, $p < 0.10$, 95% CI = 0.11, 0.37), but the substantive effect remains. Variance explained by the shared environment component also declines to 19% in the full DF model (Table 3, Model 2). Respondent sex ($b = 0.86$, $SE = 0.24$, $p < 0.001$) and age ($b = -0.04$, $SE = 0.01$, $p < 0.01$) still exert effects on the criterion variable, although it is again unclear whether variables such as sex sap the

Table 4
Determinants of frequency of social media use for communication (combined criterion variables).

	Model 1 [Eq. (1)]		Model 2 [Eq. (3)]	
	<i>b</i>	(SE)	<i>b</i>	(SE)
A (Genes)	0.51***	(0.15)	0.48**	(0.15)
C (Common Environment)	0.28***	(0.06)	0.23**	(0.07)
Female			0.63†	(0.32)
Age			−0.02	(0.02)
Black			−0.68	(0.86)
Hispanic			−0.21	(0.92)
Education			0.17**	(0.06)
Constant	1.81***	(0.49)	0.92	(1.59)
<i>N</i>	462		458	

Note: *** $p < 0.001$, ** $p < 0.01$, * $p < 0.05$, † $p < 0.10$. Unstandardized coefficients and standard errors reported. *R* is not significant and is therefore not reported (as should be the case; see Smith & Hatemi, 2013, p. 401). *E* for model 1 is 0.36 or $1 - (0.40 + 0.24)$.

predictive power of genes (*A*), the common environment (*C*), the unique environment (*E*), or all three. What the model does indicate is that there is a substantive effect of (*A*) on the criterion, i.e., $A > 0$; therefore, H1b is supported.

For purposes of comparison, Table 4 shows DF regression models predicting a combined social media use criterion. Again, the standard DF model shows a substantive impact of genes on social media use; in this case, the estimate of (*A*) explains about 51% of variation in the combined social media criterion measure. This estimate decreases to 48% after adding controls, but the non-zero influence of genetic traits on social media use remains.

4. Discussion

The goal of this study was twofold: First, this paper attempted to use a behavior genetics framework and twin study survey data to determine whether genetic traits influence frequency of social media use; second, this paper attempted to demonstrate how communication scholars with little or no exposure to highly specialized twin study data analysis techniques (e.g., SEM or Bayesian approaches) can use a simple extension of linear regression to estimate genetic influence on various media and communication behaviors. Using survey data on a nationally representative sample of twin pairs from the Midlife in the United States (MIDUS) Longitudinal Study of Health & Well-Being, I discovered that approximately one-to-two-thirds of the variance in social media use is explained by genetic traits, with the remainder of the variance explained by environment (parent-child socialization of behaviors, peer influence, unique events, etc.). In fact, the results demonstrated that the genetic component of social media use remains substantively important even after controlling for demographic factors that the literature suggests are predictive of social media use, such as respondent sex and age (McAndrew & Jeong, 2012; Perrin, 2015), although ACE estimates did decrease after adding these predictors suggesting demographics such as sex may influence social media use through both biological as well as sex-based socialization mechanisms. The analysis, in sum, is consistent with a growing body of empirical communication research evidencing genetic influence on a wide variety of media consumption behaviors (e.g., Kirzinger et al., 2012; Plomin et al., 1990; see; Sherry, 2004), and implies that unconscious and innate motivations rooted in genetic variation may affect media selection and consumption in addition to the deliberate and self-directed psychological goals hypothesized by media choice theories such as uses and gratifications (U&G).

Results from this study do not suggest a deficiency in the

¹² I again used Stata's "GSEM" program to estimate the same model treating the criterion variable as ordinal. This procedure rendered similar estimates for (*A*) genes ($b = 0.36$, $p < 0.01$), and common environment ($b = 0.17$, $p < 0.001$).

explanatory utility of U&G, but rather imply that consciously articulated, self-reported uses and gratifications sought and obtained via social media, such as “social surveillance” or information gathering (e.g., Tosun, 2012; Zhang et al., 2011) are at least partially a byproduct of genetically rooted neuroanatomy and cognition; in other words, rather than implying a shortcoming in U&G, this study suggests U&G should likely be contextualized in a broader theoretical framework as a fundamental mediating factor between, on the one hand, inherited neuroanatomical function and cognition, and observed media behavior on the other. In this sense, unique media uses and gratifications articulated by survey respondents are measurable observations of, in part, long-established and innate traits that are also shaped by social learning, enculturation, interactions within social institutions (e.g., school, church), and novel life experiences. U&G is, from this perspective, a theoretical framework that explains much but might itself be based in antecedent genetic factors that give rise to neuroanatomical differences underlying temperament and personality traits (e.g., Beatty, McCroskey, & Floyd, 2009; Beatty et al., 1998; Sherry, 2001) that ultimately drive patterns of cognitions about media. Moving forward, it would be beneficial to create a model of media behavior that reconciles functionalist communication theories (e.g., U&G) with a behavior genetics approach that emphasizes the importance of heritable traits as a foundation for human thought and action. It is notable that earlier calls for the inclusion of biological mechanisms in models of communication and media behavior (e.g., Cappella, 1996; Sherry, 2004) were made during a period when both methodological and analytical options for studying such biological mechanisms were limited; however, with the increasing availability of twin study data and a relatively straightforward analytical vehicle (i.e., DeFries-Fulker regression), it is now possible for communication researchers to more consistently and meaningfully investigate genetic determinants of communication behavior and media effects.¹³ Furthermore, large annual gatherings of twin survey respondents such as at the Twinsburg, Ohio “Twins Festival” provide opportunities for communication researchers to collect original—albeit conveniently sampled—data on both fraternal (dizygotic) and identical (monozygotic) twin pairs. Methodologically and analytically, then, there is little standing in the way of continued research on the genetic underpinnings of communication behavior and media effects, although, as Smith and Hatemi (2013) note, the theoretical hurdles involved in reconciling traditional social scientific theory with behavior genetics may at times seem insurmountable.

In the subfield of political communication, for instance, a common approach to studying child and adolescent news consumption and political behavior is to examine the role of parent socialization of these behaviors via Albert Bandura's Social-Cognitive Theory (SCT) and similar frameworks. Several recent studies of childhood political communication behaviors illustrate a consistent reliance on socially and cognitively oriented theoretical approaches such as Bandura's SCT to explore media use among youth (e.g., Edgerly, Thorson, Thorson, Vraga, & Bode, 2017; Scholl & York, 2016;

Shehata, 2016; Valenzuela, Bachmann, & Aguilar, 2016; York & Scholl, 2015); in each case, biological mechanisms for political communication behavior are mentioned in passing, if at all, which is not aberrant but entirely consistent with our discipline's traditional investigations of environmental (nurture) mechanisms rather than genes as the primary basis of human behavior (this same approach is used widely throughout the social sciences; see Smith & Hatemi, 2013). The behavior genetics paradigm, however, could enhance such investigations by supplementing traditional communication behavior and media effects models with indicators of genetic relatedness. Analytically and methodologically, there is little standing in the way of blending these approaches. The theoretical synthesis between social science and biometric models of behavior would nevertheless require more than synthesis; it would be a difficult theoretical fusion to achieve, but the payoff could potentially be a renewed understanding of communication behavior and media effects (Sherry, 2004; Smith & Hatemi, 2013).

Finally, it should be noted that while behavioral genetics models such as those used in this study offer an approach to analyzing the heritability of behavior, they also suffer several shortcomings. First, they not only rely on (relatively) rare twin data, but also often require large samples of twins (at least >1000) to achieve appropriate statistical power to detect additive genetic traits (Medland & Hatemi, 2009; Neale & Cardon, 1992), raising the possibility for Type II statistical errors (accepting a false null for the influence of genes) when sample sizes are small. Second, while the interpretation of the basic DeFries-Fulker model (Eq. (1)) regression coefficients for (A), (C), and (E) should be identical to those in structural equation approaches to ACE modeling (see Smith & Hatemi, 2013), coefficients of (A), (C), and (E) in the extended DF model with demographic predictors entered (Eq. (3)) cannot be interpreted fully because certain predictors (e.g., sex) may have both environmentally and biologically based components that sap an unknown amount of explanatory power from (A), (C), and (E) estimates. It should also be noted that while a large body of research suggests single-item measures of behavior are adequate indicators of underlying activity (e.g., Bergkvist & Rossiter, 2007; Cunny & Perri, 1991; Wanous & Reichers, 1996; Wanous et al., 1997; Zimmerman et al., 2006), caution should still be used in interpreting findings from single-item criterion variables due to possible measurement error. These limitations notwithstanding, this study provides at least preliminary evidence for genetic influence on frequency of social media use. Perhaps more importantly, it provides communication researchers with an analytical blueprint for their own investigations of genetic influence on communication behavior and media effects.

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¹³ Communication researchers have a variety of nationally representative twin datasets from which to find data, including the Minnesota Twins Political Survey (<http://www.unl.edu/polphyslab/data.html>), and the National Longitudinal Study of Adolescent Health or “Add Health” (<http://www.cpc.unc.edu/projects/addhealth>). Original twin data collection efforts have also been conducted in Denmark (Klemmensen, Hobolt, Dinesen, Skytthe, & Nørgaard, 2012) and Australia (Hatemi et al., 2015). A number of studies in behavior genetics also rely on twin pairs conveniently sampled at the annual Twinsburg, Ohio Twins Festival, which is held in August and is billed as one of the largest annual gatherings of identical and fraternal twins in the world. See <http://www.twinsdays.org/research-opportunities/>.

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